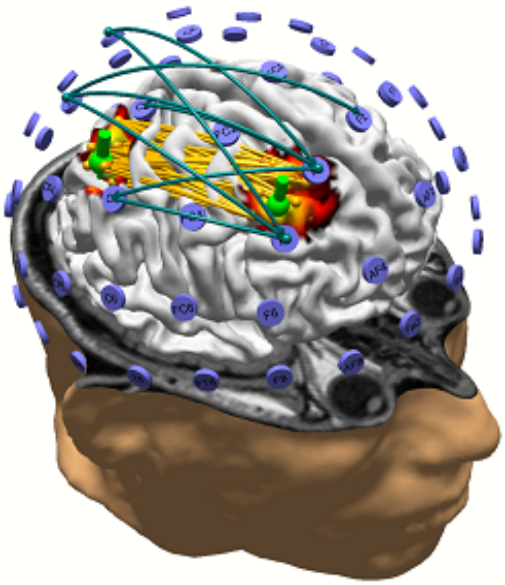

CURRY 8 User Guide

Multi-modal neuroimaging

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Year of Manufacture: 2017

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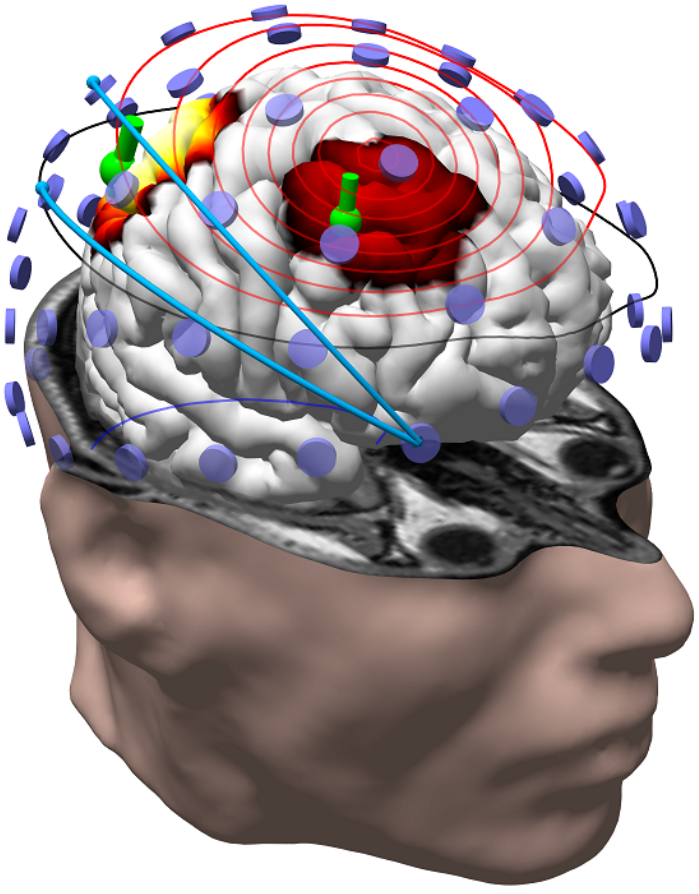
®CURRY 8

A Comprehensive Package for EEG Acquisition, Analysis, Image Data Processing, and Source Reconstruction



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1.1 Contact Information

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If you live outside the USA or Canada, and purchased your system through one of our international distributors, please contact the **distributor** first, especially if your system is under warranty.

In all other cases, please use **curry8help@neuroscan.com**, or see the other Support options on our web site (*http://www.compumedicsneuroscan.com*). Or, if you live in the USA or Canada, please call **1-877-717-3975**. International callers should use **704-749-3200**.

For Sales related questions, please contact your local distributor, or contact **sales@neuroscan.com**.

A printable PDF version of this manual can be downloaded from **www.compumedicsneuroscan.com**. A paper copy can be obtained by sending an email request to **curry8help@neuroscan.com**.

CURRY 8 User Guide [6500C]
2017-7-7

2 CURRY 8 Introduction

This latest revision of the CURRY software is an integration of the previously independent ESI (SCAN) and previous CURRY software programs, which have each been in existence for approximately two decades. Whereas they have been separate stand-alone programs in the past, they have been merged into a single program that combines the functionality of both. The resulting program is the most sophisticated and comprehensive package for acquiring and analyzing your data.

The CURRY software was created with a different type of architecture than that used in prior Neuroscan programs, such as Scan. When analyzing data within Scan, the operations (transforms) were applied in a linear or serial fashion. You might filter the data, then reduce blinks, then create epochs, perform a baseline correction, average the sweeps, and so on. In most of the steps, a new data file was created. If you wanted to go back and change an early parameter, you had to repeat all of the steps again. Individual averages were created serially - one at a time.

The CURRY software uses a *dynamic*, *constant update* method. Change a parameter setting, and the change is applied automatically throughout as much of the analyses as possible. Instead of thinking in linear terms, where operations are applied in a serial fashion, think instead of a collection of parameters that exists across transforms, where these are applied constantly and automatically whenever they are changed. You will also note that only occasionally are new files created in the process. The result is greatly reduced amount of time spent on analysis, and there are far fewer files created in the process. The parameters you select may be saved as **Study Parameters**. When you open the same original data file again, the parameters are applied automatically, giving you the results you had obtained before. If you open a like data file, you can apply the Study Parameters that were already created, and the new file will be processed in the same way as the original one.

Whereas in Scan you could automate the analysis using Tcl Batch files, in CURRY you can record a series of operations with a macro recorder, and then apply the same operations to selected data files. Macro tutorials are included to introduce you to much of the functionality in CURRY.

You will see an interface with MATLAB in various places within the program. If you wish to perform operations that are not available in CURRY, you can easily export the data to MATLAB and import the results back into CURRY.

CURRY is a modular package, meaning that it may be purchased in its entirety or in sections, or modules. The main modules are broken down into Acquisition, Basic Analysis, Image Data Analysis, and Source Reconstruction.

CURRY 8 Acquisition (X): A module that controls data acquisition from a number of Compumedics (Neuroscan) EEG amplifiers including but not limited to the SynAmps 2/RT, the NuAmps, and the Grael amplifier.

CURRY 8 Video Acquisition (V): A module that controls and synchronizes video acquisition with the acquisition of EEG data from the EEG amplifiers indicated above.

CURRY 8 Signal Processing (S): A module that controls signal processing (e.g., filtering, epoching, averaging, statistical analysis) of data acquired in the acquisition module and data acquired from other Compumedics EEG systems as well as systems of other vendors.

CURRY 8 Basic Source and Image Analysis (B): A module that performs basic source reconstruction (estimation of the location of cortical/subcortical origins) of EEG or evoked potential activity using dipole modeling with pre-calculated head models and enables overlay with individual MRI data.

CURRY 8 Advanced Source and Image Analysis (A): A module that performs advanced source reconstruction (estimation of the location of cortical/subcortical origins of EEG or evoked potential activity) and imaging processing of range of neuroimaging data including MRI, fMRI, PET, SPECT, CT, DTI, and Grid data using a variety of source reconstruction methods including simple and distributed dipole models with ability to generate individualized volume conductor head models based on each subjects structural MRI.

The license on your dongle determines which modules you will have access to. The following is a more complete description of which functionality is contained under each license.

The more modules you buy, the more you can do with CURRY. Modules are:

- X: Data Acquisition
- S: Signal Processing
- B: Basic Analysis
- A: Advanced Analysis
- D: Digitization

Add-ons enable otherwise locked functionality. Add-ons are:

- E: ELEKTA MEG Data Reader (add-on to the S module)
- R: Ricoh MEG Data Reader (add-on to the S module)
- T: Third Party EEG Data Reader (add-on to the S module)
- V: Video Acquisition (add-on to the X module)

Missing modules can be purchased and activated later. Where applicable, the relevant modules are listed with the feature descriptions below.

EEG Data Acquisition (X)

CURRY works with all current Neuroscan and Compumedics amplifiers. It supports up to 512 channels (plus 16 bipolar and 8 high level channels) at up to 20kHz sampling rate. Extensive EEG display and processing options (filtering, artifact reduction, selective averaging, different sensor montages) are available during recording. EEG data acquisition is an optional module in CURRY. Most offline Signal Processing features are also available for online data processing.

Video (V)

You may record a digital video of the subject or patient, and replay it synchronized with the data file. The license is not needed to replay previously recorded video files. Typically, videos are used in clinical recordings to correlate patient behavior with seizure activity in the EEG, but it can also be helpful in research recordings for monitoring various types of artifact.

Signal Processing (S)

After rereferencing, baseline correction, filtering, artifact detection and rejection, noise estimation, and selective averaging, CURRY can perform Principal (PCA, SVD) or Independent Component Analyses (ICA) to visualize the spatio-temporal features of EEG and MEG data. A full suite of event editing and detection tools is available. Template matching and threshold based event detection. Artifact reduction by subtraction and projection of averaged artifacts. Maps (equipotential contour lines), Source Current Density (Laplacians) and sensor coherences can be computed. Frequency domain analyses (FFT, Short Time FFT, Wavelets) are also possible.

Individual Realistic Head Models (A)

EEG signals and, to a smaller extent, MEG signals, are distorted by the electrically conducting head. CURRY can perform source reconstruction using the well-known spherical shell head models. However, one of its unique and powerful features is to create and use high-resolution realistic Boundary Element Method (BEM) or Finite Element Method (FEM) head models based on anatomical information. Such a realistic model derived from individual MRI (or CT) data increases the accuracy of source localization.

A built-in procedure performs fully automatic generation of the head model geometry (triangle nets) from T1-weighted MR images. A typical model consists of about 10.000 triangles.

Pre-computed Realistic Head Models (B)

CURRY also comes with high resolution pre-computed realistic head models that are applicable to all EEG data.

Dipole Fits (B)

Based on the measured EEG and/or MEG data, the sensor positions and the head model, a fit of one or more dipoles can be done. The position of the dipoles can be completely free (moving dipole) or can be restricted (rotating or fixed dipole, mirror or regional constraints).

Dipoles can be computed in the time and in the frequency domain.

For each fitted dipole, a confidence ellipsoid is computed which visualizes the localization accuracy.

Dipoles can be constrained to stay in the vicinity of a given location. Thus, it is possible to include prior knowledge from imaging modalities such as fMRI, PET, or SPECT.

Dipoles can be fitted to individual ICA components, thus combining the decomposition power of the ICA with source modeling.

Dipoles can also be fitted according to the MUSIC (Multiple Signal Classification) metric. If more than one dipole is computed, the fit is performed sequentially (RAP-MUSIC). After finding a dipole, its impact on the data is projected out.

For multi-dipole fits, measures that can indicate whether too many dipoles were modeled are automatically computed.

In addition to fitting dipoles, CURRY allows you to verify the dipole locations by performing, for example, dipole cross-validation, deviation scans, MUSIC scans, or current density analyses.

Dipole and Beamformer Scans (A)

During a dipole scan, many locations are scanned sequentially. For each location, a measure is calculated for the possibility that a single dipole could account for the measured EEG or MEG signal (in other words: would a dipole in this location explain the data?). The results from a dipole scan are independent from the results of a dipole fit. Therefore it provides additional and new information. If a dipole scan shows a single, sharp 'hot spot' that coincides with the location of a single dipole fit, the assumption that the measured signal can be explained by a dipole in that location is confirmed. If, however, a dipole scan shows a smeared out pattern, the underlying single-dipole model may be wrong. A dipole scan is an alternative to confidence ellipsoids to visualize the confidence volume of a dipole.

Dipole scans can be performed for one or more dipoles. Multi-dipole scans test dipole combinations.

MUSIC scans allow for the detection of multiple independent sources.

Beamformer scans for dipole sources take raw data covariances into account. In CURRY, the g2 (kurtosis) criterion for the detection of spikiness can be combined with beamforming.

Scans can be computed in the time and in the frequency domain. All scans can be performed for extended source patches instead of dipoles (point sources).

Current Density Reconstructions (R,A)

A Current Density Reconstruction (CDR) is another independent analysis. It computes a current pattern on a regular 3D grid or the cortex that would explain the measured EEG or MEG at a certain time point. In a CDR, many source locations can be active simultaneously. In order to come up with a solution, additional assumptions are needed. For example: the minimum norm constraint (L1, Lp, or L2 norm), a maximum smoothness constraint (LORETA), and statistical measures (sLORETA, eLORETA, SWARM) can be applied.

All current density methods work with an automatic calibration of the regularization parameter lambda.

CDRs can be computed in the time and in the frequency domain. They can be performed for extended source patches instead of dipoles (point sources). CDRs can be computed for selected ICA and PCA components only.

Anatomical and Functional Constraints (A)

Both a scan and a CDR provide you with the possibility to use anatomical constraints. Brain activity usually originates from the gray matter (the surface of the cortex). Using that information as a constraint improves your results.

A built-in procedure performs fully automatic segmentation of the gray matter geometry (triangle nets) using MRI data.

fMRI, PET, or SPECT images can provide anatomo-functional constraints for dipole and current density analysis. This is achieved by enhancing source probability in the vicinity of hotspots, or by seeding dipole fits from hotspot locations.

To allow for an easy inclusion of functional images, a total of three image modalities with full co-registration features are available.

Medical Images (B)

CURRY reads all kinds of medical 3D image data. Parameters are detected from image files. Source analysis results can be overlaid with image data.

Image Processing (A)

CURRY has powerful tools for processing medical 3D image data. Automatic co-registration, segmentation, morphological operations, and meshing are automated. Images from two or three modalities can be used simultaneously.

Working without Individual Image Data (B)

If no individual image data are available, CURRY automatically uses a built-in gross-average MRI data set. Alternatively, a single-subject data set, a pediatric averaged MRI, and an averaged MRI representing Asian headshape are also built into CURRY.

Talairach coordinates and Atlas support (B)

By specifying AC, PC, and the brain extensions, results can be transformed into Talairach coordinates and extensive anatomical and functional atlas information (Brodmann areas) can be accessed. Talairach coordinates and atlas information are also available without individual image data.

Statistical Analysis (B)

CURRY uses advanced and robust nonparametric statistical tests to help you determine which conditions, latencies, and source analysis results are significantly different from each other.

Viewing of Results

Results of dipole fits, scans, current density analyses and statistics can be viewed in 3D images and in 2D images. Activation timecourses for dipoles and current densities can be displayed.

Documentation of Results

CURRY provides logging to a window and to a file with selectable verbosity. A study logbook can automatically be stored with the data files. Extensive hardcopy features create image and avi movie files in a variety of file formats.

Computation results can be stored with the data files in CURRY's own format, and Excel (csv), MATLAB, and SPM result files can be created.

A built-in report generator allows you to create text documents on-the-fly.

File Formats and Compatibility

CURRY reads a broad variety of EEG, MEG, digitizer, and image file formats. CURRY is backward compatible: It will read all legacy CURRY input files, as well as all CURRY 3 and later output files.

Supported EEG data formats include Neuroscan, Compumedics, BioSemi, BESA, BrainVision, EBS, EDF, EGI, Micromed, Bio-Logic, Stellate, XLTEK, Nervus, Nexstim, Nicolet, Nihon-Kohden, Persyst, Telefactor, raw binary and raw ASCII.

Supported MEG data formats include Elekta Neuromag, Yokogawa, 4D-Neuroimaging (BTI), CTF, Philips, BESA, raw binary and raw ASCII.

Supported image data formats include DICOM, nifti, SPM, Analyze, Freesurfer, BrainVoyager, Siemens, GE, ACR-NEMA, JPEG, PNG, BMP, GIF, TIFF, raw binary and raw ASCII.

Sometimes, "Basic Source Analysis", "Basic Image Analysis", "Advanced Source Analysis", "Advanced Image Analysis" are referred to, all of which relate to aspects of functionality of the "Basic Source and Image Analysis" (B) and the "Advanced Source and Image Analysis" (A) modules.

Licenses on dongles can be combined. For example, if you have one dongle with an Acquisition only license, and another with an Analysis only license, both can be inserted and both licenses will be recognized, giving access to both modules.

Intended Use

The Curry software is intended for use in research and clinical facilities. For clinical applications, this statement describes the intended use: The Curry software is intended for use with adult and pediatric patients to aid in the evaluation of brain function and diagnosis of brain-related disorders. Use this software only under the supervision of a physician, EEG technologist or clinician.

This documents relates to the CURRY software ("CURRY software"). If other names such as "CURRY", "CURRY software package", "CURRY Neuroimaging Suite", "integration of ESI (SCAN) and CURRY software programs", "Compumedics Neuroscan CURRY NeuroImaging Software Suite", "CURRY Scan Neuroimaging Suite", "CURRY Electroencephalograph (EEG) Software" should occur, with or without the major version number ("8"), they all designate the CURRY software product.

2.1 Structure of This Manual

This manual has been written to provide the user with the reference information required to understand and perform the operation of CURRY. It is intended to be a reference, providing quick access to information on a particular window, button, or series of operations. In many cases, the operations are fairly obvious. In other instances, the utility of an option only makes sense in the context of a series of operations. Generally speaking, the *User Guide* contains all of the details about CURRY; the *Tutorials* manual shows how

many of the operations are used. If you want a description of a feature or option, use this manual. If you want to see how it is used in a larger goal-oriented process, check the *Tutorials*.

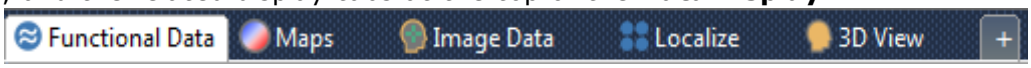
The main sections go from Acquisition, to Signal Processing, to Image Data Analysis, to Source Reconstruction, and so on.

In each section, the *User Manual* is organized in a top-to-bottom and left-to-right fashion. That is, it begins with the options on the **Main Menu** bar:

moving from **File** through **Help**, briefly describing the options under each, from top to bottom.

Then the options in the **Parameter Dialogs** including those tabs below the Database section 

, the various parameter tabs 

, and the related display tabs at the top of the **Data Display** 

are covered. The 

tabs are described near the end.

2.2 Conventions

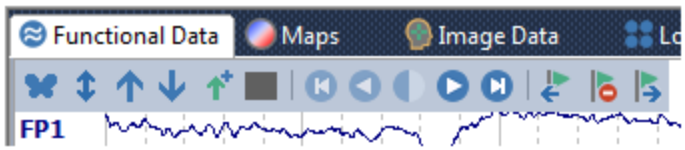
The following conventions are used in this manual or in the CURRY software.

Reduced Screen Complexity

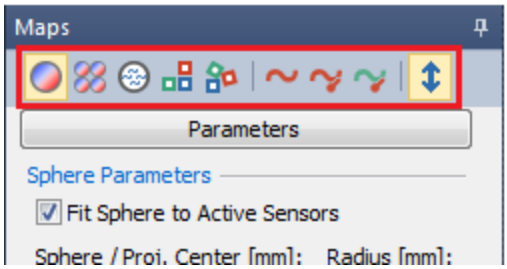
In CURRY 8, an effort has been made to reduce the complexity of the display.

Toolbars. This is most noticeable in the number of icons that are seen on the main Toolbar. You see only the icons that are used generally. You may not see all of the icons in all of the subsequent Toolbars. What you see depends on the licenses you have.

More specific Toolbars appear with each data display window. Position the mouse in the upper left area to display the Toolbar.

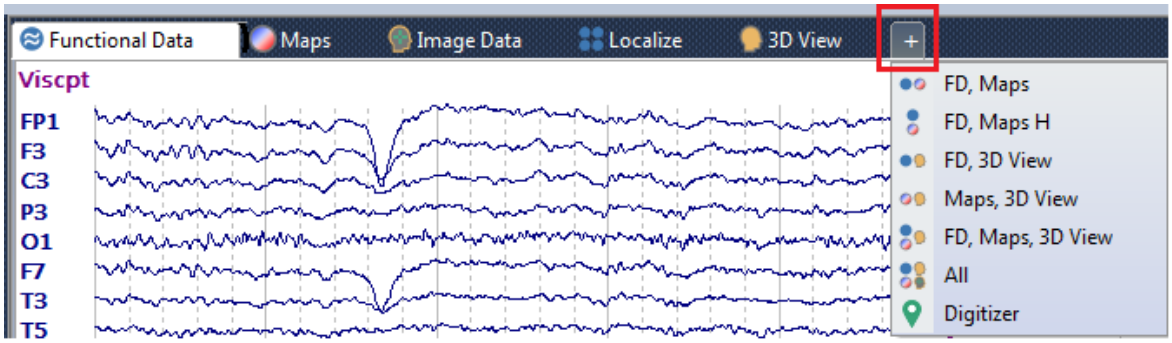


Additional Toolbars are seen at the top of most of the Parameter Dialogs.



In this way, you only see the Toolbars when you need them.

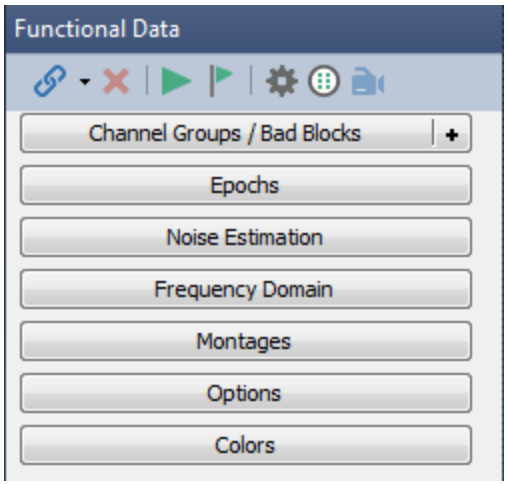
Display tabs. Similarly, the number of display tabs has been reduced. Click the **+** at the end of the line to see additional display options.



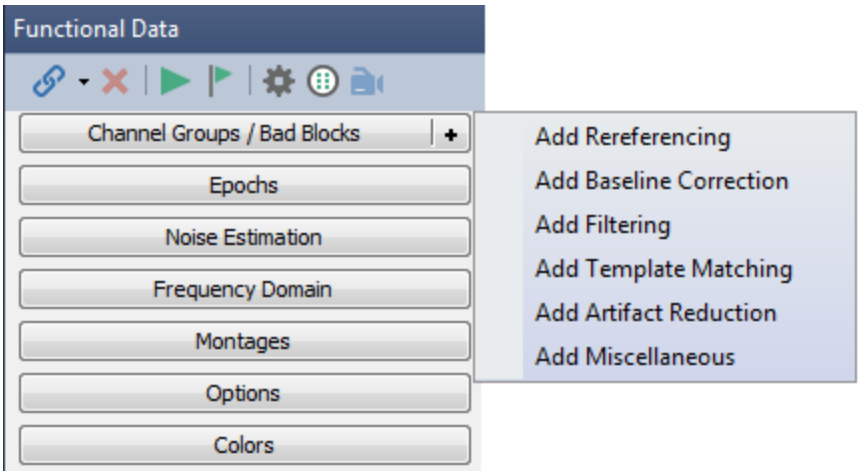
Parameter Dialogs. The Parameter Dialog tabs (at the bottom of the display), can be removed using the middle mouse button. If you don't have a middle mouse button, hold the *wheel* down and rotate it forward slightly.

Analysis Sequences

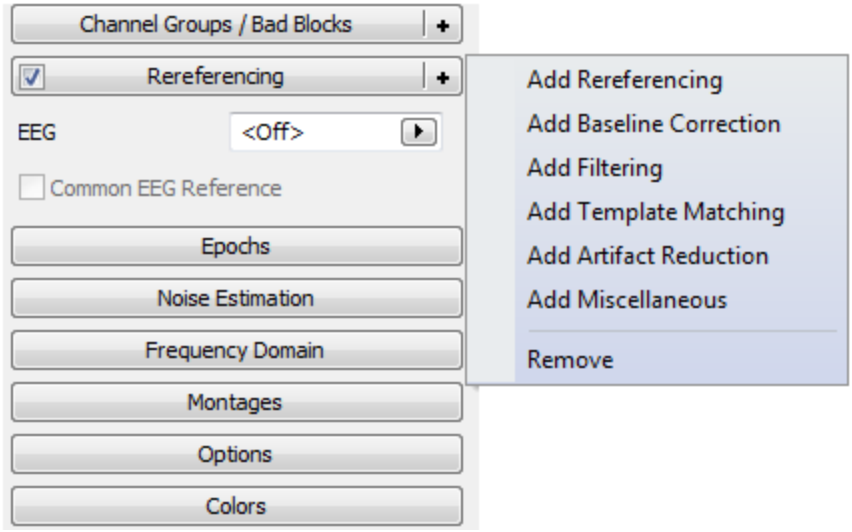
Starting with CURRY 8 you may simplify and customize the analysis sequence(s) you wish to use. This applies to Functional Data. Initially, there are few options present (in comparison to previous versions of CURRY). The operation of these will be illustrated in the *CURRY 8 Tutorials*.



If you click on the plus sign to the right of **Channel Groups / Bad Blocks**, you will see additional parameter panels that may be added. You decide the order of the operations.

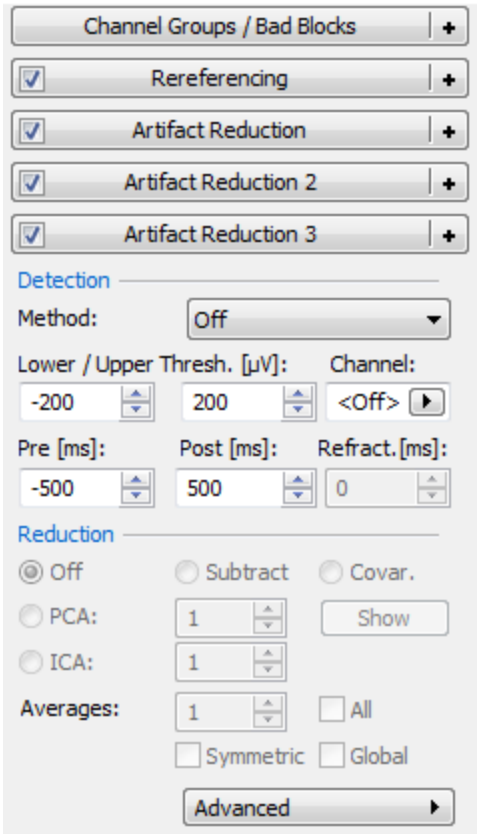


After adding one, you have the same option to add more, or to **Remove** the one you have added. The check box on the left allows you to apply or not apply the parameters in that panel, while still keeping the panel in place.

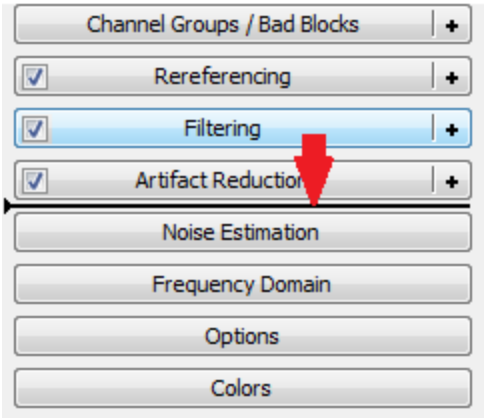


In previous versions of CURRY, you could, for example, configure up to 5 **Artifact Reduction** sequences from within the same parameter panel. Beginning with CURRY 8, you can do the same thing, but you do it by adding additional **Artifact Reduction** panels.

Each of these may be configured independently. The **Scan Artifacts** icon  at the top is used to initiate the scan(s) (to scan for artifacts, spikes, or template matches).



You may also reorder the processing steps by drag and dropping a title bar.



Once you get the display the way you will generally use it, you can save the **Study Parameters** and see that layout each time you open CURRY.

General Conventions in CURRY

Mouse Keys

The use of "click", as in *click* on a specified option, refers to the left mouse button. If the *right mouse* button is indicated instead, *right mouse* will be in *italics* to draw attention to it. Similarly, the *mouse wheel* and *keyboard* options will be in *italics*.

Options, Buttons and Displays

In general, specific reference to a named option, button or display will have the name printed in **bold** text, as when referring to, for example, **Dipole Type**. In many cases the actual button or tab will be displayed, as with Start or . *File names* and *paths* will appear in *italics*.

Icons used throughout displays serve to underscore the functional relatedness among parts of the program. That is, options relevant for the processing of Functional Data, for example, are accessed from the Parameter Dialog tabs Functional Data. The corresponding display tab has the same icon Functional Data.

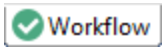
Sequence of Selections

In some instances you will be directed to perform a series of selections. For example, if you are directed to click the **File** option on the **Main Menu** bar, then the **Image Data** option, and then the **Image Data Parameters** option, that sequence will be indicated by **File** → **Image Data** → **Image Data Parameters**.

Hyperlinks

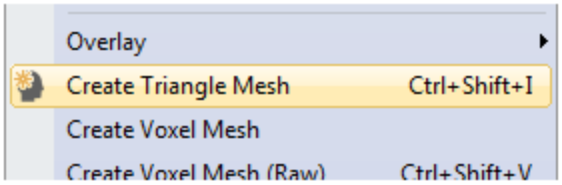
In the body of this manual, you will see underlined text in a bold font, as in **Introduction**. These are hyperlinks. Click the text to go directly to that section.

Alternate Access to the Same Option

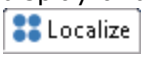
CURRY has been designed with considered flexibility, that is, there can be several ways to access the same option: from the lists under options on the Main Menu bar, from the Toolbar icons, from the 

list of options, from context menus (accessed by clicking the *right mouse* button in a window), and from accelerator keys on the keyboard. The functions are the same - the various methods are presented for easy access and for your personal preference.

For example, if you want to create a triangle mesh of a segmented surface, you can do so by clicking **Image Data** → **Create Triangle Mesh**.



You can also click the  icon on the **Image Data** Toolbar, you can use *Ctrl+Shift+I* combination from the keyboard, you can click the *right mouse* button in the 

display and select **Create Triangle Mesh**, or you can click the *right mouse* button in the 

display (in the MR images) and select **Create Triangle Mesh**. The result is the same.

Wherever possible, the software will display the Toolbar icons and keyboard combinations along with the named option for your convenience: 

.

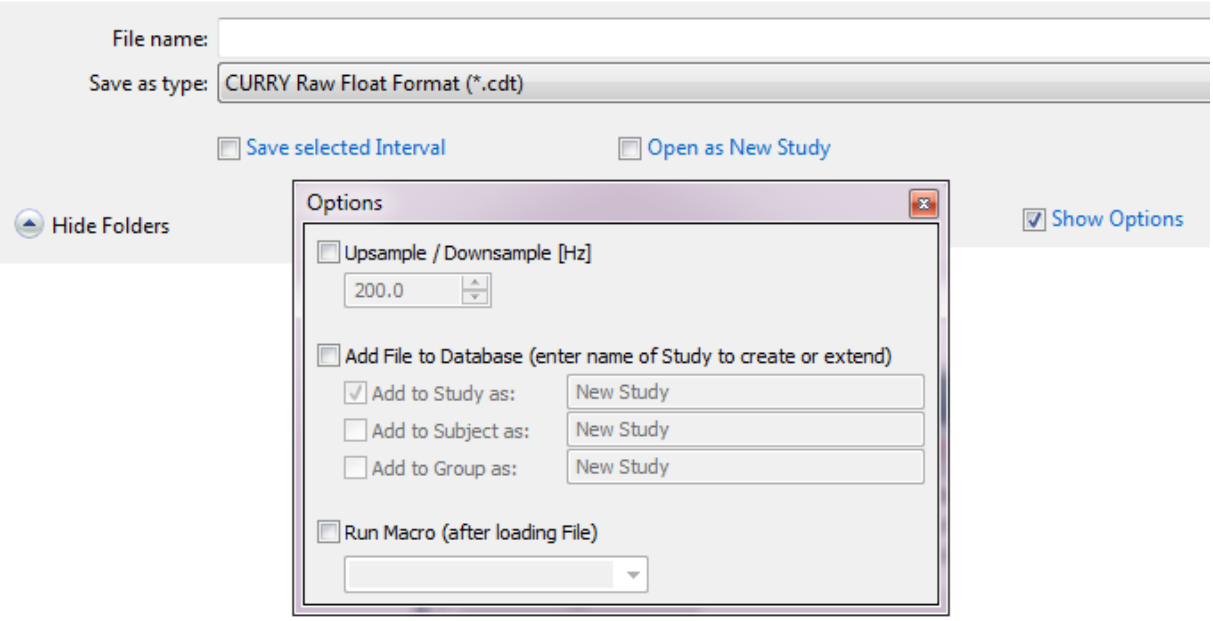
If you position the mouse over a Toolbar icon, a **Tooltip** will appear, giving the command name and keystroke combination (if present). Go to **Edit** → **Options** → **Enable Tooltips** if you do not see them.

There are two "classes" of keyboard commands - those that use the *Ctrl* key, and those that use the *Alt* key. The *Ctrl+key* commands do not change across displays. The *Alt+key* commands change viewing "properties", and therefore the same key stroke combination may have different actions in different displays. A complete list of keyboard combination strokes is found in the **Keyboard Shortcut Commands Summary** section below. If you frequently use keyboard commands, you may want to print out that section.

Saving Options

As a general "rule", CURRY saves/exports the data you see on the screen - what you see is what is saved. There are exceptions, most notably with montages. CURRY will save the original data, not the montaged data. In most instances, the changes you make will become permanent when you explicitly save/export the file.

Pay attention to the **Save As** dialogs when they appear. Often these contain important options that are not available elsewhere. For example, when you create an averaged data file and save it, you will see several options (click **Show Options** to see the **Options** dialog):

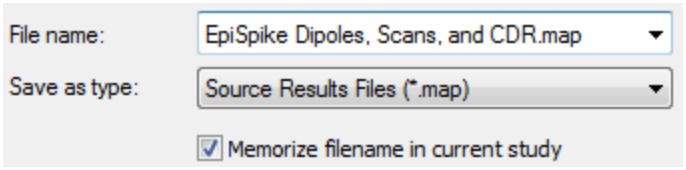


Upsample/Downsample is the CURRY option for Decimation or for Spline Fitting (as it was called in the SCAN software). There is also the option to add the results in a new Study, Subject or Group in the Database. You have the option to save just the Timerange designated between the two outer cursors, or the entire Timerange (epoch interval). You can open the file after saving it, and run a macro at that time. Other Save As windows have similar options.

Note

Change in file extensions. Beginning in CURRY 8, there are changes to the file extensions that are used. Data files that are acquired, or otherwise saved, will have .cdt extensions rather than the previous .dat extensions. This is to avoid the confusion with various other files that use .dat. Also, in prior versions of CURRY, two CURRY parameter files were created when functional data were imported - the .dap and .rs3 files. Beginning with CURRY 8, these files are combined into a single .dpa file.

Similarly, when saving source reconstruction results, there is an option to Memorize the filename in the current Study. When enabled, the results file(s) will be added to and be accessible from that Study.



Context Menus

Context menus are found throughout much of CURRY, and are accessed by clicking the *right mouse* button after positioning the cursor in various parts of the displays. Some options are found only in context menus; others are repeated elsewhere.

Icons

You will see the following icons are used in the left margin of this manual to indicate special notes.

Note

When important information is given, it is indicated by the 'Note' symbol.

Care

When care needs to be taken in performing an action, for example, it is indicated by an exclamation mark!

EEG

This indicates a note that applies to EEG data handling.

MEG

This symbol is used to indicate a remark for MEG users.

Accuracy

When information relating to accuracy is given, it is indicated by a ruler and a compass.

Performance

When information relating to performance is given, it is indicated by a tachometer. In general, there is a trade-off between performance and accuracy; as performance increases, accuracy decreases.

1. Steps indicate a sequence of actions to be undertaken,
2. and the sequence ends with a horizontal line.

Activity

When CURRY is active, i.e., a command is being carried out, the window or the button which triggered the activity may become inactive, or the mouse cursor may change to an **hourglass** or **rolling wheel** (precluding further actions). For time-consuming activities, the **Status Bar** shows the progress of the operation, the results can be seen in the **Output** panel, and the mouse cursor will show an hourglass. If, during the program's activity, further inputs are made, they will be handled as soon as the previous activity has ended, or else ignored. It is recommended that you wait for current operations to conclude before selecting new ones.

Many computations and activities run in the background, and can be stopped by pressing *Esc* or *Break*. Input may be ignored for activities running in the foreground.

Performance

CURRY allows you to perform very complex actions on large amounts of data. For that reason, it only runs satisfactorily on fast computers with large amounts of internal memory.

Processing Speed

For some operations complex algorithms are used repeatedly, e.g., for each point on a surface, or for each sample. They may take several minutes before being completed. This applies to, for example, the initialization of a realistic head model (BEM), the first dipole fit done with a new head model, and the computation of a Scan or a Current Density map for an extended Timerange.

Video Drivers

CURRY uses advanced methods for OpenGL hardware accelerated graphics presentation. We strongly recommend that you update your video drivers to avoid display problems (determine your video card, and go to the manufacturer's web site for updated drivers). In some cases it may be necessary to obtain a more powerful video card in order to use all of the video functionality (such as, Transparency with more than one object).

Memory

Large amounts of internal memory are needed for the initialization of a realistic head model (BEM), and for Scans and Current Density analyses with extended Timeranges.

Computation Time

Bear in mind that computing times depend on:

- the amount of information processed,
- the available amount of free memory, and
- the type of processor.

 **Performance**

The performance of CURRY varies from system to system. Differences of up to a factor of 10 may be found. Performance will be adversely affected if you run CURRY on a computer that does not meet the minimum specifications. Avoid running other programs at the same time (including those running in the background) if you encounter performance problems.

2.3 Working With CURRY

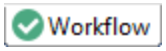
CURRY can be seen as a toolbox for data acquisition, analysis, and multi-modal neuroimaging. Its broad functionality supports the different aspects that are needed for performing the analyses in a state of the art fashion. This section provides an overview for the concepts and processes involved with CURRY.

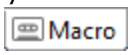
Conceptual Shift in Processing

Perhaps the most important concept to understand about CURRY is that it uses a different approach to processing your data than that used in some other software packages, including Neuroscan's SCAN software. In the SCAN EDIT program, for example, you would

apply a particular Transform, such as Filtering, and a new file was created with the filtered data. Perform blink reduction and you would get another file with the corrected data. And so on. If you wanted to go back and refilter the file, you had to redo all of the subsequent analyses, creating new files along the way. The process was a serial, step-by-step one, with a sequential progression to the final data.

Processing in CURRY is not performed in such a step-by-step manner. Rather, think of a constellation of parameter settings, where the current settings are applied automatically and immediately throughout much of the analyses. Change a parameter, and the results will change accordingly. The parameter settings are being applied all of the time, in most instances. Once you have finished analyzing a data file, you can save the **Study Parameters**. All of the parameters will be saved with the Study. When you reopen the same Study, the Study Parameters are applied automatically, and the same results will be seen as before (with some exceptions). Study Parameters you save for one file may be applied to other like files.

You can review or modify the parameter values using the 

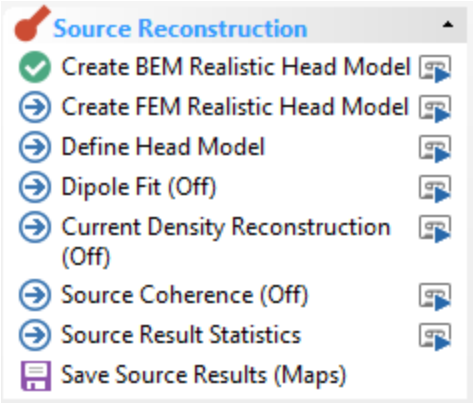
display. Individual items in the list take you to the relevant dialog screens to view or modify the parameters. If you want to apply the same sequence of operations to another similar data file, there is a 

option. You can record the operations you perform with one data file and apply the same operations to other data files you select.

This concept of the automatic application of parameter settings has been used in CURRY for some time. The **Study Defaults** in previous versions of CURRY have taken on a greater degree of importance in CURRY 7 and CURRY 8, and are now called **Study Parameters**. See the **Global, Study and Other Parameters** section below for more information.

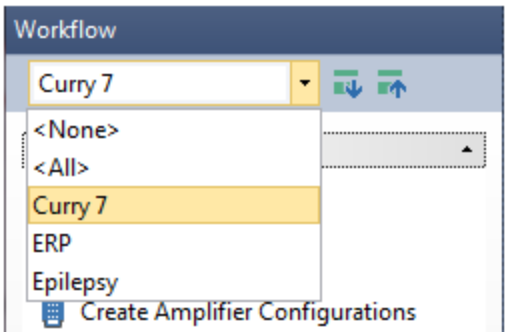
Workflow

A **Workflow** display is provided to guide you through the operation of CURRY in a logical progression of steps, remind you of current parameter settings, and take you directly to the sections in CURRY that are used for the various tasks. This is extremely useful for those in the initial orientation and familiarization phase. The icon to the right of some lines  means that there is a demonstration macro available for running.



At the top of the Workflow are **Scope Parameters**. These are sets of preset parameters that you may be using. Selecting one of these will avoid having to enter the parameters each time, or saving parameters as Study Parameters (it is an optional convenience). One

option is for CURRY 7, which will make the interface look more like you had in CURRY 7, and it will set some of the same parameters. If you wish to use one of the Scopes, it is necessary to select it *before* you open a data file.



Database

Input data that are acquired or processed by CURRY are generally defined and structured using a Database.

Database files store the filenames of the data files, as well as the logical structure of the data CURRY works on, i.e., which data files contain which type of data. Database files do *not* contain the data themselves. "Studies" are like folders that hold all information that is necessary for data acquisition, data analysis, image analysis, and source reconstruction.

Studies can contain :

- EEG/MEG data, sensor position, and functional landmark files,
- image data and anatomical landmark files,
- results files,
- CURRY configuration files (parameter files), and
- additional files.

File Loading Wizards

CURRY will assist in loading data and digitizer files, and the co-registration of the files, using three "Wizards".

Functional Data Parameters Wizard. This part of the program is used to fill in undetected parameters or to modify parameters in the functional data files. It also lets you select which files to use for co-registering functional and anatomical landmarks. The outputs are two parameters files that are read when you subsequently load the data files, thereby bypassing the wizard.

Digitizer File Wizard. The Digitizer File Wizard is used when your digitizer files cannot be interpreted accurately. Format modifications are made, and a file is created that contains information allowing CURRY to interpret the columns in your digitizer file. This wizard writes a parameter file as well - containing the 'column information'.

Image Parameter Wizard. This routine is used to assist CURRY in the loading and autodetection of parameters in the image data files. It is also used to specify the anatomical landmarks and Talairach landmarks and boundaries. The output is a parameter file that is read when you subsequently load the data file, thereby bypassing the wizard.

Functional Data

Data from EEG and MEG measurements can be processed. The information can be visualized on a time axis. Multiple options for viewing and functionality are offered. The functional data can be pre-processed by averaging, filtering, event detection, artifact rejection, and many additional data processing transforms. Different channel (sensor) selections are possible for data display and source reconstruction.

Image Data

Data such as MRI or CT show the anatomy of a subject, while fMRI or PET reveals brain activity. CURRY reads the data available in DICOM, SPM/Analyze, nifti, plain binary, and other formats. An autodetection feature scans the data set and derives as many of the image parameters as possible. This allows for an entire stack of image slices to be read and transformed into a 3D data set.

Image landmarks are defined using a manual selection process. They are used to set up an internal coordinate system that is based on the nasion and preauricular points. This makes it possible to compare results between subjects and to perform registration between different image modalities.

From this point on, image viewing and processing are available. Objects such as the skin, the skull, or the cortex can be segmented automatically. Segmented objects are displayed as a 3D image that allows visual inspection and volumetric measurement.

On the surface of a segmented object, support points can be distributed and connected to form a triangular mesh. This mesh can then be visualized, saved, and used in other parts of CURRY.

Working Without Individual Anatomical Data

CURRY comes with several built-in grand average MRI data sets. If no individual image data are available, an averaged MRI data set may be used instead.

Sensor Positions

The functional EEG or MEG data are acquired by sensors. These are either electrodes or coil arrays. In both cases the positions of the sensors must be known. This means that the location of the electrodes or the geometry and location of the coils must be available in some arbitrary coordinate system. The x, y, z position of each sensor is needed.

 **EEG**

For each set of measured EEG data the electrode positions must be known. Five methods are supported:

- A file that provides locations, as measured by a digitizer. Landmarks are used to match these locations to the coordinate system of the image data.
- CURRY can provide default sensor locations based on the electrode labels.
- CURRY can compute sensor locations based on the 10-20 system as measured along the subject's skin.
- Markers on the MR and CT can be used to select the sensor locations.
- ECoG grids can be defined by specifying the four corner points, strips by two points.

 **MEG**

In order to use MEG data the system geometry needs to be known. CURRY supports most MEG systems. The geometry is either read from the MEG data files, or taken from a predefined montage.

Landmarks are used to match these locations to the coordinate system of the image data.

Sensor position, functional landmark, anatomical landmark, and montage files are entered from the Database or via the **Functional Data Parameter Wizard**.

Co-Registration Using Landmarks

Combining the measured and pre-processed functional data with anatomical data enables multi-modal source localization. Both modalities have to be related to each other, i.e., the known sensor locations have to be linked to the available anatomy. As both modalities have their own coordinate system, the co-registration of these systems is done by identifying a few points in common to both. These points are based on landmarks and determine the (rigid) transformation between the two coordinate systems. Landmarks are positions on the head surface that can be identified uniquely.

 **EEG**

Landmarks and sensor positions are measured with a 3D digitizer and written to a digitizer file that CURRY can read.

 **MEG**

Landmarks and sensor positions are part of the MEG data files.

Often the nasion and the pre-auricular points are used as anatomical landmarks. In this case, nothing more needs to be done, as CURRY already knows their positions in the image data.

If other landmarks are used, their location in the image data is specified in CURRY. MRI markers, e.g., vitamin E capsules that show up in the image data, can be used to help identify those landmarks.

 **Care**

Using landmark-based registration, the center-of-gravity (COG) of the landmarks is the most well defined location. The further sensors or sources are away from the COG, the larger their coregistration errors are.

Source Reconstruction

Source reconstruction is about answering the question, where in the head is the source of the activity that generated the measured data? The answer lies in solving two related problems. These are known as the forward and inverse problems.

Forward Problem

In the forward problem, the strength and location of a source inside a head are known. The functional data that would be measured on the outside of the head, i.e., the field or potential distribution, are unknown.

The problem has a unique solution. Computing the solution requires information on sensor locations. The head is a volume conductor (head model) that distorts the potential of the impressed source, therefore its shape and location dependent electrical conductivities need also to be known.

The very complex shape of a human head with all its anatomical details is represented by a simplified model. Its parts such as the brain or the skull are represented by different compartments with each compartment being assigned an electrical conductivity. The shape of these compartments is either spherical, or is derived from the actual shape of the head using anatomical data. The latter improves the accuracy of the solution to the forward problem.

 **EEG**
A realistic head model can significantly improve localization accuracy for EEG data.

 **MEG**
For MEG, the magnetic fields due to volume conduction effects are relatively small compared to the magnetic field originating from the sources. A one-shell realistic head model defining the inside of the skull is normally adequate.

Inverse Problem

In the inverse problem, the signals on the outside of the head are known, while the source or sources in the head are unknown. This problem does not have a unique solution. For each set of functional data, an infinite number of sources or combination of sources generating the data can be found.

The unlimited number of solutions is a fundamental problem of source localization, and additional information (*constraints*) is required to single out one solution. Specifying the type of sources representing the actual brain activity, the source models, is an important step in providing additional information. Two different classes of source models are available, distributed and local sources. Distributed sources are found using current density methods, while local sources are computed by dipole fits.

 **Care**
Constraints are derived from the nature of the functional data and from your relevant experience. The type of source model, number of sources, as well as additional anatomical constraints to be included have to be specified before the inverse problem can be solved. Making assumptions not matching reality can lead to incorrect results.

Once the source model, the number of sources, and additional constraints have been established, the inverse problem can be solved. The problem now has transformed into determining the parameters of the source model (e.g., locations and strengths). The solution of the forward problem based on these parameters matches the measured functional data as closely as possible.

Logging Facility

There are several ways to create a History of the steps you have performed with a data file. These range from text files, to more involved files with graphics, to macros that

actually record the steps (and can be replayed). See the **History Options** section below for more details.

Report Generator

The **Report Generator** allows you to create summary reports. You can create a template for use with multiple reports, in which you can design your own information fields, add your logo, etc. Toolbar icons and context menu selections are used to copy images and text results automatically to the Report. Formatting capabilities let you design the Report using your own personal style.

Macro Feature

A macro feature allows you to record sequences of operations. That sequence can then be applied to additional data files, thus automating data analysis.

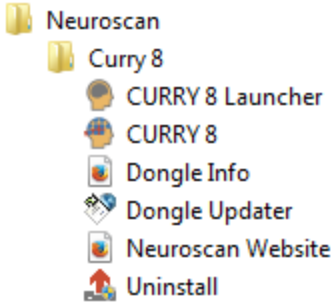
Program Launcher

CURRY 8 has the capability to control the complexity of the CURRY display. If you have licenses for multiple modules, but you wish to see only selected modules, you can set CURRY to display only the relevant functionality. Please see the *CURRY 8 Launcher* section, under *Installation*, in the *Installation and Tutorials* manual.

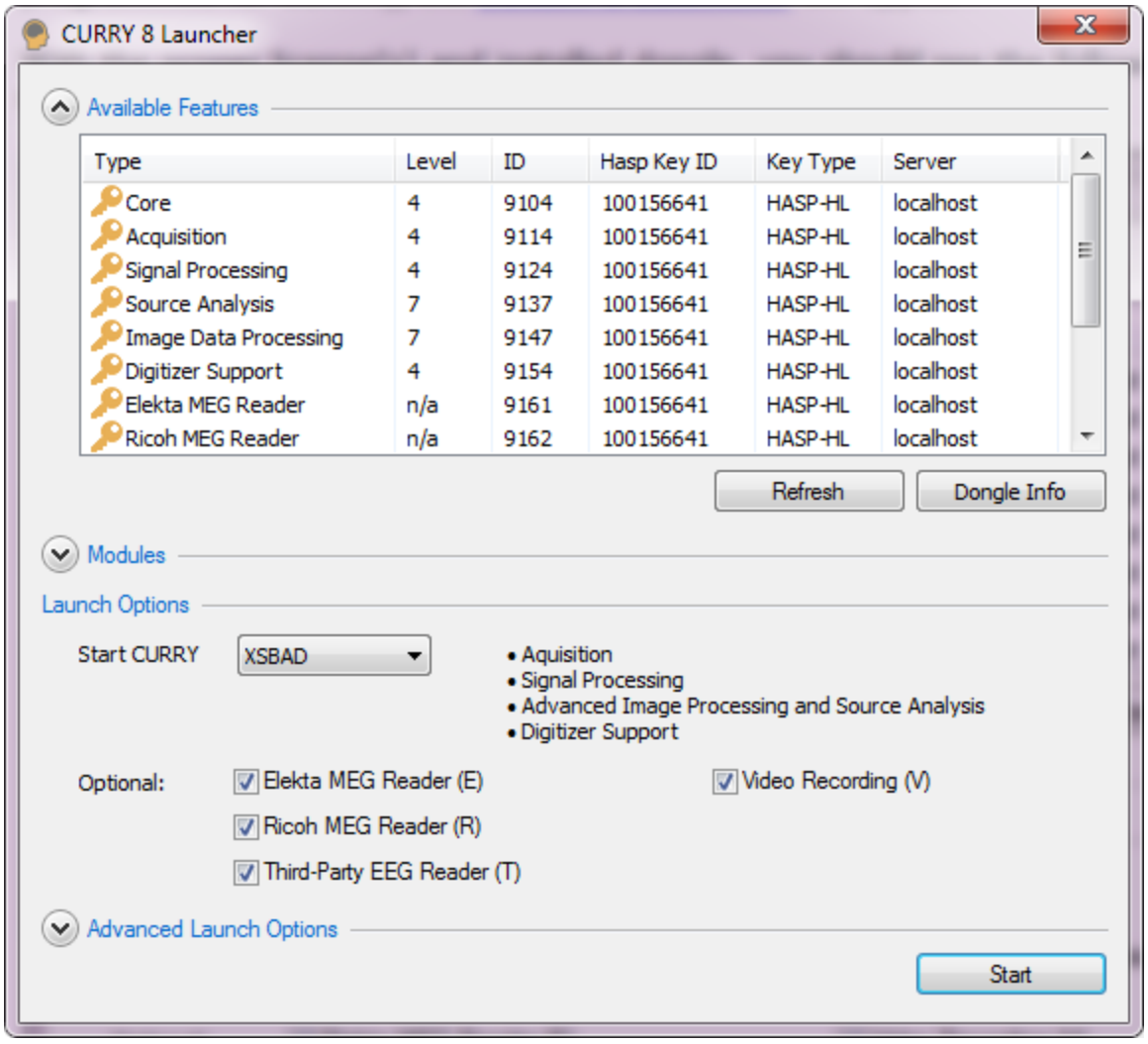
3 Dongle Updating

In order to run the CURRY program you must have a properly programmed software lock, or HASP dongle, plugged into your computer's USB port. If you are a brand new user, you will have received the HASP dongle with the system, and it will be preprogrammed with one or more licenses. If you already have a dongle, e.g., for your SCAN system, it will need to be exchanged for a HASP dongle. Contact curry8help@neuroscan.com for more information.

If you attempt to start CURRY without a dongle (or with a dongle that is not properly programmed for CURRY), the **CURRY 8 Launcher** will appear. You can also run the program by going to **Start** → **All Programs** and the path shown below.



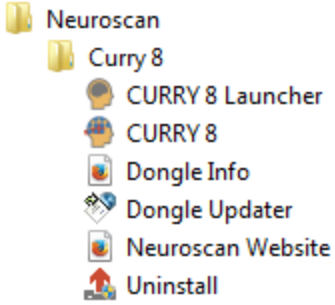
With the proper license(s) and installed dongle, you should see the following dialog. CURRY is then ready to run.



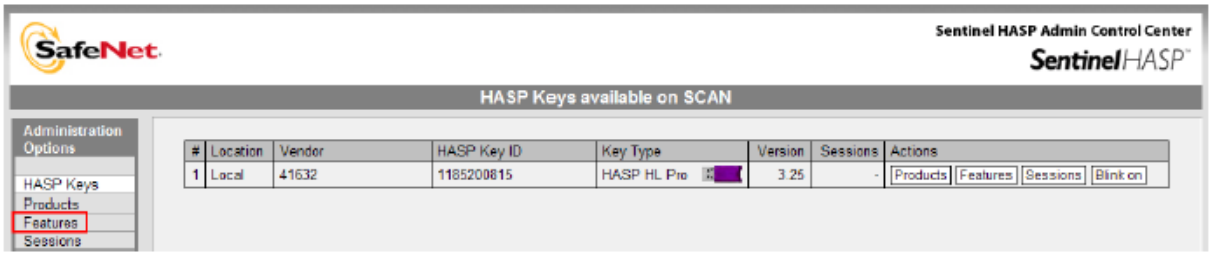
CURRY checks for the dongle periodically. You cannot start CURRY on one computer, then remove the dongle and use it to run CURRY on a second computer. The first one will not continue to function without the dongle.

HASP Dongle

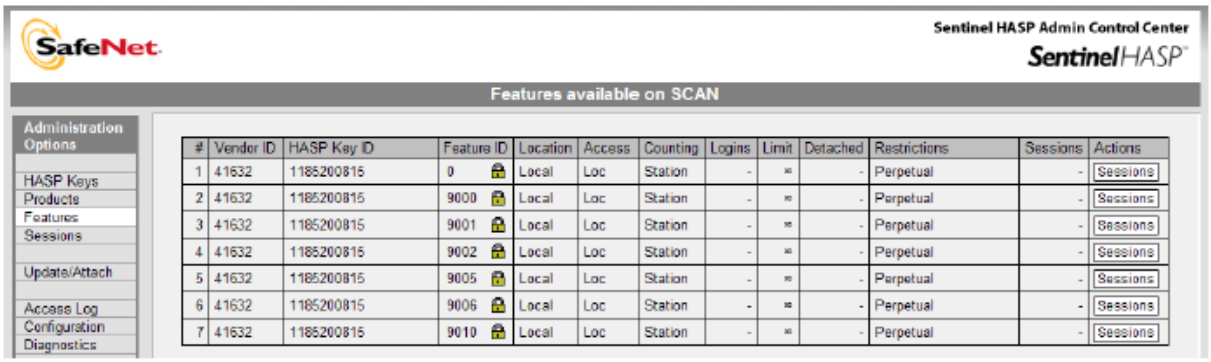
You will see two more options on the **All Programs** list: **Dongle Info** and **Dongle Updater**.



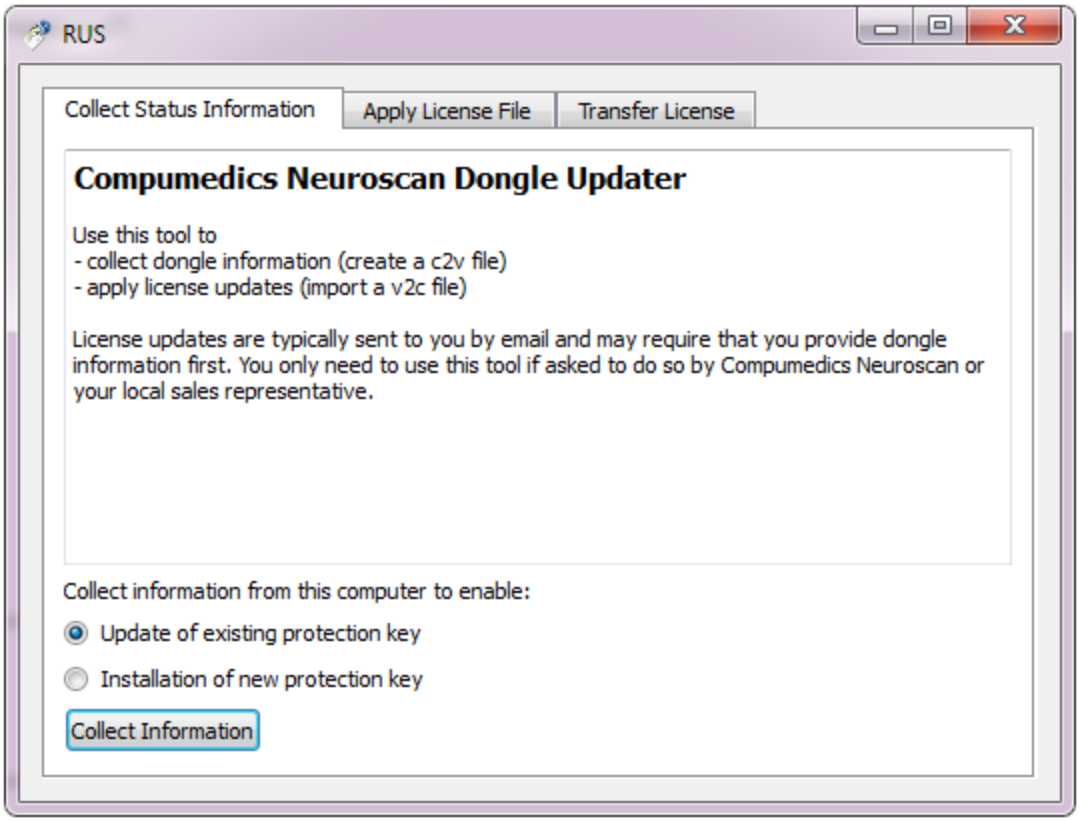
Dongle Info. This option is used to view the licenses that have been programmed onto your HASP dongle. Clicking this option takes you to the **SafeNet Admin Control Center** web site (internet connection required). You will see the type of dongle that has been found. Select the **Features** option.



You will then see the licenses that are contained on your HASP dongle (yours will differ from the one shown below).



Dongle Updater. This option is used to update the licenses on your HASP dongle. Clicking it displays the **RUS** dialog (Remote Update System). Briefly, to make changes to the license(s) on your dongle, you need to send a file to Neuroscan (the .c2v, or client to vendor file). You will receive a file in return (the .v2c, or vendor to client file), which is used to update the dongle.



Click the **Collect Information** button. You will be prompted to select a folder and a file name for the .c2v file that will be created.

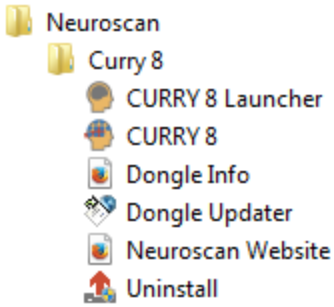
You will then see a message with the results: 09:56:37: Key status retrieved from HASP successfully. . The .c2v file has been created; e-mail it to the address given to you by tech support (or currylicense@neuroscan.com).

When you receive the .v2c file via return e-mail, go back to the **Dongle Updater** and click the **Apply License Update** tab. Use the **Browse** button to select the .v2c file, then click **Apply Update**.

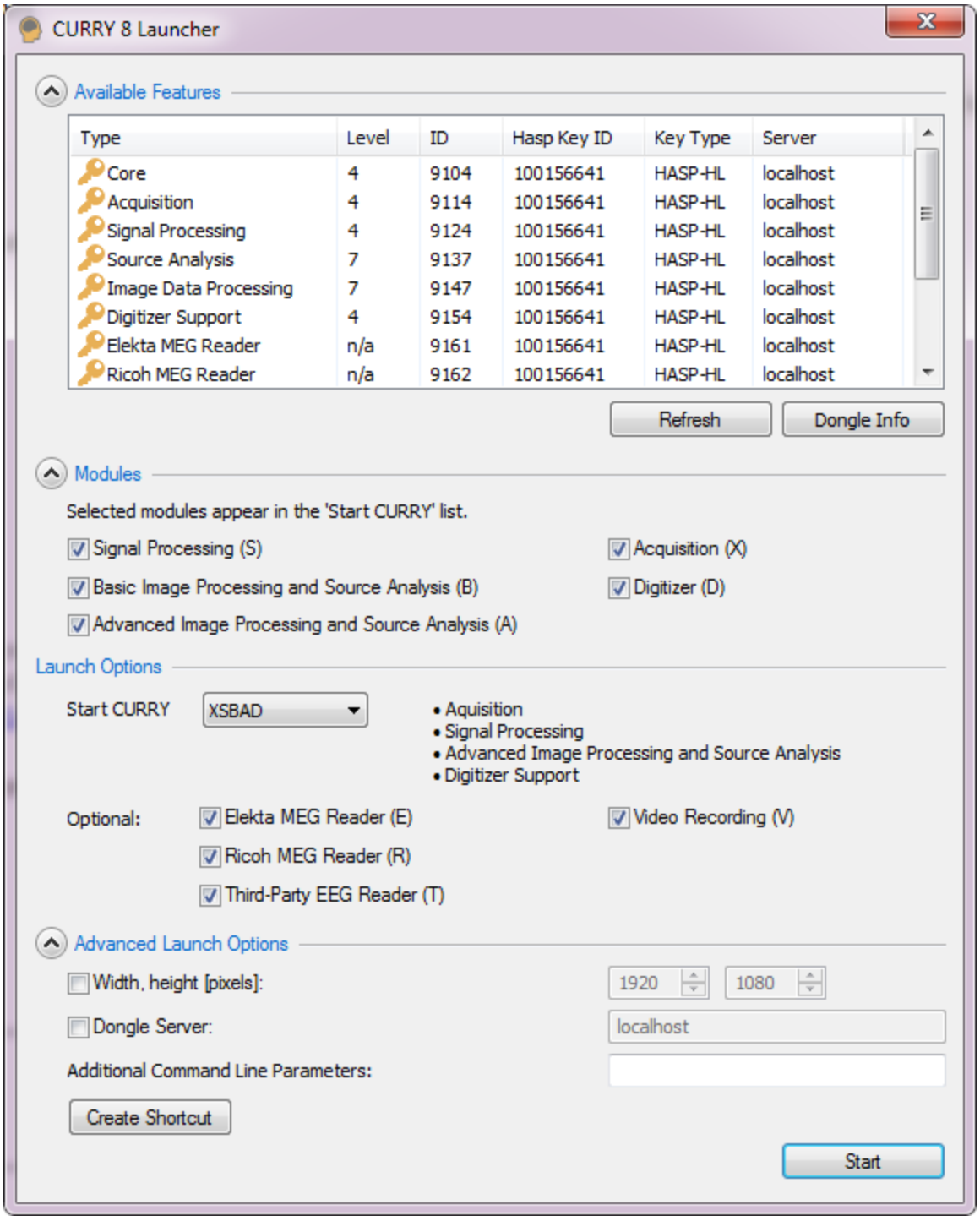
Your HASP dongle should now be updated.

4 CURRY 8 Launcher

The CURRY 8 Launcher is found from the **Start** button in the path shown, or in the *... \Neuroscan\Curry 8* folder (or similar folder depending on your OS). You cannot run CURRY and the Launcher at the same time. Close CURRY and then start the **CURRY 8 Launcher**. You can then Start CURRY from the Launcher, if desired.



Running it displays the following window.



When you start CURRY, the default setting is to display everything for which you have a license. At times, you may wish to simplify the CURRY display by hiding the sections that you are not using. For example, if you are analyzing the data only, you may decide to not display Acquisition and Digitizer panels and icons. Or, you may decide to display only the acquisition and video modules if you are acquiring the data only. You have the option to display whatever modules you wish.

Available Features
This displays the CURRY licenses on your dongle. Click the **Dongle Info** button to go to the SafeNet web site for more information about your licenses.

Modules
This displays the main modules in CURRY, with their license codes. Select the modules you want to use/display from here, and they will be displayed in the **Start CURRY** list below under **Launch Options**.

Acquisition - X
Digitizer - D
Signal Processing - S
Basic Imaging Processing and Source Analysis - B
Advanced Imaging Processing and Source Analysis - A

Launch Options
Clicking the list displays all permutations of licenses that can be used. The content of the list depends on what you selected for the Modules and which licenses are available on your dongle. If you select one with fewer licenses and click 

, you will see only the functionality that is relevant for those licenses. In other words, this is simply a way to reduce the visual information on the screen, displaying only those options that may be needed. For example, if all you are doing is acquisition, open just the X license.

Optionally, there are additional licenses available for:

Elekta MEG Reader (E)
Ricoh MEG Reader (R)
Third-Party EEG Reader (T)
Video Recording (V)

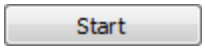
Advanced Launch Options

Width, height [pixels]. This refers to the size of the main CURRY window when opened. You can set it as desired.

Dongle Server. If you are using the dongle on a server instead of the local computer, and you wish to restrict where CURRY looks for licenses, enter the name or IP address of the server here.

Additional Command Line Parameters. This line is only meant to be used if so directed by the CURRY HelpDesk. You will be given the commands to type in. If you enter an unknown command, CURRY will interpret it as a file name (you can use a fully qualified filepath as a command) and display a warning (assuming the file does not exist).

Create Shortcut. If you want to start "Curry X" with a certain dongle server, clicking "Create Shortcut" will create a shortcut for exactly this configuration. Generally, Create Shortcut will create a shortcut on the desktop with all the settings you have just set in the Launcher.

Click the 

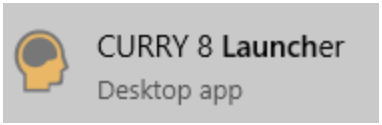
button to start CURRY.

5 What to do if CURRY does not start

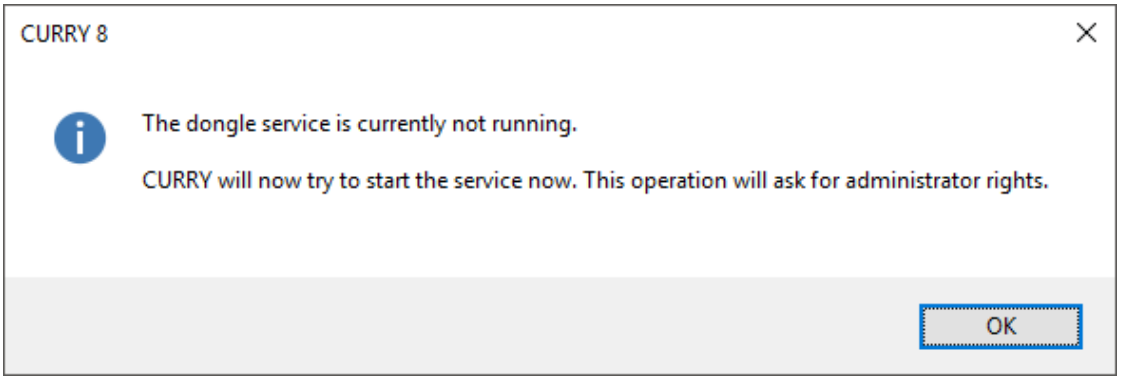
With certain Windows 10 updates (Creators Update) the dongle service may not be available automatically, which will result in CURRY not being able to start. Sometimes this service gets stopped after a Windows update, or by your in-house security solutions. Should CURRY not start, please follow the steps below.

1. Restart the computer.

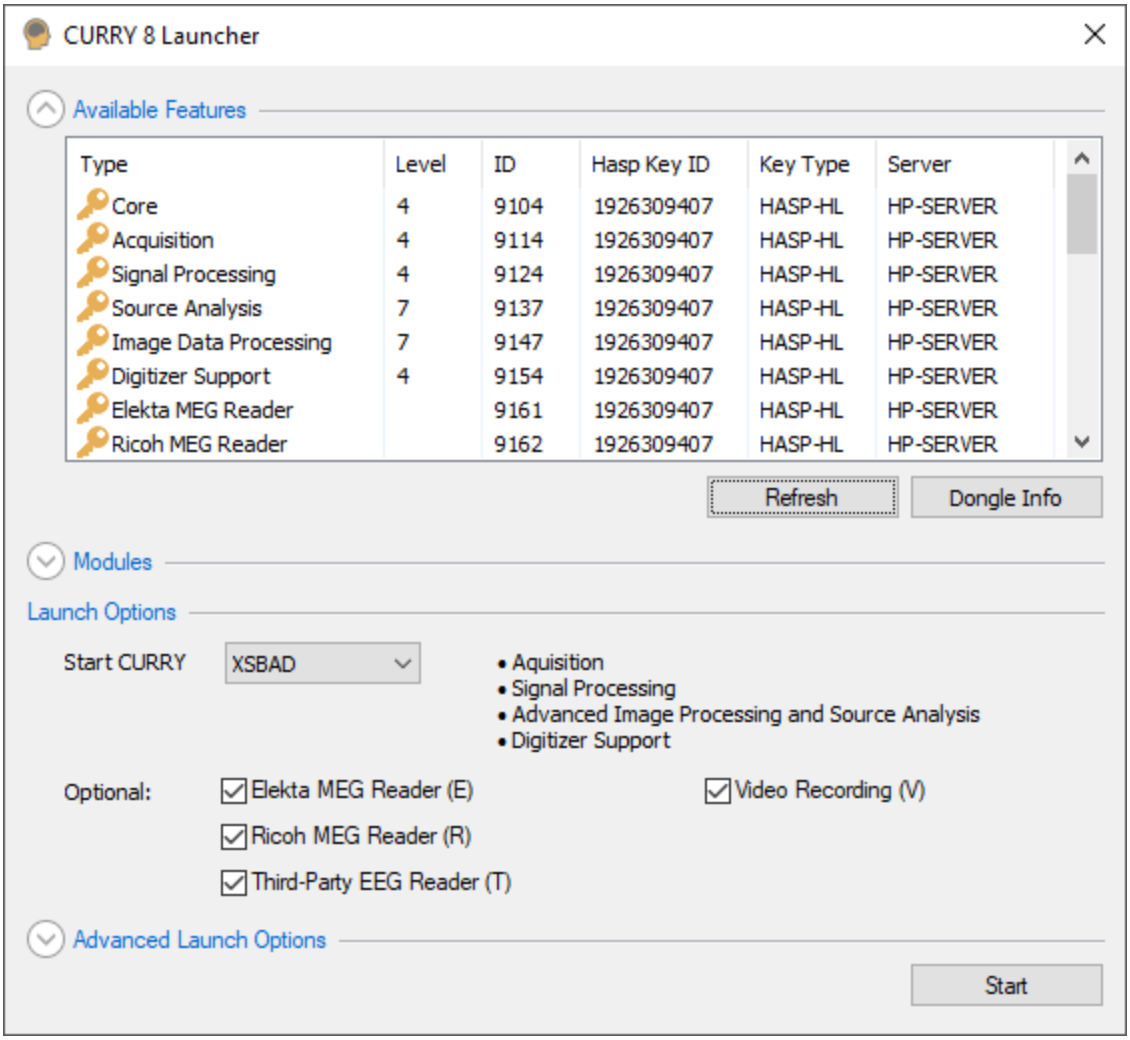
2. Start the CURRY 8 Launcher (not the CURRY 8 program yet).



The CURRY Launcher will check if the license service is running and attempt to start it (administrator privileges are required):



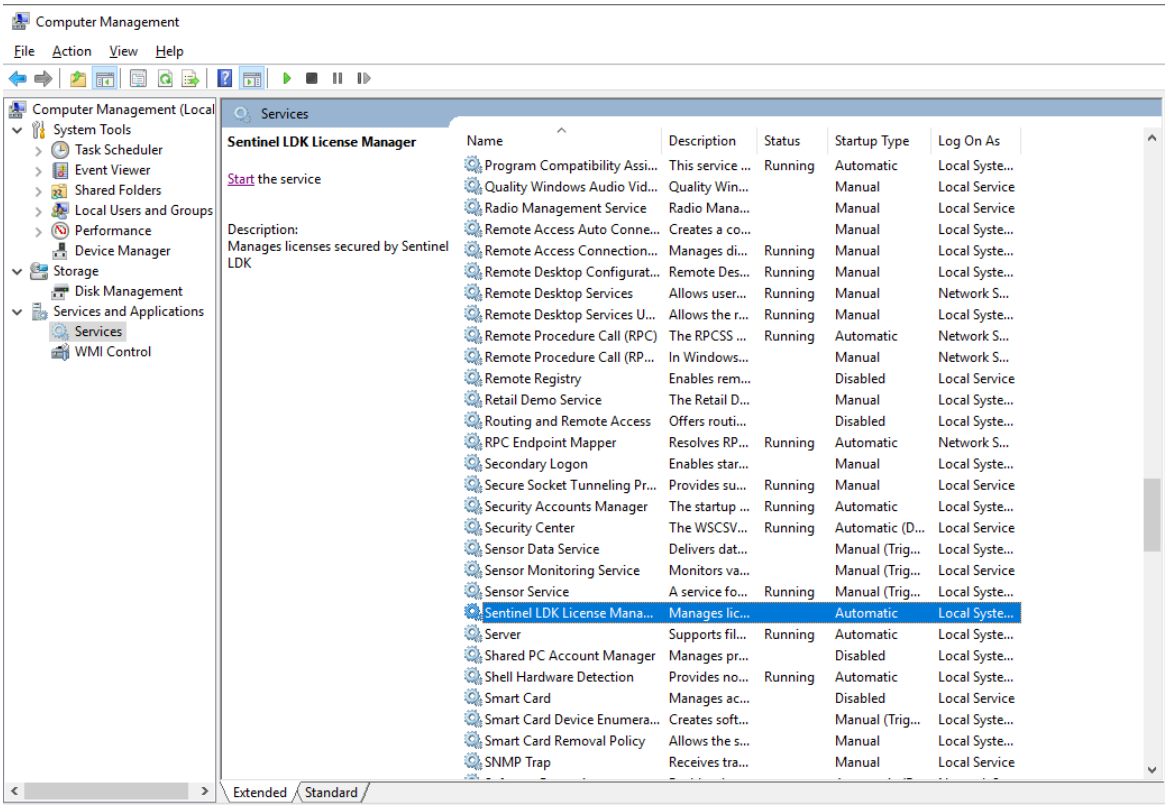
If the license service is running, you should see features available on your dongle:



Click **Refresh** if the list of features is empty after the Launcher has just restarted the dongle service.

If the CURRY 8 Launcher fails to start the license service, you can do it manually:

1. Open **Computer Management** · › **Services and Applications** · › **Services**.
2. Select the **Sentinel LDK License Manager**.
3. Click **Start the service**:



If the **Sentinel LDK License Manager** is missing or fails to start, install the dongle driver from:

C:\Program Files\Neuroscan\Curry 8\License\HASPUserSetup.exe.

If this does not work, get the latest dongle drivers from here (look for "Sentinel HASP/LDK - Windows GUI Run-time Installer"):
https://sentinelcustomer.gemalto.com/sentineldownloads/

Another option is to re-install CURRY 8.

If the license service is running, but the list of features in the Launcher remains empty:

1. Check if your USB dongle is inserted and its light is on.

2. In case a network license is used, check if the computer providing the license is available.

3. Check the chapter **Network CURRY** just below in the *CURRY User Guide* for additional information.

4. Update the license driver (see above).

6 CURRY on a Network

There are three scenarios for using CURRY and a network.

The first is to have a network license, or red network dongle, on the server, and then multiple users may access that license from computers on the network. This is described just below in the **Network CURRY** section.

Second, incoming data may be transmitted to a second computer where it may be viewed and recorded (a dongle with at least an acquisition license is needed), or, the data stream may be sent to MATLAB or other third party program, or both. The options for this use are described in the **Configure as NetView Server or Client** button in the **Amplifiers** panel.

Third, it may become advantageous for you to relocate your data files and the Database to a server that can be accessed by multiple users. This is described in the **Multiple User Access of the Database** section below.

General Network and File Size Questions

What is the difference between the network and local versions of the CURRY software?

The software, drivers and services that are installed are exactly the same in both cases.

We use technology from Sentinel HASP for licensing:

http://www.safenet-inc.com/software-monetization/sentinel-hasp/

The Sentinel drivers are part of the CURRY installer.

The client computer needs to have CURRY and the license driver installed.

The server computer may have CURRY installed as well, if it also acts as a work station, but it would also suffice to only install the license driver, which contains the process needed to distribute the license on your network.

Is the network version a floating license?

Yes. CURRY can be installed on as many work stations as you like. Whenever an instance of CURRY is started, the needed licenses will be blocked for other users and released again when an instance of CURRY closes. You can have as many instances of CURRY running in parallel as you have licenses available.

Does it have a centrally-managed license file. If so, does the license manager portion get installed on a server?

The computer that holds your license needs to run a local process (part of the CURRY installer) that lets you access the "Sentinel Admin Control Center", where you can further restrict access of licenses to certain users, see which users currently occupy licenses and so forth.

Your license comes on a USB dongle that can be used on any computer that has the Sentinel drivers installed. If needed, Compumedics Neuroscan can provide a software license that is bound to a certain computer and does not require any USB hardware.

The license code itself is managed by Compumedics Neuroscan. You will receive a perpetual license based on your order, so typically no maintenance is needed.

If your license needs to be changed/updated, this can be done remotely via small updated files you receive from us via email.

How large are the data files generated by this software?

This depends on how you use the software.

If you only read in data files that already exist (such as EEG recordings or DICOM image data sets), CURRY will only write small parameter files (smaller than 100 KB) that contain information to be able to read the files.

If you use the CURRY Acquisition module to record EEG files from a Neuroscan EEG amplifier, the resulting filesize depends on the sampling rate and number of channels you use. One minute of EEG data from a 69 channel recording at 1 kHz sampling rate occupies ca. 16.5 MB.

If you export files (such as EEG recordings or DICOM image data sets) from CURRY, the resulting file will be of a similar size to the source file you have loaded into CURRY.

If you export results, these files are typically smaller than 1 MB, however, some operations can produce results that are 1 GB or more, depending on the selected parameters.

CURRY creates a log file every time it runs, which is typically in the range of a few 100 KB.

The CURRY installation itself occupies approximately 1.2 GB.

6.1 Network CURRY

It is possible to run CURRY across a network. That is, the HASP dongle on a host computer can be used to run CURRY on a remote computer(s) over a LAN. However, CURRY can only run on as many computers simultaneously as there are licenses on the dongle. Network licenses require a special type of dongle (with a red housing), and these are typically purchased with the original order (they can be purchased later, as well).

CURRY will look for the network licenses automatically; local dongles will be preferred.

In order to "see" the dongle on a network computer in the LAN (not over the internet), you have to install the dongle driver on the that PC. The driver will launch a service that makes the dongle visible to the other computers. The firewall on the server computer has to be configured to allow remote access. The server computer should be on the same subnet.

In most cases (e.g., Windows 7 with a internet connection), all you need is to plug in the dongle on that computer and Windows will do the rest. If that does not work, it will be necessary to install the drivers manually. There are three ways to do this.

1. Install CURRY 8 on the server computer, and the drivers will be installed automatically.

2. Copy the *HASPUserSetup.exe* file from an existing CURRY 8 installation (in the *...\Program files\Neuroscan\CURRY 8\License* folder) to the server and run it. The drivers will be installed into the CURRY 8 folder that it creates. There is also a *HASPUserSetupReadme.HTML* file that contains the directions.

3. Download the drivers from Safenet: http://sentinelcustomer.safenet-inc.com/sentineldownloads/.

Then, if you are connected to a LAN, you will see the other Servers and IP addresses in the license window. The **1** in the **Licenses available** column indicates the computer that has the dongle (if more than one computer on the LAN has a dongle, all will be shown). Highlight that computer and click **OK**. If you select **Set as Default**, that computer will be accessed automatically for the dongle in the future.

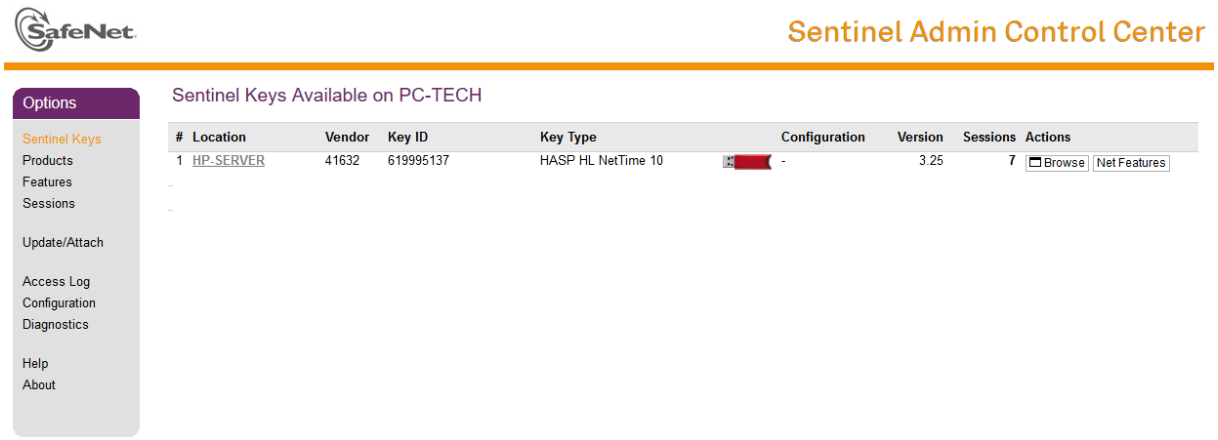
Additional Details for Running CURRY on a Client PC

First, some operational definitions:

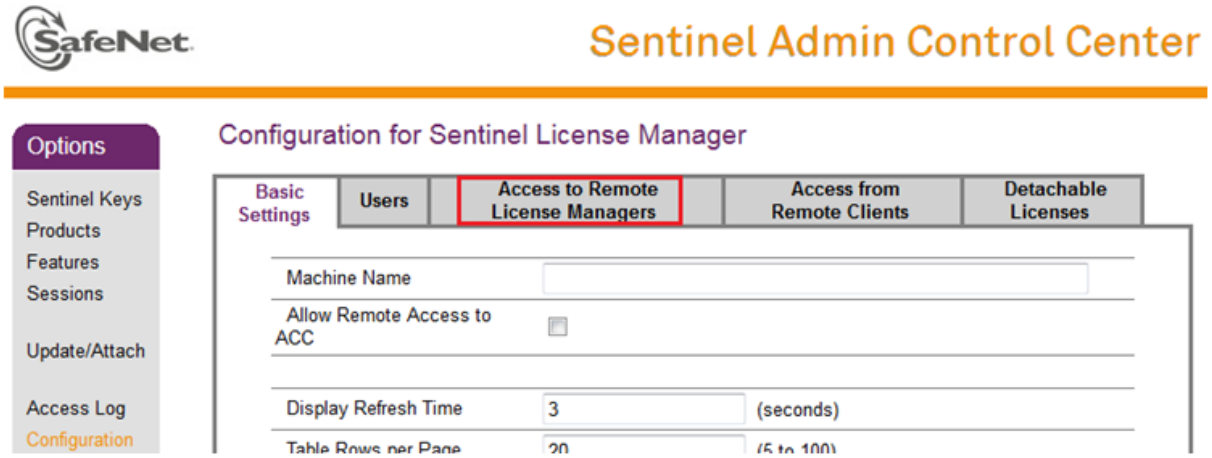
Server: the PC that will have the CURRY 8 dongle physically connected to it.
Client: any PC with the CURRY 8 software installed.
CURRY 8 network dongle: this will be a dongle, red in color.

Basically, to run CURRY 8 on any client PC, you need to fully install the CURRY 8 software on that computer.

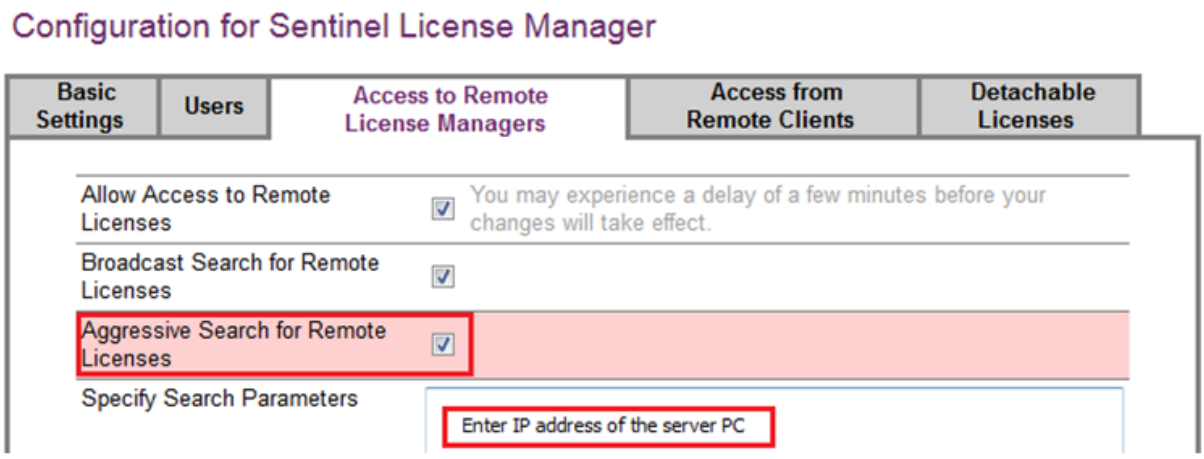
On the client, click the Windows **Start** button, and go to ***Programs*** → ***Neuroscan*** → ***CURRY 8*** → ***Dongle Info***. This calls up a local page inside your web browser, which will display information about any detected licenses. Your dongle's 'Key Type' should be 'HL Net', or HL NetTime'.



From the main page, under **Options** click the **Configuration** button. Select the **Access to Remote License Managers** tab.



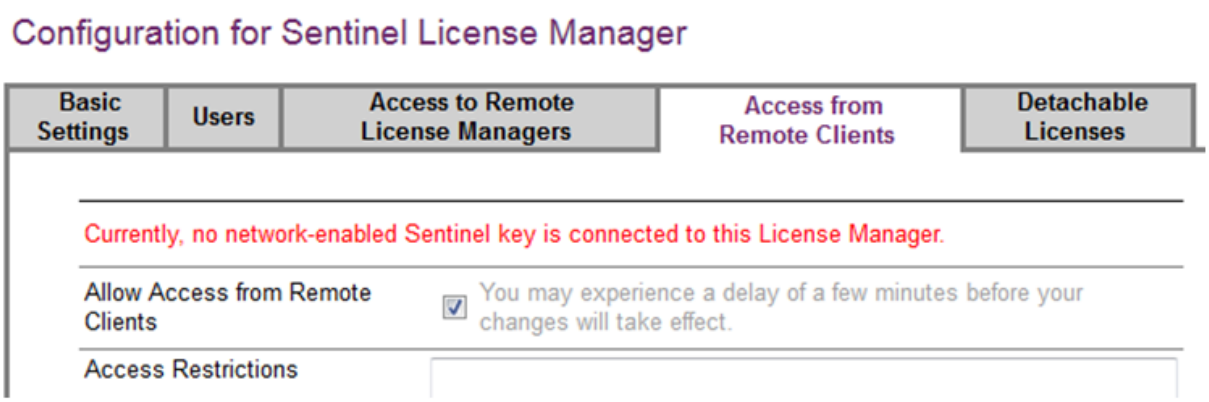
Select **Aggressive Search for Remote Licenses** and under **Specify Search Parameters**, enter the IP address of the server PC. If the client and the server are on the same Subnet, you may not need to enter the server's IP address on the client side. If on the same Subnet, the first, second, and third numbers of your client and server IP address should be identical (such as, 192.168.1.10 and 192.168.1.22) If they are on different Subnets, then manually entering the server IP address is usually needed.



On the server PC, you can run the **Sentinel Access Remote Center** to access this same field, or use the following address:

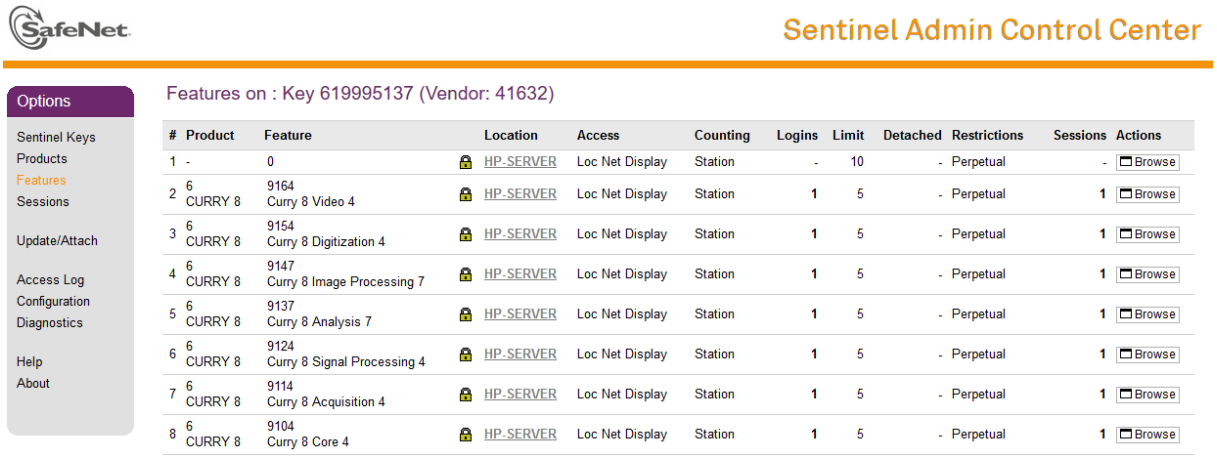
http://localhost:1947/_int_/config_to.html.

Go to **Access from Remote Clients** and make sure the **Allow Access from Remote Clients** field is selected (this is the default).



The dongle driver communicates via port 1947 - ensure the firewalls on the server and client allow this. Normally, the installation will take care of this automatically, but you could encounter a problem if you used plug and play for the installation.

To check the features installed on a license key, click the **Features** button under **Options**, and check the table. The **Limit** field will tell you how many instances of a particular module may be executed simultaneously. (Your list may appear simpler than the one below). What is called a "License" in the context of this manual, appears as "Feature" in the Admin Control Center. The license for every module (Acquisition, Signal Processing, etc.) is represented as a feature on your dongle (or Softlock).



A single-seat network license will likely show a **Limit** of **1** for 9002, 9005 and 9006. This means that, while a network license, it will only allow access to any one client at a particular time. In this particular instance, the dongle supports a maximum concurrency level of 10 (hard-coded into the dongle when purchased), and the Curry 8 "product" on it supports up to 5 simultaneous users.

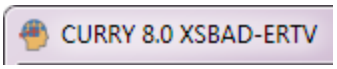
Finally, the **Sessions** page, under **Options**, will tell you what PC is accessing a network license at any given time.

After making or verifying the settings, open CURRY and the dongle on the network should be found and CURRY should open normally. If you run into problems, contact curry8help@neuroscan.com.

7 The CURRY Display

The CURRY Display
When you start CURRY and open a Study, you will see several parts in the main display. What you see will vary somewhat based upon the type of license you have. For example, if you have a basic analysis only license, you will not see the options for acquisition and source reconstruction.

If you look at the Title Bar at the top of the window, you will see letters after the program name.



These letters let you know what license(s) you have (described In the **Introduction** section above).

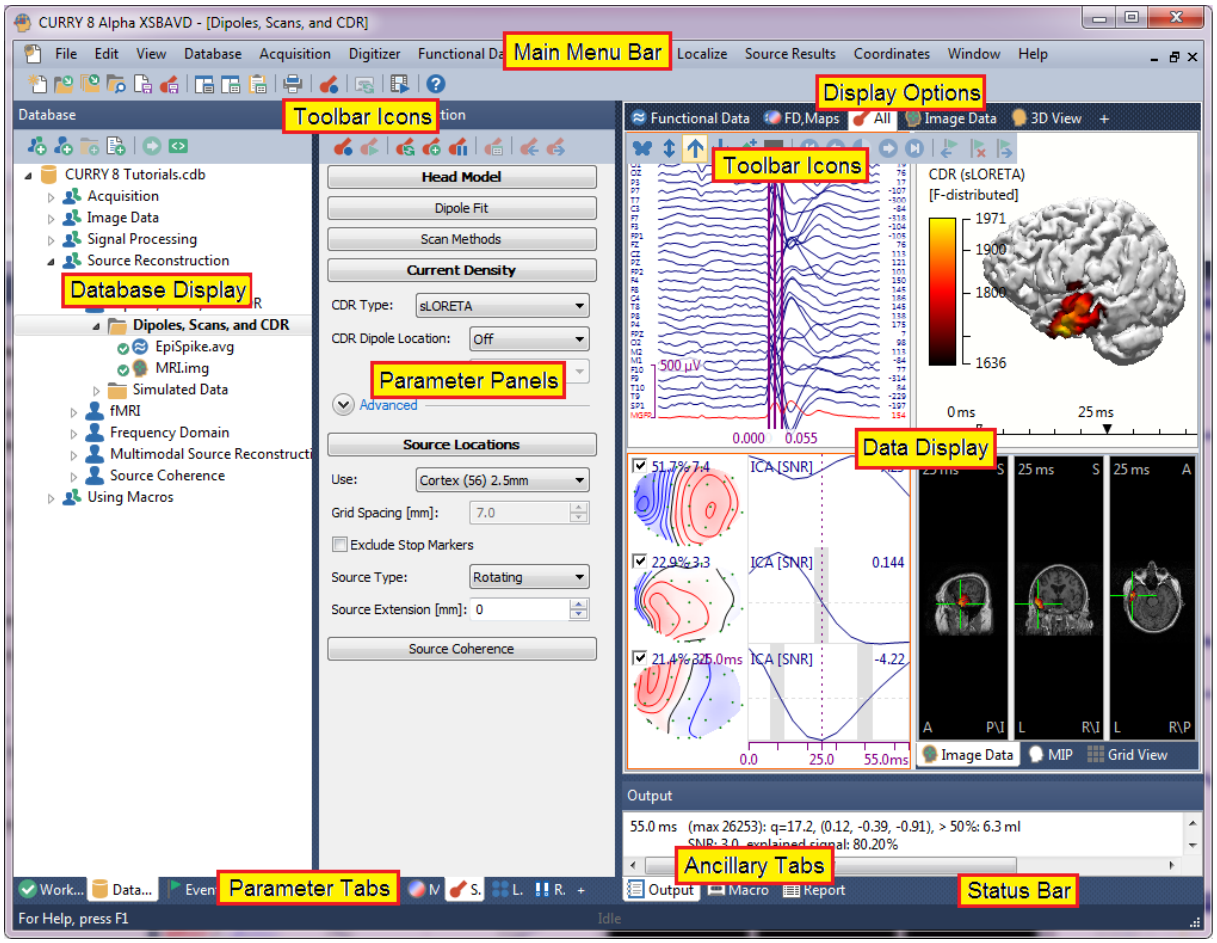
X - Acquisition
D - Digitizer
S - Signal Processing
B - Basic Source Analysis
(R) - Special Research license
A - Advanced Source Analysis

E - Elekta MEG Reader
R - Ricoh MEG Reader
T - Third-party EEG reader

V - Video Recording

An "SBA" license would therefore mean you will have access to Signal Processing and Basic and Advanced Source Analysis. The "V" license is required to record video; it is not required for the replay of existing video files.

The figure below shows all of the buttons and options that are available with a full license, along with the main parts of the display (seen once a Study is opened).



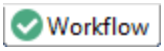
The **Main Menu Bar** is a standard feature across Windows applications. Many of the options you will use can be found in the drop-down lists. The menus will vary depending upon whether you have a Study open and the license you have. The Main Menu Bar is described in the next section below.

The **Toolbar** icons are shortcut buttons for operations that are generally performed most frequently. They are described in more detail in the **Toolbars** section below. There are Toolbar options that are accessible all of the time, and other ones that are accessible only for certain displays, such as the Functional Data Toolbar, the Image Data Toolbar, and so forth.

The **Display Options** let you select what you want to see in the data display region. For example, you may choose to view the Functional Data only, or the Image Data only, or a combination of displays. These are described in the **Display Screen Options** section below.

The **Data Display** area is where you will be viewing and working with the data files.

A **Database** is used to select the files you want to work with. Databases can contain zero or several **Groups**. Each Group can be divided into zero or several **Subjects**. Each Subject may have one or more **Studies**. Each Study contains the **Functional Data**, the **Image Data**, and other files that you wish to use. The Database is described in detail in the **Database** section below.

The **Workflow** list is seen when you click the 

tab below the Database. The items in the list will vary according to the Study you open and the operations that have already been performed. It shows you what has been done (green check) and what additional steps you may wish to perform (blue arrow). Clicking an item takes you to the section of CURRY needed to review or perform the task. The Workflow list is described in more detail in the **Workflow** section below.

The **Parameter Tabs** are grouped according function: Acquire, Functional Data, Event List, etc. Clicking a parameter tab displays the associated **Parameter Panels**, which may be expanded to see the options. These are discussed in more detail below.

The **Ancillary Tabs** - Output, Macros, and Report - are described in the **Output, Macro, and Report** section below. Briefly, the **Output** section displays the numerical results of the operations that are performed, as well as other information. **Macros** are used to record the operations you perform. The Macro can then be applied to other data files you select. The **Report** was created as a means to save text and graphics (a sort of research notebook), as well as a report for clinical users.

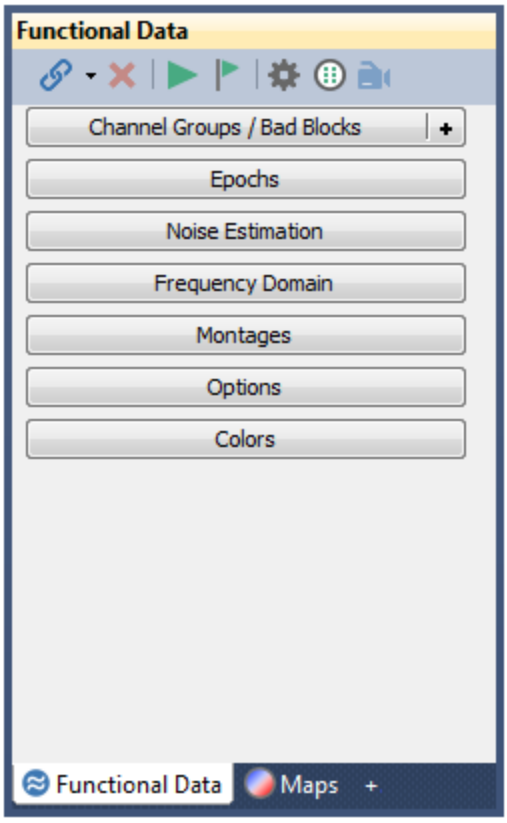
The **Status Bar** is seen at the bottom of the display, and is useful to display the progress of longer duration operations.

Repositioning the Display Screens

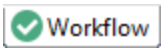
There are several ways in which you may reposition the display areas to, for example, maximize the area for the Data Display. One is to grab the divider between displays and resize the windows. Dividers occur throughout CURRY - if you see two parallel lines separating displays, chances are that you can grab and drag the divider.

You can also undock the entire display of processing options and/or the Output, Macro, and Report screens. Grab and drag one of the title bars

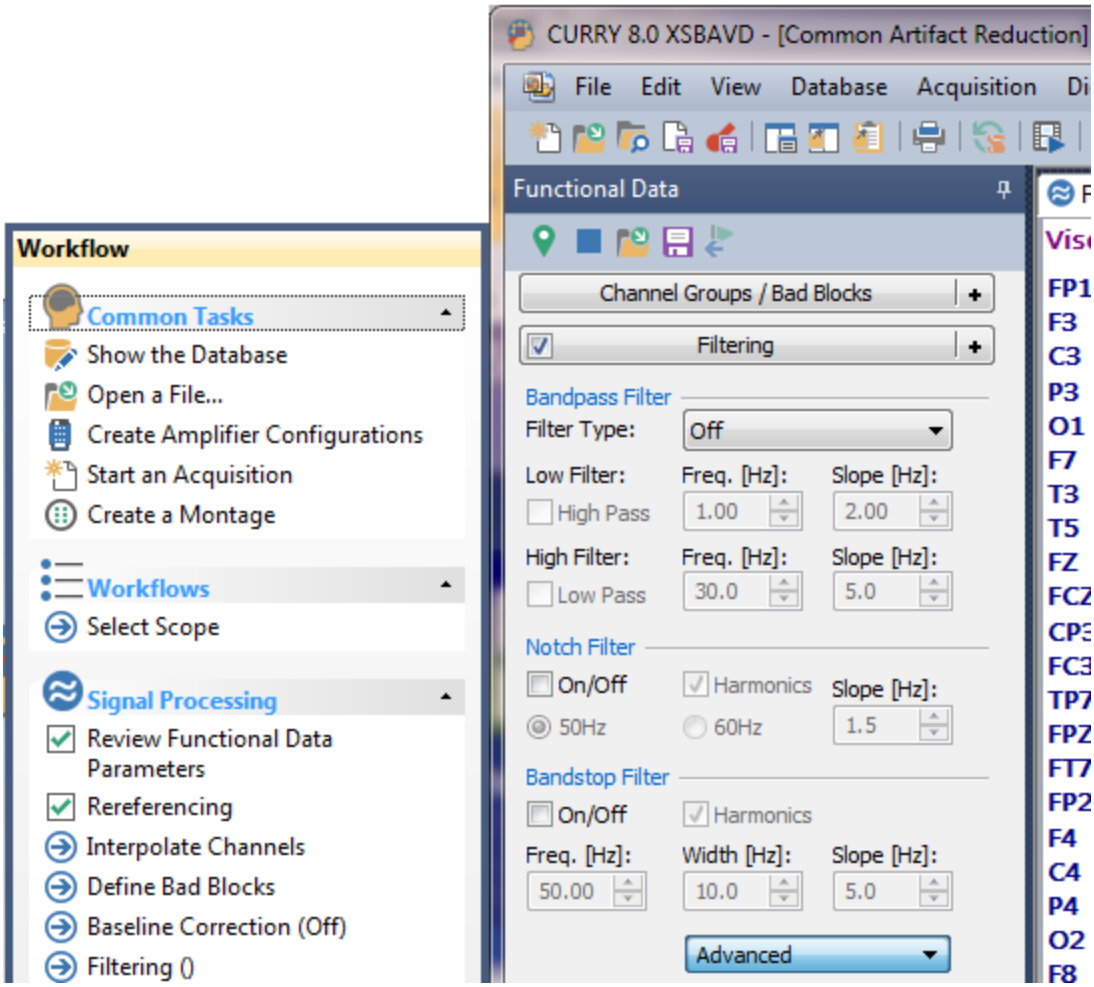
, or *double-click* the title bar, and the entire set of options or displays will appear in a free-standing display. To undock the entire display, **View → Lock Window Layout** has to be disabled. To dock it again, *double-click* the title bar.



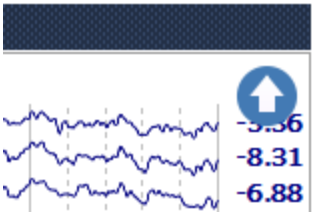
You may also reposition an individual parameter panel outside of the CURRY display (or to a second monitor), as well as to other positions within the CURRY display (assuming **View → Lock Window Layout** is not enabled) by double-clicking on its tab: 

. This allows you to access whatever panels you wish (

is a good one to leave off to the side). *Double-click* on the title bar to return the panel to its original position.

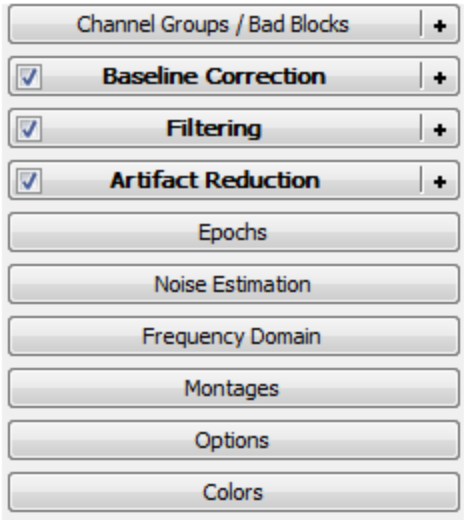


You can full-size the data display with a single click. Position the mouse in the upper right corner of the data display to see the expand button. Clicking it will expand the data display to the entire screen. After expanding the display, position the mouse in the same area to see the reduce button.



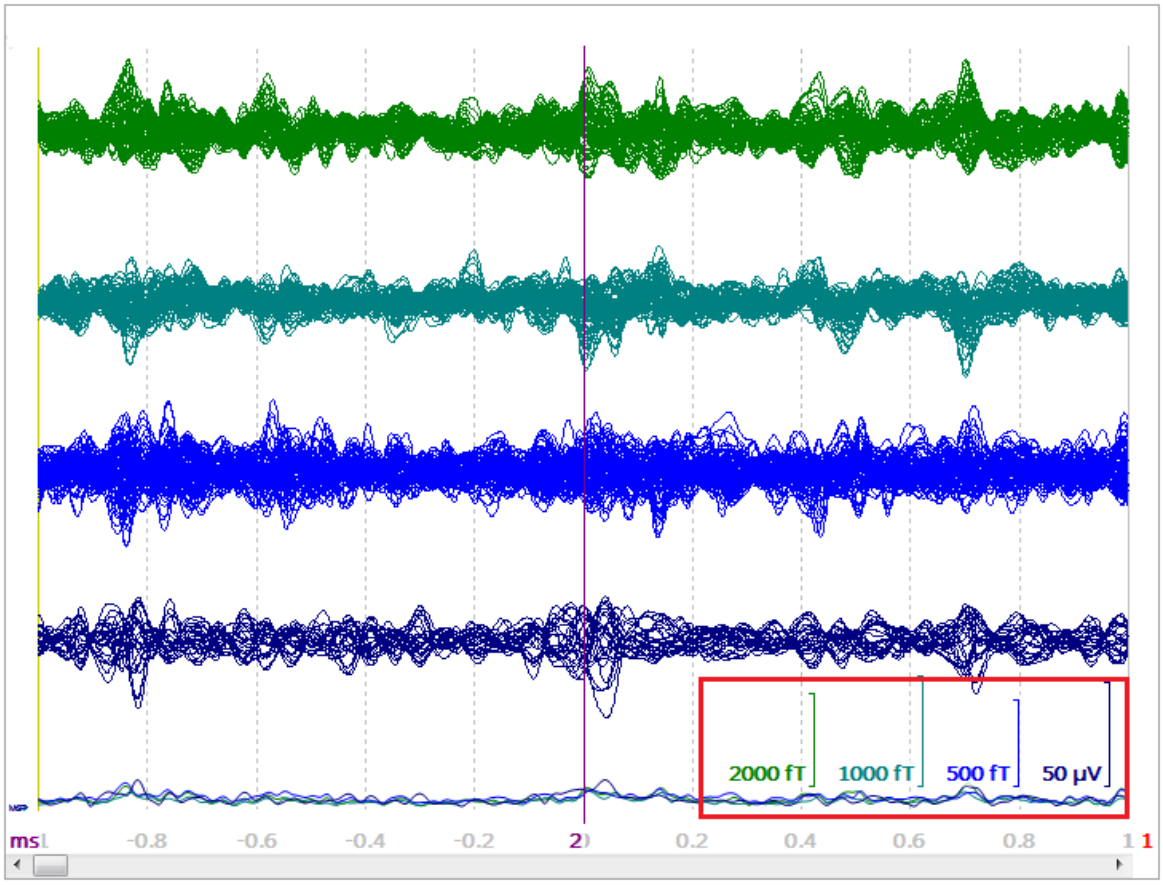
If the layout gets too "messed up", and you want to restore the original layout, select **View → Reset Window Layout**. The default layout will be restored when you restart CURRY; you will be asked whether to restart it immediately.

As you use the program, you may note that the parameter headings sometimes appear in **bold**.



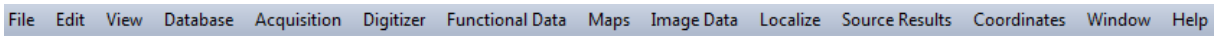
When you change a setting (from the defaults) in selected parameter panels, the heading will turn bold, letting you know that something has been changed or enabled.

If you have multiple Channel Groups, such as with MEG data or with depth electrode data, you will see separate, color-coded Scale Tools for each group.



7.1 Main Menu Bar

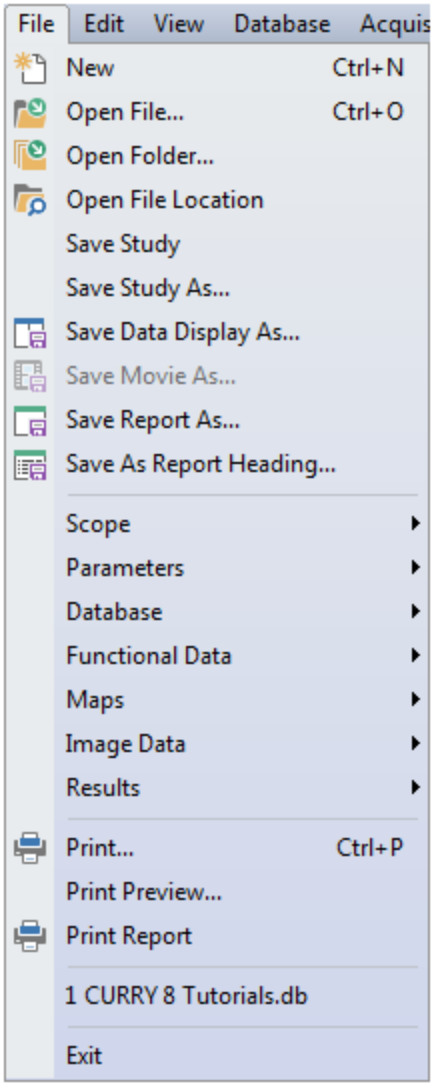
This section contains a description of the options seen at the top of the CURRY display:



These options will not all be seen until you open a Database, and then select a Study for use. Fewer options are seen if you have less than a full license.

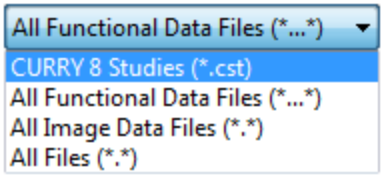
7.1.1 File

This contains the basic commands for opening, saving, closing and printing, as well as other commands specific to CURRY. The options that are seen will vary depending on whether you have Study data displayed or not. If you have Study data displayed, you will see the more complete list of options. The options that are also accessed by Toolbar icons have the icons displayed.



New. The New option is used to create a new Study (same as the  icon on the **Standard** Toolbar, or *Ctrl+N*). Selecting it will create a new "Unfiled" study in the Database hierarchy. More importantly, it accesses the acquisition part of CURRY.

Open File. The Open option is used to open different types of files (same as the  icon on the **Standard** Toolbar, or *Ctrl+O*). Clicking the option displays a standard Open file utility. Click the drop-down menu to see the types of files that may be opened or displayed.



If you select Functional or Image Data files, and then select a file, a new "Unfiled" Study will be created with the file in the proper folder. This saves the step of creating a new Study first.

Study files (.cst) provide the flexibility to open and use existing Studies at any time, without having to close an already open Database. You may open several saved Studies, and compare their data without having to create a Database containing them.

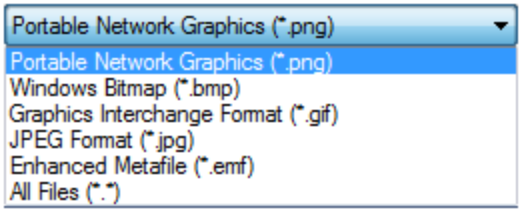
Open Folder. Use this option to open a functional data folder (such as a Compumedics folder), or an image data folder.

Open File Location. Click this option to access the Windows Explorer program to the folder containing the selected data file. This is a convenience for finding files or changing their Properties (as in Read Only). The option is also accessed from the  icon on the **Standard** Toolbar.

Save Study. The Save Study option lets you save the currently opened Study (.cst). Clicking it displays a standard Save file utility. The .cst files in the selected folder are seen. If you have already saved the file, clicking this option saves any changes to the file automatically, with the same file name.

Save Study As. Click Save Study As to save the current CURRY Study using a different file name.

Save Data Display As. Select this option to save the data display region using one of the possible graphics file types (seen in the **Save as type** list).

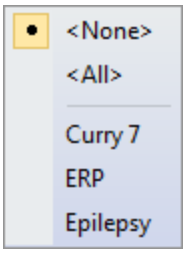


Save Movie As. A movie comprising the selected Timerange and showing the whole of the data display can be saved as an .avi file.

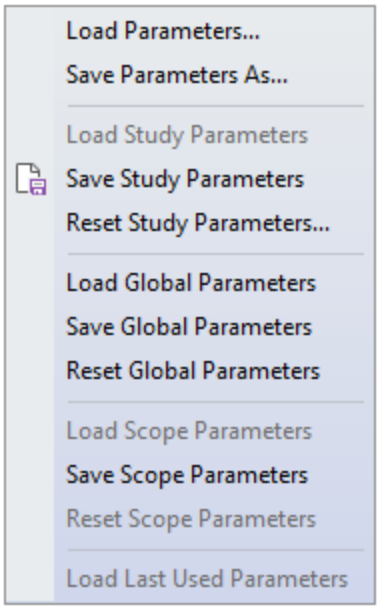
Save Report As. After completing the Report, click this option to save it in either .rtf or .txt format. The option is also accessed from the  icon on the **Report** Toolbar.

Save As Report Heading. This option is used to save the heading once it has been created in the Report display. It will then be used as the heading for subsequent Reports. The option is also accessed from the  icon on the **Report** Toolbar.

Scope. Select a Scope configuration, if desired (same as at the top of the **Workflow** panel). Scopes are predefined configurations of parameters that have been created for ERP Analyses, Epilepsy evaluations, and Source Reconstructions. They are short cuts that select the most frequently used options in those scenarios. See the **Global, Scope, Study and Other Parameters** section below for more information.



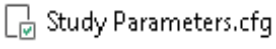
Parameters. The Parameters are an important part of CURRY. CURRY has three kinds of Parameter configurations: **Global Parameters**, **Scope Parameters**, and **Study Parameters**. Global Parameters are applied across all data files, all Studies, all Subjects and all Databases - they are applied globally. Scope Parameters contain preconfigured settings for ERP Analyses, Epilepsy, and Source Analyses (described in the **Global, Scope, Study and Other Parameters** section). Study Parameters are applied only to the particular Study. When you save the Study Parameters (.cfg configuration files), for example, all of the settings in CURRY are saved with that Study. When you reopen the Study, the parameters are applied, and you will be back where you were when you closed the Study. **Last Used Parameters** are like Study Parameters, except they are the parameters that were in place when the study was closed, and so may be more recent than Study Parameters. Last Used Parameters are controlled by **Edit** → **Options** → **Settings** selections.



Load Parameters. This option lets you select previously saved .cfg files. The settings will be applied, although the .cfg file itself will not appear in the Database.

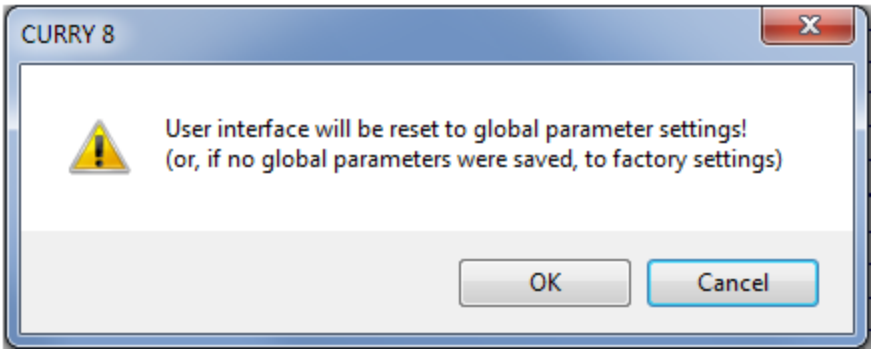
Save Parameters As. This option is similar to Save Study Parameters, except that it displays a Save As utility to name and place the .cfg file. The .cfg file is saved only, not applied. You can select it at a future time using **Load Parameters**. The option allows you to create a new .cfg file without changing the currently open one.

Load Study Parameters. In some cases, the Study Parameters may contain operations that require lengthy steps in their application (such as, some CDR computations). In these cases the parameters are not applied when you open the Study, as you may not wish to wait. The parameters are applied explicitly by selecting **File → Parameters → Load Study Parameters**.

Save Study Parameters. The current study settings will be saved and displayed below the Results folder 

. If you have not already created a .cfg file, you will be able to name it and select its folder. If you already have a .cfg open, the new settings will be written to it. The same option can be accessed from the  button on the **Standard** Toolbar.

Reset Study Parameters. Clicking this options displays the following dialog. Clicking OK will remove the Study Parameter settings, leaving the Global Parameters. The Study Parameter file remains in the Database, and will be applied when you open the study again. If you want to reapply the Study Parameters without closing and reopening the Study, go to **File →Parameters → Load Study Parameters**.

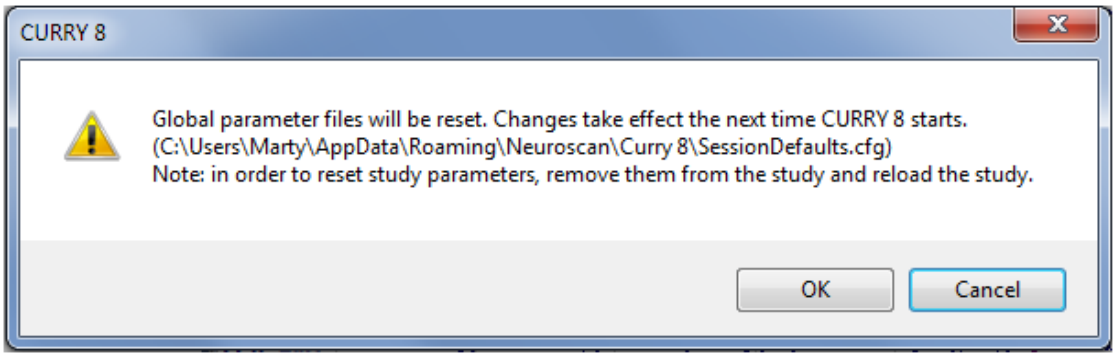


Load Global Parameters. Clicking this option will immediately apply settings that have been saved using **Save Global Parameters**.

Save Global Parameters. The settings you make will be saved and applied globally to all Databases, Subjects, Studies and data files. The settings are saved in the *GlobalParameters.cfg* file in one of two folders, depending on the operating system you have (see **Target Folders for Windows XP versus Windows 7**).

The types of settings that may be saved include:
- Colors, such as the colors of the waveforms or other components in the Colors panels.
- Most parameter settings.
- Most of the Properties in the **3D View** List.

Reset Global Parameters. Clicking this option displays the following self-explanatory message. The original Global Parameters will be restored the next time you run CURRY.



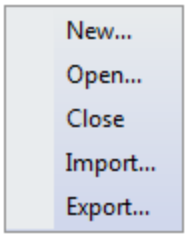
Load Scope Parameters. Clicking this option will load the Scope Parameters that have been saved using **Save Scope Parameters**.

Save Scope Parameters. You may make changes to the Scope Parameters that you have selected, and save the changes.

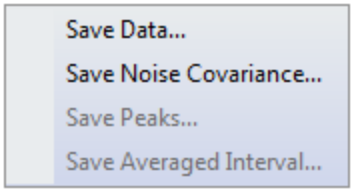
Reset Scope Parameters. Clicking this option will restore the default Scope Parameters for the selected file.

Load Last Used Parameters. If you have saved the Last Used Parameters for the study you have open, you can load them using this option. Last Used Parameters are described under **Edit** → **Options** → **User Interface**.

Database. This accesses the **New**, **Open**, **Close**, **Import**, and **Export** options. These are the same options as listed under **Database** on the Main Menu bar, and are described there.



Functional Data. This accesses the **Save Data**, **Save Noise Covariance**, **Save Peaks**, and **Save Averaged Interval** options. These are the same options as listed under **Functional Data** on the Main Menu bar, and are described there.



Maps. These options are the same as those found under **Maps** → **Save**, and are described there.

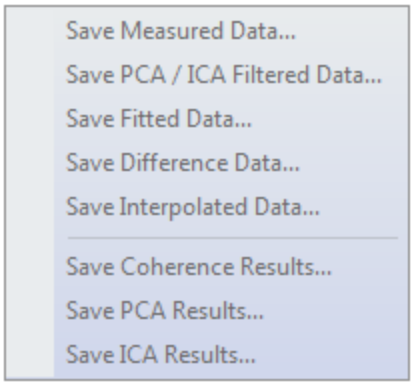


Image Data. These options, **Image Data Parameters** and **Save Image Data As**, are the same as those found under **Image Data** (on the Main Menu Bar) and are described there.

Results. These options, **Load Results**, **Save Results As**, and the source reconstruction results export options, are the same as those found under **Source Results** (on the Main Menu Bar) and are described there.

Print / Print Preview. These options open a preview of the active study's window for printing. Print is also accessed from the icon on the **Standard** Toolbar (or *Ctrl+P*).

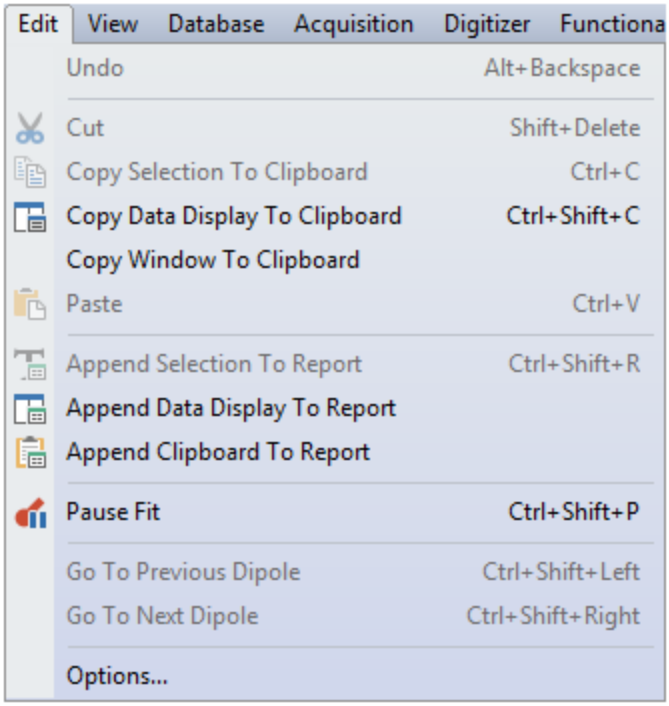
Print Report. Selecting this option prints the Report. It is also accessed from the icon on the **Standard** Toolbar and the **Report** Toolbar.

Recent Databases/Studies. The next section lists recent Databases (.cdb files), Studies (.cst files), and, most importantly, data files that have been opened. Click a Database to open it, or click a .cst or data file to open it as an "Unfiled" study.

Exit. Exits CURRY.

7.1.2 Edit

Clicking Edit displays the standard **Undo** (*Alt+Backspace*), **Cut** (*Shift+Delete*), and **Paste** (*Ctrl+V*) options common to Windows applications. Most of the options can be accessed from the **Standard** and/or **Report** Toolbar icons, or the accelerator keys on the *keyboard*, as shown.



Copy Selection To Clipboard. This option is used to copy selected text or the *part of the display having the focus* to the Windows Clipboard. The icon on the **Standard** Toolbar has the same function (or *Ctrl+C*).

Copy Data Display To Clipboard. Copies the *entire data display* to the Windows Clipboard. The icon on the **Standard** Toolbar has the same function (or *Ctrl+Shift+C*).

Copy Window To Clipboard. Copies the *entire CURRY window* to the Windows Clipboard.

Append Selection To Report. Selected text or the selected pane in the data display will be copied to the Report. The  button is found on the **Report** Toolbar (or *Ctrl+Shift+R*).

Append Data Display To Report. Co-pies the data display to the Report. The  icon on the **Standard** Toolbar and **Report** Toolbar has the same function.

Append Clipboard To Report. Pastes the Windows Clipboard contents to the Report. The  icon on the **Standard** Toolbar and **Report** Toolbar has the same function.

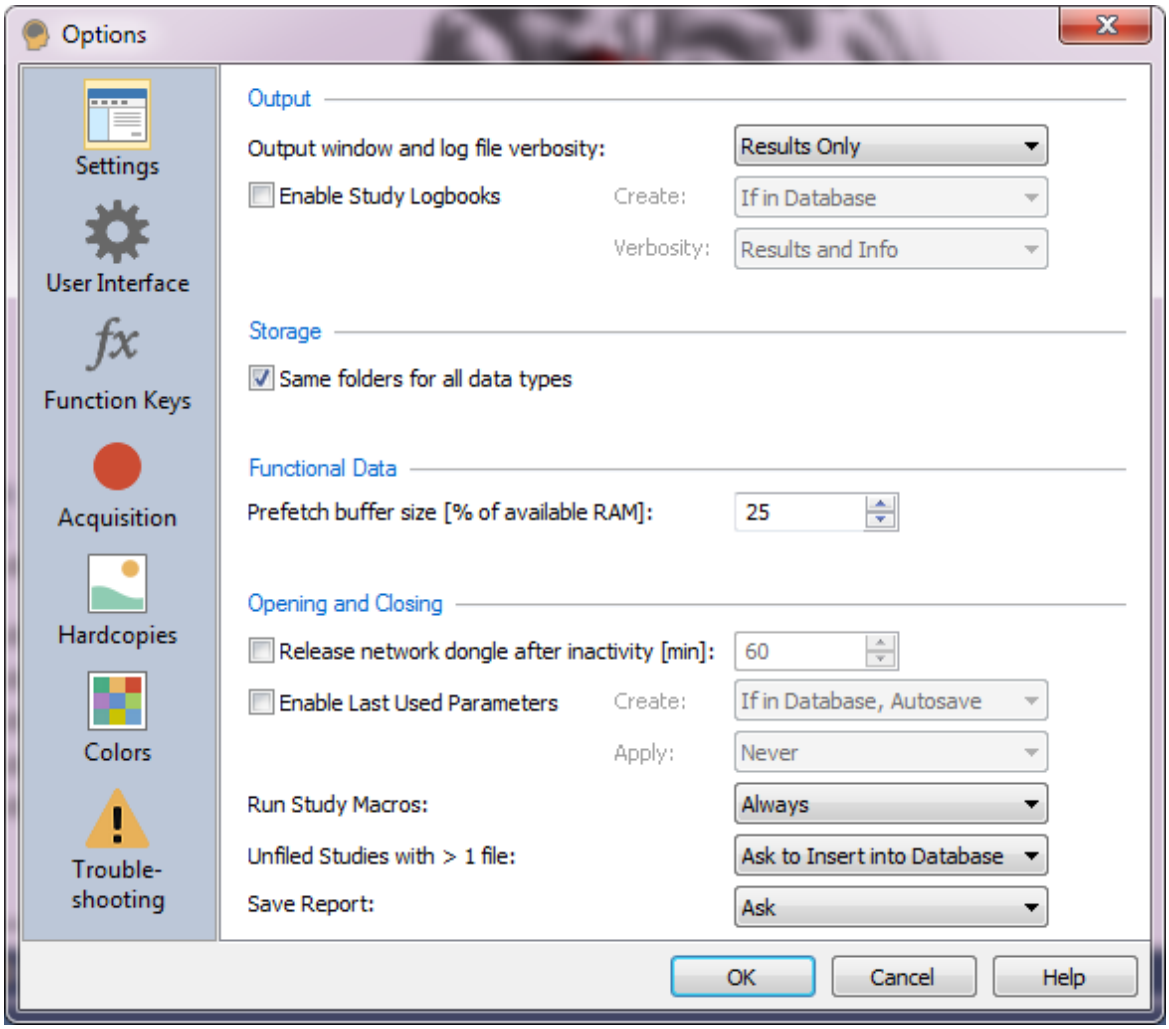
Pause Fit can be used to pause lengthy source reconstructions, e.g., in order to adjust parameters before continuing. The  icon on the **Source Reconstruction** Toolbar has the same function (or *Ctrl+Shift+P*).

Go To Previous Dipole. If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the previous dipole. The  icon on the **3D View** Toolbar has the same function (or *Ctrl+Alt+left arrow*).

Go To Next Dipole. If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the next dipole. The  icon on the **3D View** Toolbar has the same function (or *Ctrl+Alt+right arrow*).

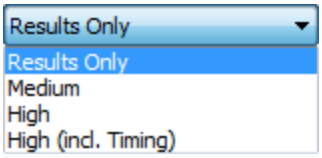
Options. Options contains a variety of user selections. Use the buttons on the left to access the various options. If you wish to return these options to their default settings, go to **File → Parameters → Reset Global Parameters**. (This deletes the *SessionDefaults.cfg* file in the User folder. This file is written each time CURRY is closed, and contains these Options as well as the acquisition parameters).

 **Settings**



Output
These settings control the degree of detail contained in the Output file, as well as the use of and content in the Logbook files.

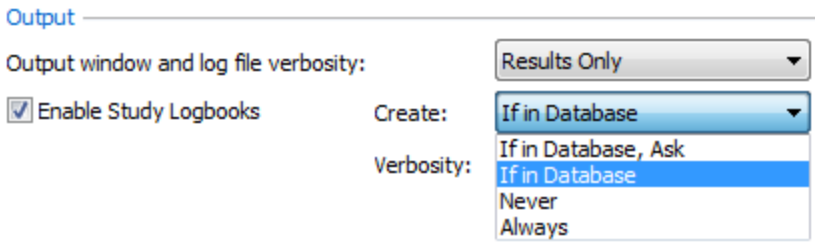
Output window and log file verbosity. This refers to the amount of information that is displayed in the Output window and the log file. Select Results Only, Medium, High, or High including timing information. When the latter most option is selected, many of the processing results (dipole fits, etc.) will have timing information included in the Output.



Enable Study Logbooks. Logbooks are a variation on the Output files. These are contained in the Studies in the Database, where there is ease of access. Logbooks are a record of the operations that have been performed to the file(s) in the Study and the results that were obtained, and thus are a form of

History. Like Output files, Logbook files are merely records. They have no effect on the data files. Parameter files, on the other hand, are in a sense historical records also, with the main difference being that they restore the last saved state.

Create. You may create Logbooks or not. If you elect to create them, you can control when they are created. There are slight differences depending on whether you are opening a data file directly, or from within a Database.



If in Database, Ask. If you have this option selected, and are opening a data file not within a Database, no Logbook file will be created.

If you have this option selected, and are opening a Study within a Database, a Save As dialog will appear and you have the option to save a Logbook file if desired. If you already have a Logbook file in the Study, the new information will be written to that file.

If in Database. If you have this option selected, and are opening a data file not within a Database, no Logbook file will be created.

If you have this option selected, and are opening a Study within a Database, one will be created based on the data file name. If you already have a Logbook file in that Study, the new information will be added to it.

Never. No Logbook will be created when you open a data file directly or from within a Database.

Always. If you have this option selected, and are opening a data file not within a Database, a Logbook file will be created using the data file name.

If you have this option selected, and you do not have a Logbook file already started in the Study you are opening, a new Logbook file will be created using the data file name. If you already have a Logbook file in that Study, the new information will be added to it.

In all cases where a Logbook file is created, and a Logbook file with the default name already exists on the hard drive in the target location, a Logbook file with a name containing date and time information will be created, to avoid overwriting the existing file.

Verbosity. You can save just the Results, the Results plus additional information, or All possible details.

Storage

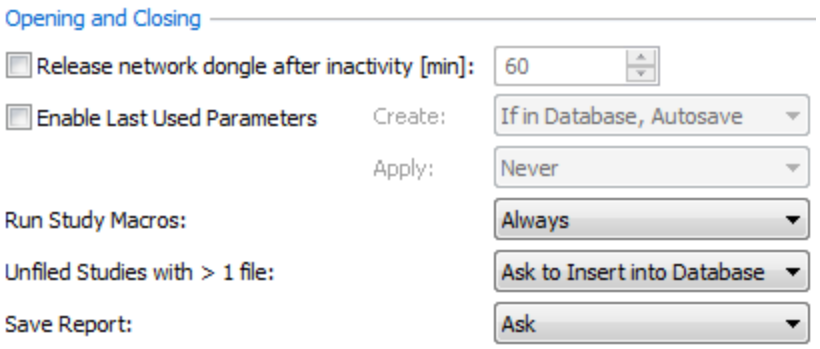
Same folders for all data types. This is a convenience option. If the option is enabled (default), then say, for example, you have functional and image data in the same folder, and then you load the functional data. When you go to load the image data, you will be taken to the same folder where the functional data was. If you have the option disabled, and you have the functional and image data in separate folders, when you load either the functional or image data, its folder will be memorized. If you load more functional or image data, you will be taken to each respective folder. In other words, if you have all of your data files in the same folder, enable the option so that the folder will appear when you want to load more files. Disabling the option may be helpful in cases where the additional file(s) you want to insert are located on different drives, across a network, etc.

Functional Data

Prefetch Buffersize [% of available RAM]. This controls the amount of available RAM that is used to speed up data processing. This is a useful option for the 64 bit version of CURRY 8, where a file may be read completely into memory. CURRY will check the available RAM and only use this percentage to prefetch data. For example, if you have 8 GB RAM and a 2 GB file, CURRY will load the entire file into RAM with the 25% setting. This will make file processing go much faster. There are lower and upper limits (<100%) for the Buffersize (e.g., 20-70%).

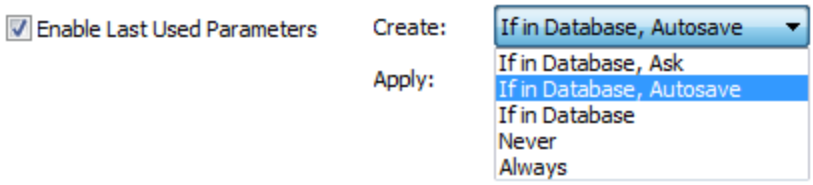
Opening and Closing

These are the options that are available when you open or close the CURRY program.



Release network dongle after inactivity [min]. This allows the network dongle to be released for others to access if it has not been active for N minutes.

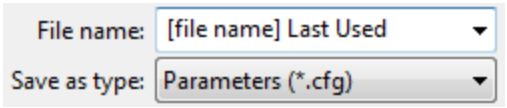
Enable Last Used Parameters. When this option is enabled, the most recently used parameter settings can be saved and are applied when you reopen the Study. These supersede the Study Parameters you may have saved (should there be conflicts between the two). A .cfg file will be created (*Data File Name + Last Used.cfg*) and placed in the Study.



There are options for creating last used parameter files, and for applying them.

Create. When you close the Study, you can control what will happen with the Last Used parameters.

If in Database, Ask. When you close a Study, a Save As dialog will appear in which you can save the Last Used parameters. If a Last Used parameter file already exists, the recent changes will be saved when you close the Study. If you open a data file directly (without using a Database), there will be no option to save the Last Used parameters.



If in Database, Autosave. When you close the Study, a Last Used parameter file will be created automatically, using the data file name. That file will be updated automatically every 5 minutes. If you open a data file directly (without using a Database), there will be no option to save the Last Used parameters.

If in Database. When you close the Study, a Last Used parameter file will be created automatically, using the data file name. It will not be updated automatically. If you open a data file directly (without using a Database), there will be no option to save the Last Used parameters.

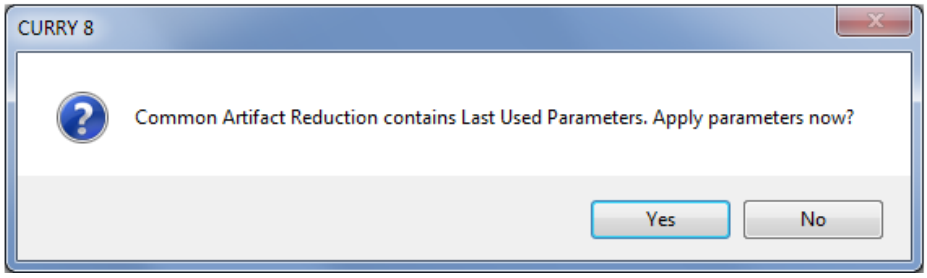
If that file already exists (but is not in the Database), an extended file name that includes data and time information will be created automatically. If the file exists and is in the Database, it will be overwritten.

Never. Never save the .cfg file.

Always. When you close the Study, a Last Used parameter file will be created automatically, using the data file name. If you open a data file directly (without using a Database), there will be no option to save the Last Used parameters (depending on the selection you have made for **Unfiled Studies with >1 file**).

Apply. Choose when to apply the last used parameters.

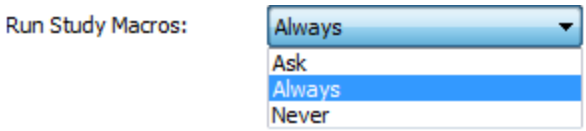
Ask. When you open the Study, you will be asked if you want to Apply the Last Used parameters.



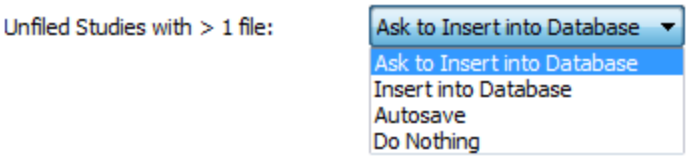
Never. The Last Used parameters are never applied.

Always. The Last Used parameters are applied automatically.

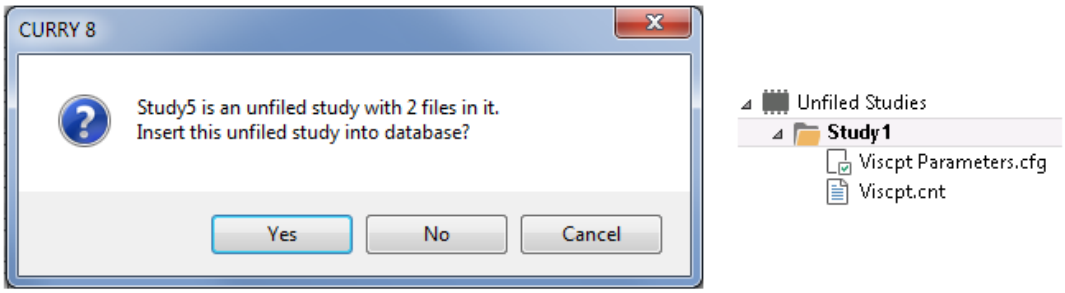
Run Study Macros. If you have used the **Insert Study Macro** option (context menu) in the Database, You can have the program **Ask** if you want to run the macro, **Always** execute it, or **Never** execute it.



Unfiled Studies with >1 file. If you have opened a data file outside of a Database, it will be displayed as an Unfiled Study. When you close the Study, nothing is saved. If, however, you have created a .cfg file, or a subfolder with derived results, there is a greater likelihood that you will want to insert the Unfiled Study into a Database. This option, therefore, applies when there is more than one file in an Unfiled Study. Otherwise, the file will appear at the bottom of the **File** menu.



Ask to Insert into Database. When you close the Unfiled Study, you will be asked if you want to insert it into a Database. If you say Yes, an autosaved Subject will be added to your Database.



Insert into Database. The Study will be inserted automatically.

Autosave. The unfiled study will be saved as a .cst file (to the default folder for .cst files).

Do Nothing. The Unfiled Study is closed with nothing being saved.

Save Report. This refers to the Report section of CURRY seen in the 

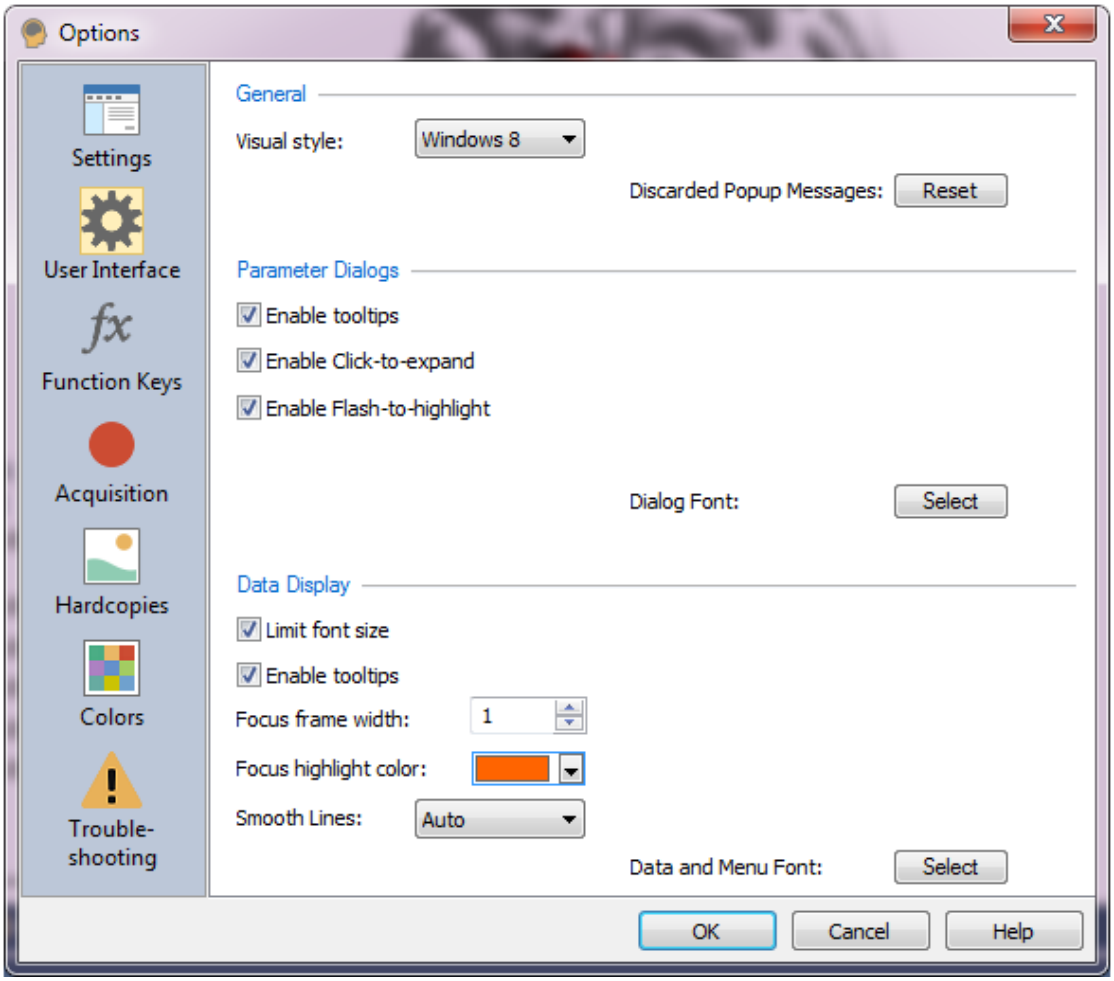
display. If you have made changes to the Report (without explicitly saving the Report), you may set CURRY to respond in different ways when you close the Study.

Ask. You will be asked if you wish to save the changes.

Autosave. The changes will be saved automatically to the report that was open.

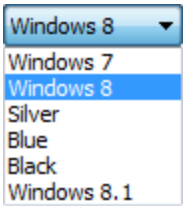
Never. The changes will not be saved.

User Interface

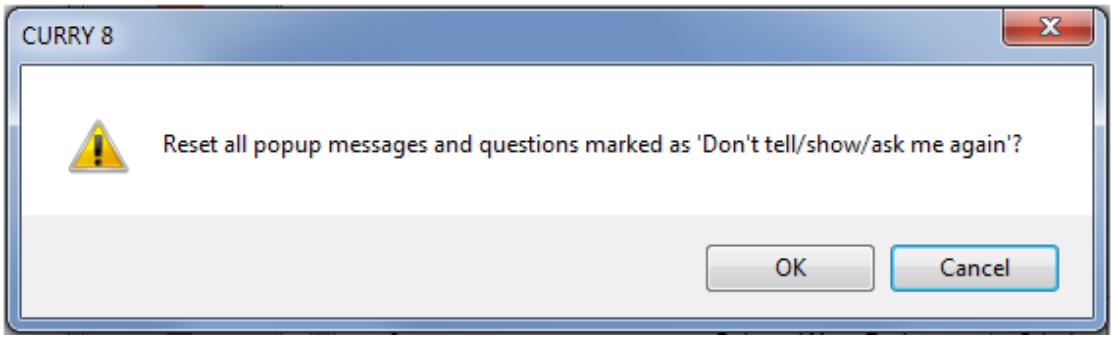


General.

Visual style. Select one of the styles for the display.

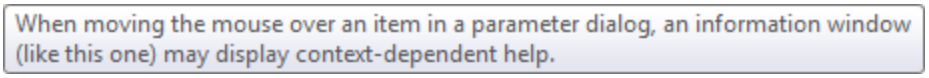


Discarded Popup Messages. Clicking this option displays the following dialog. This will restore discarded messages with the option not to display them again.

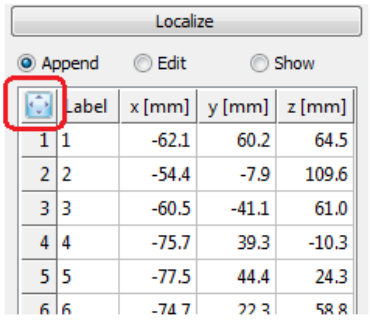


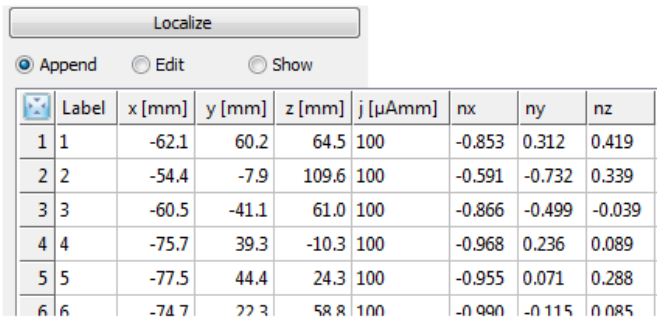
Parameter Dialogs. These options affect display aspects of the parameter dialogs.

Enable tooltips. Positioning the mouse over many options *in the Parameter Dialogs* will display a Tooltip. These can be enabled/disabled independently from the Data Display Tooltips.

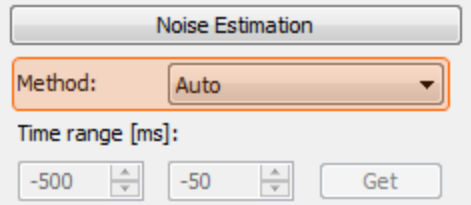


Enable Click-to-expand. When enabled, an expand button will appear in the top left corner of tables in some of the parameter displays. These allow you to see the entire table. Position the mouse in the left corner to see the button. Other places where the expand button will appear are in the online Averages panel, and in the matrix in the Result Statistics panel.





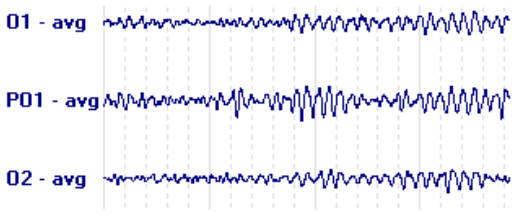
Enable Flash-to-highlight. If you select an operation from the Workflow, such as, Noise Estimation (Auto) , you will see a flashing region in the corresponding panel, when this option is enabled.



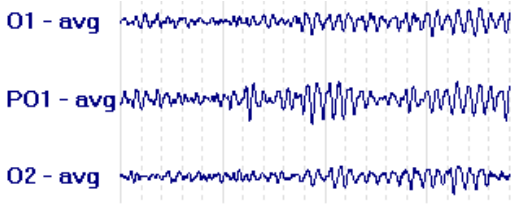
Dialog Font. Select a font that you wish to use for the dialog text.

Data Display. These options affect the appearance of the User Interface (UI). They are saved as part of the most recently used parameters (configuration) file.

Limit font size. When enabled, the font size in various places will be smaller than if disabled. For example, if you decrease the number of channels displayed, the font size will be larger with **Limit font size** disabled.



Font size limited

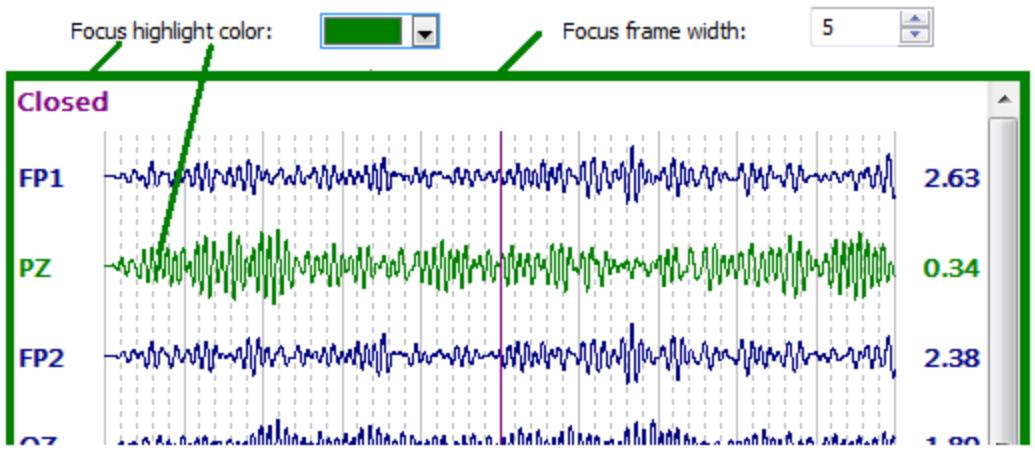


Font size not limited

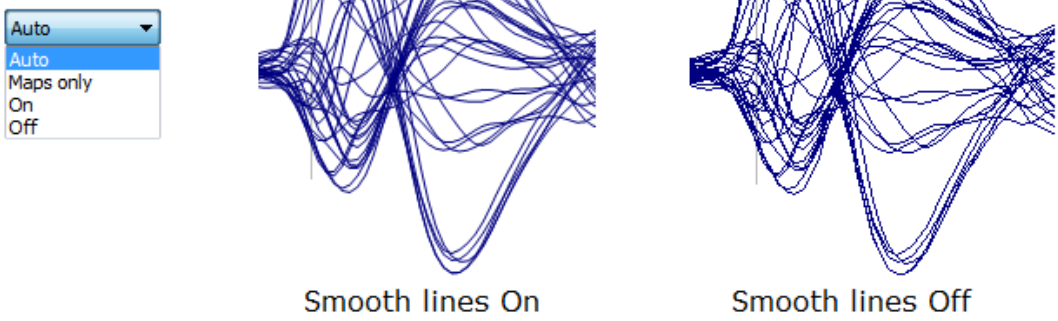
Enable Tooltips. When enabled, a Tooltip will appear when you position the mouse cursor over many objects *in the data display screens*.

Focus frame width. This refers to the width of the outline shown in the figure below.

Focus highlight color. This refers to the highlighted box that indicates which pane has the focus. The color is used for that as well as the channel that gets highlighted when you move the mouse over it.



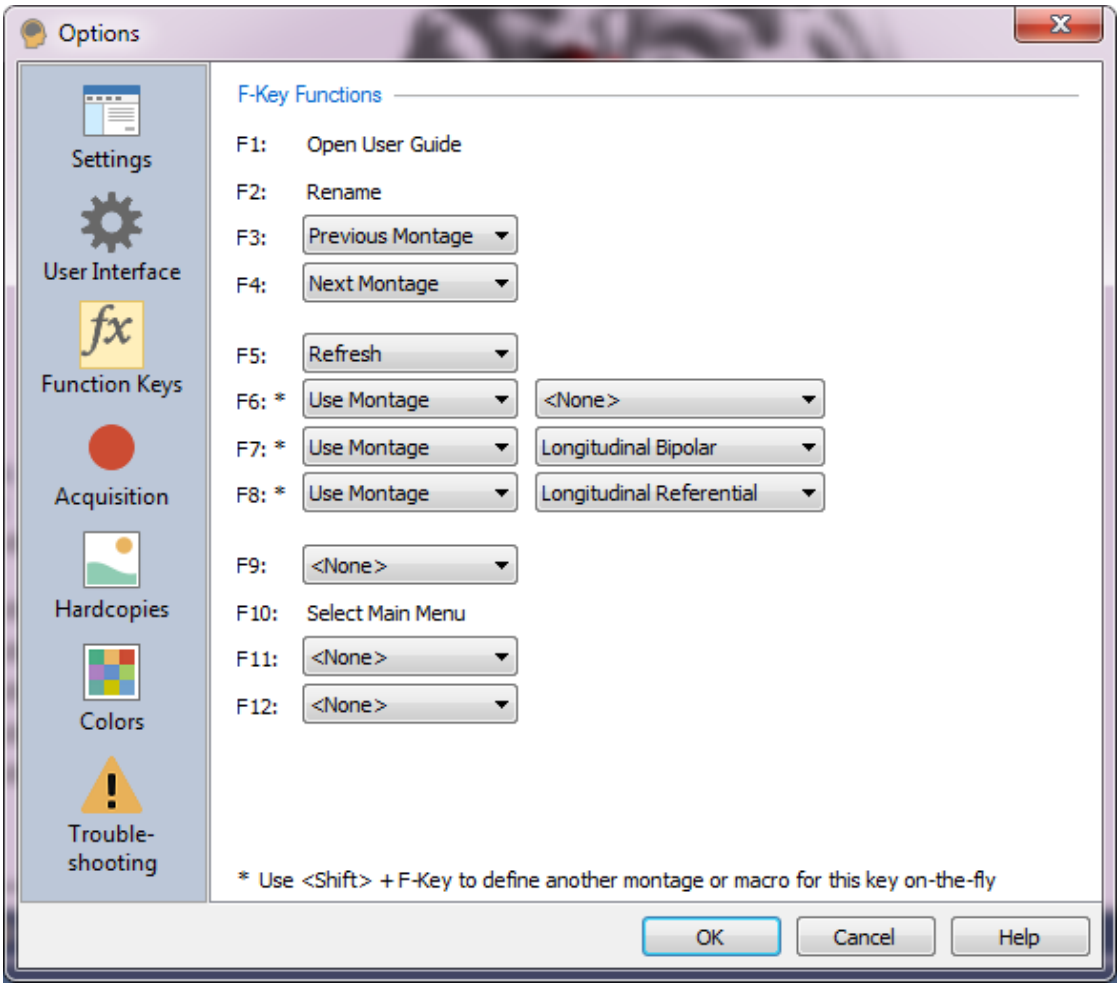
Smooth Lines. This option controls the smoothness of lines (such as waveforms and contour lines). **Auto** draws smooth waveforms when performance allows it. **On** always draws smooth lines, even if it decreases performance. **Maps only** does not draw smooth lines for waveforms.



Data and Menu Font. Select a font to use for the data display and menu text.

Function Keys

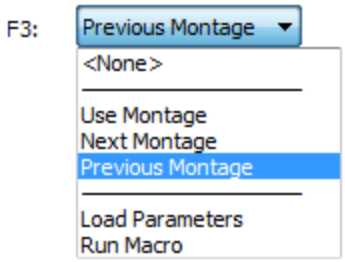
You can assign functionality to the Function Keys.



F1. This is the standard function key reserved for opening the *User Guide*.

F2. This is the standard function key used for renaming files, etc.

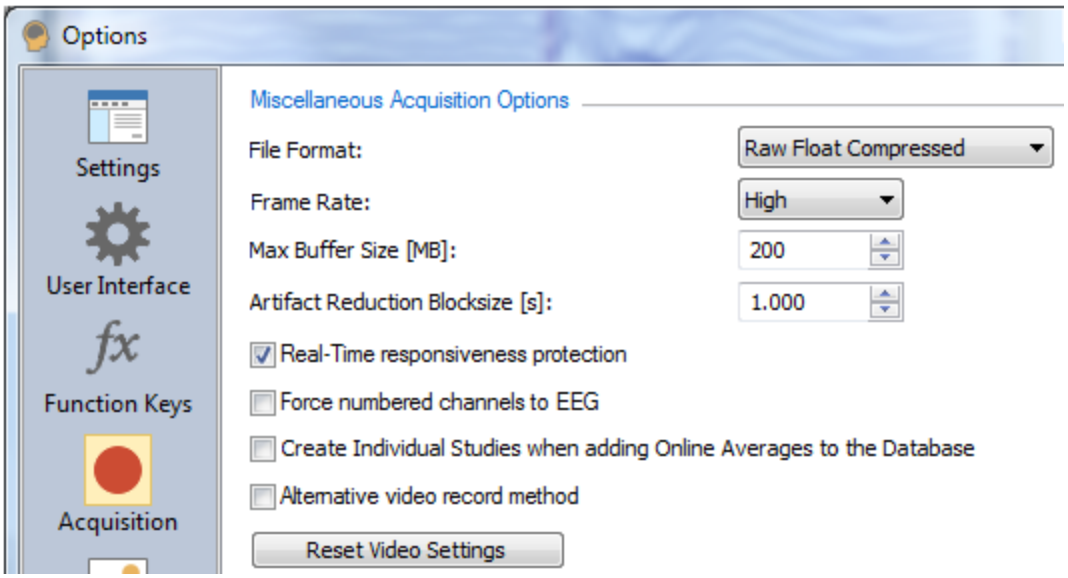
F3-F9, F11, and **F12**. Functionality may be assigned to these keys. See the pull-down list for the available operations.



F10. This is a standard key for activation the Main Menu bar (from there you can use additional keys).

Acquisition

These are miscellaneous options that are used in acquisition. These options are only seen if you have the X license for acquisition.



File Format. CURRY can record data either in the Raw Float format, as in prior versions, or in the Compressed format (default), which will save disk space (saves about 30%). There is no loss of data with the compression. This does not affect the saved file if you save it as a CNT or EDF file. It is compatible with CURRY 7 (CURRY 7 reads compressed files, but does not write them). If you plan to load your recordings directly into MATLAB, select Raw Float, because the MATLAB-script provided by CURRY does not support the compressed format. If you have already recorded the data using compression, resave the file where you select Raw Float in the Save As dialog. Generally, compressed files are recommended due to the smaller file sizes.

The remaining options are more for Troubleshooting when problems arise. You should leave them with their default settings unless directed to change them.

Frame Rate. This option allows you to reduce the frame rate during acquisition, which may help with freezing while acquiring data.

Max. Buffer Size [MB]. This determines the size of the buffer that is used for the rollback, or lookback, capability in Acquisition (moving the scroll bar backward to go to an earlier section of the recording). CURRY will automatically adjust the buffer size depending on the amount of RAM available.

Artifact Reduction Blocksize [s]. This is the number of seconds that are passed into the Artifact Reduction pipeline (online only). Shorter values may reduce the delay before you see the corrected data, but CPU usage increases

in the process. The default is 1 s, meaning CURRY will wait 1 s before looking for the particular artifact, and you should leave it at that unless directed otherwise. With values <1 s, you will see the data faster (less of a delay). For BCI applications, please see the **NetView Server or Client** section under **Amplifier Control**, as those settings can supersede the Artifact Reduction Blocksize.

Real-Time responsiveness protection. During acquisition, if CURRY detects that the CPU usage is becoming to high, it will automatically start disabling online processing steps (such as artifact reduction or template matching) to ensure that CURRY remains responsive and that the recording is uninterrupted. You have the option to disable the option if it is not performing properly.

Force numbered channels to EEG. Ordinarily, electrodes that have numbers for labels and no 3D positions will be moved to the Other group. If you want them to be considered EEG channels, enable this option.

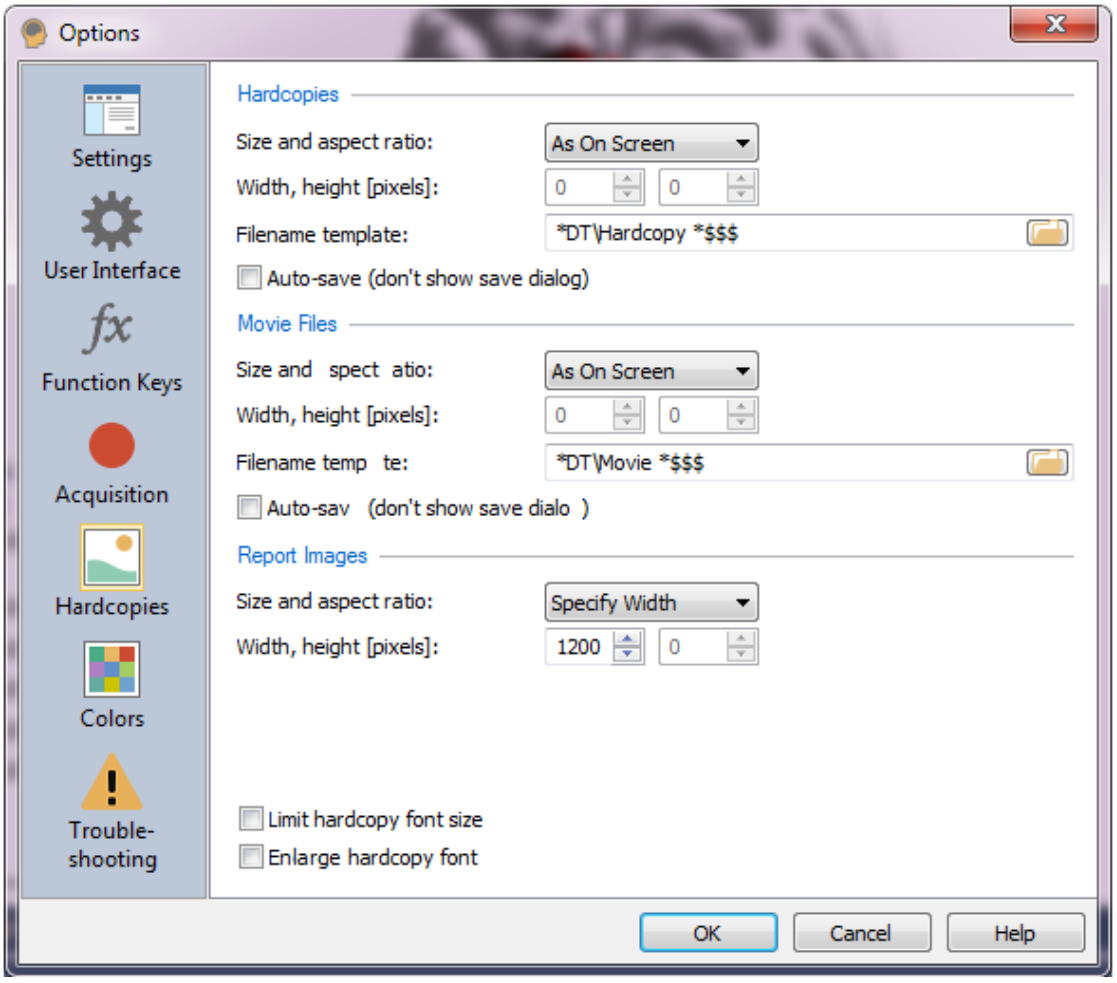
Create Individual Studies when adding Online Averages to the Database. Usually when online averages are created, they will be added to a single Study called Averages. These are typically averages of the same thing (epoch interval), and when the Study is opened the averages will be seen as individual epochs. If, however, you have epoch intervals of different lengths, CURRY will concatenate the epochs, which is usually not what is desired. If you enable this option, CURRY will place the averages not in a single Study, but rather in separate Studies beneath the Averages study.

Alternative video record method. If your video does not record (and you get an error message), try enabling this option. When disabled, a more automatic method is used. The alternate method is a little stricter, where CURRY has more control.

Reset Video Settings. Try this option if the video window does not open. Enabling it will delete from the *SessionDefaults.cfg* file the settings that pertain to video and restore the defaults. For example, if you have set up a camera on a network, and then remove it or change to a different one. CURRY may retain the settings for the initial camera, which can then be removed with this option. When you attempt to restart video, you will again see the video selection dialog.

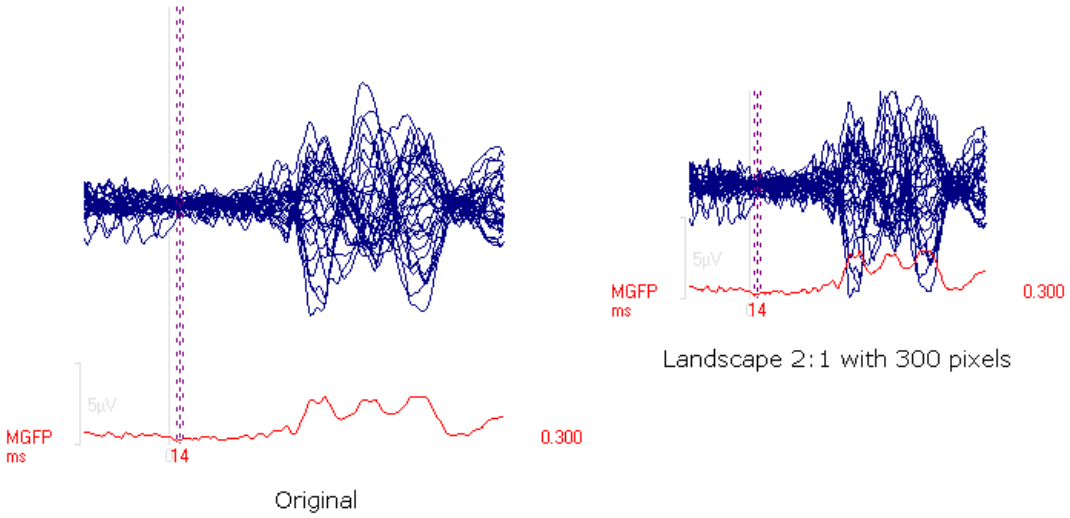
Hardcopies

These options let you resize the hard copy, movie files, and report image graphics that you save (*right click* in one of the data displays and select one of the **Copy** or **Save Image** options).



Hardcopies

Size and aspect ratio. For example, if you want a figure to be seen as a Landscape with a 2:1 ratio, with a Width of 300 pixels, set the parameters and click OK. When you make a **Hardcopy** (such as, **Copy Image to Clipboard** and paste into another application), the figure will have the appearance as selected.



Width, height [pixels]. Enter the desired pixel width, and the pixel height will be set automatically. The values vary depending on the Size and Aspect ratio option you select.

Filename template. These options for Hardcopies and Movie Files instruct CURRY to create file names for you, using the same file naming convention as that used with Acquisition and in Macros (see **Macro** for more details).

Auto-save (don't show save dialog). When enabled, the files will be saved automatically, using the **Filename template**, without displaying the Save As dialogs.

Movie Files

Size and aspect ratio. Same as Hardcopies above.

Width, height [pixels]. Same as Hardcopies above.

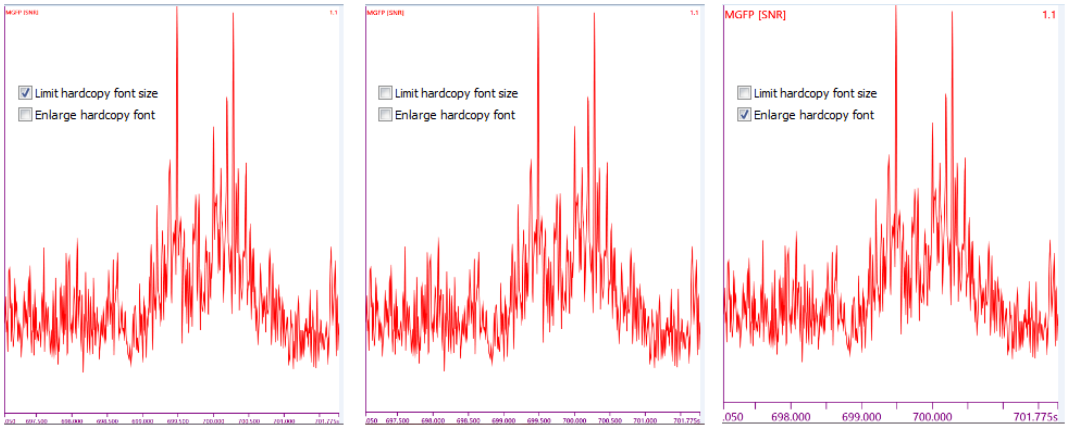
Filename template. Same as Hardcopies above.

Report Images

Size and aspect ratio. Same as Hardcopies above.

Width, height [pixels]. Same as Hardcopies above.

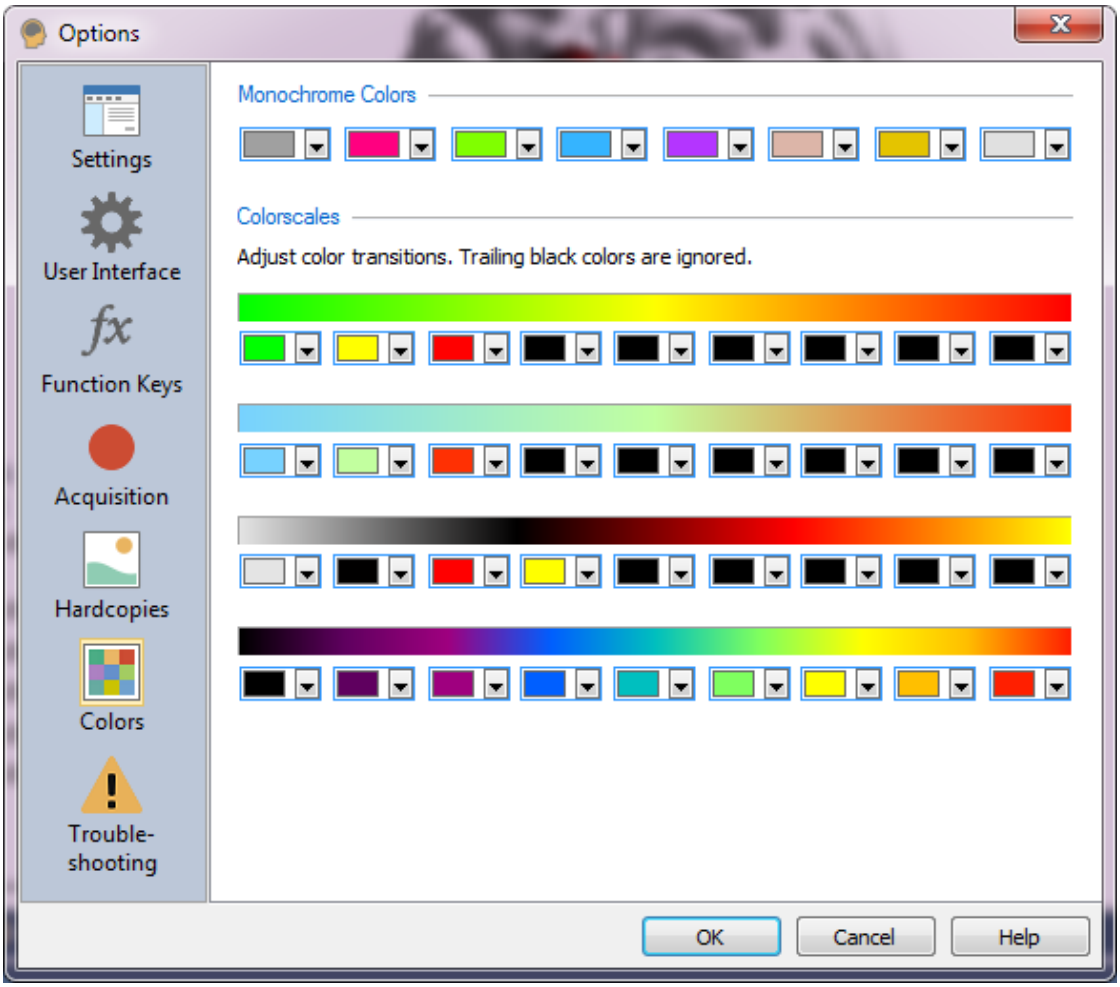
Limit hardcopy font size. This option, along with **Enlarge hardcopy font**, allows you to control the font size in, for example, figures for presentation. To get the best text for printing, leave **Limit hardcopy font** size disabled, and enable **Enlarge hardcopy font**.



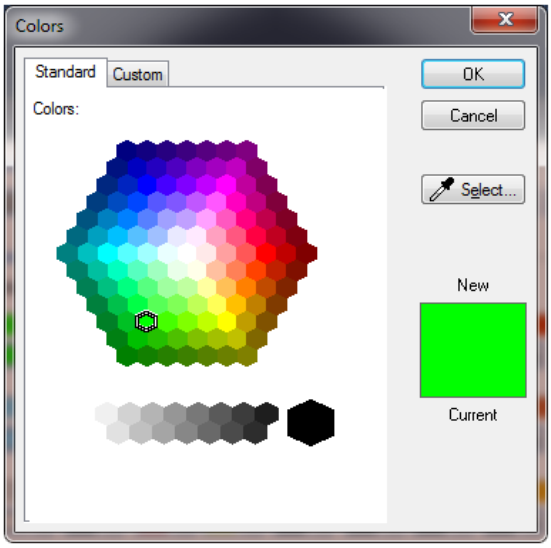
Enlarge hardcopy font. Please see preceding description.

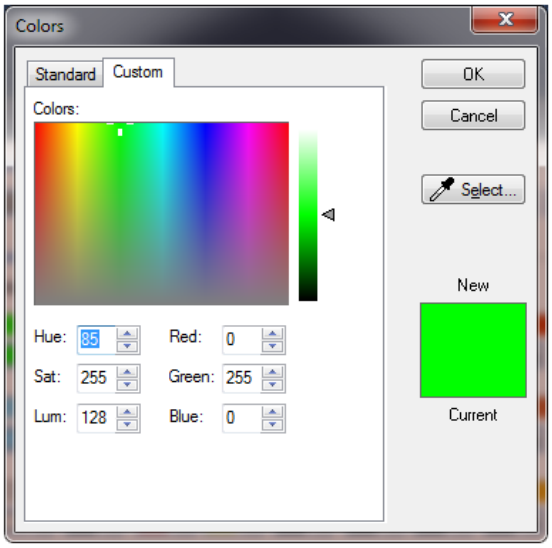
Colors

User Defined Colors. There are multiple places in CURRY where you may specify colors. These options here allow you to add additional color options. The color options are organized into two groups. The first contains single **Monochrome** colors. After you set these, they will be seen in the color selection grids throughout CURRY. The **Colorscales** are the last four scale options. These fields are used to create your own color scales. Note that the black colors will be ignored if they fall at the ends of the scales (black in the middle is OK).



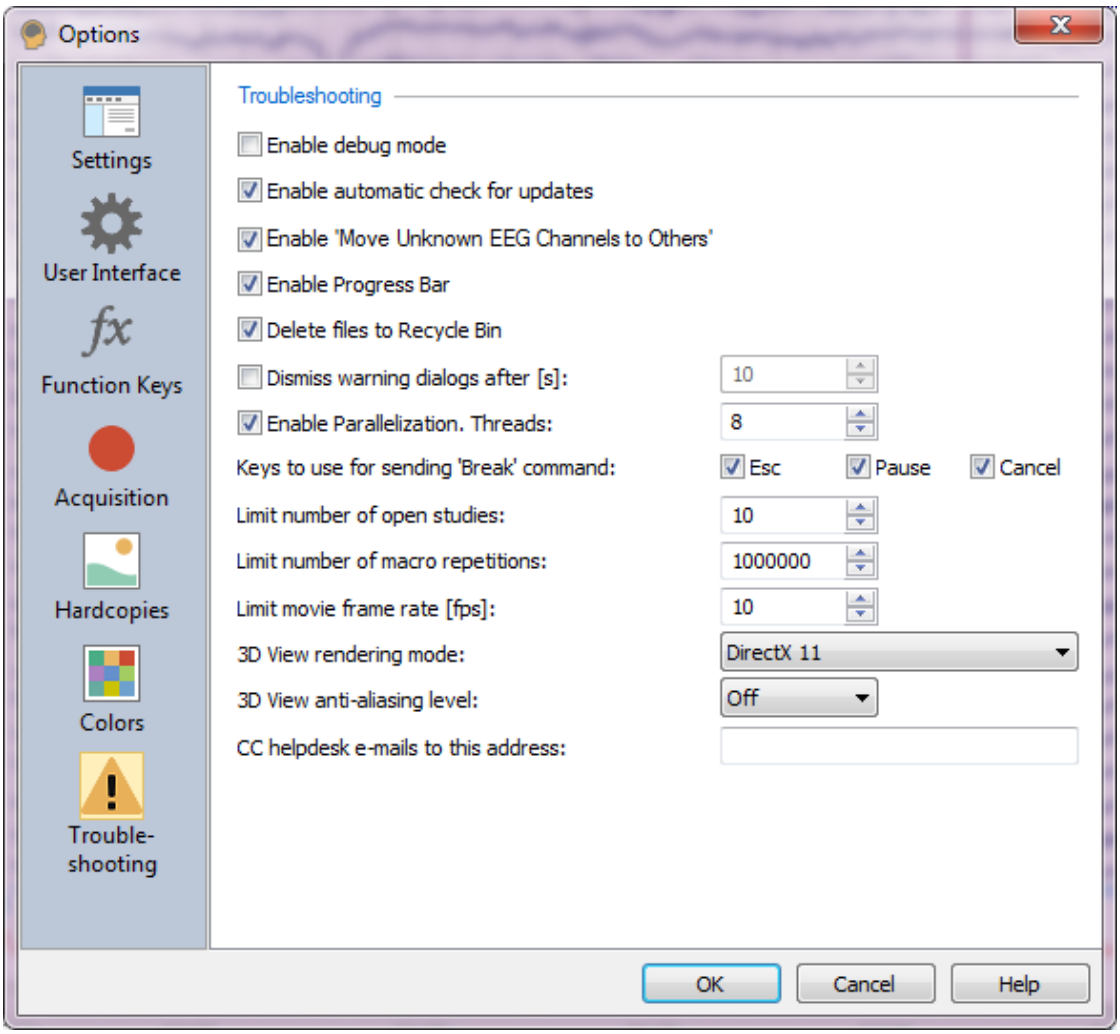
If the colors that are offered are not sufficient, you may specify your own colors. Click the More Col... button from the drop-down grid, and then select one of the **Standard** colors, or create colors using the **Custom** option.





Troubleshooting

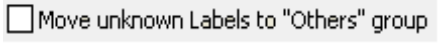
Generally, you should leave these options disabled or unchanged unless directed to enable or change them (other than the first one).



Enable debug mode is used to help diagnose certain problems. When enabled, additional text in gray will appear in the **Output** display following operations.

Enable automatic check for updates. CURRY will automatically checks or software updates on a weekly basis. If you do not wish this to occur, disable the option.

Enable 'Move Unknown EEG Channels to Others.'. On the first screen of the Functional Data Import Wizard, there is the following option:



. When enabled (default), channels that would not be detected via Label Matching are set as "Other" channels. "Other" channels are excluded from many of the operations in CURRY, where their inclusion would distort the results.

The purpose for this option was the fact that only the wizard moves, e.g. VEOG, to the "others" group. If a file happens to contain all needed information (positions, landmarks), then the wizard will not be invoked, and therefore VEOG stays in the EEG group (since the CTF, Neuromag, etc. reader claims it to be EEG).

If the **Enable 'Move Unknown EEG Channels to Others.'** option is checked (default), the Wizard will appear if there are EEG labels that are detected as "belonging to the others group".

More completely, the wizard comes up if:

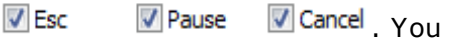
1.) one or more sensors contain invalid positions,
2.) one or more groups cannot be transformed into the Curry coordinate system ("coregistration"), or
3.) the checkbox is disabled and "other" channel labels are found in any EEG group.

Enable Progress Bar. This is a debugging option that should only be disabled when so instructed by technical support.

Delete files to Recycle Bin. When enabled, deleted files will be sent to the recycle bin (where they may be restored), as opposed to deleting them completely.

Dismiss warning dialogs after [s]. When enabled, warning dialogs will be seen for as many seconds as you enter.

Enable Parallelization. **Threads**. The number of virtual cores on your system determines the number of Threads. There is generally no need to change this or to disable it, unless so directed by technical support.

Keys for sending 'Break' command. Any of the following may be used to send a Break command 

. You may disable any or all of them, if needed.

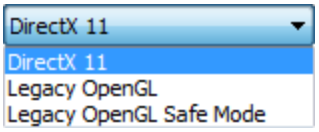
Limit number of open studies. This sets the maximum number of Studies that may be opened at the same time. This option should be left at 10.

Limit number of macro repetitions. If you wish to limit the number of times a macro will repeat in "play infinitely" mode, you can set the limit in this field.

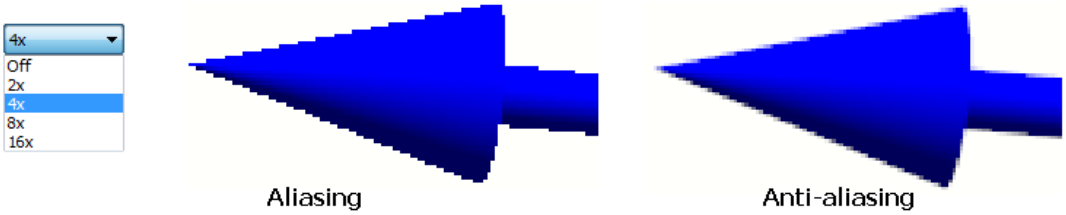
Limit movie frame rate [fps]. The movie frame rate will not exceed the value of frames per second that is entered here.

3D View rendering mode. Here you decide whether to use DirectX 11 or OpenGL for 3D View. The default is DX11, and when it is not available (older graphics cards may not support DX11), CURRY automatically reverts back to OpenGL. "Legacy OpenGL" and "Legacy OpenGL Safe Mode" are the same graphics modes that existed in CURRY 7. If you needed the Safe mode in CURRY 7, and your graphics board did not support DX11, you will also need the OpenGL Safe mode in CURRY 8. Again, CURRY chooses the needed mode on its own.

Only for troubleshooting would you want to switch the mode (when either 3D View is very slow, or you see "artifacts", or get crashes).



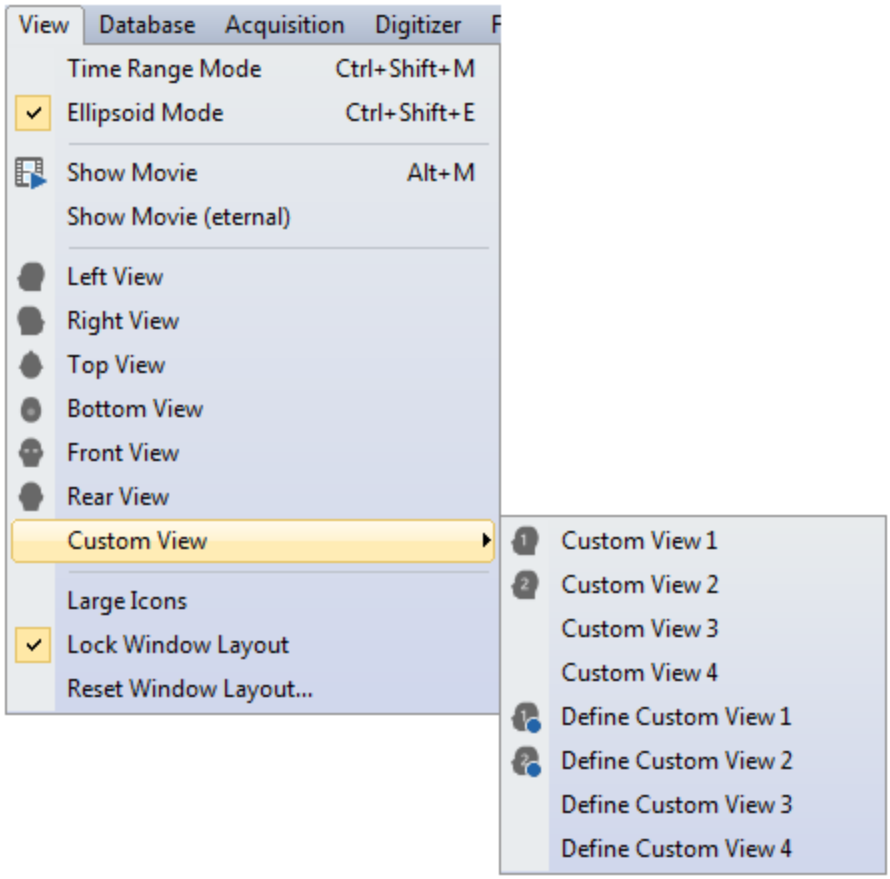
3D View anti-aliasing level. Enabling anti-aliasing has a slightly softening effect of the edges of the objects in the 3D View. Anti-aliasing does not work with **Transparent** objects. It is set to **4x** by default. You may need to restart CURRY to see the effects.



CC helpdesk emails to this address. Under **Help** on the **Main Menu** bar, there is an option called **Send E-mail to Helpdesk**. This will send a screen shot and needed version information to the Helpdesk. You can have a copy sent automatically to the address you enter in this field.

7.1.3 View

The View option consists of toggles for the Toolbars, Dialog screens, the Status Bar, etc.



Time Range Mode. This toggles between Movie Mode and Trace Mode. It may also be accessed from the icon on the **3D View** Toolbar (or *Ctrl+Shift+M*).

Ellipsoid Mode. This toggles the display of the Confidence Ellipsoids on and off. It may also be accessed from the icon on the **Standard** Toolbar (or *Ctrl+Shift+E*).

Show Movie. Use this option to play a movie. Source solutions are displayed sequentially for each time point in the Timerange. It may also be accessed from the icon on the **Standard** Toolbar (or *Alt+M*).

Show Movie (eternal). Selecting this option will play the movie continuously. Press the *Esc* button to stop it, or bring another window to the foreground.

Left View, **Right View**, **Top View**, **Bottom View**, **Front View**, and **Rear View**. Select one of the standard views. These may also be selected from the 3D View and Localize Toolbars .

Custom Views . Custom views are those intermediate perspectives that you wish to use repeatedly. You may define and retrieve up to 4 Custom Views. The **Define** options set the current orientation (size, perspective, etc.) of the display as Custom View 1-4. Click one of the **Custom View** options (1-4) to retrieve the custom

view you had set. Note that there are icons for the first two views, and these are available in the toolbars for the **3D View** and **Image Data** (rendered view only).

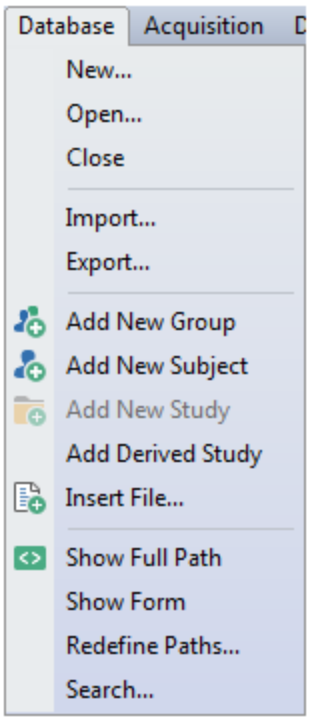
Large Icons. Selecting this enlarges the icons, making them easier to see.

Lock Window Layout. When enabled, you will be unable to undock the dialog screens (Database, Output, etc.). If disabled, you may *double-click* the title bar to undock it. *Double-click* the title bar to dock it again.

Reset Window Layout. Clicking this option restores the original layout of the dialog screens when CURRY was installed (changes take effect the next time you start CURRY).

7.1.4 Database

The Database options are used to create new Databases, open existing ones, Import/Export Databases, and additional functions described below. See also the **Database** section below.

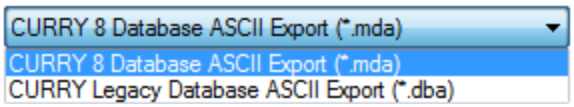


New. The New option is used to create a new Database (.cdb extension). Clicking it displays the "Create new Database" utility window, where you may select a folder and enter a file name. You do have the option to create the older .mdb format, although the .cdb format is recommended.

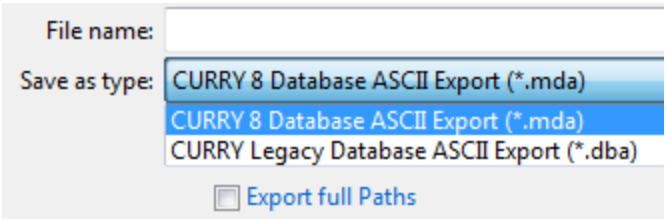
Open. The Open option is used to open an existing Database file (.cdb extension). Clicking it displays the standard Open file utility. You may also select pre-existing .mdb Database files. It is recommended that you save existing .mdb files as .cdb files.

Close. Closes the open Database (also accessed from **File** → **Database** → **Close**).

Import. Select this option to import a CURRY 8 Database that had been exported (.mda), or one of the legacy Database exports (.dba). Clicking it displays the standard utility for locating and retrieving a file.



Export. Select this option to export the currently open Database as a CURRY Database (.mda or .dba extension). Selecting the option displays a Save As screen. Files can be saved with the current .mda extension for CURRY 7 or 8, or with the .dba format for use with earlier versions of CURRY (.dba does not recognize Groups or Derived Studies, and so should be avoided unless you really intend to use the Database in the prior versions of CURRY).



You have the option to **Export only selected experiments and subjects** (*Ctrl+click* to highlight them), or all. You may **Export fully qualified file paths** or not.

The paths for the files stored in Database can now be relative. That is, if you happen to insert a file that is stored "below" the Database file, it will replace the absolute path with a relative one.

Example:
C:\Program Files\Neuroscan\TestDatabase\MyDatabase.cdb
C:\Program Files\Neuroscan\TestDatabase\TestFiles\MyFile.cnt → $\TestFiles\MyFile.cnt

Note that this enables you to move your Database (plus files) around or share it with colleagues without having to modify the Database.

If the checkbox is checked, it will "backtransform":

$\TestFiles\MyFile.cnt → C:\Program Files\Neuroscan\TestDatabase\TestFiles\MyFile.cnt
(or whatever the current path of the Database is *at the moment*).

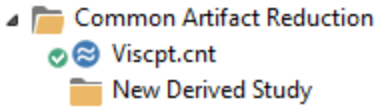
Note that you can always "Search and Replace" the paths with "Redefine Paths" (which creates a backup file). That is, you can make the paths absolute again by replacing "$" with "C:\....".

Add New Group. Adds a new Group to the Database (see the **Database** section below for more details). This has the same function as the  icon on the Database toolbar.

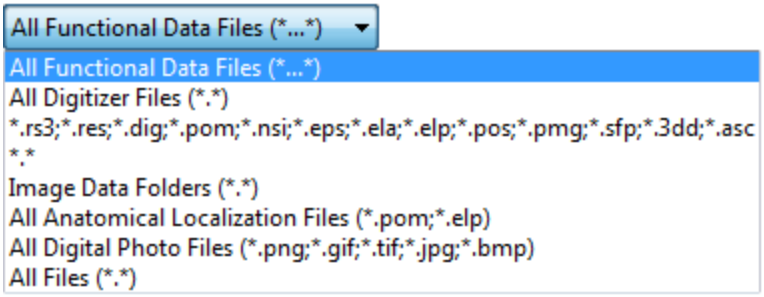
Add New Subject. Adds a new Subject to the Database. This has the same function as the  icon on the Database toolbar.

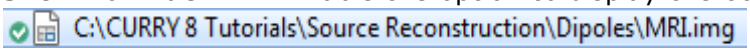
Add New Study. Adds a new Study to the Database. This has the same function as the  icon on the Database toolbar.

Add Derived Study. A derived Study is one that exists within an existing Study (a sub-study). Clicking this option adds a "New Derived Study". (CURRY 6 will read CURRY 7 and 8 Databases as well, but will display experiments as "empty subjects" and will place derived studies in the same level as the parent study).



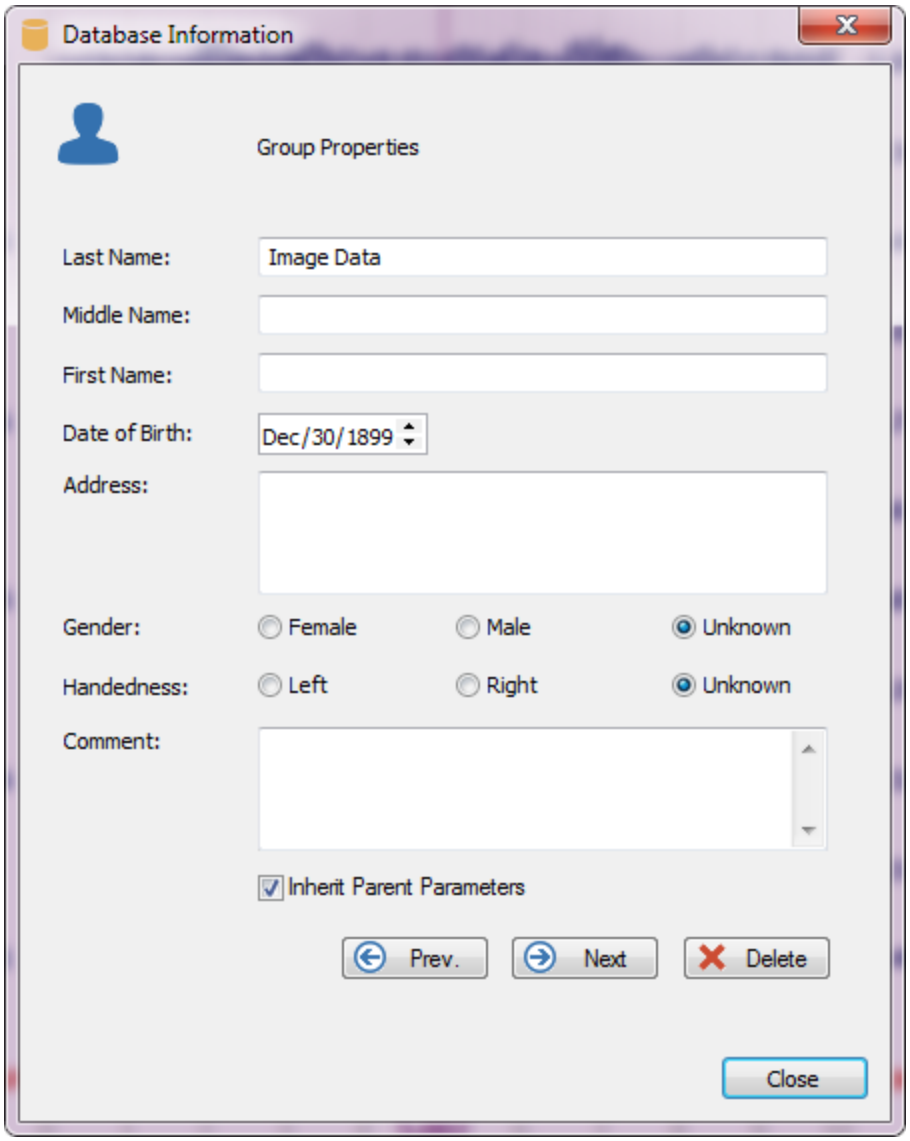
Insert File  . This field is active when you highlight a Study, Functional Data folder or Image Data folder. An Open File utility will allow you to select the data file. Click the Files of Type drop-down list to see the types of files that can be inserted; the types of files depends on what was highlighted to start with.



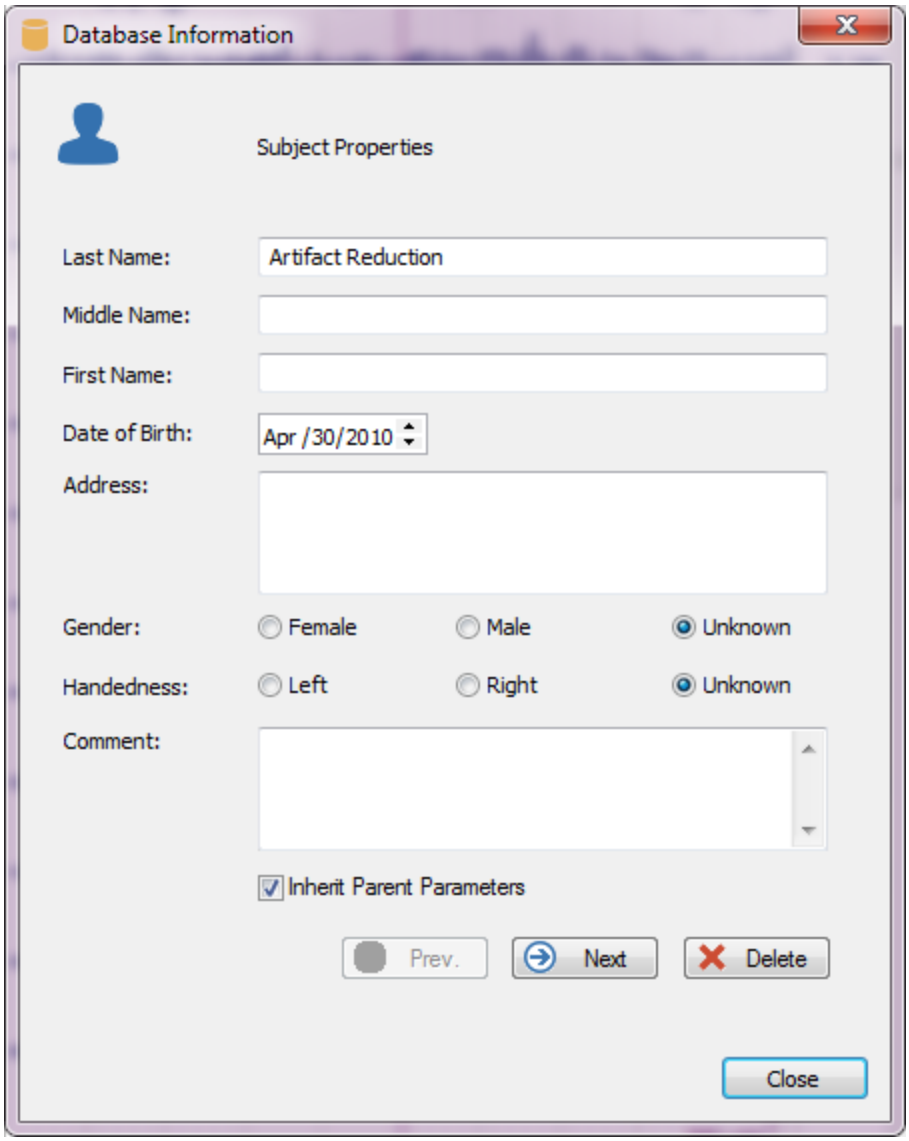
Show Full Path  . Enable the option to display the complete path to the files: 

. Disable it to display the file name only. The same option can be accessed by clicking the *right mouse* button on the Database file in the Database.

Show Form. Group, Subject, Study and File information can be entered and stored from the Database. Select the option and an empty screen will appear. Click on the Group line in the Database to see the following dialog. Enter the desired information in the fields as shown. Note that this is another place where you may enable the **Inherit Parent Parameters** option. This is described in the **Global, Study and Other Parameters** section below.

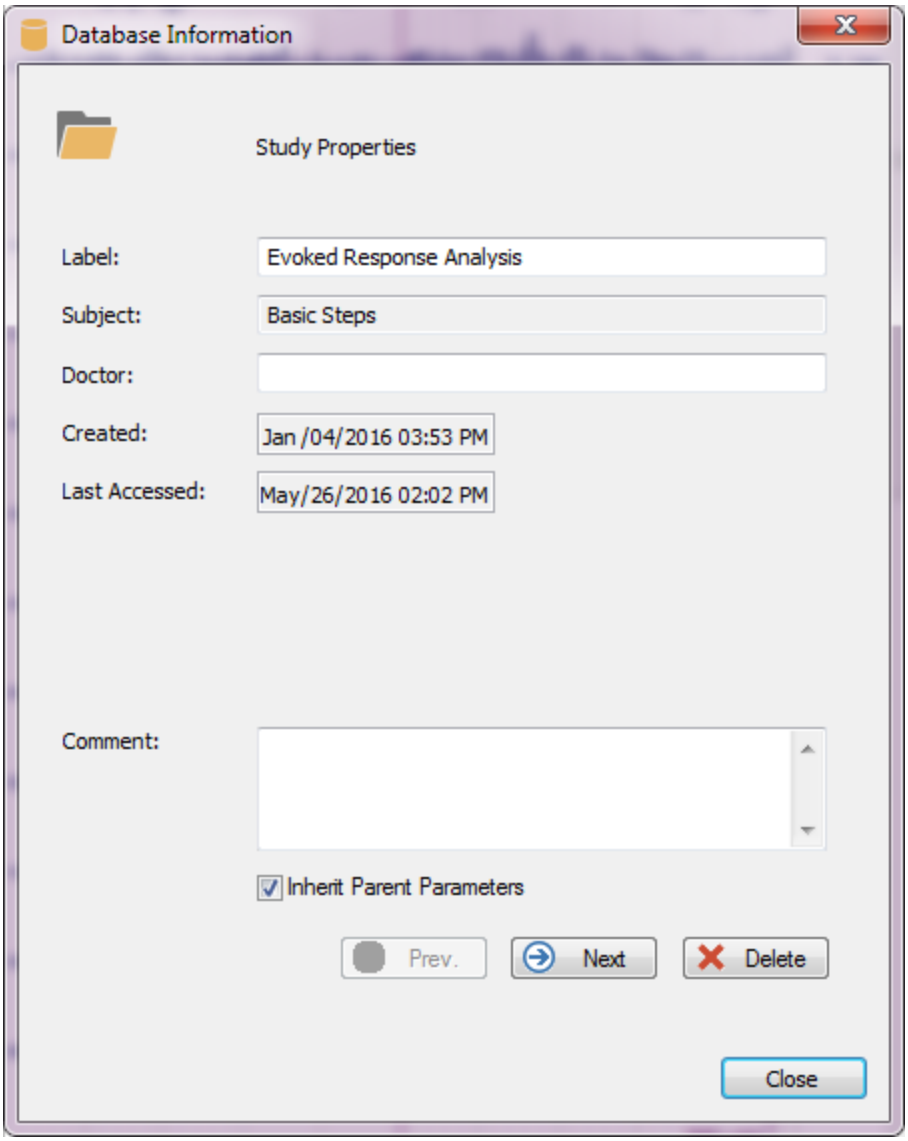


Click on the *Subject* line, and the fields to enter the Subject information will appear. Fill in the fields as desired. This is another way to change the Subject name; the names you enter will appear as **Last, First M.** in the Database.



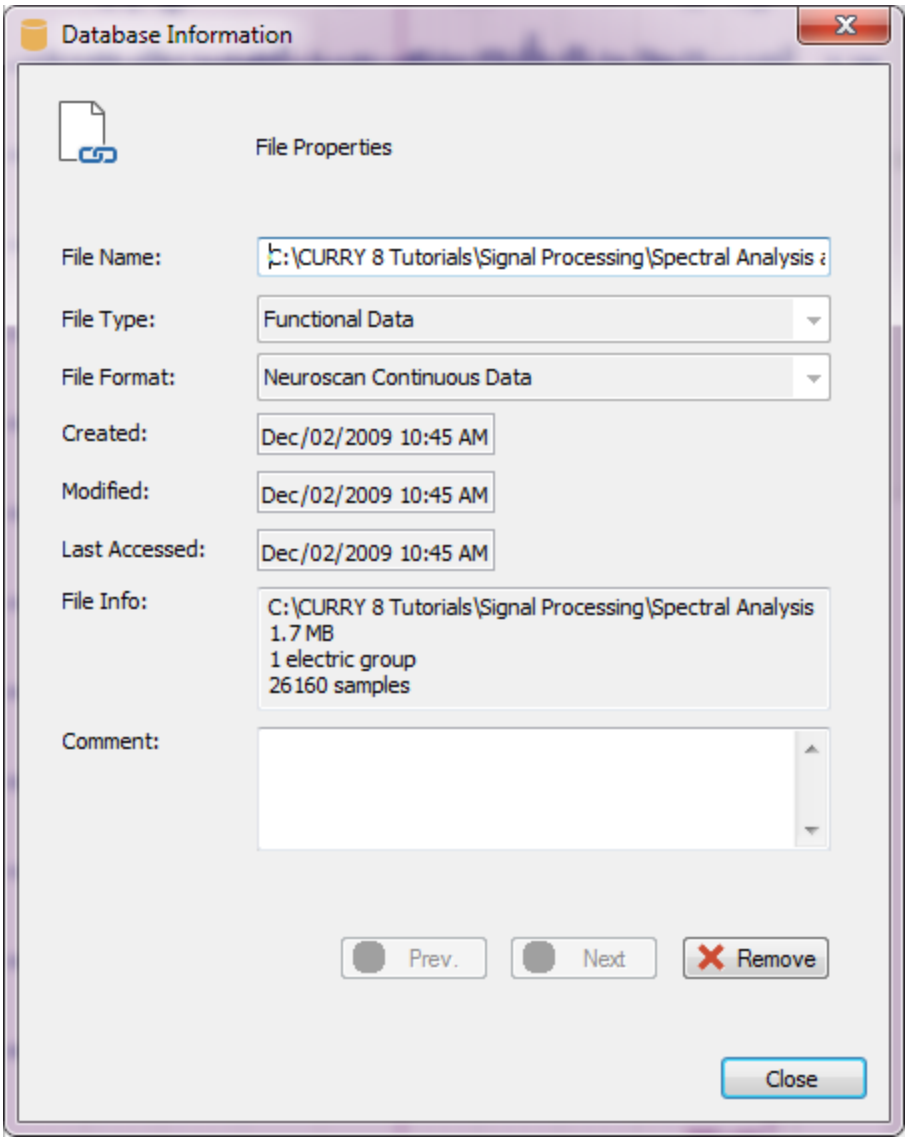
If you have multiple Subjects, you can move among them using the Prev. and Next buttons. Click the Delete button to delete the Subject from the Database.

Click on the *Study* line to see the Study information.



The Study information screen allows you to enter additional information, and functions similarly to the Subject information screen.

Click on the *Data File* line (functional or image data), and you can enter information specific to that file.

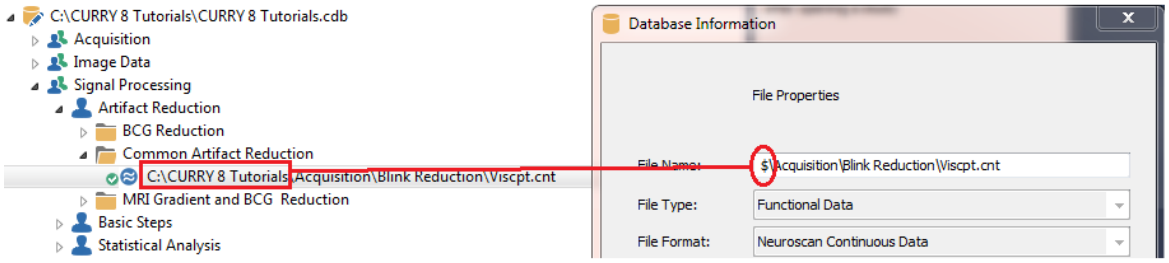


When you have the information entered, you can click Close, the X in the upper right corner, or else click **Database** and deselect **Show Form**.

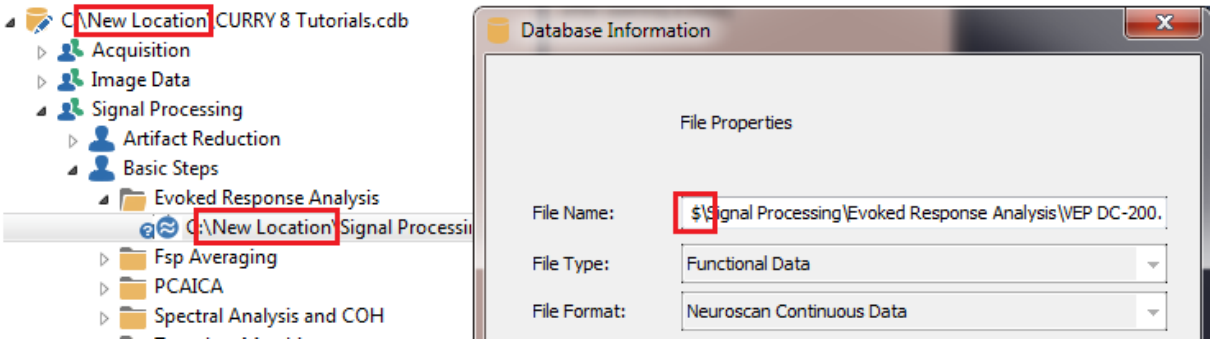
Redefine Paths. There will be times when you move an entire Database - the .cdb file and all of the folders and files with it - to a new drive or other location. There may be other times where you want to move just a Study to a different location. Recall that the Database does not *contain* any of the files it uses; it merely contains the paths to where the files are stored on the hard drive. If you move the files on the hard drive, does that mean the paths in the Database will all be incorrect, and you have to reinsert the files manually? No.

1. For example, if you take the Database used for the *CURRY 8 Tutorials*, and move it to a different drive (from C to D), what happens? Load the .cdb Database file from the D drive, and all of the files are found. You do not have to change the paths for each file. Hows does it work?

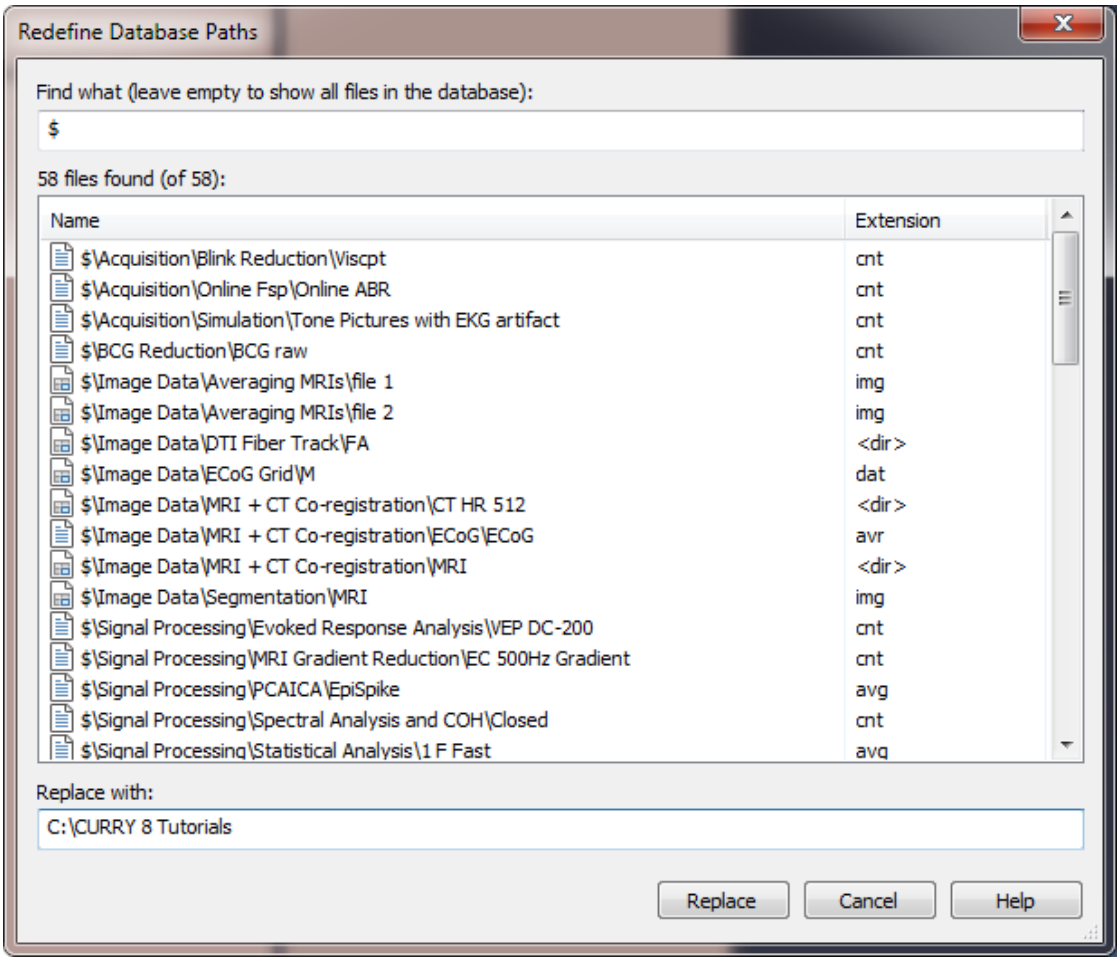
Expand the folders to see one of the data files. Select the **Show Full Path** icon <> above the Database. *Right click* on the data file and select **Properties**. At the beginning of the path for the file is a $ - a substituted variable. The $ is a substitution for the path for the Database, in this case *C:\CURRY 8 Tutorials*. When you select the Database, the substituted text is applied throughout the Database files. The paths with the $ are referred to as "relative" paths.



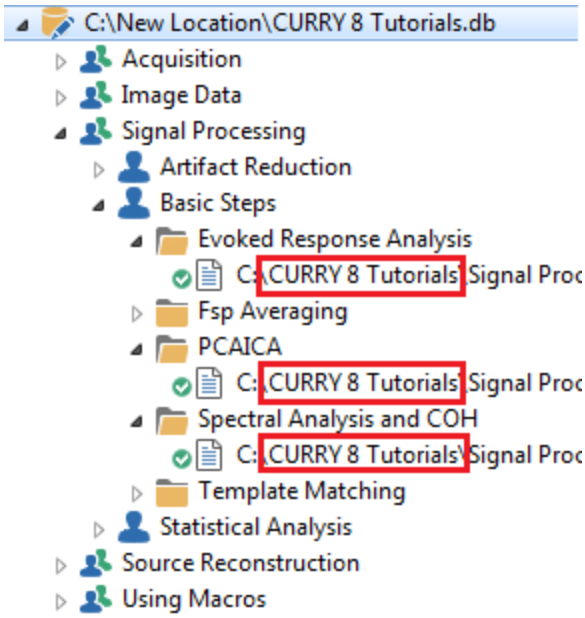
2. For another example, we have moved just the .cdb Database file to the New Location folder, leaving all of the other files where they were. We then loaded the Database file, and now none of the data files are found. That is because the paths are relative, and were changed automatically. They no longer match where the files are actually stored on the hard drive.



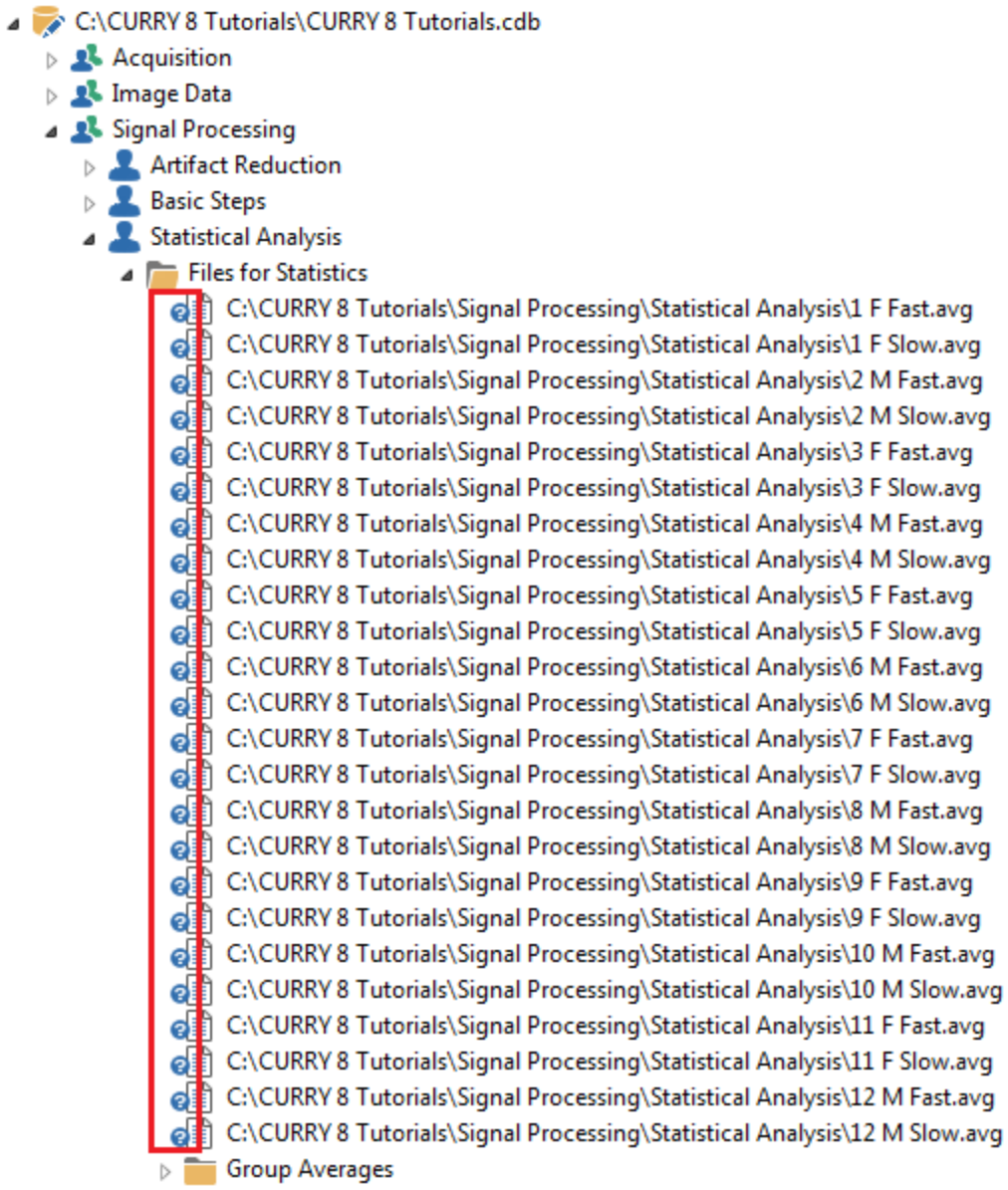
This is an example where the **Redefine Paths** option is used. After selecting the option, you will see all of the files being used in the Database, with the path for each one. **Redefine Paths** is basically a search and replace tool. In this case, the problem we have is that the $ is not correct, so we need to replace it with the correct path information. Type in "$" for **Find What** and "C:\CNS 7 Tutorials" for **Replace with**.



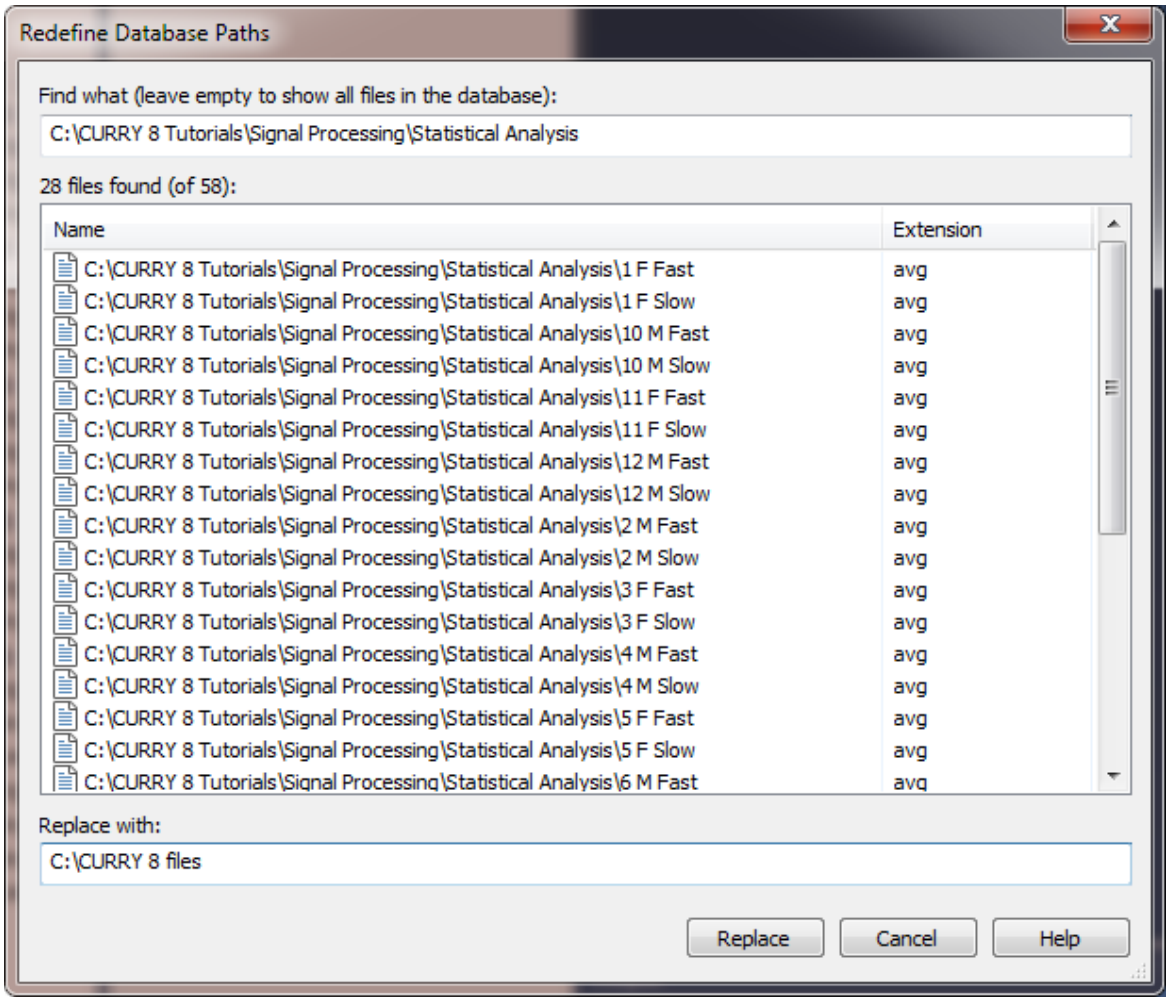
After clicking **Replace** you will get a message saying how many files were modified. With the correct paths, the files are now found. The new path is referred to as an absolute path, since it contains no substitutions, and it differs from the Database path (.cdb file).



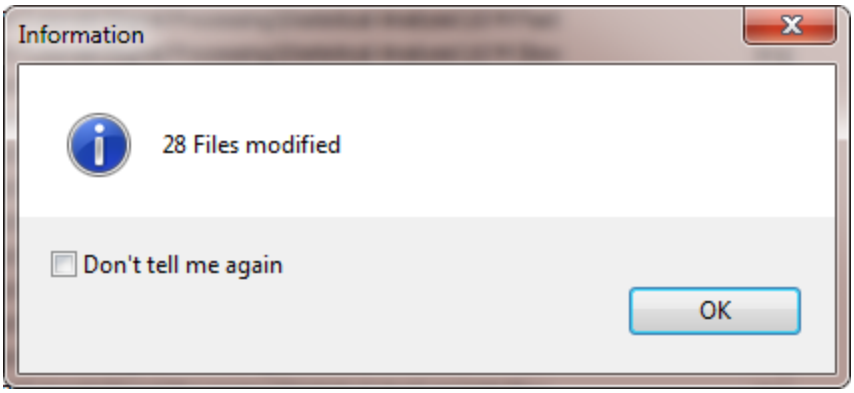
3. There may be occasions where you need to change the paths in only a single Study. The process is much the same. In this case, the data files were in the desired location when the Database was made, and then were moved elsewhere. We want to define the new location of the files. Note the question marks before the files, indicating that the files are not found.



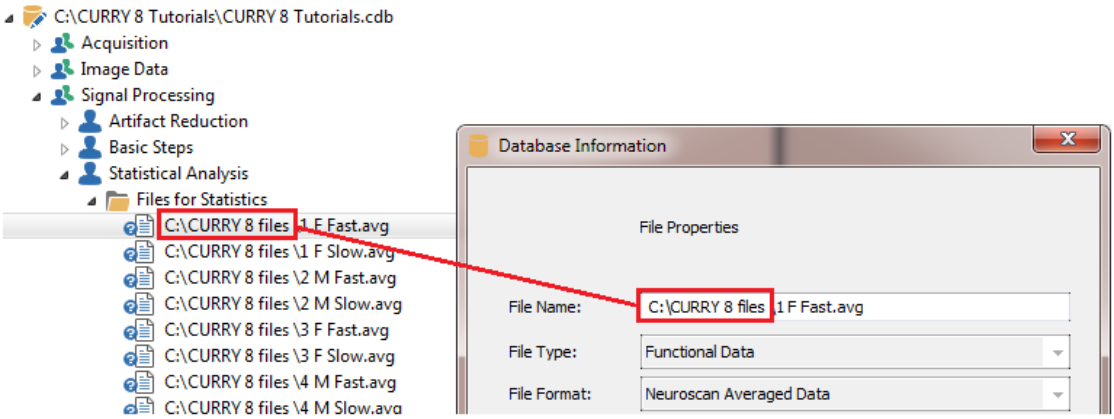
On opening **Redefine Paths**, we see the relative paths for the data files still in place, which is why they are not found. We need to change them to absolute paths. "C:\CURRY 8 Tutorials\Signal Processing\Statistical Analysis" is entered into the **Find what** field, and "C:\CURRY 8 files" - the correct location on the hard drive - is entered for the **Replace with** field. Click **Replace**.



A message informs us that, in this case, 28 files were modified.

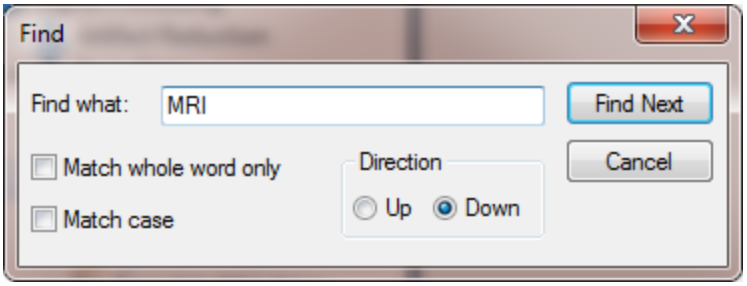


We now have absolute paths for these files only. If we were to *right click* on one of the data files and select **Properties**, we would see the absolute path, rather than the relative one with the $ substitution.



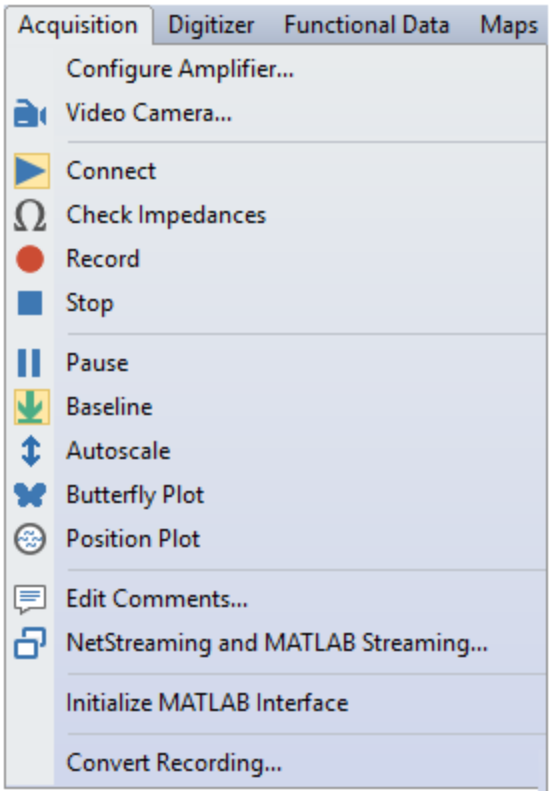
The **Redefine Paths** feature, therefore, is basically a simple search and replace method, affecting the paths for the data files in the Database.

Search. Select the Search option to search the existing Database for a specified file. You can elect to have it search for the whole word only, and to match the case. You may also specify whether you want to search to go up or down from the current highlighted location. The option is useful if you have multiple Subjects/Studies in the Database, and you are looking for a particular file.



7.1.5 Acquisition

These are options used during EEG acquisition. See the **Acquisition** section for details.



Configure Amplifier. Accesses the amplifier configuration dialogs (see **Configuration Options** below).

Video Camera. This option will show or hide the video camera window, and has the same function as clicking the Video icon on the Acquisition toolbar.

Connect. Connect to the selected amplifier.

Check Impedances. Click this option to view the impedance display. If you perform an impedance test while recording the EEG data, the results will be stored and seen in the **Show Information** field, under **Functional Data** (offline). From there they may be copied/pasted elsewhere.

Care

*Impedance tests should only be performed with surface EEG, and never if you are recording from cortical grid or depth EEG electrodes. There is an option in the Configure Amplifiers section to disable impedance tests (**Allow Impedance Test**), which is intended for use with grid and depth recordings.*

Record. Click the Record button to start saving the data to the hard drive.

Stop . Disconnect from the amplifier (or stop Impedance, stop Digitizer, or stop Recording, and then disconnect).

Pause . Pause display.

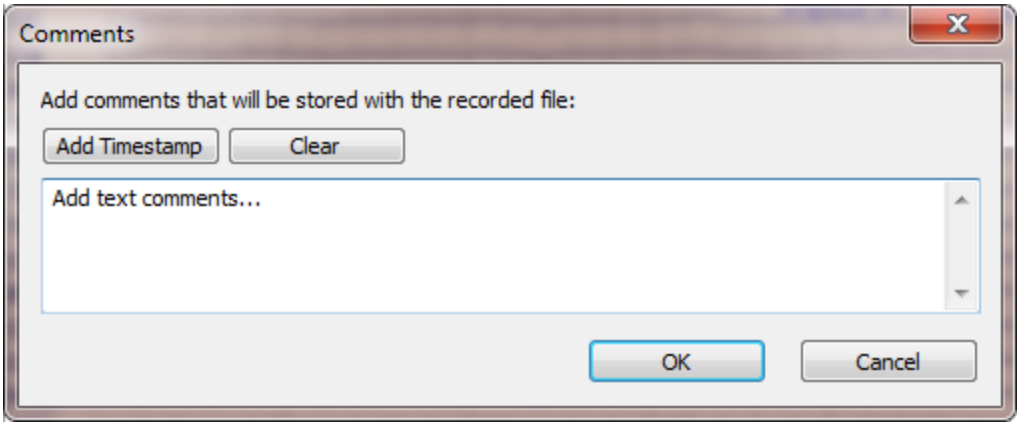
Baseline . Centers traces in their display space (removes DC offsets from the display). Data are not affected.

Autoscale . Autoscales the display of all traces (data are not affected).

Butterfly Plot . Superimposes all channels.

Position Plot . Displays channels in separate windows about the head.

Edit Comments . This allows you to add text comments that will be saved with the file. You can include a Timestamp if desired. When you open the file offline and go to **Functional Data → Show Information**, you will see the comments there.



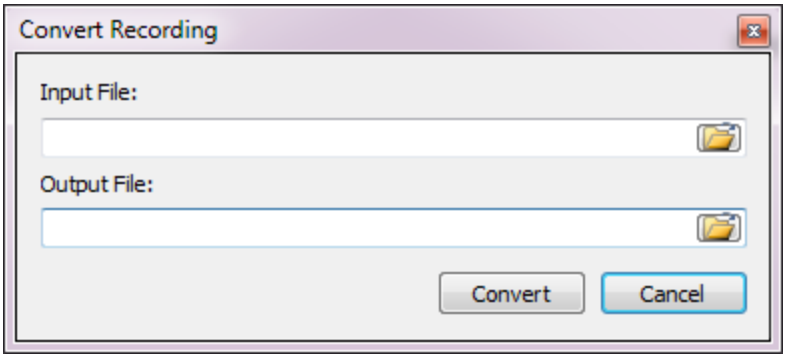
NetStreaming and MATLAB Streaming. This is a shortcut to the **NetStreaming and MATLAB Streaming** dialog, also accessed from the icon in the Amplifier Control panel.

Initialize MATLAB Interface. This option can be used to start and initialize MATLAB manually if you plan to use it during acquisition. Otherwise, MATLAB will be initialized when it is needed, which might interrupt acquisition since it can take quite a while. This is especially the case with NuAmps where there is a danger of a buffer overrun. The option can also be used for troubleshooting to check whether the MATLAB interface is working correctly.

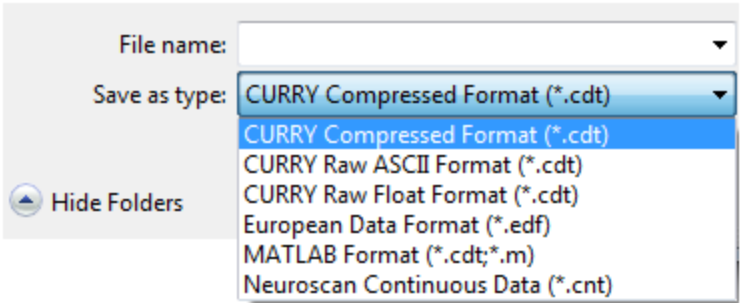
Convert Recording. This option was added to the Acquisition part of CURRY so that those with Acquisition Only licenses may export files to other formats (this was formerly available offline only and required an additional license). Input and Output file

types are seen in the format lists. The **Convert** button will show a green check mark when the conversion is successful 

.

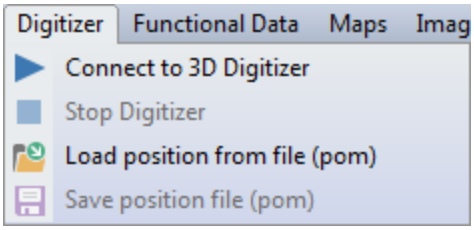


Note that in the Output File window, in the Save as type field, there are options for several types of file formats. While the Neuroscan Continuous file type remains (.cnt), it is becoming less stable and is not recommended.



7.1.6 Digitizer

This section refers to the digitization of the electrode positions using a Fastrak or Polaris digitizer. Details are found in the **Digitizer** section below.



Connect to 3D Digitizer. Initiate digitization.

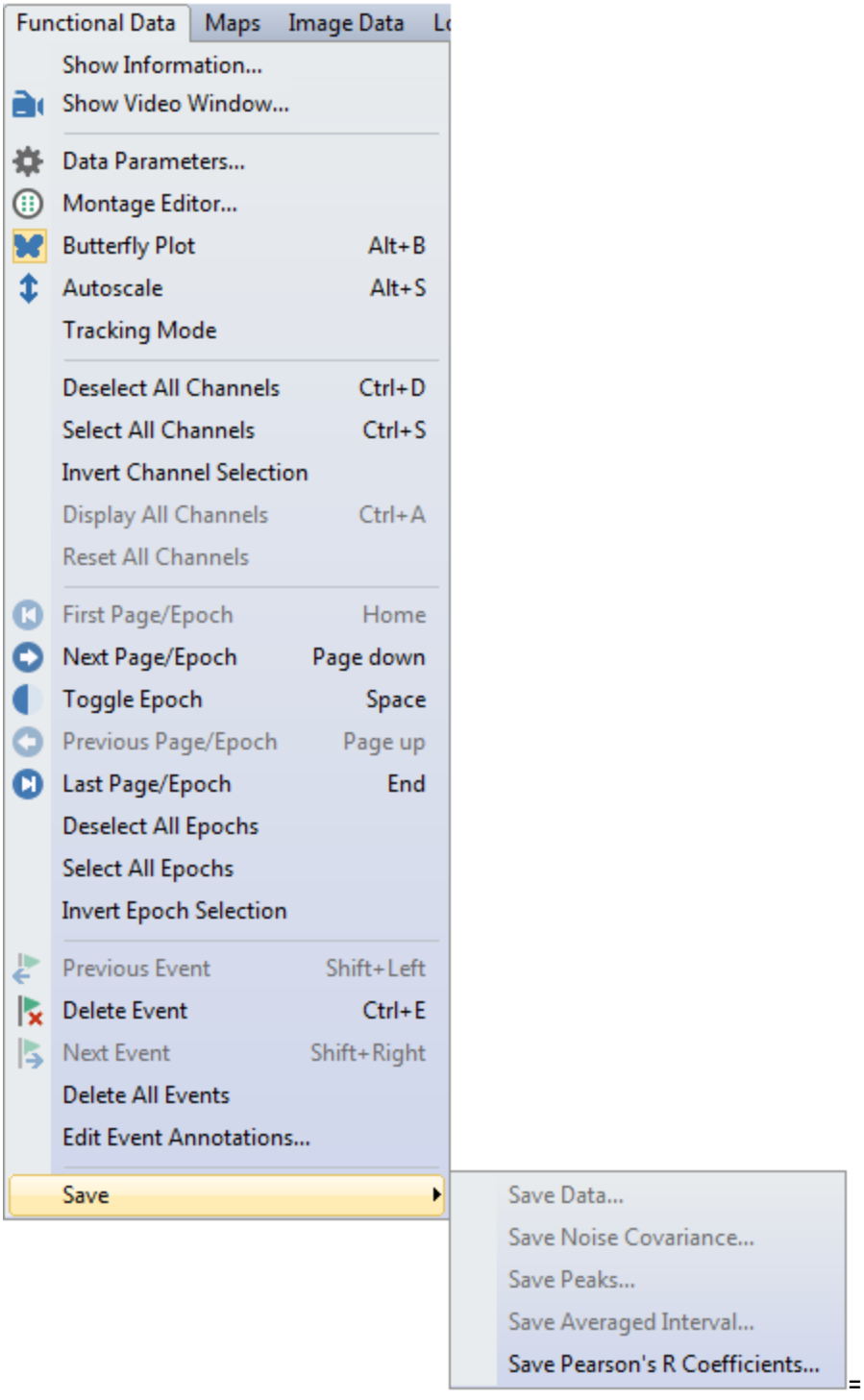
Stop Digitizer. Stop digitization.

Load positions from file (pom). Select an existing .pom file.

Save position file (pom). Save the XYZ position information in a file with a .pom extension.

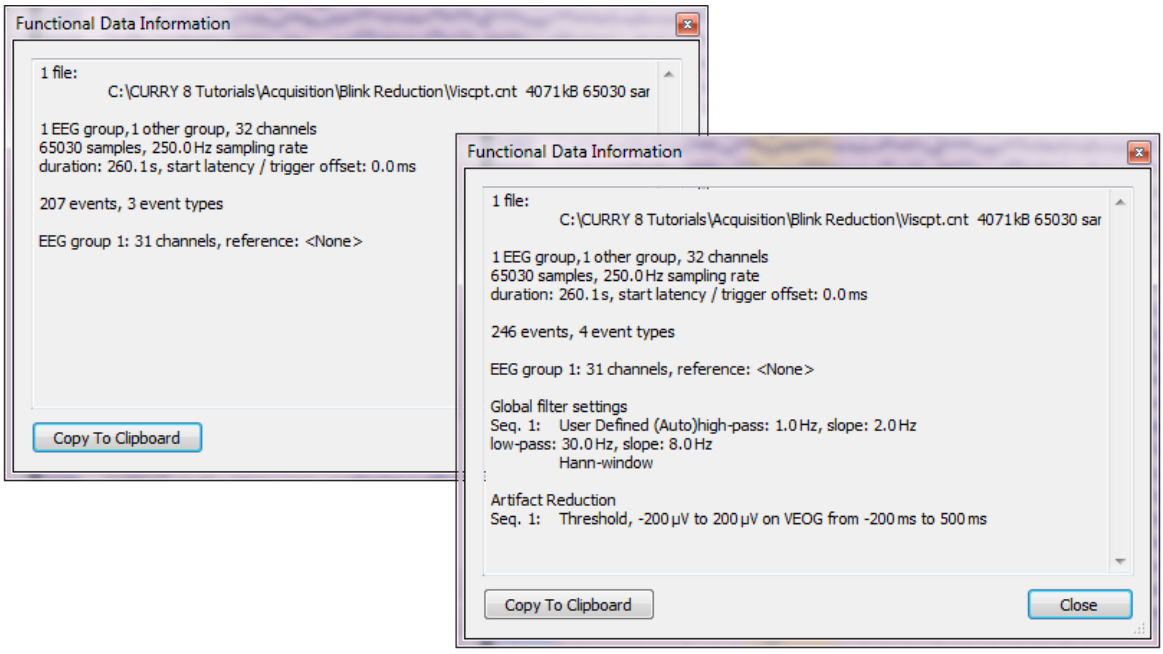
7.1.7 Functional Data

The items pertain to the display of waveform data, navigation through the file, and exporting data or events.



Some of the options will not be accessible unless you have retrieved a continuous or epoched file, and have identified events.

Show Information. This displays information about the file(s) in the currently open Study. As you perform analysis steps, these will be added to the file. The contents may be copied to the Clipboard. If you save the Study Parameters and later reopen the file, the history is retained.



Show Video Window. Displays Video window.

Data Parameters . Invokes the **Functional Data Parameters Wizard**.

Montage Editor . Accesses to the Montage Editor (described below in the **Options** section).

Butterfly Plot . Toggles the Butterfly Plot display on and off (or *Alt+B*).

Autoscale . Autoscales the display of the functional data (or *Alt+S*).

Tracking Mode. When enabled, a single vertical cursor may be positioned by clicking the mouse on a position, or by grab-and dragging the cursor to a position. The voltages for each channel at the cursor position are displayed on the far right of the Data Display. *Shift+left mouse* also disables Tracking Mode; double-clicking the left mouse button enables it.

If you disable Tracking Mode, there will be three vertical cursors for positioning. The two outer cursors are used to define the Timerange. the middle cursor defines the specific time point within the range. The Timerange is used for Noise Estimation, Source Reconstruction, Zooming, etc.

Deselect All Channels. All selected channels will be deselected.

Select All Channels. All deselected channels will be selected.

Invert Channel Selection. Selected channels will become deselected channels, and deselected channels will become selected channels.

Display All Channels. Restores the display of all channels.

Reset All Channels. This will reset to the default settings the changes you have made to channel attributes, such as filtering, zooming in, color changes, interpolation, etc.

First Page/Epoch  (or *Home*), **Last Page/Epoch**  (or *End*). Moves to the First or Last displayed page (continuous data files) or Epoch (epoched data files).

Next Page/Epoch  (or *Page down*), **Previous Page/Epoch**  (or *Page up*). Moves to the Next or Previous Page (continuous data files) or Epoch (epoched data files).

Toggle Epoch (Space)  . Toggles the Accept or Reject state of the current epoch (or *Space bar*).

Deselect All Epochs. All epochs will be deselected.

Select All Epochs. All epochs will be selected.

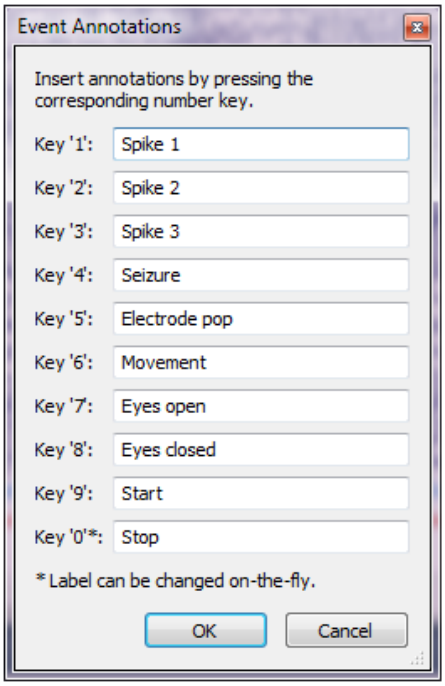
Invert Epoch Selection. Selected epochs will become deselected epochs, and deselected epochs will become selected epochs.

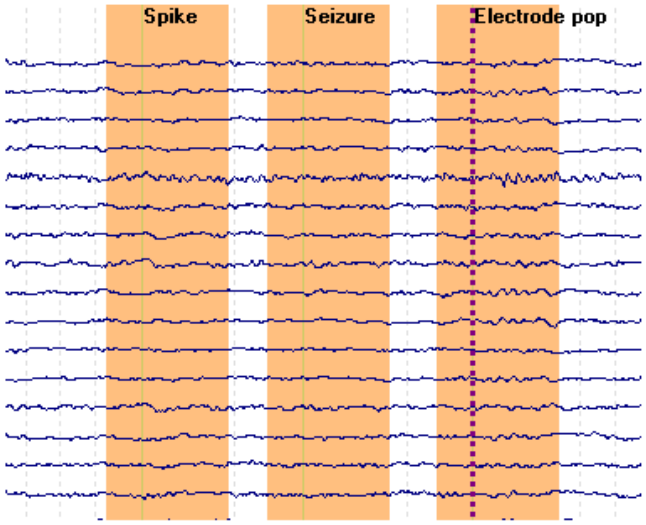
Previous Event  (or *Shift + Left arrow*), **Next Event**  (or *Shift + Right arrow*). Move to the Previous or Next Event (in continuous data files where events have been detected).

Delete Event  . Removes the highlighted event from the (continuous) data file.

Delete All Events. All Events in the data file will be removed. Click the  button at the top of the  panel to restore the original events.

Edit Event Annotations. When you are inserting events manually (using the  option under the Event List and the *number* keys on the keyboard), the default labels will be 1, 2, 3, etc. You may define the events using **Edit Event Annotations**. The new text will be seen in the data display when you insert the events. You can edit the annotations after they have been inserted using the **Event List** dialog. Details for using Annotations are found in the **Manual** option in the **Event List** section.



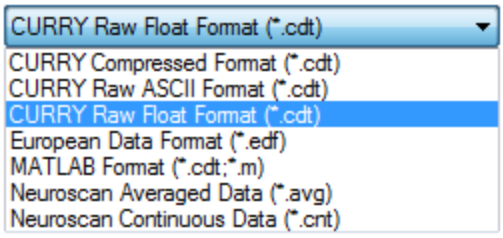


Save

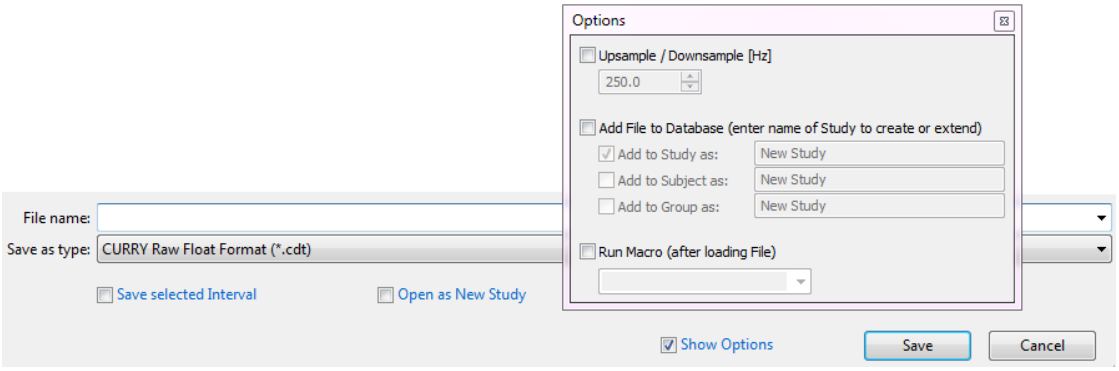
Save Data. As a general "rule", CURRY saves/exports the data you see on the screen - what you see is what is saved (such as, re-referencing, filtering, baseline correction, etc.). There are exceptions, most notably with montages. CURRY will save the original data, not the montaged data. In most instances, the changes you make will become permanent when you explicitly save/export the file.

CURRY can save data either in the Raw ASCII format, as in prior versions, or in the Compressed format, which will save disk space. There is no loss of data with the compression. This does not affect the saved file if you save it as a CNT or EDF file. It is compatible with CURRY 7 (CURRY 7 reads compressed files, but does not write them). This is an issue when reading files into MATLAB, since the script CURRY uses does not recognize to more complex compressed format. In that case, use the Raw Float format. If you have already recorded the data using compression, resave the file where you select Raw Float in the Save As dialog. Generally, compressed files are recommended due to the smaller file sizes.

The functional data may be exported as a Neuroscan Continuous Data or Neuroscan Averaged Data file. In general, the CURRY file types may have speed advantages over the Neuroscan file types; use the Neuroscan file types if you are planning to open the files in the Scan software. EEG data (not MEG data) may be saved in EDF files (European Data Format).



There are several additional options in the lower part of the window.



Save selected Interval. By default, the entire displayed interval will be saved. If you want to save less than that, set the two outer cursors to define a Timerange that you want to save, and then enable the option.

Open as New Study. Enabling this option will open the file (or Study containing the file) automatically.

Show Options. Enabling this displays the Options window.

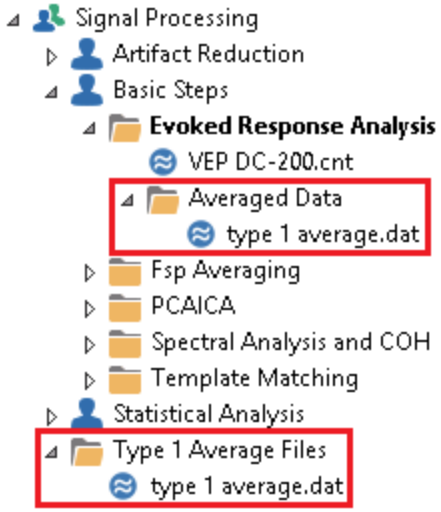
Upsample or Downsample. This is where decimation occurs. For example, you can save a file sampled at 5000 Hz to 500 Hz (every 10th point would be saved). Low pass filtering should be used first with downsampling to avoid aliasing. Upsampling uses a spline fit for the added points.

Add File to Database. These are very useful options when you are using a Database to organize your files.

Add to Study as. Imagine you start with a continuous data file, and from it you have created an averaged file. You want to save this file in a subfolder (derived folder) under the Study with the continuous data file. You would then enable the option and add a new file name (Averaged Data). If you had used an existing Study name (under the continuous data Study), the averaged file would be added to that folder.

Add to Subject as. In this case, you could also create a new folder under the Subject, or add this averaged file to an existing folder under the Subject.

Add to Group as. This option, as well as the previous one, are used, for example, when you want to create grand averages of the average files we are creating. Recall that you can only average files when they are found in the same Study folder. In this case, we are saving the averaged data file under the continuous data file from which it was created, as well as in a new Study called "Type 1 Average Files" that will be created at the Group level. Other averages could then be saved to the same Group level folder so that all averages would then be in the same Study, and could then be averaged to get the grand average. (Note: the files are not saved in the Database - only the paths to the file that are stored on the hard drive).



The averaged file is added as a new subfolder under **Evoked Response Analysis**, as well as under the Group.

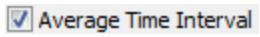
Run Macro. If you enable this option, you can select a macro file to run automatically when the file opens (this is used to, for example, link two macros together without user intervention).

Save Noise Covariance. Noise covariance can be saved to an .noi file, which can then be recalled for **Noise Estimation** using the **From File** option.

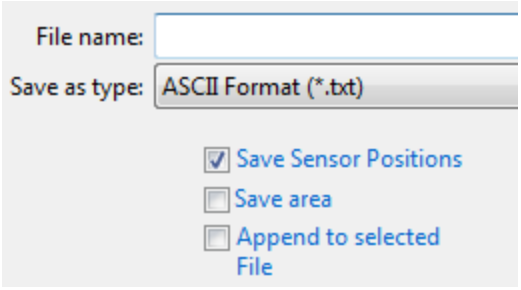
Save Peaks. After you have defined a Timerange and selected **Maximum Peaks** and/or **Minimum Peaks** (under **Options**), you will see the peaks marked. Use this option to save the information. A text file is created that contains the maximum and minimum voltages for each channel, using the Timerange that has been defined. A section of the text file is shown below.

The header displays whether the file contains time or frequency domain data, how many channels were in the file, and how many samples were in the Timerange. The Timerange limits are shown. Following that are the channel labels, the XYZ coordinates of the electrode, the minimum and maximum values, with their respective latencies.

```
# time domain
# channels, tested samples
   28    35
# -10.0 - 165.0 ms
# channel labels, positions[mm] [x y z], min max[µV], latencies[ms]
O1    42.41    89.90   -22.07  -41.660   74.237  165.000   80.000
OZ     2.31   105.41   -13.35  -77.856  123.474   30.000   90.000
P3    50.05   103.18    40.49 -106.807  133.718   10.000   80.000
P7    71.86    67.31     6.47 -114.699  160.610  110.000   40.000
T7    82.98    20.07    31.22 -291.703  317.704   95.000   30.000
C3    59.11    55.26    84.52  -81.522  135.944    5.000   35.000
F7    66.92   -14.84    58.08 -289.796  318.092   90.000   25.000
F3    46.40     7.96    99.55 -122.205  114.874   85.000   30.000
FP1    30.69   -37.77    88.94 -110.196  105.032   90.000   25.000
FZ   -15.30     7.64   117.27 -107.602   44.049    5.000  110.000
```

Save Averaged Data. After setting a Timerange, use the 

option under **Options** to see the averaged values in the column on the far right. Save these values using Save Averaged Data. At the bottom of the Save As dialog, you will see options to Save Sensor Positions and Append the results to an existing file (as opposed to overwriting it).



For time domain data, you will see a file similar to the following. The average for each channel across the -10 to 65ms Timerange is found in the column on the right.

```
# time domain
# channels, averaged samples
   28    15
# -10.0 ... 65.0 ms
# channel labels, [µV]
O1 - avg          15.893
OZ - avg         -22.083
P3 - avg          10.732
P7 - avg          84.218
T7 - avg         149.003
C3 - avg          23.067
F7 - avg         109.829
F3 - avg           6.727
```

For frequency domain data, there are columns for each frequency band (delta, theta, etc.), showing the averages for each band, and the overall average in the far column on the right. In the example below, the cursors defined a frequency

range of 0 to 70.4Hz. The numbers in brackets are the number of frequency bins in each band, as well as the overall number of bins.

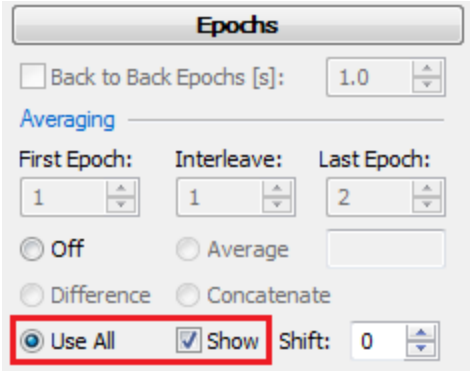
```
# frequency domain
# channels: 28
# averaged frequency ranges [bins]:
# 0.000...3.000 Hz [50]
# 3.000...8.000 Hz [83]
# 8.000...12.000 Hz [67]
# 12.000...30.000 Hz [296]
# 30.000...70.000 Hz [656]
# 59.000...61.000 Hz [33]
# averaged frequencies (cursors):
# 0.000...70.374 Hz [1154]

# channel labels, [µV]
FP1-avg    0.020    0.229    0.695    0.172    0.018    0.010    0.111
PZ - avg   0.018    0.286    1.474    0.255    0.013    0.005    0.179
FP2-avg    0.020    0.255    0.739    0.168    0.017    0.008    0.113
OZ - avg   0.013    0.251    0.710    0.172    0.015    0.007    0.112
F3 - avg   0.016    0.255    0.681    0.161    0.013    0.006    0.106
FC5-avg    0.012    0.170    0.571    0.137    0.012    0.003    0.087
F4 - avg   0.019    0.299    0.729    0.170    0.014    0.005    0.115
FC6-avg    0.013    0.197    0.615    0.139    0.011    0.004    0.091
C3 - avg   0.010    0.164    0.482    0.140    0.011    0.004    0.082
CP5-avg    0.012    0.174    0.520    0.142    0.011    0.005    0.085
C4 - avg   0.010    0.190    0.538    0.136    0.011    0.003    0.086
CP6-avg    0.010    0.173    0.474    0.150    0.011    0.004    0.084
P3 - avg   0.015    0.257    0.840    0.204    0.012    0.005    0.126
CP1-avg    0.012    0.197    0.631    0.188    0.012    0.004    0.106
P4 - avg   0.013    0.256    1.212    0.223    0.014    0.004    0.153
CP2-avg    0.012    0.203    0.914    0.198    0.011    0.003    0.125
O1 - avg   0.015    0.301    0.916    0.224    0.022    0.009    0.144
PO1-avg    0.018    0.347    1.388    0.280    0.015    0.005    0.185
O2 - avg   0.014    0.247    0.744    0.180    0.012    0.005    0.114
PO2-avg    0.016    0.300    1.442    0.230    0.014    0.005    0.171
```

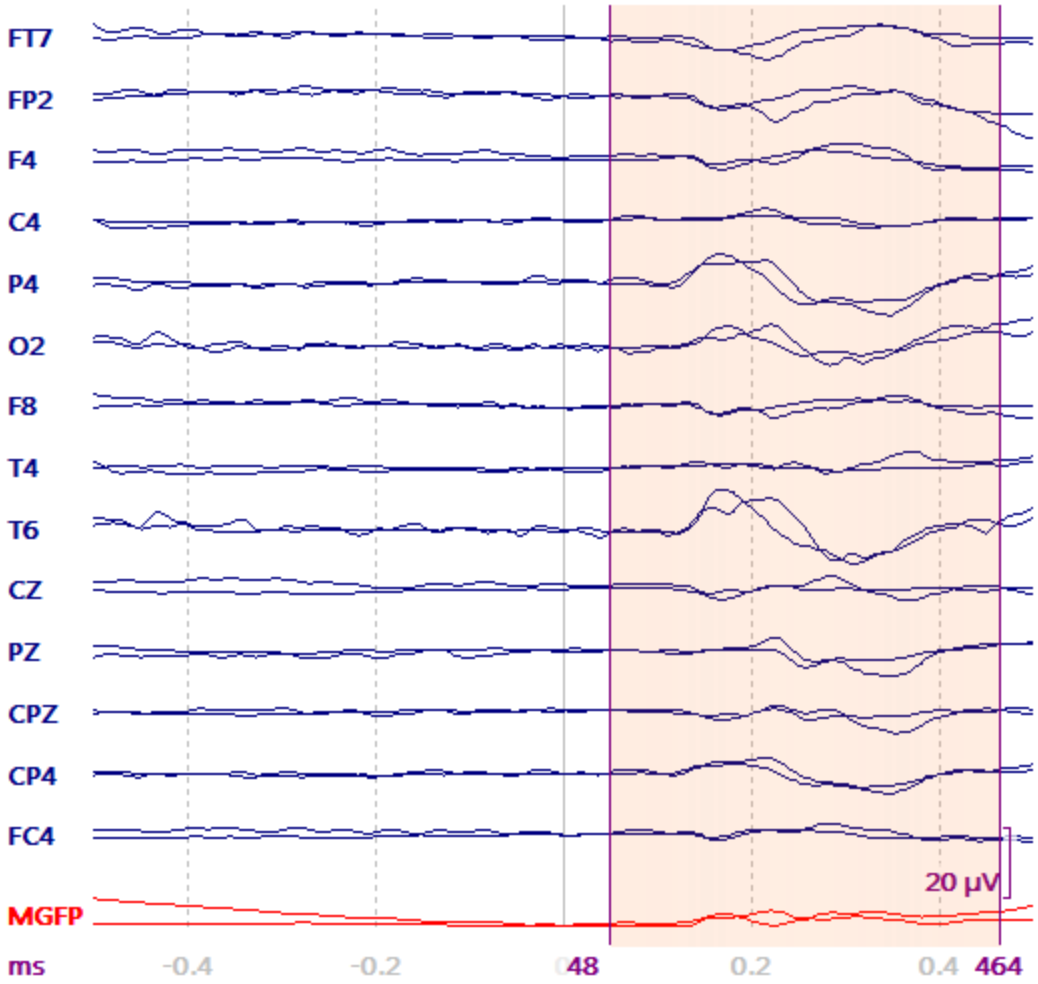
Save Pearson's R Coefficients. Pearson's r correlation coefficients may be computed between pairs of electrodes across two compatible data files (time or frequency domains). The files must have the same number of channels, same labels in the same order, number of points, and start and stop times. To compute the correlations, please do the following:

1. Place the two files in the same Study and open it to see the two files as epochs.

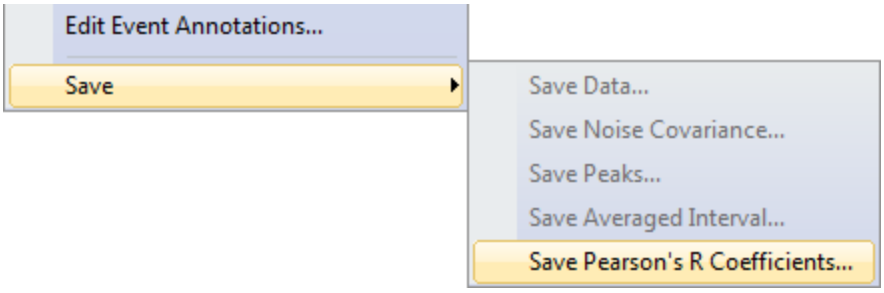
2. In the Epochs panel under **Functional Data**, select **Use All** and **Show**.Now you should see the two files superimposed.



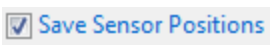
3. Set a Timerange of interest using the outer two cursors (which may be the entire file).



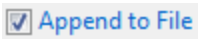
4. On the Main Menu bar, go to **Functional Data → Save → Save Pearson's R Coefficients**.



5. In the Save dialog, note that there are additional options at the bottom.

Save Sensor Positions 

. When enabled (default), the xyz coordinates for the electrodes will be exported also. If you do not want these (to simplify the file), disable the option.

Append to File 

. This option is enabled when you wish to append the current results to a pre-existing text file.

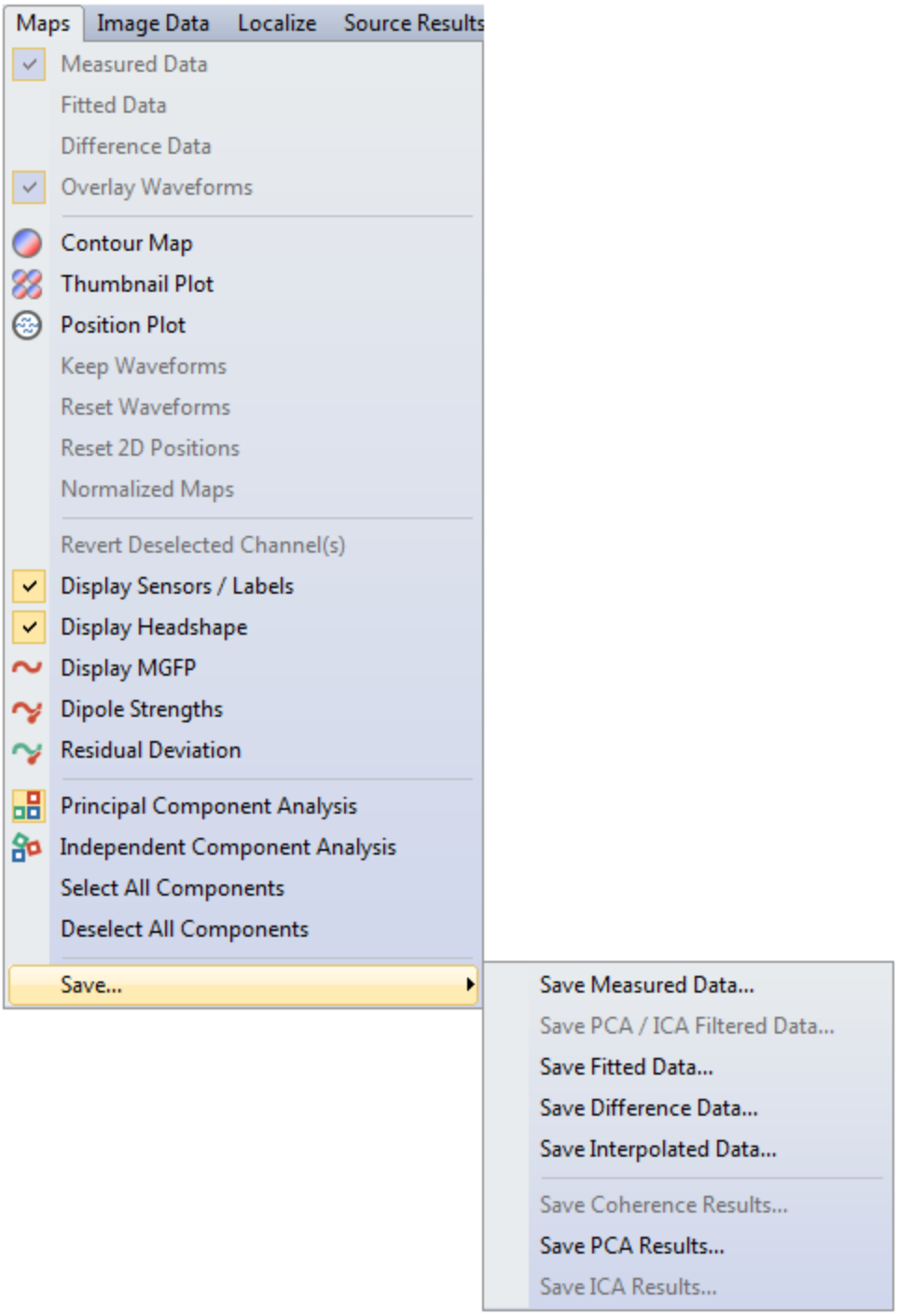
6. The resulting text file will appear similar to the following, where the r's between pairs of electrodes are listed.

```
# time domain
# channels, tested samples
  32    85
# 84.0 ... 420.0 ms
# channel label, Pearson's R
FP1          0.861
F3           0.890
C3           0.830
P3           0.241
O1           0.713
F7           0.877
```

7.1.8 Maps

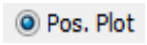
These options are used to select different displays in the 

display, select PCA or ICA analyses, or export Measured, Fitted, Difference data or PCA/ICA results. Position Plot, PCA, ICA, MGFP, Dipole Strengths, and Residual Deviation are only possible if a Timerange is selected (not possible for a single timepoint). These are discussed in more detail in later sections.



Measured Data. This is the actual data in its original form.

Fitted Data. Fitted Data are those that are generated by the best fit dipole reconstruction.

Difference Data. Difference Data are the differences between the Measured and Fitted data. These can be viewed either as 2D contour maps or as waveforms using the 

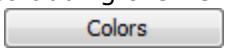
option.

Overlay Waveforms. This option allows you to overlay Measured, Fitted, and Difference waveforms.

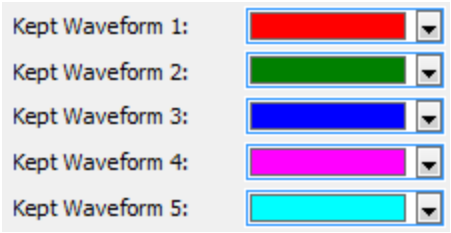
Contour Map  . Displays a single contour map corresponding to the position of the middle cursor in the Functional Data display (or *Alt+C*).

Thumbnail Plot  . Displays the maps in a series of Thumbnails (the number of thumbnails is set in the **Parameters** panel under **Maps**; or *Alt+T*).

Position Plot  . Select this option to display the data on a 2D head shape (or use *Alt+P*).

Keep Waveforms. Select this option to "keep" the current waveforms seen in the Position Plot view. Make a change, such as, apply a filter or move to a different epoch, and the new display will be superimposed on the kept one. This allows you to compare the effects of an operation you have applied. It is also used to compare multiple average files or epochs (up to 5). For overlaying multiple displays, click **Keep Waveforms** each time prior to adding the new display. The colors are assigned automatically, as seen in the 

panel for **Maps**. The most recent waveform - not yet "kept" - will always be the color you have selected for the EEG (or MEG) waveforms.



Reset Waveforms. Removes "kept" waveforms.

Reset 2D Positions. If you have changed any of the electrodes in the Position Plot (repositioned or resized), clicking this option will restore the original positions and sizes.

Normalize Maps. This option is used in conjunction with the **Average Time Interval** option, found under **Options**, under **Functional Data**. If you select a Timerange and click the **Save** button, the **Normalize Maps** option will become active. If you click it and move to another Timerange, the 2D Maps will show the difference with respect to the "saved" maps.

Revert Deselected Channel(s). If you click on a channel(s) from the Maps display to deselect it, the channel(s) will disappear (and be removed from the maps computations). Clicking this option will restore the deselected channel(s). The last deselected channel will be restored if they were deselected individually. If you

deselected channels by dragging a rectangle around them, all of those will be restored. If you want to have all channels selected, use **Select All Channels** in the Functional Data context menu (or *Ctrl-S*).

Display Sensors / Labels. Toggles the sensors or sensor labels on and off.

Display Headshape. Toggles the display of the background headshape on and off.

Display MGFP  . Display the Mean Global Field Power (*Alt+G*).

Dipole Strengths  . Display the dipole strengths (*Alt+D*).

Residual Deviation  . Displays the residual deviations (*Alt+R*).

Principle Component Analysis  . Select PCA (or *Ctrl+A*).

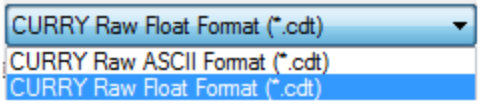
Independent Component Analysis  . Select ICA (or *Ctrl+I*).

Select All Components. All components will be selected.

Deselect All Components. All components will be deselected.

Save...

Save Measured, **PCA / ICA Filtered Data**, **Fitted**, or **Difference Data**. These options may be used to export the measured, PCA/ICA filtered, fit or difference data to a float-format or ASCII-format .dat file (Export Fit and Export Difference are active after a source reconstruction has been performed). Parameters and sensor locations are written to the accompanying .dpa file.



Save Interpolated Data. If you have data files that have, for example, different numbers of channels, yet you wish to combine them into a grand average, you can use the sensor positions from one file to interpolate and extrapolate the channels in the first file to match those in the second file (with more channels). Obviously, this is a fairly drastic thing to do, since you are changing data on existing channels and creating new channels that did not exist. This option should only be used with care. The required steps are explained in the following sub-section **Interpolated and Extrapolated Channels**.

Save Coherence Results. The Coherence results, including sensor positions, are saved to an ASCII file (.coh extension). These .coh files are not interchangeable with the .coh coherence files created in Scan's EDIT program.

```
# frequency domain
# sensors frequencies
   28    11
# 8.972 - 10.254 Hz
# sensor positions[mm] [x y z]
   29.00  -106.50    32.90
   -0.00    55.00   141.30
  -29.00  -107.50    32.80
   -0.00    94.50    70.40
   51.00   -81.50    86.10
   77.00   -44.30    69.30
  -53.00   -82.30    84.00
  -77.00   -44.20    68.30
   71.00    17.60   116.70

   85.00    -6.50    38.50
  -84.00    -8.50    38.30
   74.00    51.60    49.30
  -73.00    50.60    49.20
   -1.00   -23.30   156.40
   -0.00   -92.60   112.00
# coherence matrix
1.000 0.250 0.967 0.704 0.920 0.871 0.904 0.870 0.665 0.016 0.6
0.250 1.000 0.268 0.120 0.144 0.283 0.198 0.260 0.197 0.196 0.0
0.967 0.268 1.000 0.726 0.879 0.798 0.939 0.918 0.629 0.020 0.7
0.704 0.120 0.726 1.000 0.828 0.583 0.858 0.711 0.614 0.133 0.8
0.920 0.144 0.879 0.828 1.000 0.877 0.914 0.772 0.754 0.033 0.6
0.871 0.283 0.798 0.583 0.877 1.000 0.766 0.682 0.793 0.026 0.4
0.904 0.198 0.939 0.858 0.914 0.766 1.000 0.921 0.666 0.045 0.8
0.870 0.260 0.918 0.711 0.772 0.682 0.921 1.000 0.524 0.053 0.8
0.665 0.197 0.629 0.614 0.754 0.793 0.666 0.524 1.000 0.084 0.4
0.016 0.196 0.020 0.133 0.033 0.026 0.045 0.053 0.084 1.000 0.2
```

Save PCA Results. Select this option to export the PCA results to a text file (.pca extension). The file contains the number of sensors, number of data sample points in the Timerange, the number of patterns, their weights, and the normalized results (shown in part below). The PCA ASCII file can be read by **Functional Data** → **Artifacts and Baseline** → **PCA Projection** for artifact suppression.

```
# sensors samples
   28    15
# selected patterns
  1   2   3
 PCA PCA PCA
# weights
   148.851    58.6908    30.2899
# normalized patterns [SNR]
 -0.008332  -0.065820  -0.048511   0.126843   0.410721   0.053407   0.276939   0.047862   0.080806
-0.140650  -0.130257  -0.135422  -0.182963  -0.216449  -0.170724  -0.211995  -0.140648  -0.152823
-0.186454  -0.063362  -0.110865  -0.105570   0.132416  -0.061023   0.357499  -0.057831   0.404430
0.298778
```

Save ICA Results. Select this option to export the ICA results to a text file (.ica extension). The file contains the number of sensors, number of data sample points in the Timerange, the number of patterns, their weights, and the normalized results (shown in part below).

```
# sensors samples
   28    15
# selected patterns
  1   2   3
 ICA ICA ICA
# weights
   135.155    73.2262    58.6704
# normalized patterns [SNR]
  0.008562  -0.055202  -0.018730   0.159422   0.421678   0.053415   0.245966   0.026375   0.043786
-0.161477  -0.133521  -0.126659  -0.195367  -0.230175  -0.171509  -0.216405  -0.134325  -0.142888
-0.181933  -0.099141  -0.102812  -0.093167   0.152253  -0.049550   0.330275  -0.044492   0.415267
0.300355
```

7.1.8.1 Interpolated and Extrapolated Channels

If you have data files from, for example, different labs, and you want to combine them, but you can't because the sensor positions are different and/or the number of channels is different, you can force fit the files using an interpolation (changing the waveforms on existing channels) and extrapolation (creating new channels) procedure. Obviously, this is something you would only do as a last resort, and with the recognition that you are changing the existing data. Similarly, the number of channels could be the same, but the placement scheme was different, and you wish to interpolate the data as if the same placement had been used.

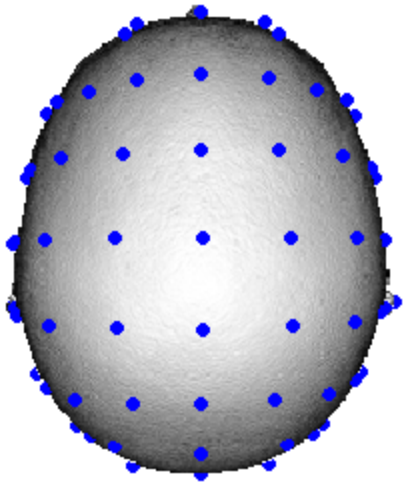
Interpolation uses a spherical spline interpolation, where the sphere center of new electrodes is subtracted before the interpolation.

This option is used only with a single EEG Group, not with multiple EEG Groups.

Also, use care if you are interested in something that is occurring near or at the peripheral electrodes, such as a temporal lobe spike. Adding more electrodes that extend below the original electrodes can distort the spike topography, and that may have unpredictable effects on source localization.

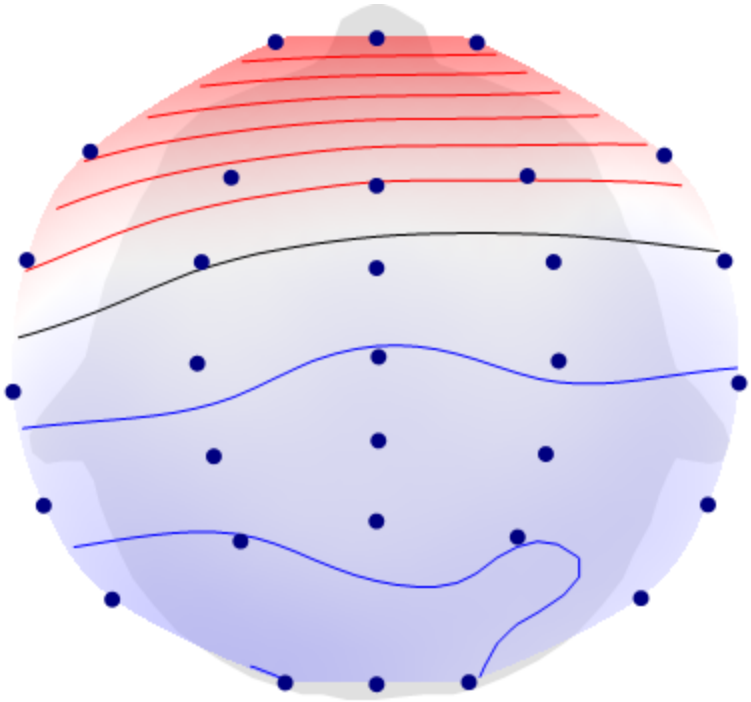
For example, let's say that File 1 has 32 channels, and File 2 has 66 channels. You want to combine them, and so you wish to approximate 66 channels in File 1.

1. Open File 2 and go to the **Localize** display. *Right click* and select **Import Electrodes**.



2. Click the **Save** button at the top of the **Localize** list, then select a folder and enter a file name, such as *66 channels.pom*.

3. Close that Study and open the Study with File 1. Select a display option that includes Maps (to see the effect).

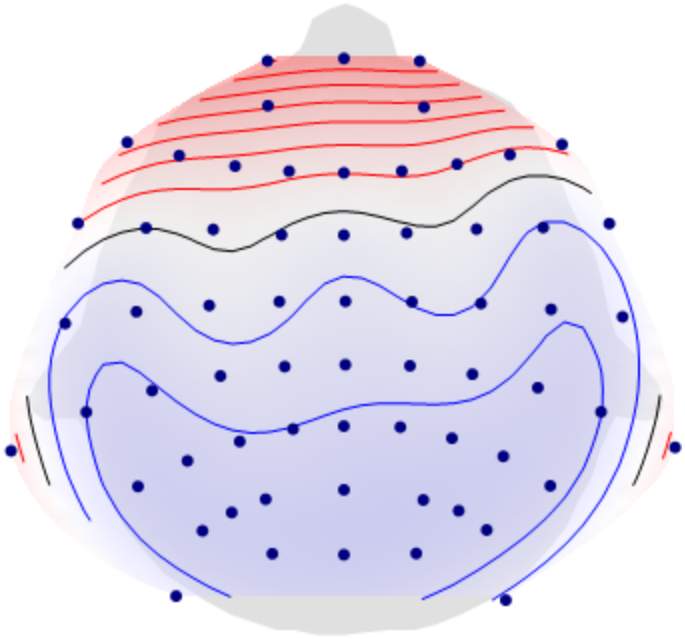


4. Select that part of the data file that you wish to save (the Timerange). For continuous data, that may be many seconds; for averaged data it may be the entire epoch interval.

5. On the Main Menu bar, go to **Maps** and click **Save**. Click the **Save Interpolated Data** option. An **Open** file window will appear. Select the .pom file you just created (*66 channels.pom*). The **Save Interpolated Data** window will

appear. Select a folder and enter a file name for the new file that will be created (*New File 1.cdt*).

6. Open that file in a new Study. You will then see the interpolated and extrapolated data. You will see the same section of the waveform data, only now there are 66 channels instead of 32 channels. Typically, the waveform data will display a spatial smoothing as well as an increase in noise. Features in the old data may now appear less pronounced since the channels have been interpolated and extrapolated using all channels.



7. You can then go ahead and average the now similar data files, keeping in mind that the data have been altered considerably.

7.1.9 Image Data

These options are used to import raw MR data, perform segmentation, and additional options. Refer to the **Image Analysis** sections below for more details. Fewer items will be seen if you do not have the advanced analysis license.

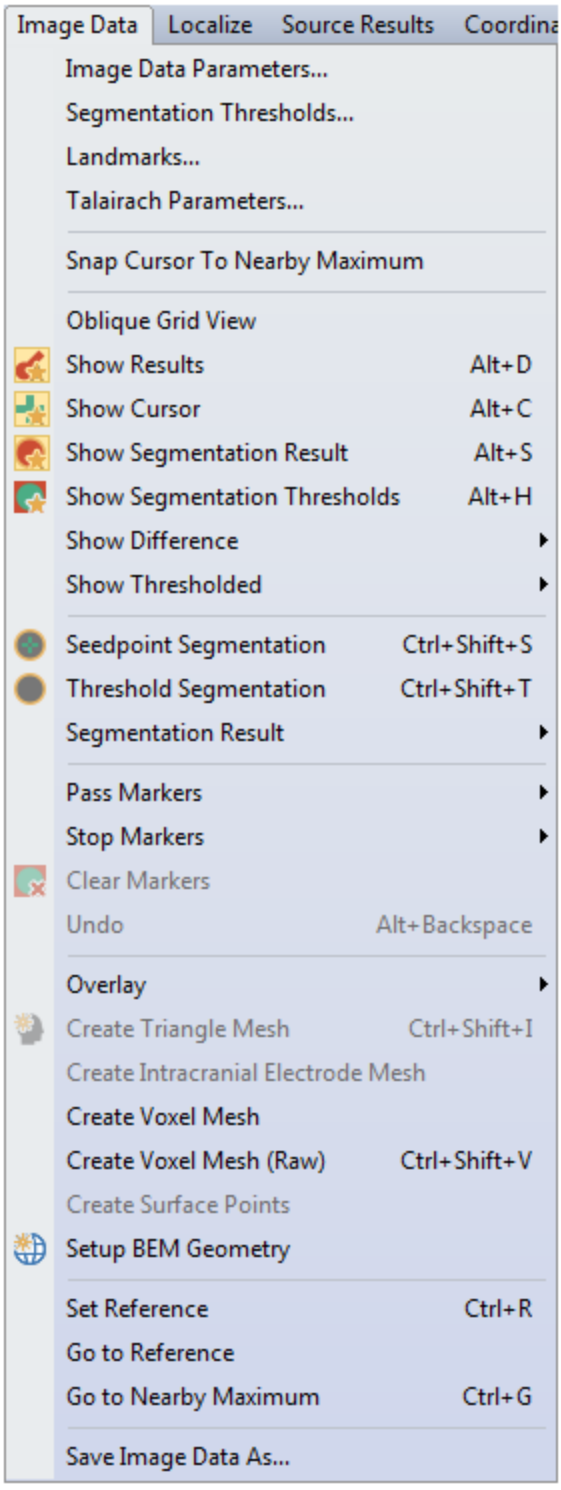


Image Data Parameters. This option opens the **Image Data Parameters** windows (described below).

Segmentation Thresholds. **Step 5** from the **Image Data Parameters** windows is accessed, allowing you to review or modify the segmentation thresholds.

Landmarks. **Step 6** from the **Image Data Parameters** windows is accessed, allowing you to review or modify the anatomical landmarks.

Talairach Parameters. Click this option to review or modify the anatomical landmarks (AC, PC, and MS) and the brain region boundaries as related to defining the Talairach parameters (**Steps 6** and **7** of the **Image Data Parameters** windows will appear).

Snap Cursor to Nearby Maximum. This feature, when enabled, will move the image data cursor to a nearby intensity maximum after clicking in the image data. It is, in a way, a sibling feature to the "magnetic cursor" that can be enabled for manual event marking. It is typically used for defining electrode locations in CT data that are usually rendered as small bright dots.

Oblique Grid View. This option allows you to apply the oblique view you set in the iso-images to the Grid View as well. The Oblique Views are described in the **Image Data Context Menu** section.

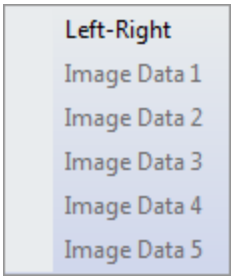
Show Results. This option toggles the display of the source localizations on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+D*).

Show Cursor. This option toggles the display of the cross-hair cursor on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+C*).

Show Segmentation Result. This option toggles the display of the segmentation results on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+S*).

Show Segmentation Thresholds. Toggles on and off the display of the segmentation thresholds. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+H*).

Show Difference. You may subtract the right side from the left, or, if you have more than one set of image data opened, you may subtract, for example, Image Data 2 from Image Data 1.



Show Thresholded. The option is used to superimpose the image data from one set upon another. It will be active after you load at least two image data sets. If you select it from one data set, you will have the option to select either of the other data

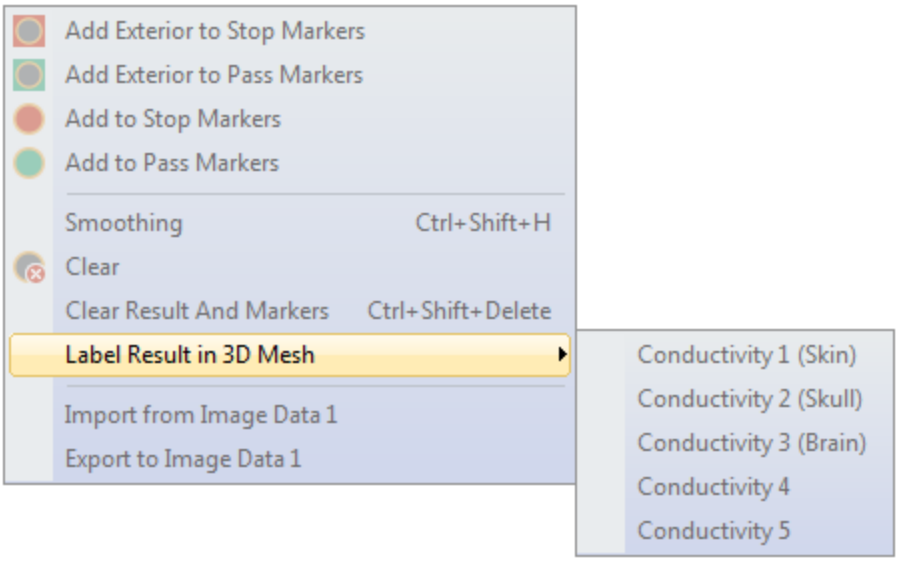
sets for superimposition. Note that only the portions above the threshold set in the modality to be added are shown.

This option may also be used to superimpose DTI data on the MR data (from the same subject). Load the MR data first in the Database. Make sure the MR data has the focus, then select **Image Data 2** to display the DTI data on the MR data. The same result may be obtained by selecting the **Threshold** option from the **Options** panel. Use the **Transparency Atlas** option to adjust the transparency.

Seedpoint Segmentation. This option performs **Region Growing** segmentation. Clicking it has the same function as clicking the Start button in the **Segmentation** panel after Region Growing has been selected. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+S*).

Threshold Segmentation. This option performs **Threshold** segmentation. Clicking it has the same function as clicking the Start button in the **Segmentation** panel after Thresholding has been selected. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+T*).

Segmentation Result. This accesses a secondary menu with the following options. Pass Markers are generally seen in green, and Stop Markers are in red (you can change the colors in the **Colors** panel under **Image Data**). Most of the same options are seen in the **Segmentation** panel after clicking the Result button.



Add Exterior to Stop Markers. Exterior regions will be filled with Stop Markers (regions will turn red). It is also accessed by the icon on the **Image Data** Toolbar.

Add Exterior to Pass Markers. Exterior regions will be filled with Pass Markers (regions will turn green). It is also accessed by the icon on the **Image Data** Toolbar.

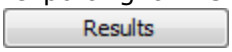
Add Segmentation Result to Stop Markers. Click this option to include the segmented region with the Stop Markers (regions will turn red). It is also accessed by the  icon on the **Image Data** Toolbar.

Add Segmentation Result to Pass Markers. Click this option to include the segmented region with the Pass Markers (regions will turn green). It is also accessed by the  icon on the **Image Data** Toolbar.

Smoothing (*Ctrl+Shift+H*). This option is meant to be used to obtain a quick Smoothing result, and so always uses a **12mm Dilation**. Use the **Morphology** panel options for any other parameters, and its **Start** button to apply them.

Clear. This clears the segmentation result. It is also accessed by the  icon on the **Image Data** Toolbar

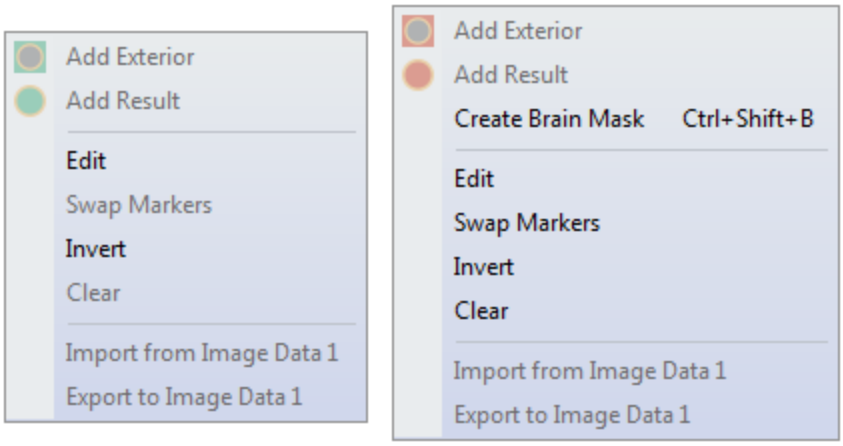
Clear Result and Markers. This clears the segmentation result and markers.

Label Result in 3D Mesh. This feature is related to the creation of FEM models. Between creating a tetrahedra/cube mesh and exporting it in CAUCHY format (which can be done from the context menu in 

), one might wish to "label" tetrahedra with respect to which tissue type they represent. This is based on the segmentation result currently in **Image Data**. Because compartments enclose each other, the program starts with the skin, then the outer skull, then the inner skull, overwriting in each step the labeling for the enclosed tetrahedra.

Import from Image Data 1/Export to Image Data 1. You must have two (or more) image data sets loaded to use these options. The second or third data set can import results from the first, or export results to the first.

Pass Markers/Stop Markers. Pass and Stop Markers determine the boundaries or regions used in segmentation.



Add Exterior. Adds the complement of the segmented volume to the markers of the selected **Marker Type**. It is also accessed by the icon on the **Image Data** Toolbar.

Add Result. Adds the segmented volume to the markers of the selected **Marker Type**. It is also accessed by the icon on the **Image Data** Toolbar.

Create Brain Mask. Stop markers will be added to everything but the cortex, creating a mask about the brain.

Edit. Selecting this option expands the Markers panel, and sets the **Edit Mode** to **Pass/Stop Markers**.

Swap Markers. Swaps Stop and Pass Markers.

Invert. Inverts **Pass/Stop Markers**.

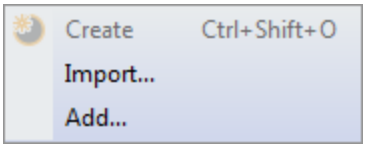
Clear. Clears all **Pass/Stop Markers**.

Import from Image Data 1/**Export to Image Data 1**. You must have two (or more) image data sets loaded to use these options. The second or third data set can import markers from the first, or export markers to the first.

Clear Markers. Select this option to clear the Markers (same as the button on the **Image Data** Toolbar).

Undo. The most recent step is undone.

Overlay. The options are used to Create, Import, or Add overlays. Overlays store segmentation results and markers for later use.



Create. This creates an overlay of the most recently segmented surface(s). It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+O*).

Import. This selects the Doubleclick: Import Overlay mode in the **Properties** panel under Results. Import Overlay shows all Overlays (segmentation results) that can be imported to **Image Data**. Creating a new overlay will *replace* an existing one. Double-click an overlay to import it.

Add. This selects the Doubleclick: Add Overlay mode in the **Properties** panel under Results. New overlays will be *added* to the list. Double-click an overlay to import it.

Create Triangle Mesh. After segmentation, click this option to create a quick triangulated mesh surface, using a fixed **Dilation** of **12mm**. The results will appear in the **Properties** panel as Surface**#** (where # is the number of the next available Surface). The results are displayed in the 3D View. The option is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+I*). Use the parameter fields in the Create panel for other settings, and then click its **Start** button to apply them.

Create Intracranial Electrode Mesh. This is a convenience option that is only available for CT data with depth electrodes, saving you from performing the steps manually. It consists of the following operations.

1. Create brain mask.
2. Find thresholds suitable for intracranial electrodes.
3. Creates a voxel mesh (raw).

The result in the **3D View** Objects list is called Electrode Mesh, and displays the segmented depth electrodes.

Create Voxel Mesh. A voxel mesh is created (see also Create).

Create Voxel Mesh (Raw). This feature is similar to the Create Voxel Mesh command, which transforms the yellow segmentation result into a voxel mesh and therefore has an inherent resolution of 256x256x256 (the resolution of markers and segmentation result). However, especially for CT, the raw image resolution may be higher, usually 512x512x512, and the "raw" voxel mesh will have the resolution of the raw image data, not using the segmentation result at all, but simply including all voxels that satisfy the threshold (and marker) criteria into the voxel mesh. This results in higher-quality 3D View renderings of e.g., intracranial electrodes.

Create Surface Points. After segmentation, click this option to create a surface consisting of points (see also Create). The results will appear in the

Properties panel as Points**#** (where # is the number of the next available set of points). The results are displayed in the 

.

Setup BEM Geometry. This is a shortcut to the 

panel for using the automated BEM Realistic Head Model algorithm. It is also accessed by the  icon on the **Image Data** Toolbar.

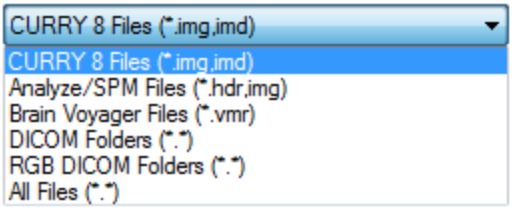
Set Reference. Click this option (or *Ctrl+R*) to set the reference point at the current cross-hair cursor position. A small plus will appear, with the color determined by the **Infos** color setting under 

. The distance from the cursor to the Reference is displayed in the Tooltip and in the **Options** panel.

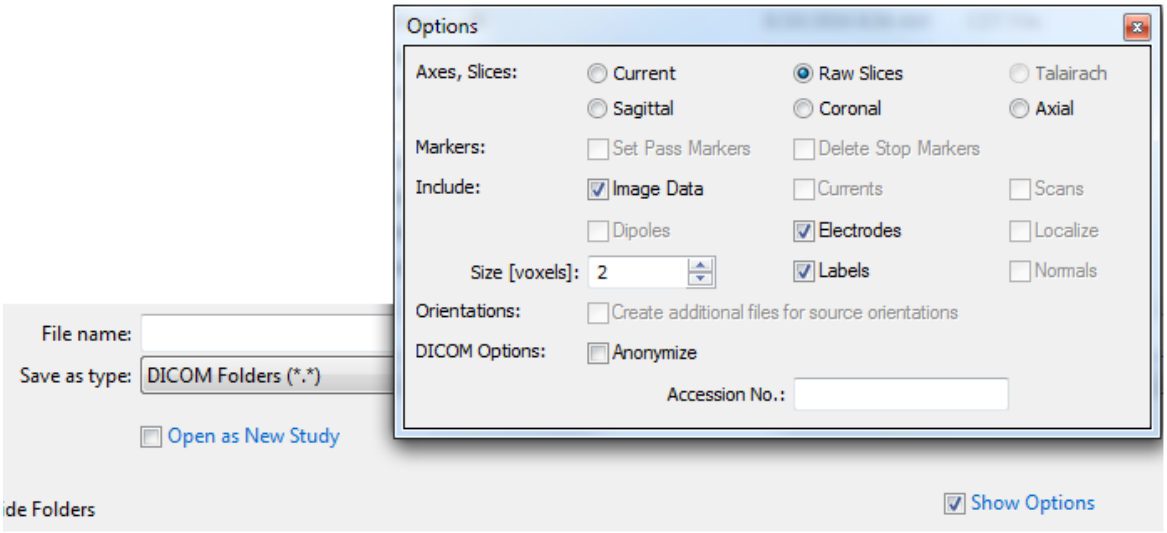
Go To Reference. Select this option to return the cross-hair cursor to the reference point in all three iso-images.

Go To Nearby Maximum (*Ctrl+G*). This is used for finding the exact center of bright dots in an MRI or CT, such as vitamin E markers or ECoG electrodes. "Nearby" translates to a 5mm radius, wherein the center-of-mass is computed. A similar routine in Localize performs the operation for all Localize locations. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, the **3D View**, click the border of the bright area, and this functionality brings the cursor to its center (this can be applied repeatedly).

Save Image Data As. This option allows you to save the MR images in one of several output file formats:



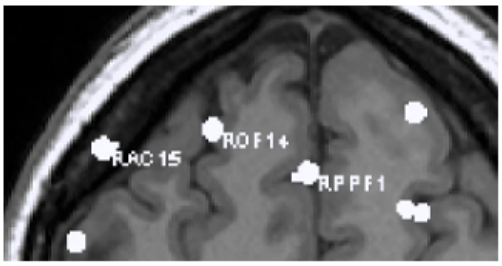
In the **Show Options** part of the Save As dialog are additional options that you may use.



Axes, Slices. If you have changed the axes or resliced the image data, you have the option to save the **Current** axes and slices, or the **Raw Slices**. The **Talairach** option will be active if you have selected the Talairach coordinate (**Coordinates → Talairach (R,A,S)**). If **Raw Slices** is not selected, a 256x256x256 image cube will be exported. You also have the option to save the Sagittal, Coronal, or Axial orientations (DICOM only). When the file is opened, you will see the images on the film strip on the left in the orientation you selected.

Markers. If you have included Pass Markers and/or Stop Markers, you can save these. Pass Markers will be seen in white if you select **Set Pass**. Stop markers will be seen in black, unless you enable **Delete Stop Markers**.

Include. Dipole results (etc.) can be exported to surgical navigation system with or without **Image Data** (enabled by default). You can include the **Currents** (thresholded current densities exported as high-intensity markers in 3D images), **Scans**, and **Dipoles** results, the **Electrodes**, and any **Localize** points you have created. You can vary the Symbol **Size** (in voxels). The electrode labels can be saved in the written image data file. The labels will be seen in the view selected in the **Axes, Slices** selections. For example, select **Axial** if you want the labels to appear in those slices (the labels are one slice thick). The figure on the right shows all of the labels with all of the electrodes (Intensity of the labels is 250). If **Size** of the electrodes is up to **10**, the labels will be seen to the side of the electrodes. If it is **11** or greater, the labels will be inside the electrodes. (The **Interpolate** option may need to be disabled).



If the **Size** is **3** or larger, you can include the **Normals**. Normals are imprinted in orthogonal slices, which means that a 3D rendering may show more than one tail per dipole.

For whatever components (Dipoles, Localize, Electrodes) are visible in Image Data (controlled by the respective checkbox in **3D View**), the respective checkbox in the Save Image Data dialog becomes active.

Orientations. This option is used when saving CDR results in SPM (image) format. Three additional images for the normal components are created. If not checked, only the strengths are saved.

Options. Generally speaking, CURRY 8 includes the following meta-information (read from the original image data file) when writing DICOM: modality, field strength, patient name, gender, birthday, age, series description, and study description. The exported information may be modified as follows.

> **Anonymize**. The Anonymize option results in patient name and birthday not being written to the saved files (not just DICOM).
>
> **DICOM Accession No**. The accession number is a way to store an additional, manually entered 16-character string (usually a number) with the written DICOM files.

After saving. If you enable **Open as new study**, the .imd file will be added to the Database as an unfiled Study, and this image data-only study will be opened.

Exporting results to surgical navigation systems (e.g., Stryker). Please follow the steps below to export the image data and other results to surgical navigation software.

> 1. Make sure **Show Results** has been enabled  (Toolbar or Image Data context menu).
>
> 2. The **Save Image Data As** dialog shows checkboxes for including Dipoles, Electrodes, and Localize (or any) locations in the saved MRI. Formats can be DICOM, etc. (select under **Save as type**).

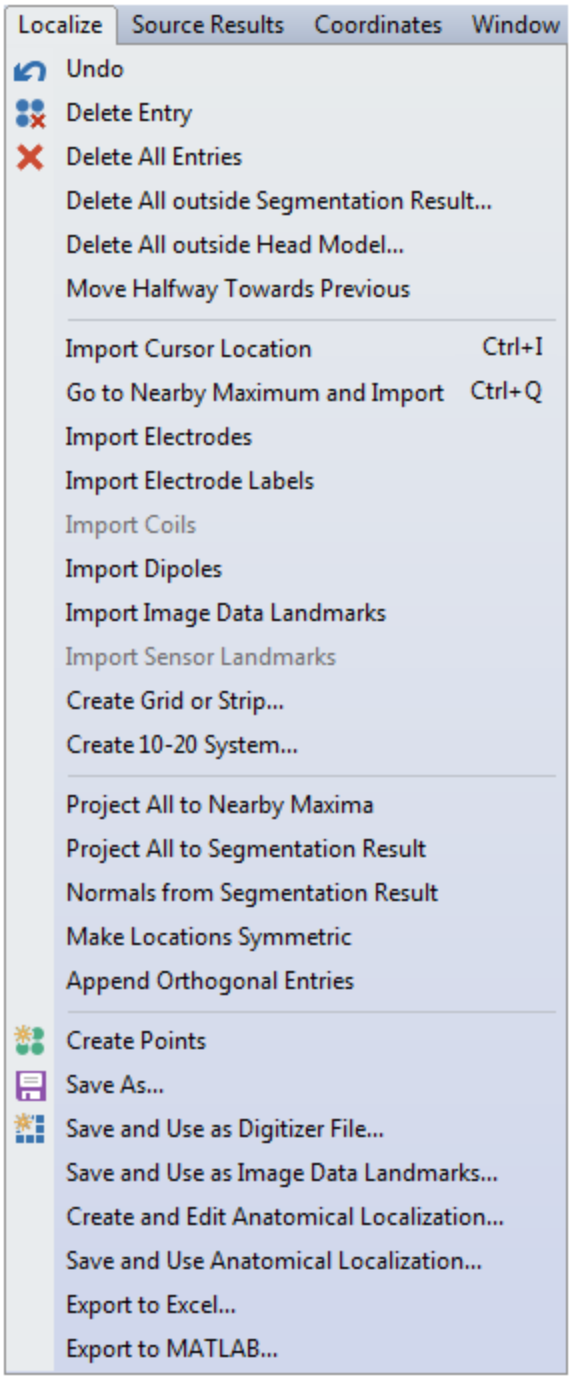
3. The items that are checked are included with the saved structural MRI as high-intensity markers (their size can also be selected).

4. No overlays are necessary, and coregistration is not an issue.

5. If a second version of the image without markers is desired, resave the image data without the items being checked. The navigation system needs to be able to deal with two 3D images (one with structural data only, one with additional bright spots where the CURRY results are).

7.1.10 Localize

These options are used in conjunction with the Localize display.

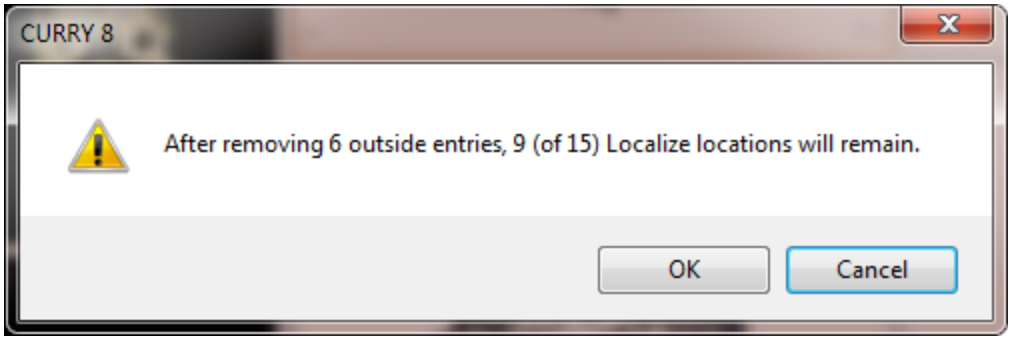


Undo. Undo last step or entry.

Delete Entry. Click this to delete the most recent entry in the list. Delete Entry is grayed out in Append Mode; deselect Append Mode to access Delete Entry.

Delete All Entries. All entries in the list will be deleted.

Delete All Outside Segmentation Result. If localize positions exist outside of the segmentation result, you may delete these. A message will appear telling you how many such positions were detected.



Delete All Outside Head Model. Locations outside of the head model will be deleted.

Move Halfway Towards Previous. When digitizing grid electrodes in Localize, sometimes an electrode cannot be seen. In this case, click the next electrode instead and select Move Halfway Towards Previous. The value of the estimated position will be entered into the list.

Import Cursor Location. Use this option to set the edited point to the 3D Cursor location. This is used to fill the Localize cells with information you might wish to work on (typically, modify).

Go to Nearby Maximum and Import. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, the **3D View**, click the border of the bright area, and this functionality brings the cursor to its center (this can be applied repeatedly).

Import Electrodes. Selecting this option imports the electrode positions from the digitizer file to the Localize panel, and displays the positions on the iso-images in the Localize display. For example, if we want to modify electrode locations, we can:

1) import them
2) change them (using the Change Locations parameter panel)
3) Save and use as Digitizer File.

Import Electrode Labels. The electrode labels from the open data file will be imported in the same order as they appear in Functional Data. These labels will replace the labels in the Localize matrix.

Import Coils. Selecting this option imports the MEG coil positions from the digitizer file to the Localize panel, and displays the positions on the iso-images in the Localize display.

Import Dipoles. Selecting this option imports the dipole positions from the digitizer file to the Localize panel, and displays the positions on the iso-images in the Localize display.

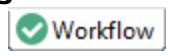
Import Image Data Landmarks. The anatomical landmarks that were determined when the image data were loaded are imported to the Localize list and displayed on the Localize images.

Import Sensor Landmarks. The sensor landmarks that are determined from digitization or other sources are imported to the Localize list and displayed on the Localize images.

Create Grid or Strip. Opens the **Create Grid** panel. To define a grid, enter its four corner points (either clockwise or counterclockwise). To define a strip, enter its first, any intermediate, and its last point. Then, call the appropriate item of this submenu. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  .

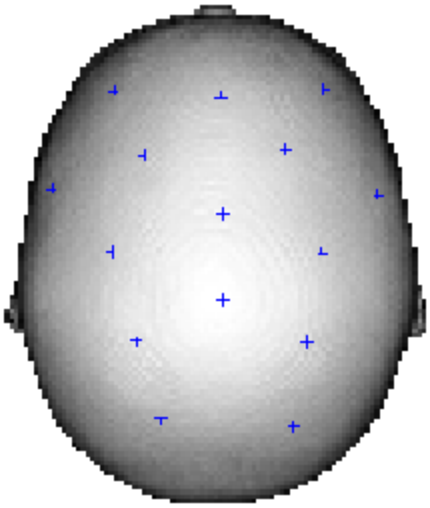
Create 10-20 System. This option is used to create the positions of the extended 10-20 system. If electrodes with recognized labels are found in the study, you may choose to create their positions only. Otherwise, the ordering and selection of the positions is based on the **NUMBER_POM_xxx** entries in the Study Parameters file, if present, or the *GlobalParameters.cfg* file. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  . Then select the new .pom file for the Digitizer File. This option uses the **Image Data** segmentation result for measuring distances along a curved surface, so a skin surface (e.g., the **Skin overlay**) should typically have been imported first.

Project All to Nearby Maxima. Projects the locations onto the nearby maxima. Maxima are the centers-of-gravity of the spherical volumes around the **Localize** locations. A radius of 5mm is used.

Project All to Segmentation Result. This option projects the locations onto the **Image Data** segmentation result, radially towards its center-of-mass. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  and select the option from the  window. This option uses the **Image Data** segmentation result for projection, so a skin surface (e.g. the **Skin overlay**) should typically have been imported first.

Normals from Segmentation Result. The normals (nx, ny, nz) are replaced with those from the segmentation results (assuming locations were projected onto the segmentation result, but not actually changing the locations).

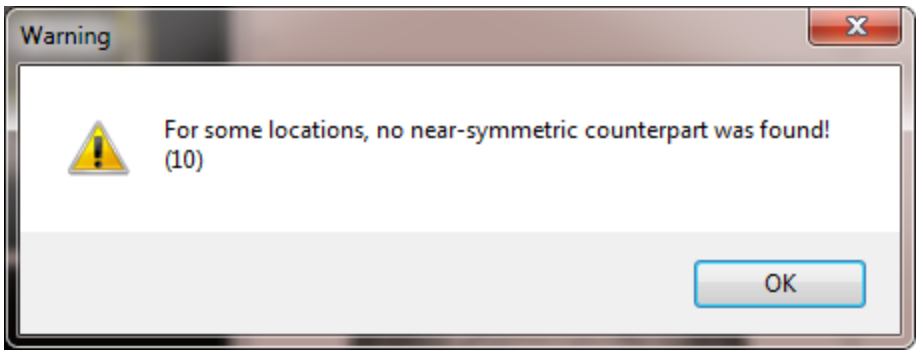
Make Locations Symmetric. This option is used when creating a standardized location file that will be used with multiple subjects. In that case, you will likely want the positions to be symmetrically located. In **Localize**, click to create the positions as closely as possible.

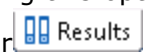


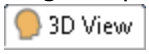
Append Orthogonal Entries. In some cases, you have a location/orientation, and you wish to have (actually, or in addition) representations of the other two orthogonal orientations. This is typically used for dipole simulations, for example, when (for MEG simulations) tangential sources are of interest.

Then click **Make Locations Symmetric**. This will make the homologous positions symmetric, and move the midline electrodes to the exact midline. Normals are not adjusted. A given electrode and its counterpart position must be within 10mm to be recognized as homologous. The new positions given to both will be the average of the two. Midline electrodes must be with 5mm of the midline to be recognized as midline electrodes. You may see a message such as the following that will tell you how many locations did not fall within the location criteria, and therefore not made symmetric (the lowermost pair above is an example). Move one of the positions manually by selecting the 

option under **Localize**, and click **Make Locations Symmetric** again.



Create Points. Points can be used to backup or individually display several sets of Localize locations. Clicking this option will create a new entry in the Points list in the **Properties** panel (under 

), containing the point locations in the list. It will also create an entry under **Objects** in the 

options. Enabling it will display the locations as small 3D stars in the 3D Display. In the **Points x properties**, you can change the Color, Size, Shape and Transparency.

Save As. Saves the locations to a .pom file. This has the same function as the  icon at the top of the **Localize** panel.

Save and Use as Digitizer File. This uses the entered locations as sensor (electrode) positions and modifies the current study. This has the same function as the  icon at the top of the **Localize** panel.

Save and Use as Image Data Landmarks. This allows you to change image data's NAS, PAL, PAR landmarks based on what you have in Localize. Three locations with these labels must exist for the button to work. Other locations are ignored. This is used in cases where, for example, a digitized skin (including landmarks) is moved around in Localize, and these landmarks shall finally be used. (Note that the Load button, when Files of type is set to All Files, will let you select the 3dd and 4D (BTI) hs_file formats).

Create and Edit Anatomical Localization. Selecting this option prepares an anatomical localization file for editing or opens an existing one for review. Labels from the digitizer file are used. If the landmarks cannot be created automatically, you will need to identify them individually. After selecting the option, a Save As utility will appear, allowing you to specify the folder and file name (.pom extension).

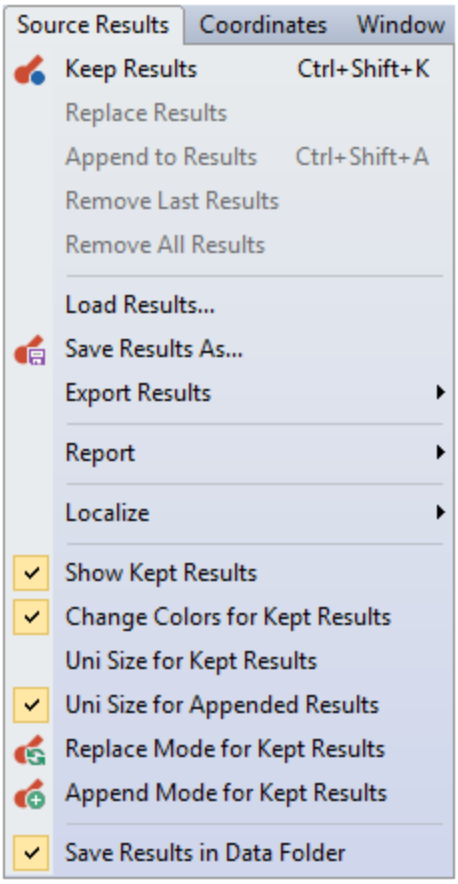
Save and Use Anatomical Localization. This uses the entered locations as anatomical landmarks (.pom file is saved) and modifies the current study.

Export to Excel. Localize points may be exported to Excel (.csv files).

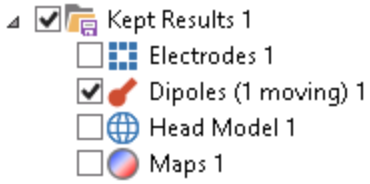
Export to MATLAB. Localize points may be exported to MATLAB (.mat files).

7.1.11 Source Results

The Source Results options are accessible after you have performed source reconstruction, and allow you to keep, save, load, export,etc. the results.



Keep Results  . The current results will be seen as a new set of display items (labeled Kept Results x). It is also accessed by the  icon on the Source Reconstruction Toolbar (or *Ctrl+Shift+K*).



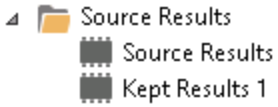
Replace Results. When selected, the last Kept Results will be replaced with the latest results.

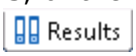
Append to Results. When using continuous data files, where there are multiple source results that are Kept, use this option to save the results to a single Kept Result.

Remove Last Results. When selected, the last Kept Results will be removed.

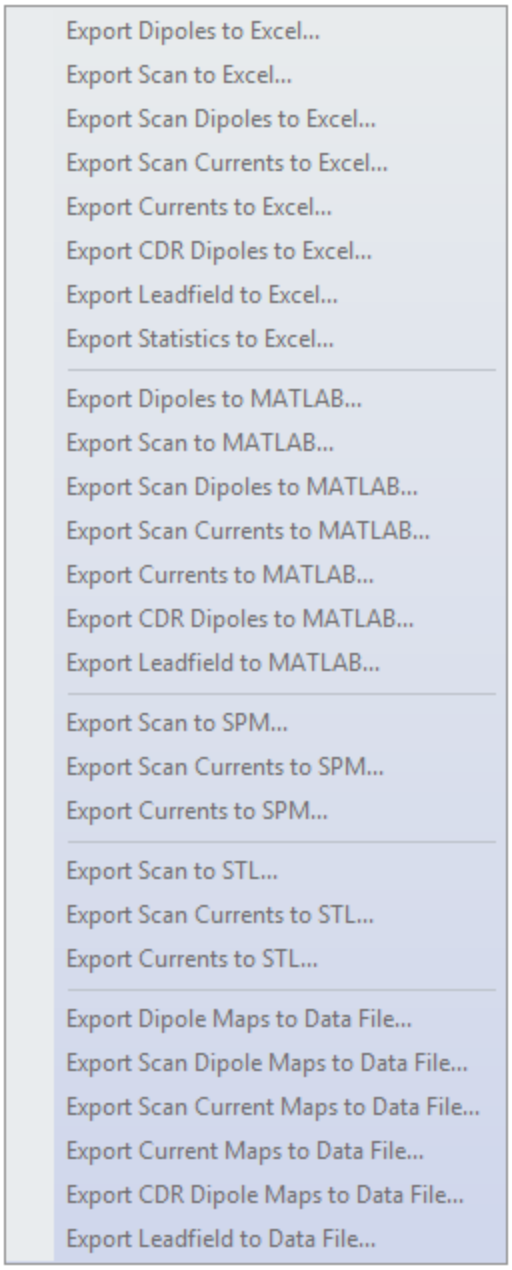
Remove All Results. All Kept Results will be removed.

Load Results. This option allows you to load previously saved results. The results will appear under the Source Results folder in the **Results** panel.



Save Results As  . Use this option to save results files. It has the same function as **File** → **Results** → **Save Results As**, or the  button when Results are selected in the **Result Properties** panel under  . The option is also accessed from the  icon on the **Standard** Toolbar.

Export Results. The source reconstruction and statistics results may be exported to Excel, MATLAB, or SPM, as shown.



If you export the CDR results, for example, to Excel, you will see a large matrix with the time points for the columns and several variables for the rows, including the following:

Residual Deviation (normalized),
Residual Deviation (original),
Explained Variance (normalized), and
Explained Variance (original).

Residual Deviation is rDev = 1 - [goodness of fit].

The explained variance is eVar = 1 - rDev * rDev, so for 10% rDev (=90% explained field), this gives 99% explained variance. Since 99% is closer to 100% than 10% is to 0%, the latter is sometimes preferred, although both are exported.

The difference between (normalized) and (original) is due to the SNR transformation: If performed channelwise (user-defined time range), each channel is "multiplied" by it's individual SNR, thus downweighting noisy channels. Fit algorithms are applied in SNR (normalized) space, resulting in Residual Deviation (normalized) or Explained Variance (normalized). The best fitting (normalized) result is then backtransformed to "µV" (original) space. Note that in a perfect world (where all channels have the same amount of noise), normalized and original give exactly the same values. The same is true if you specify a global noise level for all channels. Typically, the difference is not that great, since one tends to switch off bad channels before performing noise estimation.

These are followed by the Strengths, Locations (XYZ coordinates), and Normals (direction information, in XYZ coordinates).

If you export dipole results to Excel, you will see similar fields:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	t [ms]	x [mm]	y [mm]	z [mm]	j [µAmm]	nx	ny	nz	ellipsoid	a [mm]	b [mm]	c [mm]	atlas	res.dev.n	res.dev.o	var.norm.	var.orig. [%]
2	0	-10.3	-9.6	1.2	4835	0.19	0.31	0.93	71.4	15.5	20.2	54.5	-	11.7	12.7	98.6	98.4
3	5	-11.8	-1.5	13	4480	0.26	0.19	0.95	29.1	12	15.9	36.6	-	12.9	13.7	98.3	98.1
4	10	-18.5	12.7	28.8	3634	0.43	0.03	0.9	13.4	10.2	12.6	25	Parahipp	15.4	15.7	97.6	97.5
5	15	-26.5	24.6	41	3226	0.65	-0.11	0.75	7.1	9.6	10.4	17.1	Lentiform	15.1	15.1	97.7	97.7
6	20	-29.9	31.1	49.4	3248	0.82	-0.18	0.54	5.2	8.9	10	13.9	Extra-Nuc	14.1	14.3	98	98

The columns of the dipole output are as follows:

a: dipole time stamp [ms]
b,c,d: dipole position [mm] (with respect to the current coordinate system)
e: dipole strength [µAmm]
f,g,h: dipole orientation (normalized vector [x, y, z])
i: volume of confidence ellipsoid [ml]
j, k, l: main axes length of confidence ellipsoid [mm]
m: atlas structure
n: residual deviation, "normalized" (i.e. taking SNR transformation into account)
o: residual deviation "original" (i.e. in µV data space)
p: variance, "normalized"
q: variance, "original"

Export <Results> to Excel. The Dipoles, Scan Dipoles, Scan Currents, Currents, CDR Dipoles, Leadfield, and Statistics results can be exported to Excel.

Export <Results> to MATLAB. The Dipoles, Scan Dipoles, Scan Currents, Currents, CDR Dipoles, and Leadfield can be exported to MATLAB.

Export <Results> to SPM. Scans, Scan Currents and Currents can be exported to SPM as 3D images. For Currents, the intensities represent the strengths of the CDR. If there are many samples, one 3-dimensional image is saved per sample. In the **SPM Timeseries File** option (**Save as type**), a file containing a 4-dimansional image is created. The fourth dimension is time. In the **SPM Timeseries Folder**

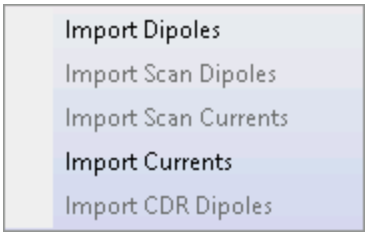
option, one image per sample is created. **Statistical Parametric Mapping** (SPM) is third-party software for the construction and assessment of spatially extended statistical processes used to test hypotheses about functional imaging data.

Export <Results> to STL. STL is the file format used for 3D printing. There are several variations of this file format, which can be selected from the drop-down list.

Export <Results> to Data File. Source results contain forward calculated ("explained") data, which can also be shown in Maps. This option will create a CURRY-format data file that contains, as data, the forward calculated maps.

Report. The source reconstruction results may be appended to the Report.

Localize. The selected source reconstruction results may be imported to the Localize display.



Show Kept Results. If enabled, the Kept Results will be displayed automatically. If disabled, the checkmark for Kept Results will be off.

Change Colors for Kept Results. When enabled, the Kept Results will automatically be assigned a new color to better distinguish them (which can be changed in its Properties).

Uni Size for Kept Results. This option is typically used when doing Dipole Clusters. When enabled, the Kept Results all have the same size dipoles.

Uni Size for Appended Results. This option is typically used when doing Dipole Clusters. When enabled, the Appended Results all have the same size dipoles.

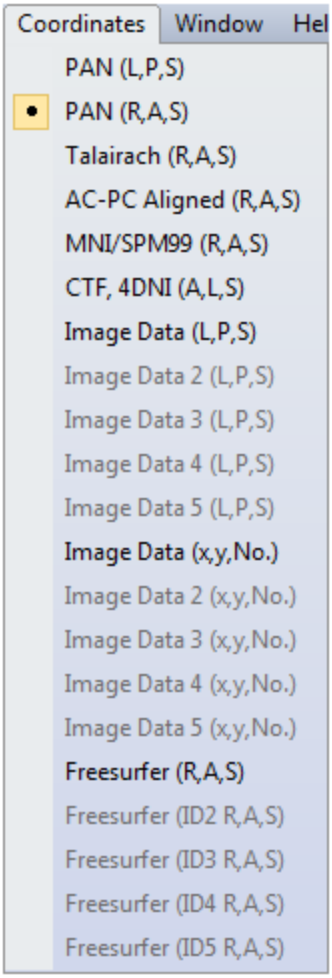
Replace Mode for Kept Results  . The most recent results will *replace* the existing Kept Results.

Append Mode for Kept Results  . The most recent results will be *appended to* the existing Kept Results.

Save Results in Data Folder. When enabled, the Results will be saved in the Data Folder (where the data file came from).

7.1.12 Coordinates

The Coordinates options are used to select various coordinate systems (L - Left, R - Right, A- Anterior, P - Posterior, S - Superior). (See also the **Coordinates** description in the **Results** panel under **Results**).



PAN (L,P,S). This is CURRY's Internal Coordinate system, with the x axis going through PAL and PAR and pointing left, the y axis extending through the back of the head (on a line with the nasion site), and the z axis pointing upward.

PAN (R,A,S). The x axis goes through PAL and PAR and points right, the y axis goes through the nasion, and the z axis points up.

Talairach (R,A,S). Uses the Talairach atlas coordinate system. AC is the origin, the y axis points anterior and goes through AC and PC. The x,y plane is defined by AC, PC, and MS, and the x axis points to the right. All readings are scaled to match the atlas, based on the extensions of the brain as specified in the **Image Data Parameters** windows.

AC-PC Aligned (R,A,S). Used to be called Talairach [mm]. The origin is AC. y axis goes through PC and points anterior. x axis points right. z axis points up. Axes are **not** normalized according to brain dimensions.

MNI/SPM99 (R,A,S). Uses the Montreal Neurological Institute / Statistical Parametric Mapping (99) coordinates. The x axis points right, the y axis points anterior, and the z axis point upward.

CTF, 4DNI (A,L,S). Uses the coordinate definition from the CTF MEG software. The x axis extends through the nasion, the origin is halfway between PAL and PAR, and the x,y plane is defined by PAL, PAR, and Nasion. The z axis points upward.

Image Data (L,P,S). The axes are aligned with the raw image data slices. Axes point approximately in the left (X), back (Y), and up (Z) directions.

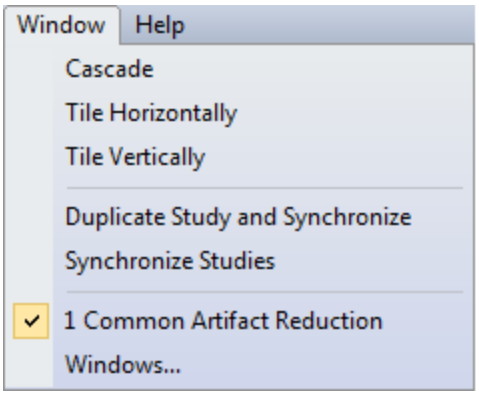
Image Data 2 (L,P,S) through **Image Data 5 (L,P,S)**. These options allow you to select among the Image Data sets you have loaded (up to 5).

Image Data (x,y,No.) through **Image Data 5 (x,y,No.)**. x and y are in-slice coordinates and No. is the slice number. These options are useful if the results need to be placed in relation to the original MRI slices.

Freesurfer (R,A,S) through **Freesurfer (ID5 R,A,S)**. CURRY 8 (in Results) allows you to load Freesurfer-created segmentation results (triangle meshes) such as lh.pial or rh.pial (these are their typical file names), and automatically co-register them into CURRY's coordinate system. An external tool plus some manual editing of files need to be used to achieve the same goal in the context of CURRY 7. In order to offer this new functionality, the co-registration between Freesurfer image data, Freesurfer triangle mesh data, and CURRY coordinates needs to be known. This is enabled by automatically detecting all required co-registration parameters when loading a Freesurfer T1.mgh or T1.mgz image data file (these are their typical file names). As a byproduct of and in order to verify the just described capability, CURRY 8 can output results in Freesurfer coordinates, where x points towards the right, y points anteriorly, and z points up.

7.1.13 Window

The Window option functions primarily the same as with any Windows application, with the exception of New Window.



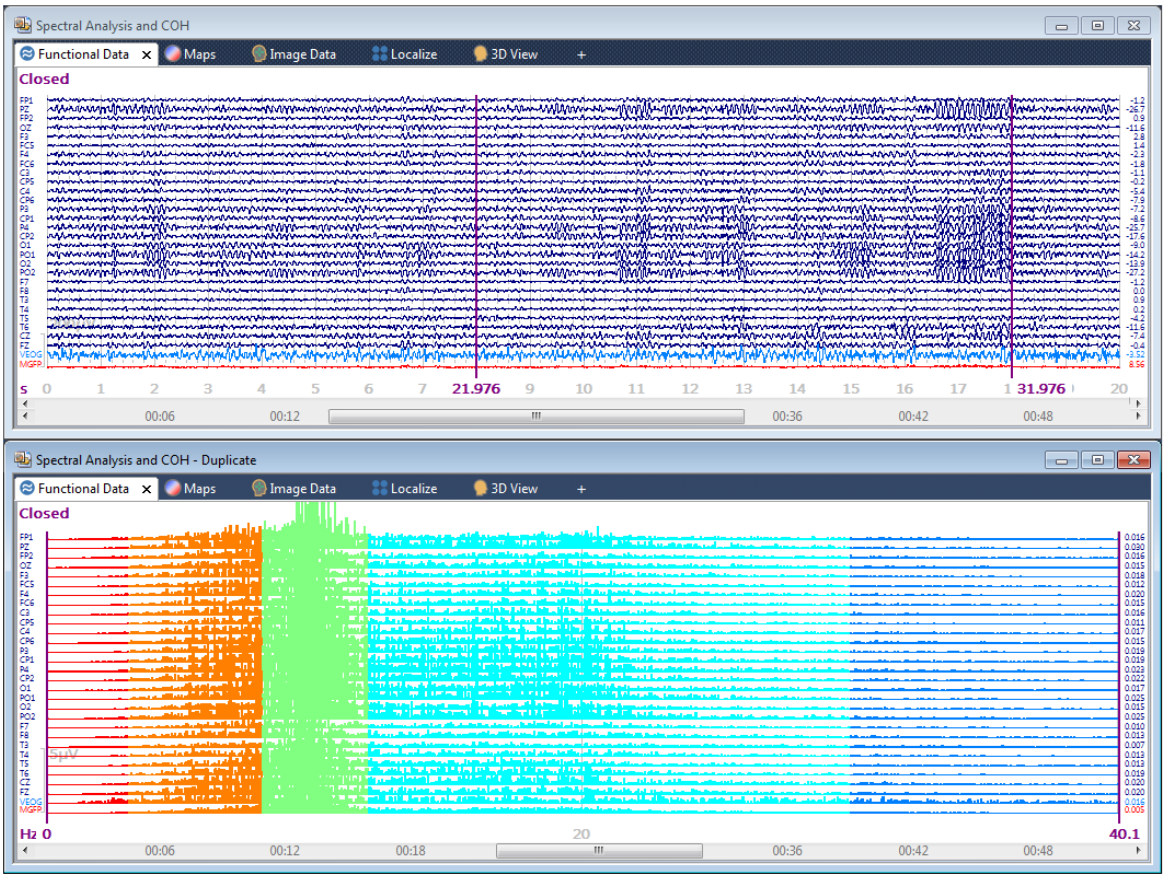
Cascade. Standard Windows option for cascading multiple windows.

Tile Horizontal. Standard Windows option for Tiling multiple windows (Horizontal Tile). The tiling options may be needed if you resize the total CURRY display.

Tile Vertical. Standard Windows option for Tiling multiple windows (Vertical Tile). The tiling options may be needed if you resize the total CURRY display.

Duplicate Study and Synchronize. If you have one continuous data file open and select this option, a second Unfiled study will be created with the same file in it. As with Synchronize Studies, moving either time slider will move both of them. You can also change the number of seconds being displayed between synchronized studies. You can, for example, select fewer seconds displayed and then select Spectra to display the FFT results on a section of the continuous data displayed in the other window.

For example, 10s are displayed in the upper window, and 2s was selected in the lower window. Note the difference in the sizes of the sliders below the data displays. The 2s in the lower window correspond to the interval between the cursors in the upper window. This lets you focus the FFT on selected sections of the upper display.

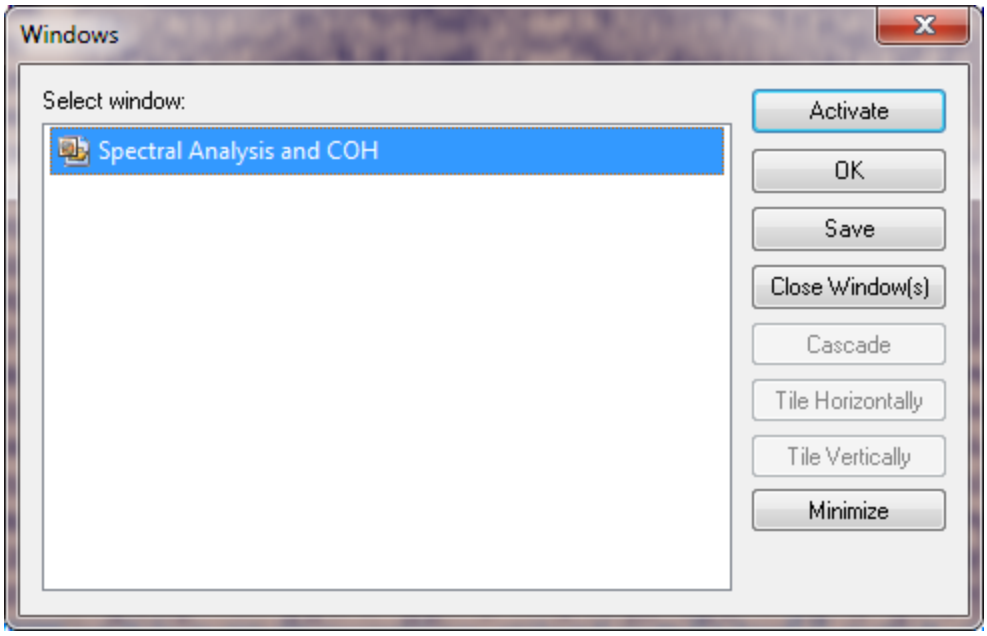


If you create in-place averages for both files, the cursors will be synchronized. If you look at Image Data for both files, the cursors will be synchronized.

Synchronize Studies. If you have two Studies open, each with like continuous data files (or the same file), you may synchronize the files so that the files will track together as you navigate through them. This option is also useful in comparing the same file before and after artifact correction, for example. See **Duplicate Study and Synchronize**.

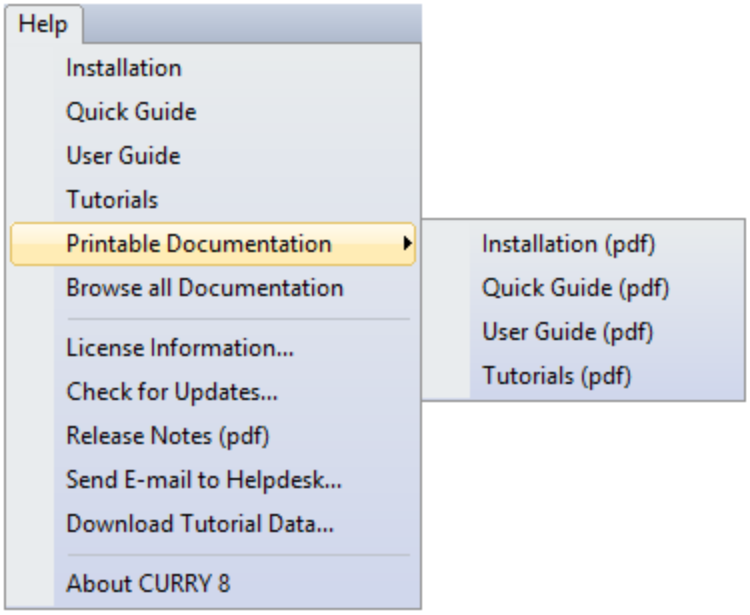
Open Study List. If you have Studies open, they will appear in the list and you may switch among them by selecting the Study.

Windows. A list of open Studies is shown. Click the **Windows** item to see the displayed screen. Highlight a Study and you have access to the options shown on the right side of the display.



7.1.14 Help

Selecting the Help option displays the following list of options.



Installation. Clicking this displays the CURRY *Installation* manual in CHM format (Compiled Help Manual), which contains information for installing the software as well as the amplifiers.

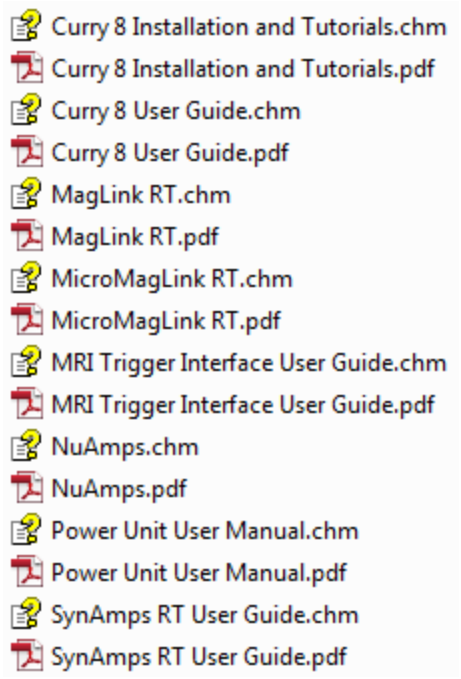
Quick Guide. The *Quick Guide* provides an overview introduction to CURRY (in CHM format), as well as an easy, step-by-step guide to get you started quickly.

User Guide. This displays the *CURRY User Guide* manual in CHM format. Context sensitive Help is available throughout CURRY. Position the mouse over a parameter panel, for example, and press the *F1* key. The *User Guide* will open to that section.

Tutorials. This displays the *CURRY Tutorials* manual in CHM format. The *User Guide* contains the details for all of the functionality in CURRY; the *Tutorials* illustrate how to combine the options to achieve a desired outcome.

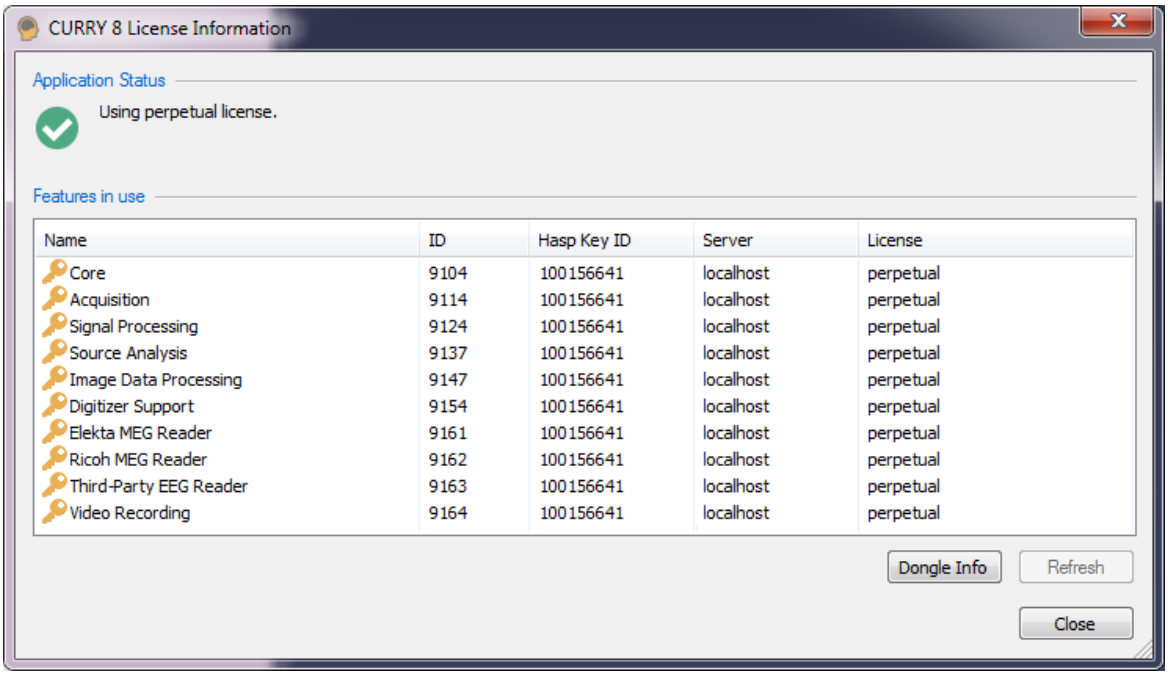
Printable Documentation. Accesses the above documents in PDF format for printing purposes.

Browse all Documentation. Click this to access other files related to CURRY 8, including MagLink RT and the Neuroscan amplifiers.



Release Notes. Accesses the Release Notes.

License Information. This displays the licenses and license information you have on your hasp dongle. If you have multiple licenses that can be detected by a computer on a network, click this option to display the CURRY License Server Selection window. All detected licenses will be displayed. Select the one that you wish to access.

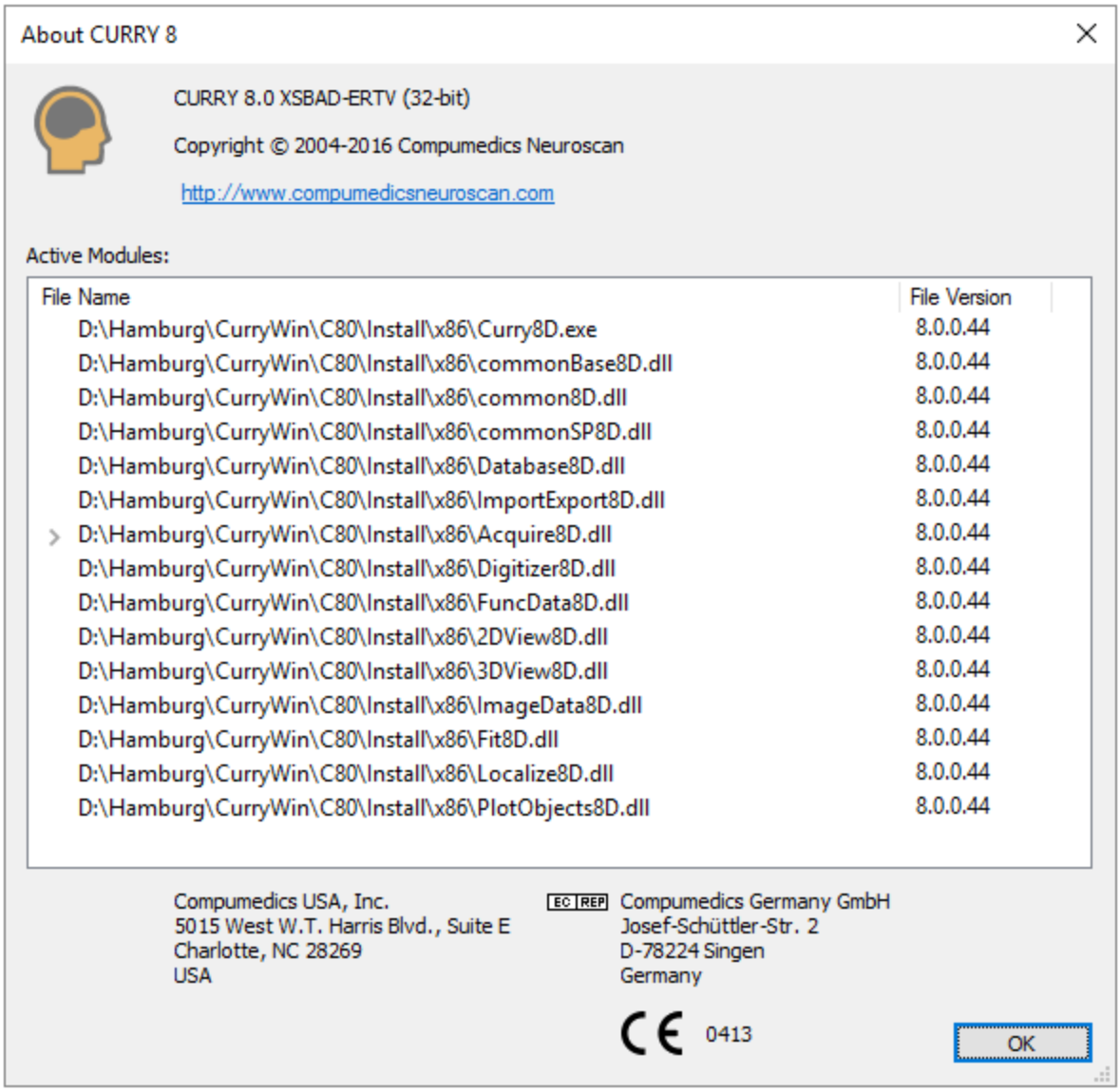


Check for Updates. Select this option to go to the web site to search for updated versions.

Send E-mail to Helpdesk. Selecting this option will transfer to your e-mail software whatever part of the display has the focus, and prepare to send the e-mail to the CURRY 8 Helpdesk. An additional file is attached that contains information about the CURRY version you are using, graphic card information, etc. (for diagnostic purposes). Add whatever explanatory text or questions you have, and send the e-mail. If CURRY crashes or if you have found an apparent bug, please include a list of steps to permit replication (using the CURRY example data files, if possible).

Download Tutorial Data. Use this option to download the data files needed for the *CURRY Tutorials*. Run the .exe file, extracting the files to the default *C:* location.

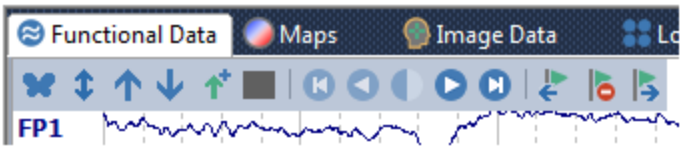
About. This option displays copyright and version information about CURRY. The Active Modules window displays the application modules CURRY is using. You may be directed to this information by Technical Support to resolve version related questions.



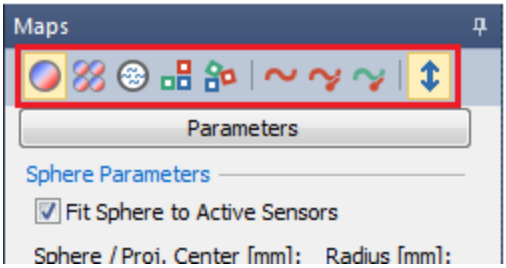
7.2 Toolbars

All of the options contained on the Toolbars can also be found in the menu lists. The Toolbar icons are shortcuts for the more frequently used menu options. There are the Standard Toolbar icons that are seen at the top of the display. You may not see all of the icons in all of the subsequent Toolbars. What you see depends on the licenses you have.

There are also the Toolbars that appear with each data display window. Position the mouse in the upper left area to display the Toolbar.



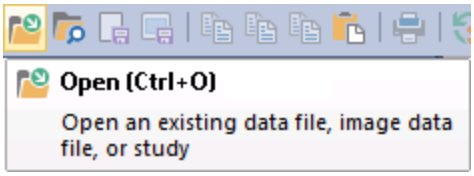
Toolbars are also seen at the top of some of the Parameter Dialogs.



7.2.1 Standard Toolbar

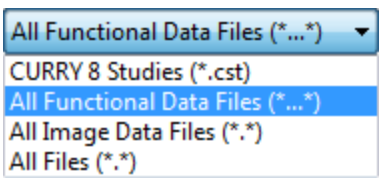
The **Standard** Toolbar consists of the following icon buttons:

Position the mouse cursor over an icon, and a Tooltip will display its name. If you do not see the Tooltips, go to **View** → **Show Tooltips** and enable the option.



New  (*Ctrl+N*). Clicking this option adds a new "Unfiled" study to the Database, and accesses the Acquisition part of CURRY (assuming you have an acquisition license). The icon will be slightly different if you do not. You have the opportunity to save all Unfiled Studies (automatically) when closing CURRY - this can be configured in **Edit** → **Options**.

Open File  (*Ctrl+O*). The **Open File** option allows you to select any of the displayed types of files: Databases, studies, and data files or folders. CURRY will place the file in a new Unfiled Study.



Open File Folder  . Open an existing image data folder.

Open File Location  . Selecting this option opens the Windows Explorer program to the folder containing the files in the selected Study.

Save Study Parameters  . This is the same as **File** → **Parameters** → **Save Study Parameters**. Various parameters can be saved as the study parameters, thereby avoiding having to enter the same settings each time you open the study. The settings are saved to a .cfg file, which will then appear in the Database under the Results folder. If the .cfg file is already present and you click the Save Study Parameters button, the .cfg will be overwritten with the new settings. See the **Global, Study and Other Parameters** section for more details.

Save Results As  . Source reconstruction results can be saved 

.

Copy Data Display to Clipboard  (*Ctrl+Shift+C*). The entire data display window(s) will be copied to the Windows Clipboard as a .bmp image. You may then paste it into another Windows application.

Append Data Display To Report  . The data display will be copied directly to the Report (select 

to see it). The same option is found on the **Report** Toolbar.

Append Clipboard To Report  . The content of the Windows Clipboard will be pasted to the Report (select 

to see it). The same option is found on the **Report** Toolbar.

Print  (*Ctrl+P*). Standard **Print** option. The data display will be seen in the Windows Picture and Fax Viewer, from where it may be printed.

Keep Results  . The current source results will be seen as a new set of display items (labeled Kept Results x).

UI Update  *(Ctrl+Shift+U)*. This is the same option as found on the Macro toolbar. Clicking it will update the macro to reflect modifications you have made during the recording.

Show Movie  (*Alt+M*). With Moving dipoles, and when in Movie Mode, selecting this option will play a Movie (sequential display of each dipole throughout the Timerange). Movies may be played in the Maps, 3D View, and Image Data displays.

Help  . Accesses the manuals and additional information.

7.2.2 Acquisition Toolbar

Acquire Online. These options are used when configuring the system and acquiring EEG data,  and  . More complete descriptions of these options are found in the sections under **Acquisition**.

Configure Amplifier  . Accesses the amplifier configuration dialogs (see **Configuration Options** below).

Video Camera  . This option will show or hide the video camera window.

Connect  . Connect to the selected amplifier.

Check Impedances  . Click this option to view the impedance display.

 **Care**

*Impedance tests should only be performed with surface EEG, and never if you are recording from cortical grid or depth EEG electrodes. There is an option in the Configure Amplifiers section to disable impedance tests (**Allow Impedance Test**), which is intended for use with grid and depth recordings.*

Record  . Click the Record button to start saving the data to the hard drive.

Stop  . Disconnect from the amplifier (or stop Impedance or stop Recording, and then disconnect).

Edit Comments  . Add text comments that will be stored with the data file.

Select Average  . Used with online averages to select another average to Overlay or take the Difference. (See **Select Average**).

Pause  . Pause display. In an **Average** view this will pause adding epochs to the average.

Restart Average  . Clear average and set epoch counter to zero.

Baseline correction  . Centers traces in their display space (removes DC offsets from the display). Recorded data are not affected.

Butterfly Plot  . Superimposes all channels.

Autoscale  . Autoscales the display of all traces (data are not affected).

Scale Waveforms Up or Down  . Rescales the waveforms (display only).

Position Plot  . Displays channels in separate windows about the head.

Send Page to Functional Data  . Sends the displayed page to Functional Data for further online processing.

7.2.3 Digitizer Toolbar

The Digitizer toolbar contains the following icon buttons  . For more details, see the **Digitizer** section below.

Connect to Digitizer  . Initiate digitization.

Stop Digitizer  . Stop digitization.

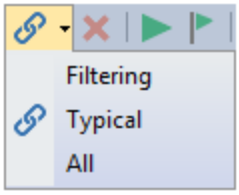
Load positions from file (pom)  . Select an existing .pom file.

Save Positions  . Save the XYZ position information in a file with a .pom extension.

7.2.4 Functional Data Toolbar

The **Functional Data** Toolbars relate to the Functional Data display, and consists of the following icon buttons (see the **Functional Data** section below for more information). The Toolbars are found at the top of the Functional Data parameter panels and in the upper left corner of the Functional Data Display.

Processing Sequences  . Clicking these options will display different sets of parameter panels. This is purely a convenience option. If you click the **Typical** sequence, you will see the same set of parameter panels that was present in CURRY 7. The other options will display fewer or all panels.



Delete Processing Sequence  . Click this option to remove any processing sequence you have selected.

Scan Artifacts/Templates  . This option is used to scan the data file after you have configured the artifact reduction screen(s) or configured a template.

Open Events

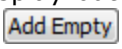
. This is a shortcut convenience option to open the 

display.

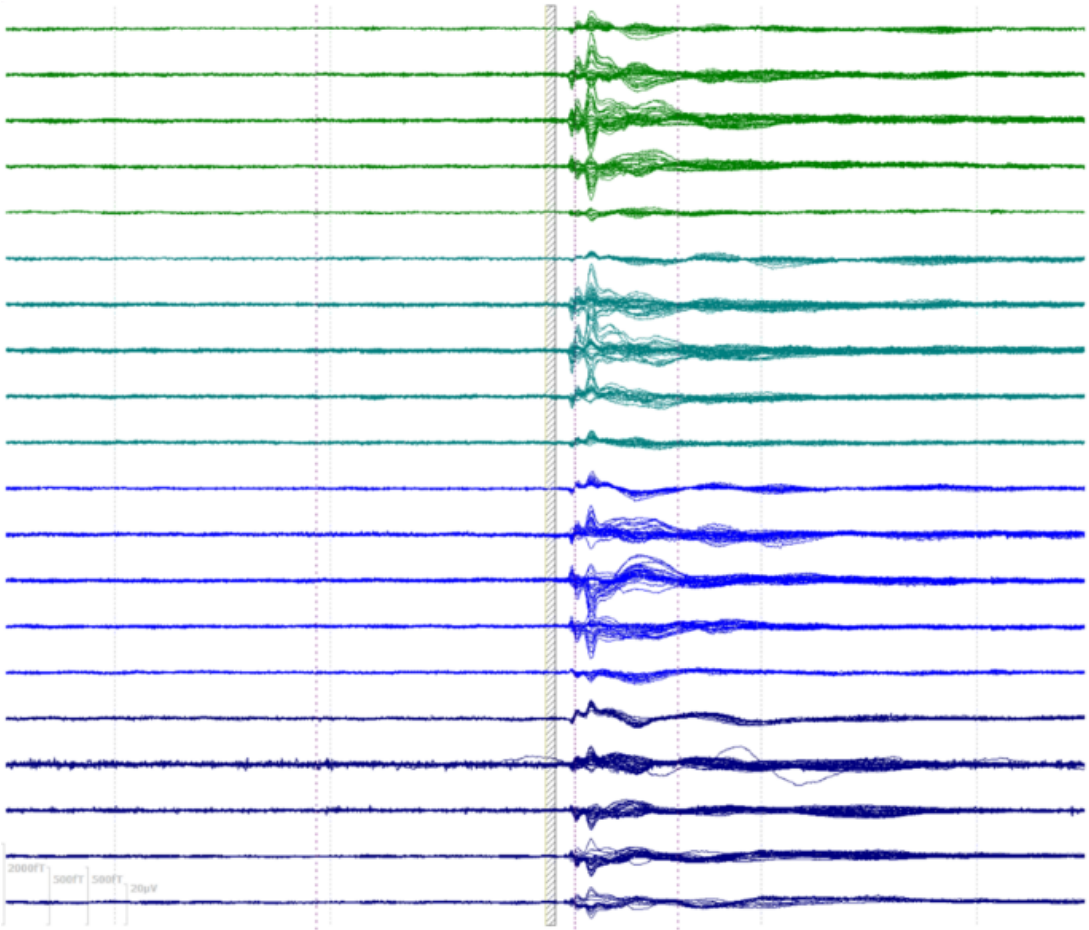
Data Parameters  . Opens the **Functional Data Import Wizard**.

Montage Editor  . Provides access to the Montage Editor (described below in the **Options** section).

Video Camera  . This option will show or hide the video camera window.

Butterfly Plot  (*Alt+B*). Toggles the Butterfly Plot display on and off. Enabling this option superimposes all channels. If you have multiple Channel Groups (EEG and MEG, or multiple groups of either), clicking Butterfly Plot will display butterfly plots for each channel group. In the Montage Editor, you can click the 

button to add a blank space between subgroups of sensors. When you select the Butterfly Plot, you will see butterfly plots for each of the subgroups. In the figure below, there are 4 Channel Groups, and each one has five subgroups of sensors. Butterfly Plots are created for each.



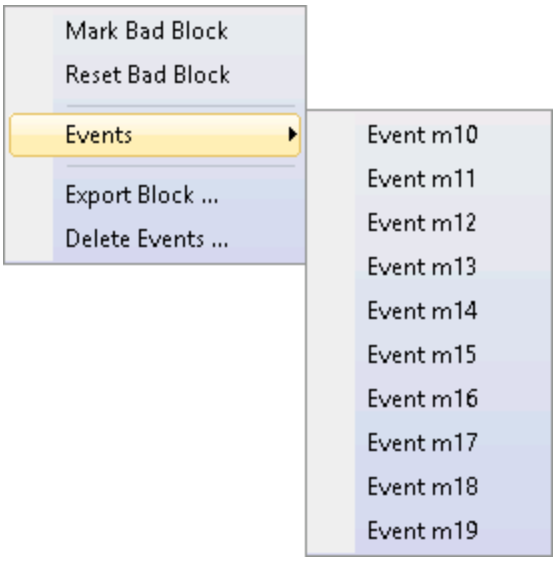
Autoscale (*Alt+S*). Autoscales the display of the functional data.

Scale up. Increases the waveform size.

Scale down. Decreases the waveform size.

Plus is up. Inverts polarity so positive is up.

Mark Blocks. Mark blocks or Timeranges by selecting the option then clicking the left mouse button once for the beginning and end of the block, or click once and drag to the end of the block. The duration of a block may extend beyond the time span that is displayed. The following options will be seen when the block has been defined.

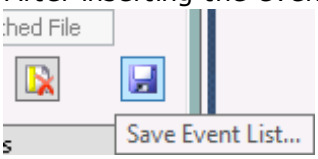


Mark Bad Block. Bad Blocks will be excluded from subsequent analyses. After marking the Bad Blocks, when you close the Study you will be asked if you want to save the changes to the file, namely, the bad blocks. If you say **Yes**, these will be saved to the .dap parameter file. If at a later time you want to remove the bad blocks, click the Reset button to reset all manually selected bad blocks, or use the next option for individual blocks.

The Bad Blocks are seen as shaded regions in the event line.

Ctrl+Alt+mouse drag can be used to create Bad Blocks more efficiently.

Reset Bad Block. Converts Bad Blocks back to unmarked blocks.

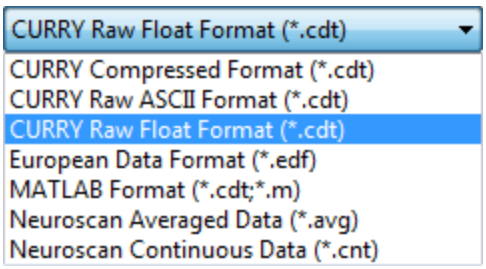
Event m10 - Event m19. These are special purpose events that include the durations of the blocks. You may also use the number keys on the keyboard to select the event to be inserted (1 = Event m10, etc.). After inserting the events, you may save the new .cef file using **Save Event List** 

at the bottom of the **Events/Epochs** display. The durations will be contained in the .cef file.

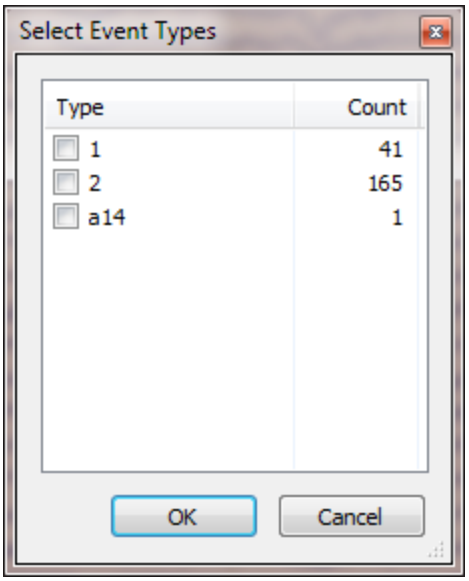
Export Block. CURRY can export data either in the Raw ASCII format, as in prior versions, or in the Compressed format, which will save disk space. There is no loss of data with the compression. Compressed data is compatible with CURRY 7 (CURRY 7 reads compressed files, but does not write them). This is an issue when reading compressed files into MATLAB, since the script CURRY uses does not recognize to more complex compressed format. In that case, use the Raw Float format. If you have already recorded the data using compression, resave the file where you

select Raw Float in the Save As dialog. Generally, compressed files are recommended due to the smaller file sizes.

The functional data may be exported as a Neuroscan Continuous Data or Neuroscan Averaged Data file. In general, the CURRY file types may have speed advantages over the Neuroscan file types; use the Neuroscan file types if you are planning to open the files in the Scan software. EEG data (not MEG data) may be saved in EDF files (European Data Format).

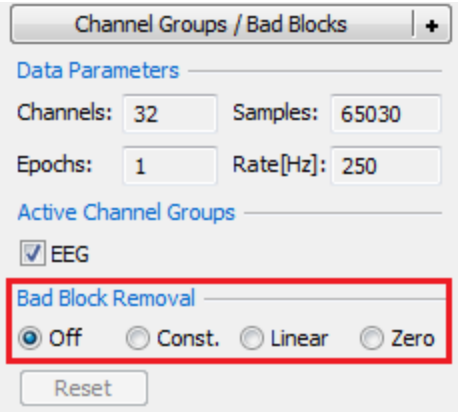


Delete Events. Delete selected events within the block.



See also the **Bad Blocks** section under 

(Functional Data parameters).



Off. No action is performed.

Constant. Flat lines (zero slope) connect the last data point before the bad block to the first data point after the block.

Linear. Sloping lines will connect the last data point before the bad block to the first data point after the block.

Zero. Zero will set the data samples within the Bad Blocks to 0Vs.

First Page/Epoch , **Last Page/Epoch** . Moves to the First or Last Page (continuous data files) or Epoch (epoched data files).

Previous Page/Epoch , **Next Page/Epoch** . Moves to the Previous or Next Page (continuous data files) or Epoch (epoched data files).

Toggle Epoch . Toggles the Accept or Reject state of the current epoch.

Previous Event , **Next Event** . Move to the Previous or Next Event (in continuous data files where events have been detected).

Erase Event (*Ctrl+E*). Removes the event from the continuous data file.

7.2.5 Maps Toolbar

The **Maps** Toolbar contains frequently used options in Mapping, PCA, and ICA (see the **Maps** **Parameters** section below for details). Position Plot, PCA, ICA, MGFP, Dipole Strengths, and Residual Deviation are only possible if a Timerange is selected (not possible for a single timepoint).

Contour Map (*Alt+C*). Displays a single contour map corresponding to the position of the middle cursor in the Functional Data display. If you are in **Tracking Mode** (Functional Data context menu) and you select Contour Map, the three

separate cursors will be replaced with a single cursor (actually the three cursors are superimposed), and you will seen a single contour map for that time point.

Thumbnails (*Alt+T*). Enables the Thumbnails display (the number of thumbnails is set in the Parameters panel under **Maps**.

Position Plot (*Alt+P*). Enables the Position Plot display.

PCA (*Ctrl+A*). Select PCA analysis.

ICA (*Ctrl+I*). Select ICA analysis.

MGFP (*Alt+G*). Enable Mean Global Field Power display.

Dipole Strengths (*Alt+D*). Enable Dipole Strengths display.

Residual Deviation (*Alt+R*). Enable Residual Deviation display.

Autoscale (*Alt+A*). Autoscale Map contours (you can also use the *mouse wheel* for rescaling).

7.2.6 Image Data / Localize Toolbars

The **Image Data** and **Localize** Toolbars have many icons in common, and are therefore combined.

The **Image Data** Toolbar relates to the Image Data display only, and consists of the following icons. The first row is seen in any of the three image data views. After that are the options seen in the fourth rendered view.

Seedpoint Segmentation (*Ctrl+Shift+S*). Initiates seedpoint segmentation (same as the Start button in the **Segmentation** panel, when **Region Growing** is selected).

Threshold Segmentation (*Ctrl+Shift+T*). Initiates threshold segmentation (same as the Start button in the **Segmentation** panel, when **Thresholding** is selected).

Clear Segmentation Result. Clears the segmentation result from the Image Data and 3D View displays.

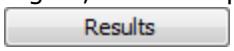
Add Exterior to Stop Markers  . Stop Markers are added to the exterior of the segmented region(s).

Add Exterior to Pass Markers  . Pass Markers are added to the exterior of the segmented region(s).

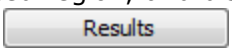
Add Segmentation Result to Stop Markers  . Stop Markers are added to the segmented region(s).

Add Segmentation Result to Pass Markers  . Pass Markers are added to the segmented region(s).

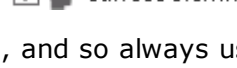
Clear Markers  . Clears Stop and Pass Markers.

Create Overlay  (*Ctrl+Shift+O*). An Overlay is created from the segmented region, and is displayed in the Overlay section of the **Properties** panel under 

(with the Default **Label**).

Create Triangle Mesh  (*Ctrl+Shift+I*). A triangulated surface is created from the segmented region, and displayed in the Surfaces section of the **Properties** panel under 

, as well as in the 

panel under **3D View** 

. The Toolbar option is meant to be used to obtain a quick result, and so always uses a **3mm Resolution**. Use the 

panel options for any other parameters, and use its **Start** button to apply them.

Setup BEM Geometry  . This takes you to the BEM Geometry panel to create a BEM model using the automated routine.

Rotate 360°  . Rotate the image 360° about the z-axis.

Show Results  (*Alt+D*). The dipole results can be toggled on and off in the Image Data display.

Show Cursor  (*Alt+C*). The cross-hair cursor can be toggled on and off in the Image Data display.

Show Segmentation Result  . Toggles the display of the segmentation results.

Show Segmentation Thresholds  (*Alt+H*). Toggles on and off the display of the segmentation thresholds.

Timerange Mode  . This toggles between displaying results for a single time point and for all time points within the Timerange.

Ellipsoid Mode  . This toggles on and off the display of the Confidence Ellipsoids (the 1 SD ellipsoid volume displaying the certainty of the source results).

Go To Previous Dipole  . If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the previous dipole.

Go To Next Dipole  . If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the next dipole.

Position the mouse near the top left corner of the MRI film strip in the **Localize** display, or any of the **Localize** panes, and you will see the following Toolbar icons. These are described just above, with the exception of the Views below.

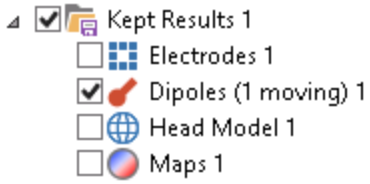
Left, Right, Top, Bottom, Front, Rear Views  . Select one of the standard viewing perspectives.

Custom Views  . Custom views are those intermediate perspectives that you wish to use repeatedly. You may define and retrieve up to 4 Custom Views (using the options under **View** on the **Main Menu** bar). The **Define**  options set the current orientation (size, perspective, etc.) of the display as Custom View. Click one of the **Custom View**  options to retrieve the custom view you had set. The icons displayed here access the first two Custom Views.

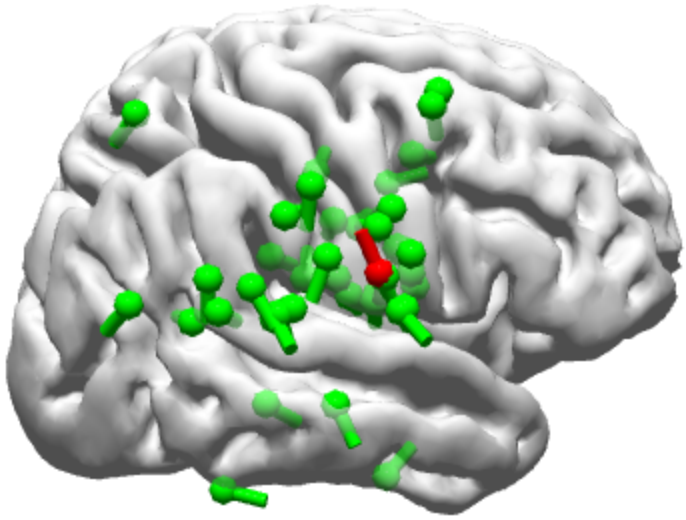
7.2.7 Source Reconstruction Toolbar

There are various Toolbar icons  at the top of the **Source Reconstruction** panel.

Keep Results  . The current results will be seen as a new set of display items (labeled Kept Results x).



Dipole Cluster  . This option lets you calculate and superimpose source reconstruction results from multiple epochs. It is the same functionality that was previously accessed from **Keep Source Reconstruction Results** and the Scan Epochs button, under Epochs. To use it you will need an epoched file with spikes at the same latency (usually 0 ms). Set the Timerange on the first epoch. Select a **Head Model** and **Dipole Type**. Then click the icon. See the *Template Matching and Dipoles Clusters* and *Epileptic Spike Detection and Dipole Clusters* tutorials for examples of its use.



Replace Kept Results  . The most recent results will *replace* the existing Kept Results.

Append Kept Results  . The most recent results will be *appended to* the existing Kept Results.

Pause Fit  . This is used to pause or resume source reconstruction computations.

Append Dipole Description to Report  . Append the dipole description that is seen in the Output section to the information in the Report section.

Move to Previous Dipole  . Move cursor to previous dipole.

Move to Next Dipole  **.** Move cursor to next dipole.

7.2.8 3D View Toolbar

Position the mouse in the upper left area of the 3D View display to see the 3D View Toolbar icons.

Rotate 360°  . This will rotate the 3D View display one complete cycle about the z-axis.

Left, Right, Top, Bottom, Front, Rear Views  . Select one of the standard viewing perspectives.

Custom Views  . Custom views are those intermediate perspectives that you wish to use repeatedly. You may define and retrieve up to 4 Custom Views (using the options under **View** on the **Main Menu** bar). The **Define**  options set the current orientation (size, perspective, etc.) of the display as Custom View. Click one of the **Custom View**  options to retrieve the custom view you had set. The icons displayed here access the first two Custom Views.

Timerange Mode  . This toggles between displaying results for a single time point and for all time points within the Timerange.

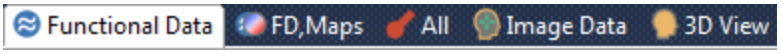
Ellipsoid Mode  . This toggles on and off the display of the Confidence Ellipsoids (the 1 SD ellipsoid volume displaying the certainty of the source results).

Go To Previous Dipole  . If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the previous dipole.

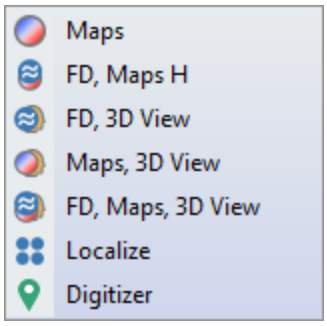
Go To Next Dipole  . If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the next dipole.

7.3 Display Screen Options

This section refers to the tabs at the top of the data display region. The tabs are used to switch among the data views, or to combine views to facilitate the operation of CURRY. Initially, you may see only a few tabs.



The one at the end will have a + sign. Click it to see the additional display options. Clicking them will add them to the display options.



For example, clicking the Functional Data tab displays the waveform data. Clicking Maps displays the 2D contours and PCA/ICA components. Clicking 3D View displays the objects in the 3D View, and so forth.

Other options show combinations of display views. For example, FD, Maps displays the Functional Data plus the Maps view. FD, Maps H displays the Functional data and the Maps in a Horizontal orientation. FD, Maps, 3D View displays the Functional Data, plus Maps, plus the 3D View display.

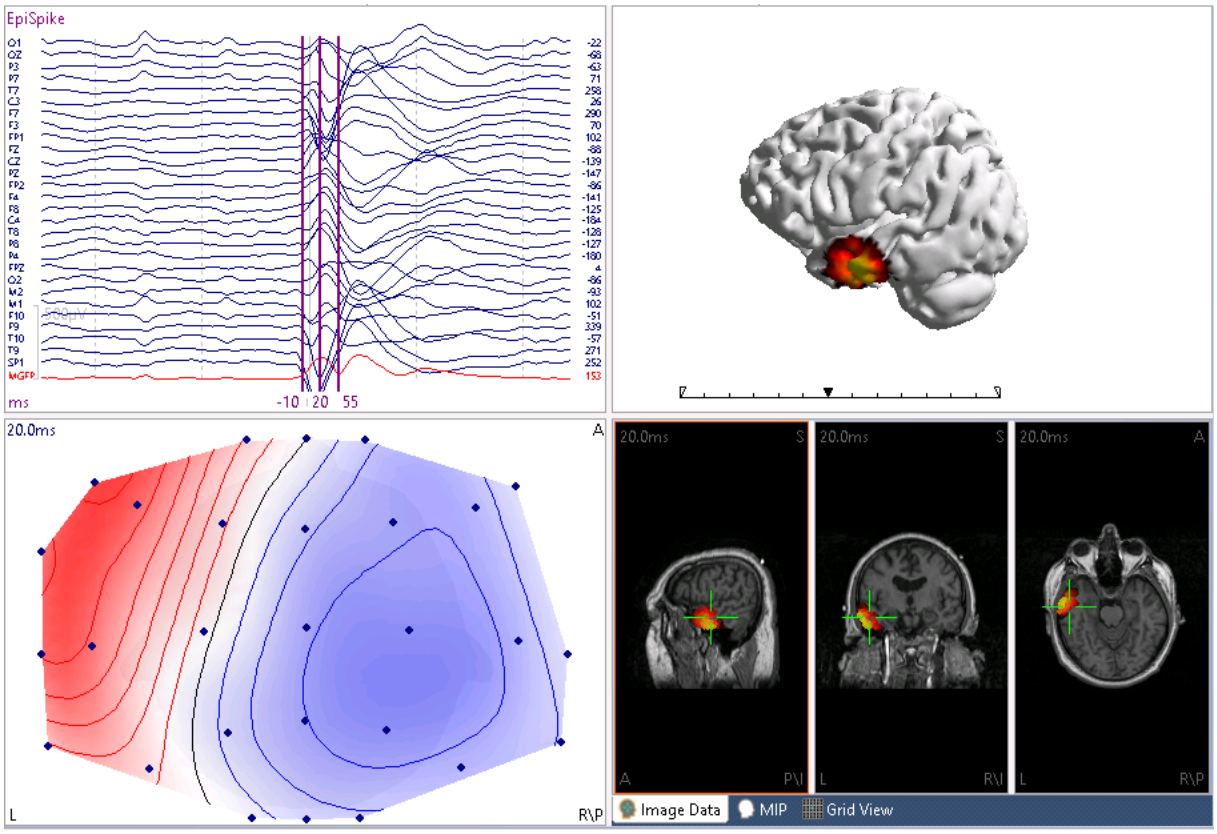
If you have loaded two MR image data sets, you will see two Image Data tabs, as well as a ID 2 tab used for displaying either or both data sets.

When you select a display tab, you will also see an option panel in expanded form. For example, when you select Functional Data, the expanded Objects panel is displayed automatically, anticipating the options that you may wish to access. Similarly, clicking the 3D View tab will display the expanded Objects panel, anticipating your desire to select the objects to be displayed, or to modify the object's properties.

There may be instances in which you wish to keep a processing panel open and change the Data Displays. For example, you might wish to keep the **Source Reconstruction** panels in view while selecting the 3D View or Image Data display. If you click on Image Data, the **Image Data 1** processing options will open automatically. You can override this by using *Ctrl+ left mouse* when clicking the Display tabs. This "disconnects" the linking of the display tabs to the processing panels.

You can also switch among tabs using *Ctrl+x* (or *Ctrl+Shift+x*), where x is a number between *1* and *0* (1, 2, 3, ... 0). The difference between *Ctrl* and *Ctrl+Shift* is that the latter does not switch the parameter tabs.

The All tab combines the **Functional Data**, **Maps**, **3D View**, and the **Image data**.



In the **Image Data** pane, you can select the  views.

There are several places in CURRY (Image Data, Localization, etc.) where you have display option tabs at the bottom.

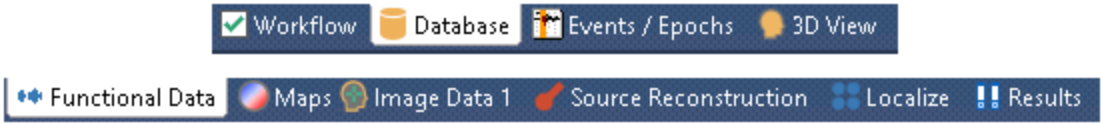
See **Edit** → **Options** for additional data display options.

7.4 Parameter Dialog Tabs

The Parameter Dialog Tabs access the majority of CURRY's functionality. The tabs are located in the lower left part at the bottom of the mainframe display area:

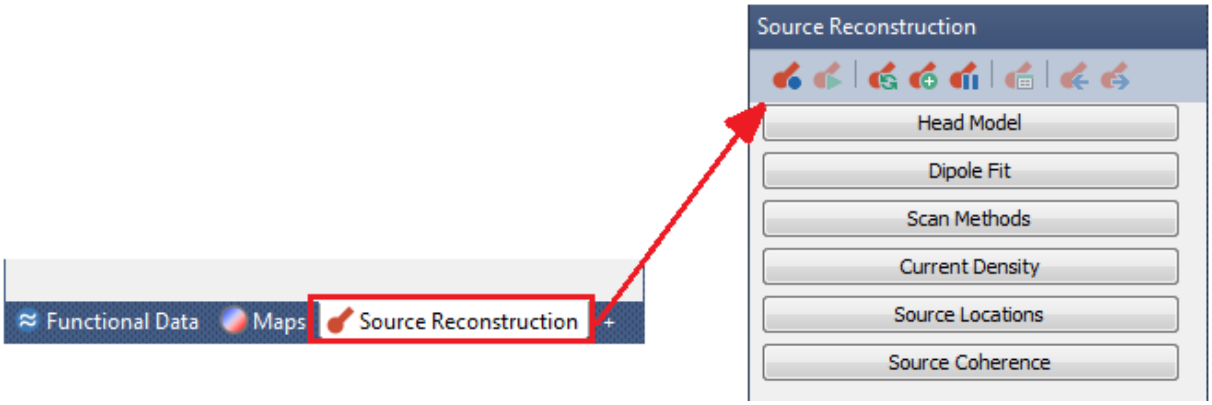

. You may see slightly different tabs. They are divided into two parts: one part is seen below the Workflow, Database, etc. display, and the other is below the Functional Data, Maps, etc. display. Note that the tab at the right of each group has a + sign. Click it to see additional parameter tabs.

Expand the viewing area, if desired, to see the full labels for each.



The icons on the tabs are paired with the icons on the Display tabs (for example, the Maps display tab is associated with the Maps parameters).

When you click one of the tabs, you will see the related option bars. For example, clicking **Source Reconstruction** displays the **Head Model**, **Dipole Fit**, etc., option bars. Clicking one of the option bars will expand the panel. Use *Ctrl+click* to expand/collapse a panel without collapsing other expanded panels.



The Parameter Dialog Tabs are laid out from left to right in the order that they are generally used.

See **Edit** → **Options** for additional Parameter Dialog options.

7.5 Ancillary Tabs

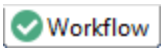
These are the tabs found just below the data display, typically in the lower left corner: Output Macro Report. Their functions are described in the **Output, Macro, and Report** sections below. Briefly, they are used as follows.

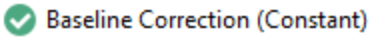
Output. This is the text output from CURRY, containing much of the results and other information. Verbosity can be selected from the context menu.

Macro. The Macro recorder is used to record a sequence of operations that you perform. Once recorded, the same set of operations may be applied to other like data files that you select. Macros thus provide a record of what steps were performed on a file, and they are a way to automate process of like data files.

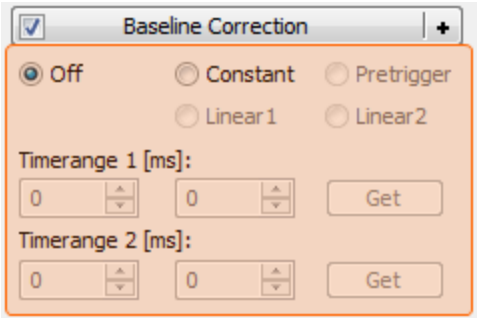
Report. The Report function is included for those wishing to create a clinical report. It can also be used to create lab notes for those wishing to document steps and results.

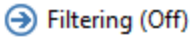
8 Workflow

The Workflow 

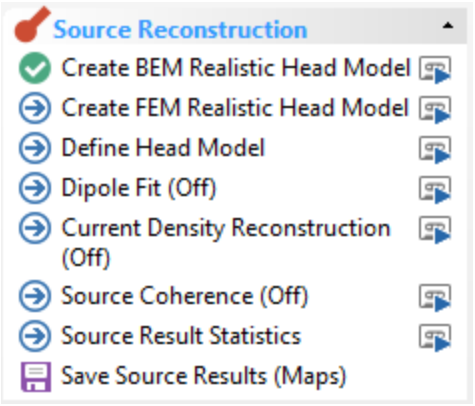
display will guide you through data file selection, parameter review, and processing steps in CURRY. You can review completed steps by clicking one of the green arrows 

, and CURRY will take you to that section of the program, with the relevant part of the screen flashing, or provide instructions.

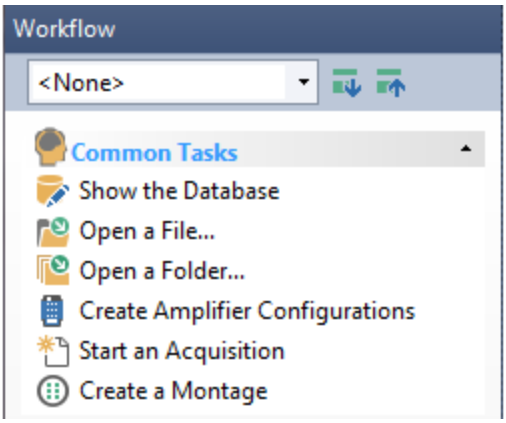


Click one of the blue arrows 

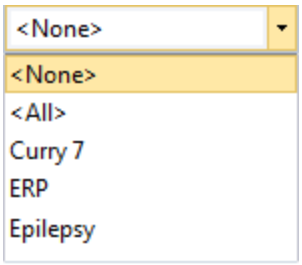
to go directly to the part of CURRY used to complete that step. Green check marks  indicate steps you have completed; blue arrows  are steps that you may yet wish to do. The  icon means that there is a demonstration macro associated with this operation. In many places, there is parenthetical information for the current settings, thereby letting you see at a glance how some parameters have been set. The icons at the top  will expand or collapse the **Workflow**.



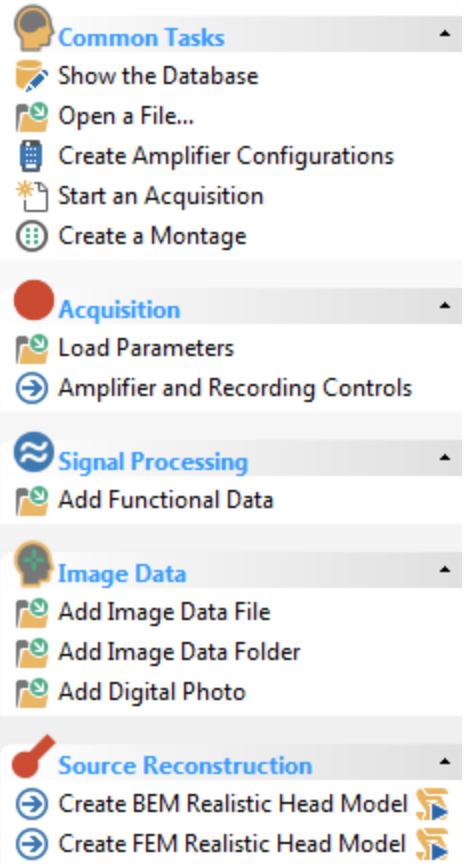
What you see in the Workflow display will change, depending on what steps you have performed. When you first open CURRY, you will see an abbreviated list of options.



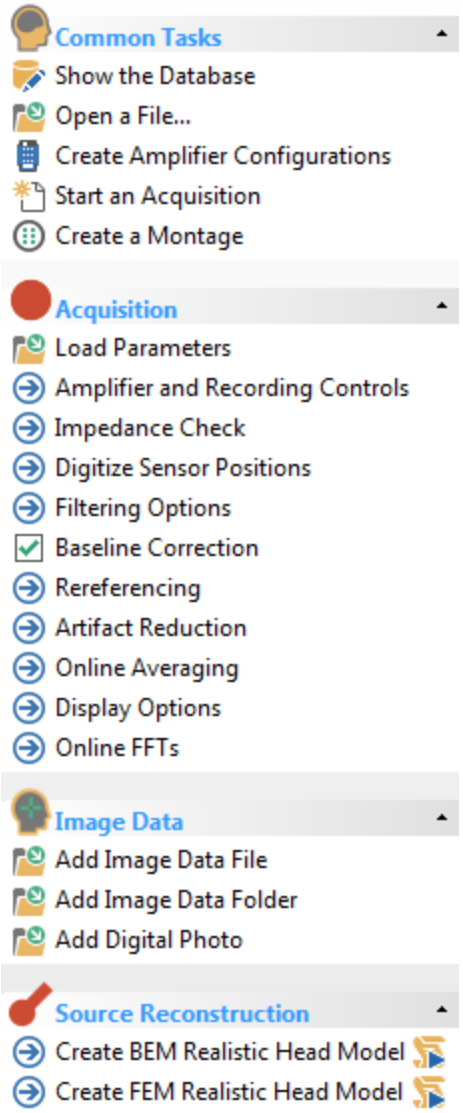
One of the first things you may want to do is to select a Scope from the drop-down list at the top. Scopes are predefined configurations of parameters that have been created for CURRY 7, ERP Analyses, and Epilepsy evaluations. They are short cuts that select the most frequently used options for those scenarios. See the next section below for more information.



If you **Start an acquisition**, you will see more items.



When you start the actual recording, you will see more items.



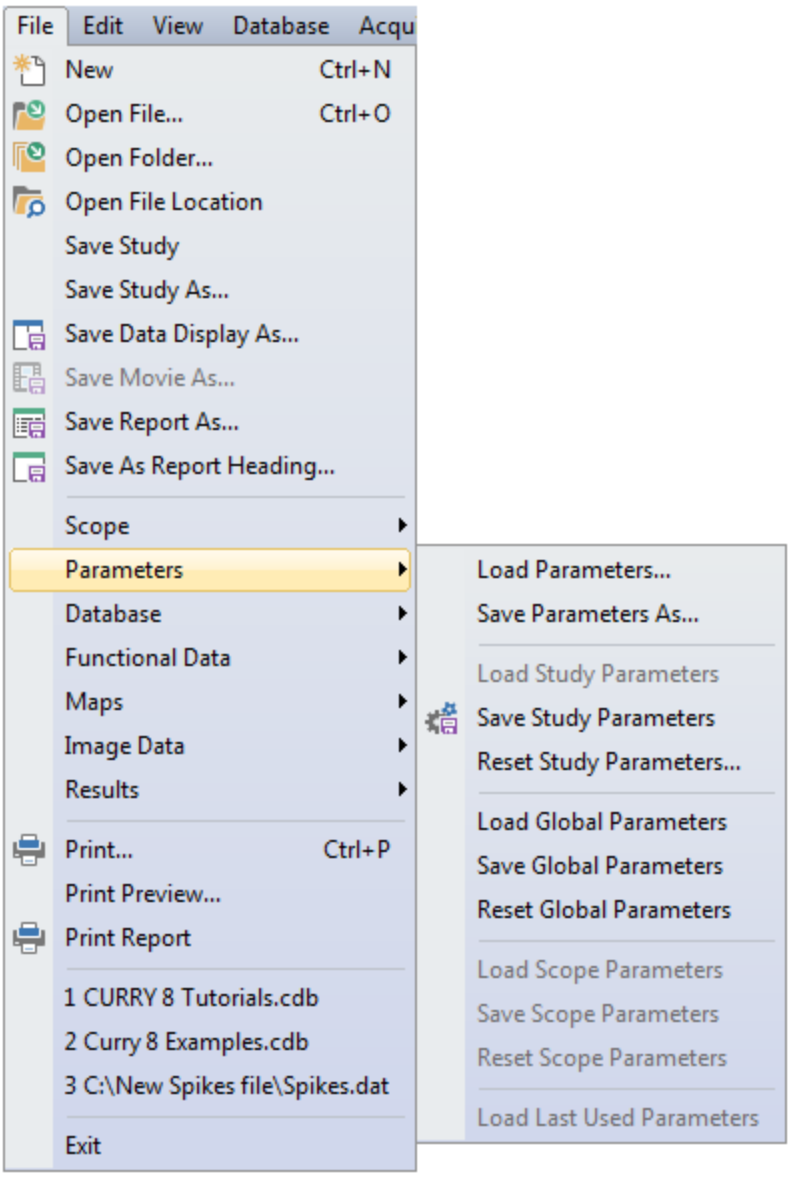
There are other additional items in the list that are seen offline depending on previous operations.

The Workflow is also meant to be a quick way to locate functionality, especially during the familiarization period with CURRY 8. Instead of searching through the parameter panels for a particular option, check the Workflow list, click the option there, and go directly to that section.

9 Global, Scope, Study and Other Parameters

Most simply stated, Parameter files are the means for saving the settings that you have selected in the program. CURRY uses several different types of parameter files: Global, Scope, Study, and Last Used Parameters. See the *Using Parameter Files* tutorial for examples using all types of parameter files.

The Parameters options are accessed from **File** → **Parameters**, and also in the **Workflow**.



Global Parameters are applied across all data files, all Studies, all Subjects and all Databases - they are applied globally. If there are certain colors or processing parameter settings, you can save these as Global Parameters and they will be applied to all data files when you open the Study. Global Parameters include only a relatively small subset of all possible parameters. If you find you cannot save some parameters as Global Parameters, save them as Study Parameters instead.

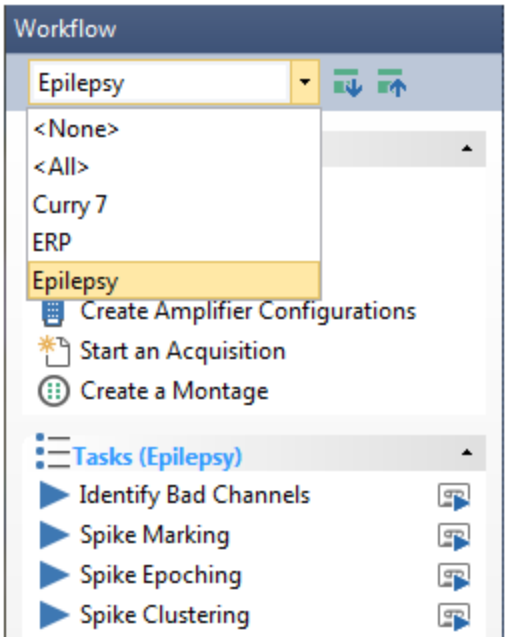
In the **Macro** section, there is an option under **Insert Action** called **UI Parameter Dump**. This will literally dump all of the parameter settings into the macro, which you can view in a text editor. A small section is shown below.

```
Study.Action                = MacroDump
```

```
STEP END
Mainframe.Action          = None
Mainframe.MacroParameterTab =
Mainframe.MacroText       = Delete unwanted channels and hide them.
Mainframe.MacroUseDelay   = 0
Mainframe.MacroFilenameNumber = 1
Mainframe.AviFramerate    = 10
Mainframe.PrintLevel      = 4
Mainframe.HardcopyWidthUsed = 0
Mainframe.HardcopyHeightUsed = 0
Mainframe.PrintWidthUsed  = 0
Mainframe.PrintHeightUsed = 0
Mainframe.MovieWidthUsed  = 0
Mainframe.MovieHeightUsed = 0
Mainframe.ReportWidthUsed = 0
Mainframe.ReportHeightUsed = 0
Mainframe.MacroDelay      = 3
Database.Action           = None
Database.AreaId           =
Database.AreaAction       = 0
Window.Action             = None
Window.TabId              =
Window.TabLabel           =
Study.Action              = None
Study.FileName            =
Study.FileIndex           = 1
Study.FileCheck           = 0
Study.FileData            = 0
Acquire.Action            = None
Acquire.AreaId            =
Acquire.EventArrayAvgNames = Stimulus 1|Accept 14|
...
```

There are hundreds of parameters in the list. If you were to open a Study that has no other parameter files associated with it, these are the parameters that would be applied. As mentioned, Global Parameters contain a relatively small subset of these, and in the absence of any other parameter file, the Global Parameters will be applied. Use care when saving the Global Parameters to be sure you are saving just the intended parameters. Once you decide what changes you want to make, enter CURRY, make those changes only, and then save the Global Parameters.

Scope Parameters. Scope Parameters are preconfigured settings designed for specific purposes, including Curry 7, ERP, and Epilepsy. Selecting one of these will avoid having to enter the parameters each time, or saving parameters as Study Parameters (it is an optional convenience). One option is for **Curry 7**, which will make the interface look more like you had in CURRY 7, and it will set some of the same parameters. If you wish to use one of the Scopes, it is necessary to select it *before* you open a data file.



To see what settings are included in a Scope, go to ...\Neuroscan\Curry 8\Workflow and see the folders for each. In each folder you will see a *ScopeDefaults.cfg* file. Open that with a text editor (Notepad, Wordpad, etc.) to see what settings are included. Here for example are the settings in the Curry 7 folder (your settings may be different).

```
Mainframe.FileVersion          =  8
FunctionalData.EventPreLatency = -200
FunctionalData.EventPostLatency =  500
SourceReconstruction.FitConductivity = 0.33 1 0.0042 0.33
ImageData1.ScriptBemFemConductivities = 0.33 0.0042 0.33 0.3301 0.3302
ImageData2.ScriptBemFemConductivities = 0.33 0.0042 0.33 0.3301 0.3302
ImageData3.ScriptBemFemConductivities = 0.33 0.0042 0.33 0.3301 0.3302
ImageData4.ScriptBemFemConductivities = 0.33 0.0042 0.33 0.3301 0.3302
ImageData5.ScriptBemFemConductivities = 0.33 0.0042 0.33 0.3301 0.3302
```

If you need to alter the preset parameters, you can do so and then use the **Save Scope Parameters** option (above) to save the new settings.

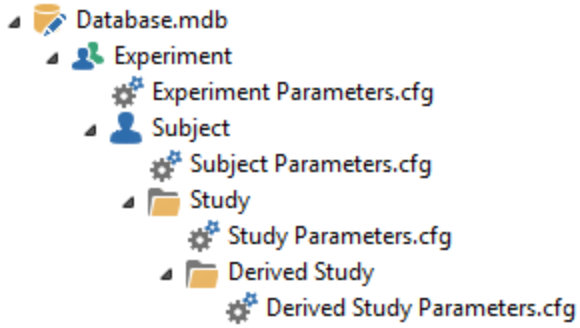
The purpose of the Scope Parameters is to automatically apply the parameter settings that are typically or frequently used in the three paradigms. They are meant to be a convenience. You do not have to use the Scope Parameters if you do not wish to.

Scope Parameters fall in between Global and Study Parameters, in that Scope Parameters take precedence over Global Parameters, and Study Parameters take precedence over both Global and Scope Parameters.

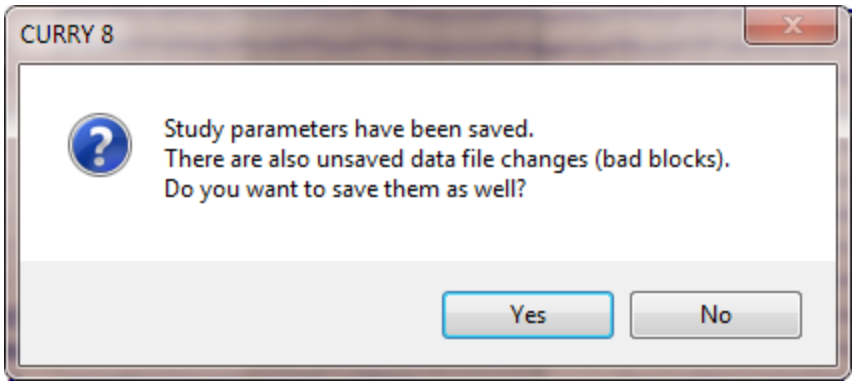
Study Parameters are typically applied to the particular Study (or Subject). The Study Parameters file contains only those changes that have been made to the Global Parameters, or Scope Parameters (if used). When you start CURRY, the Global Parameters are read first, then the Scope Parameters, and then the Study Parameters. The Study Parameters therefore take precedence over the Global and Scope ones.

Study Parameters have additional value, and it is recommended that you make use of the option to save them.

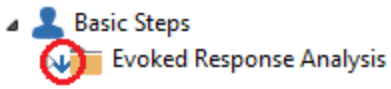
It is possible to save Study Parameters at any level in the Database hierarchy, from Group to Derived Studies. The same rules apply: Global Parameters are applied first, then Scope Parameters, and then Study Parameters in descending order. That is, "Subject" level parameter files supersede "Group" level parameters, "Study" level parameters supersede Group and Subject parameters, and so forth. In the absence of a parameter file at a given level, the nearest upper parameters are applied. If there are no parameter files at all, the Global and Scope Parameters are applied.



If you save the Study Parameters, make some changes, and then save the Study Parameters again, you may see a confirmation message, depending on what the changes were (bad blocks, inserted events, changes to events). The regular changes are already saved, and you are being asked if you want to save the special case changes as well.

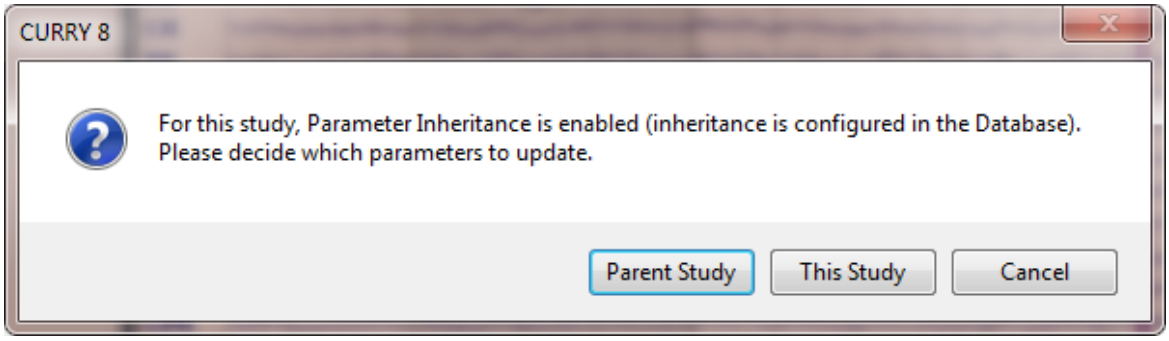


At the Subject and Study levels, you have the additional option to "inherit the parent parameters" or not. *Right click* on a Subject or Study and select **Inherit Parent Parameters**. Small down arrows will appear to indicate the parameters from the parent file can flow into the child file. The default setting for Subjects is enabled; for Studies the default setting is disabled.



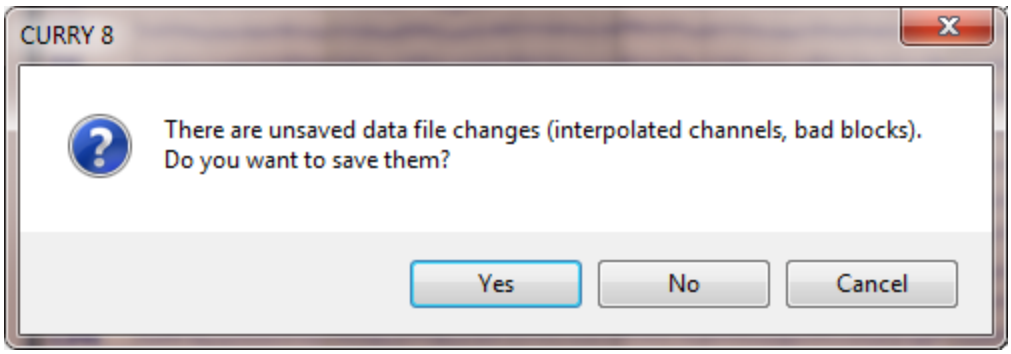
If you have Inherit Parent Parameters enabled for a Study, and then you save the Study Parameters from the Toolbar, you will have the option to save the file (or

update the file) in the Parent folder (so that the single parameter file can be applied to all of the child folders under it), or in the current study.



Last Used Parameters are the settings that were in place when the Study was closed. The Last Used Parameters settings are found under **Edit** → **Options**. When enabled, you will have the option to save a new .cfg file, similar to the Study Parameters. You can also set it so that when you open a Study, you will be asked if you want to apply the Last Used parameters (or have them applied automatically, etc.). If Study Parameter and Last Used Parameter files are in the same Study, the Last Used Parameters take precedence.

Special Case Parameters. There are some parameters that will be specific to the file you are analyzing. These include, bad blocks, interpolated channels, and deselected epochs (with epoched files). If you were to apply these parameters to a different file, the results would be incorrect for that file. To avoid this situation, changes that are made involving these parameters are saved to the .dpa file that is stored in the same folder as the data file in the Study you had opened. (This is the same .dpa file that is created in the Functional Data Import Wizard). When you close the Study, you will be asked if you want to save these changes.



There are a few conventions to be aware of when using Parameter files.

1. Parameter files are used both online for acquisition and offline for data processing and source reconstruction. When you have determined the parameters you wish to use for acquisition, save the Study Parameters file and then use it with subsequent files to acquire data with the same parameters. When you wish to analyze the data offline, you can begin with the same Study Parameters file. If you change the offline Study Parameters, you may wish to save those settings for offline use - files can be named as desired.

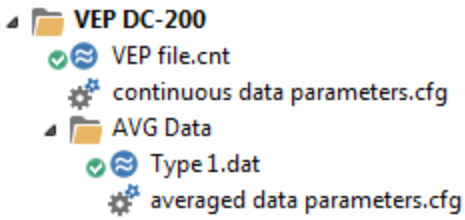
2. There are limits to how far you can go in the analyses and still save the settings in the parameter files. For example, the parameter *settings* are saved, but not the *operations* that may be performed. Whenever you Scan the data (Templates, Artifact Reduction, creating Averages, etc.), and save a parameter file, the parameter file does not go beyond the Scan, aside from saving the parameter settings. You will still need to perform the Scan(s) manually, and make any subsequent selections that require the Scan to be completed first. For example, if you perform Artifact Reduction and save the parameter file, when you reopen the Study you will see the parameter settings up to the point you scanned the data file. The reduction methods you used will not be saved with the parameters, since these are not [all] active until you have performed the scan.

Note

If your analysis sequence includes the creation of averaged data files, you should save the Study Parameters before you actually create the average(s). Once the average is displayed, CURRY is in a different state, so to speak. Study Parameters cannot be saved at that point. You can, of course, save the average data to a subfolder, open that Study, and save its own parameter file. A similar case exist with Last Used parameters - once you get to the averaged data file(s), you cannot save the Last Used parameters, unless you **Revert to Continuous** and then close the Study. Then you can save the Last Used parameters up to that point. If you save the average file and open it in its own Study, you can then save its Last Used parameters when you close the Study.

If you want to save the entire procedure that you are using to analyze the data, including scans, you can do that using macros (macros include the various settings as well as the operations).

The typical way to manage the Study Parameters is to have the averaged data in a derived folder below the continuous data. This is the default way in which averaged data files are saved. You can create Study Parameters for the continuous data, stored in the parent folder, and Study Parameters for the averaged data, stored in the child folder. The continuous data parameters are applied only to the continuous data file, unless you enable **Inherit Parent Parameters** for the child study. The averaged data parameters are applied only to the averaged data file.



3. The next convention to know is that the Study Parameters in a child folder always take precedence over those in the parent folder, if conflicts are encountered. If there were no averaged Study Parameters in the example above, CURRY will attempt to apply the continuous Study Parameters to the averaged data - to the extent that it is relevant. This convention has the advantage of letting you apply one Study Parameters file to all of the files in the subfolders beneath it. For example, the subfolders could each contain a continuous data file

to be analyzed. Study Parameters in the parent file above them could then be applied to all of the continuous data files, assuming you have enabled **Inherit Parent Parameters** for the Studies.

4. When using Study Parameters from one data file to other like data files, it is important to realize that ALL of the parameters you have changed will be applied to the subsequent data files (excluding Bad Blocks, Interpolated channels, and deselected epochs, with epoched files, which are all stored in the .dpa file, as mentioned above). There are other parameters that are saved. For example, if you have set any of the various voltage thresholds, these settings will also be applied to subsequent data files. This may or may not cause problems. For example, the voltage threshold you use for blink detection may be applicable to all or most of the files you are analyzing; whereas, the Min and Max thresholds you use for SNR based sweep rejection may be specific to each particular data file.

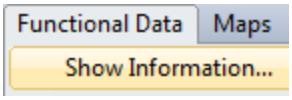
5. In some cases, the Study Parameters may contain operations that require lengthy steps in their application (such as, some CDR computations). In these cases the parameters are not applied when you open the Study, as you may not wish to wait. The parameters are applied explicitly by selecting **File → Parameters → Load Study Parameters**.

6. When you save the Study Parameters (or Global or Last Used Parameters), you are taking a snapshot of ALL of the parameter settings, and using those settings either for the Study or Globally. Be certain that you are saving only the desired parameter settings. For example, if you have been performing various operations with the data file, and then you want save specific settings, realize that ALL of the settings that have changed will be saved - those that you intend, plus those that you may have forgotten you set earlier.

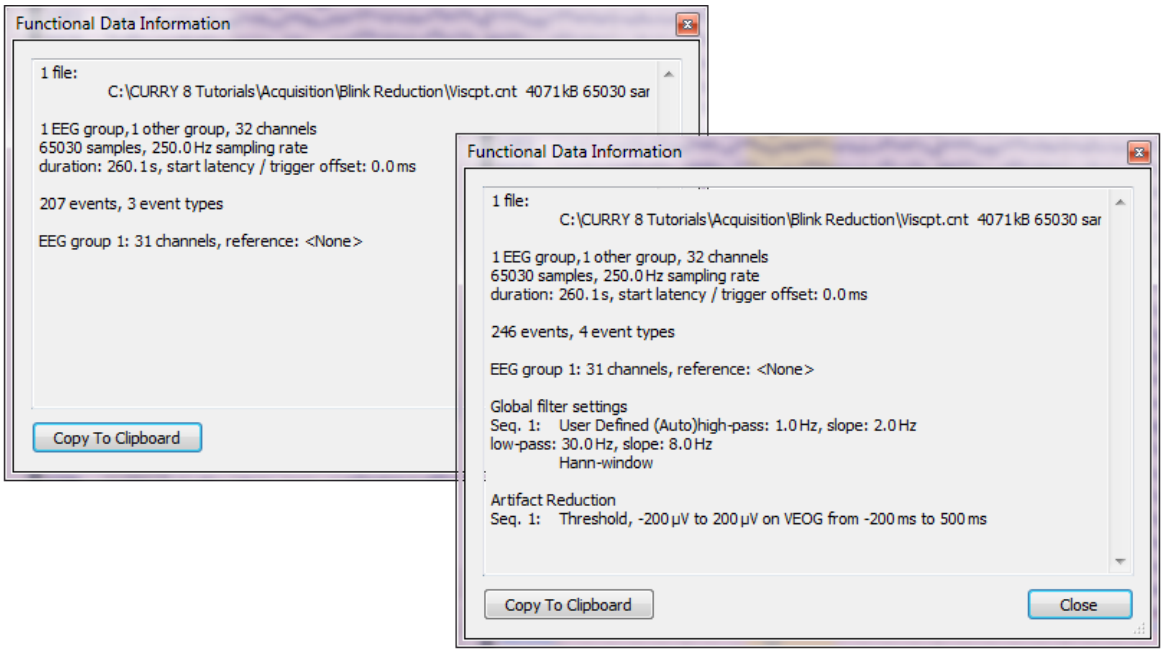
Once you understand these few conventions, you will find that parameter files can save you a lot of time by "remembering" the settings that you wish to use frequently. See the *Using Parameter Files* tutorial for examples using all types of parameter files.

10 History Options

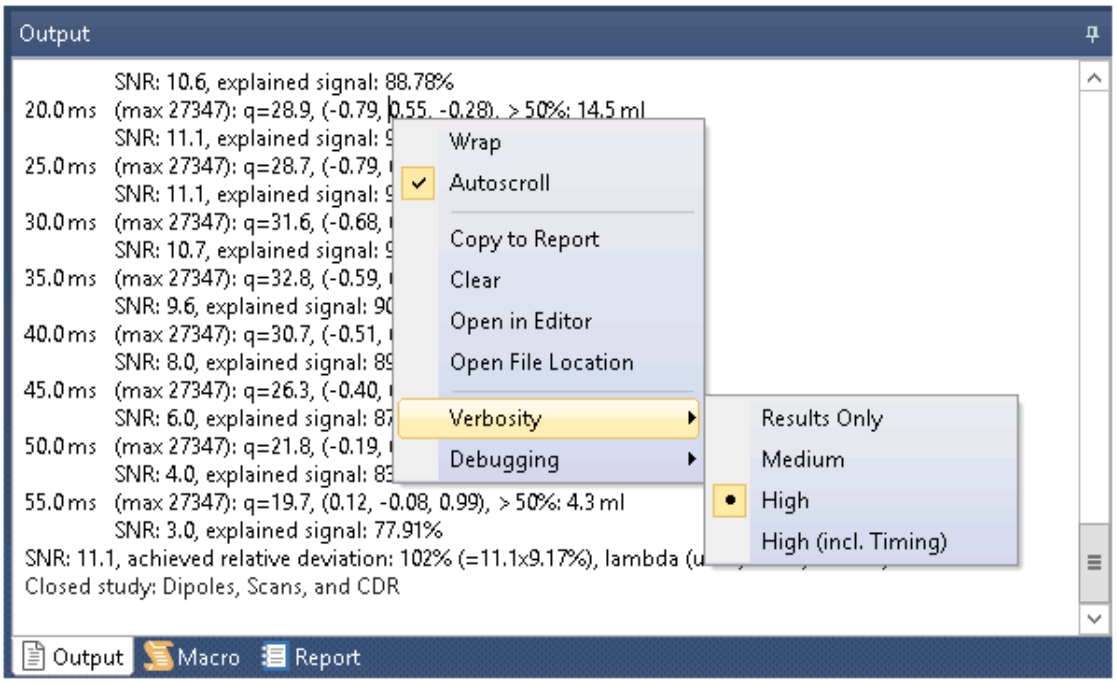
It is very important to be able to capture the series of operations you have performed with a given data file - its History. There are several ways you can do this within CURRY.



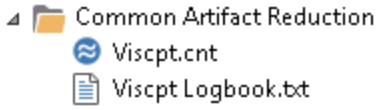
1. The **Show Information** option under **Functional Data** will show initial information about a file you open. As you perform more analysis steps, these will be added to the history. You can copy the text to the clipboard if you want to make a written record. If you save the Study Parameters, you will see the history again when you reopen the file. Exporting a data file will retain the history, and new processing steps are then added to the history.



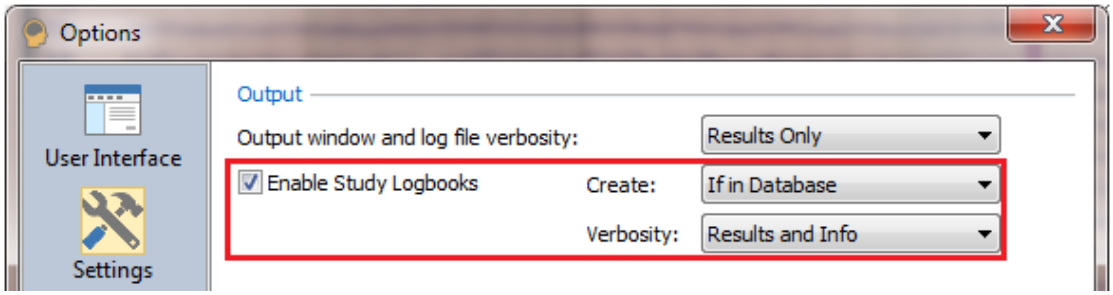
2. **Output**. The first creates a running log of operations you have performed, with a user-determined level of detail. This is seen in the **Output** panel and saved in a text file. This is described in more detail in the **Output** section below.



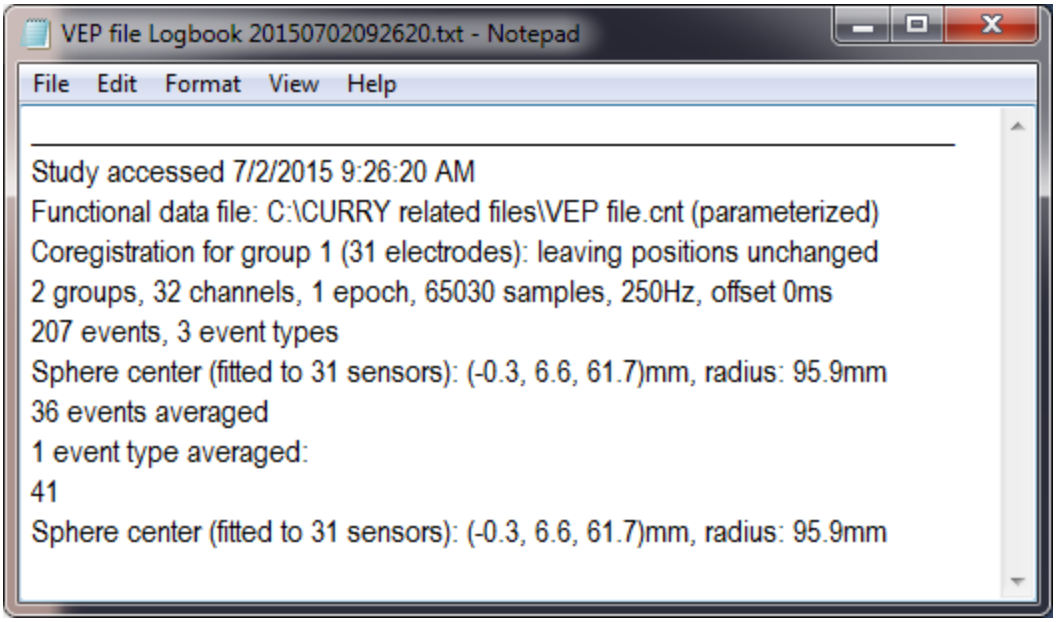
2. **Logbooks**. While the Output section contains a history of the operations and results, it can become lengthy and somewhat difficult to locate to find the history for a given file. It is used primarily to obtain the immediate results. The second method uses **Logbook** files. These are text files that can be created automatically and included in the Database. A date and time code is added automatically if an existing Logbook file is detected.



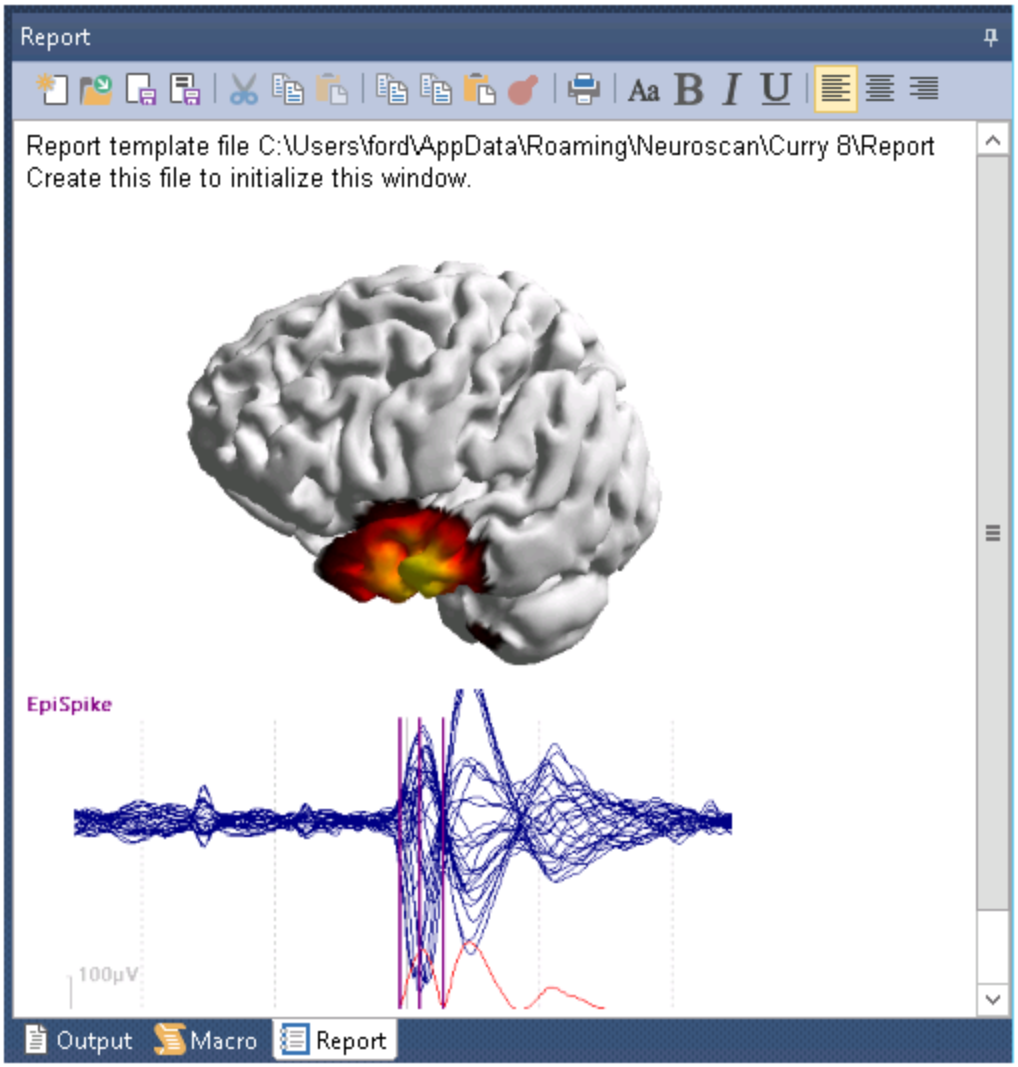
To use Logbooks, you must activate the capability from **Edit** → **Options** → **Settings**. There you will see options for when to save the Logbook, and how much content to include.



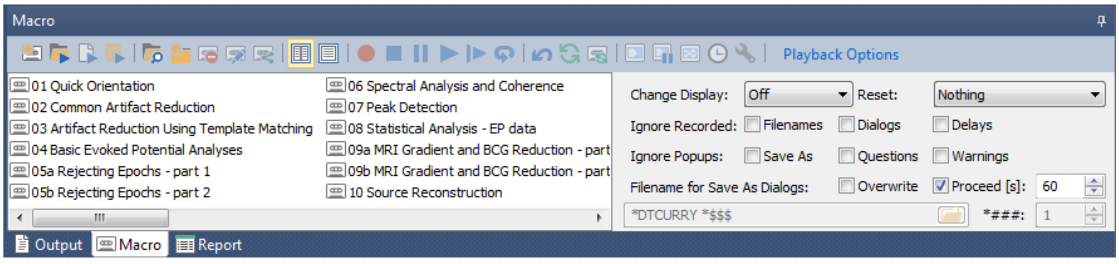
This option allows you to save basically the information seen in Output to a text file that is found within Studies in the Database. The file will be updated each time you open the Study.



3. **Report**. In various places in CURRY, you will see options to save results and figures to the Report. Results, seen in the Output section, can be transferred to the Report. The Report files can be saved and retrieved, and they contain more information - and user-selected information - than in the simple text files. Reports are described in more detail in the **Report** section below.



4. **Macros**. Macros record the steps as you perform them. When you reopen a data file again, you can apply the macro you saved, and return to the same end point in the analysis. The macro itself - which can be viewed as a text file - thus provides another form of History. In this case, it is a dynamic one that can be reapplied to the same file or to other like files.



Macros are described in the **Macros** section below.

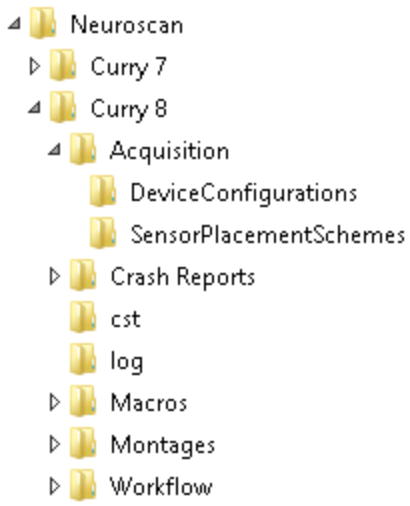
11 Target Folders for Windows 7 (and newer versions)

There are multiple places in CURRY 8 where you may retrieve files supplied by Neuroscan, as well as similar files that you create. For example, there are Configuration Files for acquisition that we supply, and these can be modified and saved with a different name, or created from scratch. The files supplied by Neuroscan are installed into certain folders. Those that you save are stored, by necessity, into different folders (this is a Microsoft requirement).

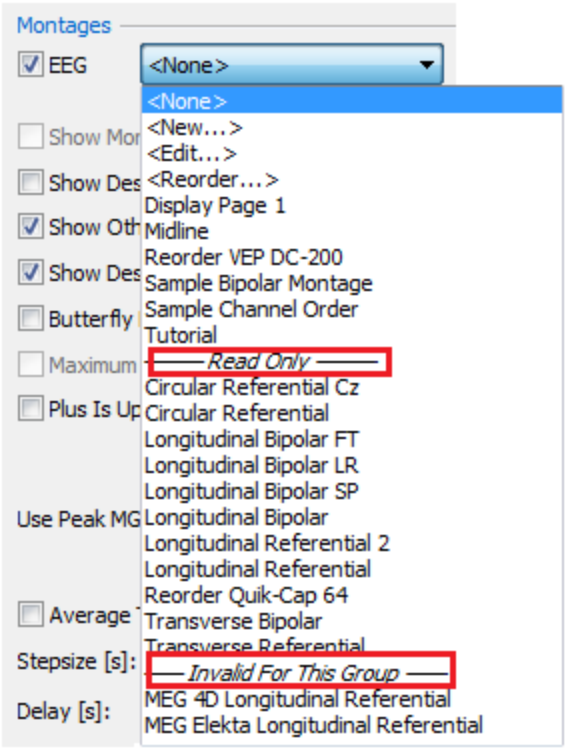
In Windows 7 (and later versions and Vista), the folder is:

C:\Users\<User Name>\AppData\Roaming\Neuroscan\Curry 8\Acquisition\DeviceConfigurations folder. The *AppData* folder may be hidden and you need to enable **Show Hidden Folders** in Windows Explorer in order to see this folder.

Similarly, sensor placement, Crash Reports, log, macros, and montage files have their own folders.



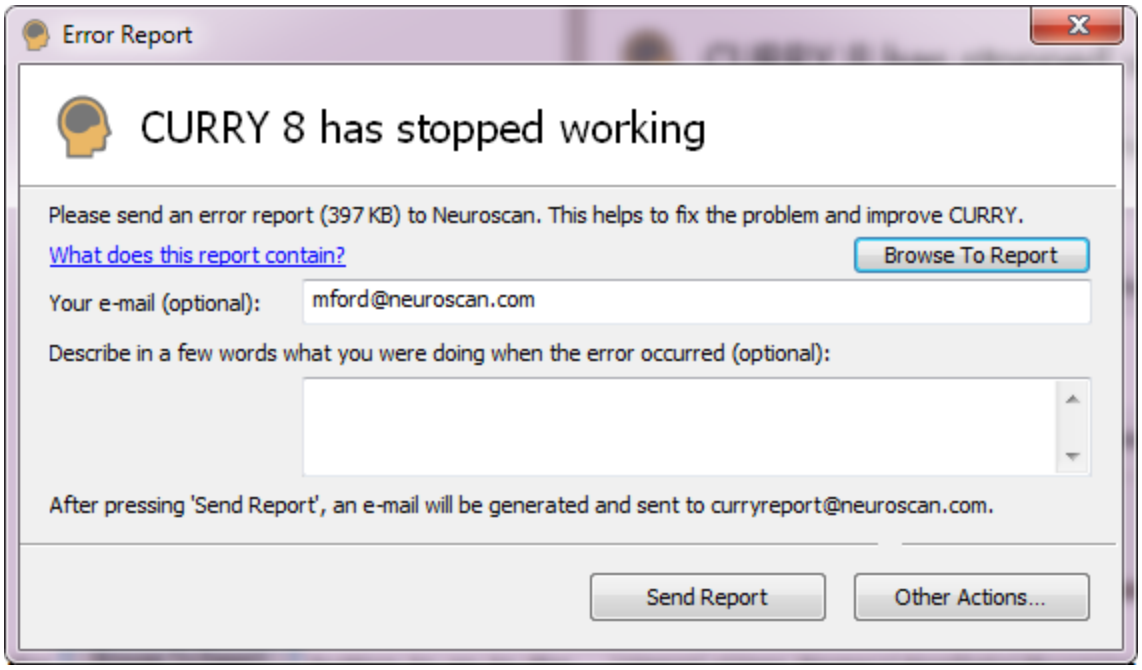
Wherever this distinction occurs, you will see a drop-down list that has files in three sections. Those above the *Read Only* line are ones you have saved. The ones we supply are *Read Only* files. You can modify them, but not overwrite them. Save them with a different file name. They will be saved to the appropriate target folder. If you save them to a different folder, they will not appear in the list, although in many instances you will be able to retrieve them manually with a browse button. Montages that do not contain any channels of the current device group are sorted out and placed in the *Invalid For This Group* section (so you can see directly which files can be meaningfully applied to a group).



12 Error Reports

CURRY will automatically generate an Error Report whenever CURRY crashes. This will be sent to the CURRY development team, for use in diagnosing the cause of the crash.

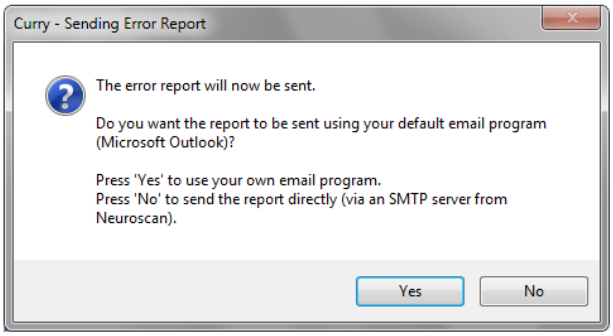
When a crash occurs, you will see the following screen.

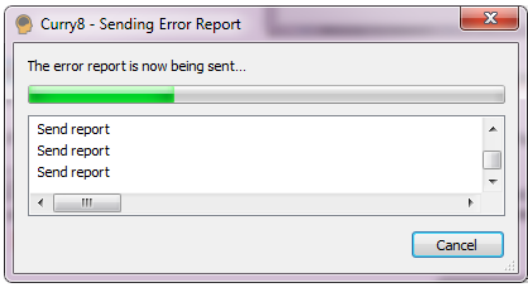


Click the Browse To Report button to go to the ...*Users**<User Name>**AppData**Roaming**Neuroscan**Curry8**Crash Reports* folder, where these files are stored. This is useful if you need to send one or more reports manually.

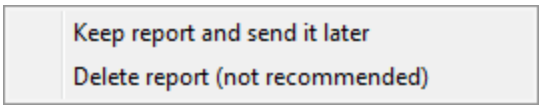
It will be helpful if you include your email address and a brief description of what you were doing when the crash occurred.

If you select Send Report, you will see the following options. If you select **Yes**, then your own email program will be used. This can be problematic because the email will include a couple of attached files, and these are sometimes blocked within some institutions. If you say **No**, then the report will be sent directly via an SMTP server for Neuroscan (recommended). You may also see only that the report is being sent.

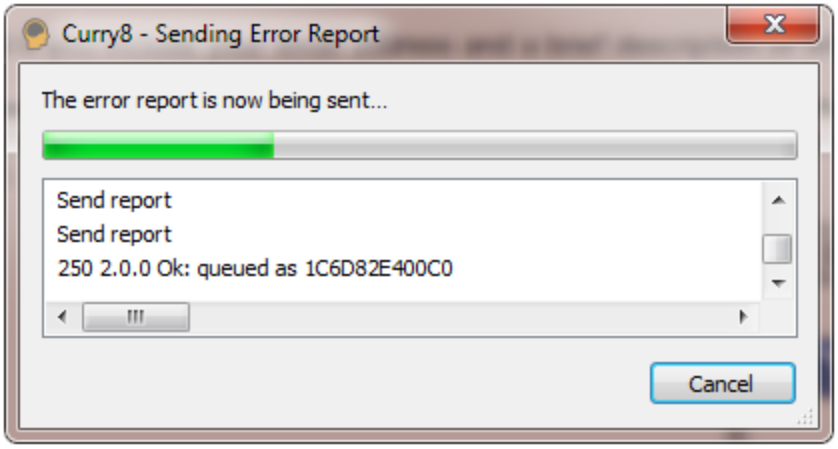




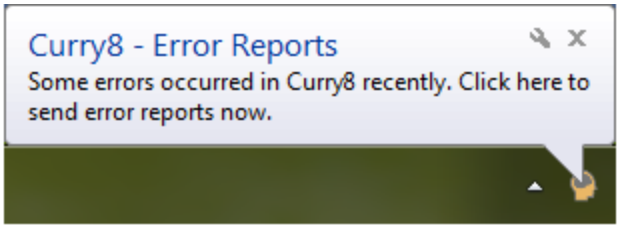
Instead of clicking Send Report, you can click **Other Actions**. Then you will have the options to Keep the report and send it later, or to Delete the report. We prefer that you do not delete the report since the information it contains may be helpful in finding the cause of the crash.



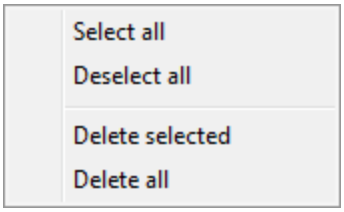
You will see a confirmation window when the report is being sent.



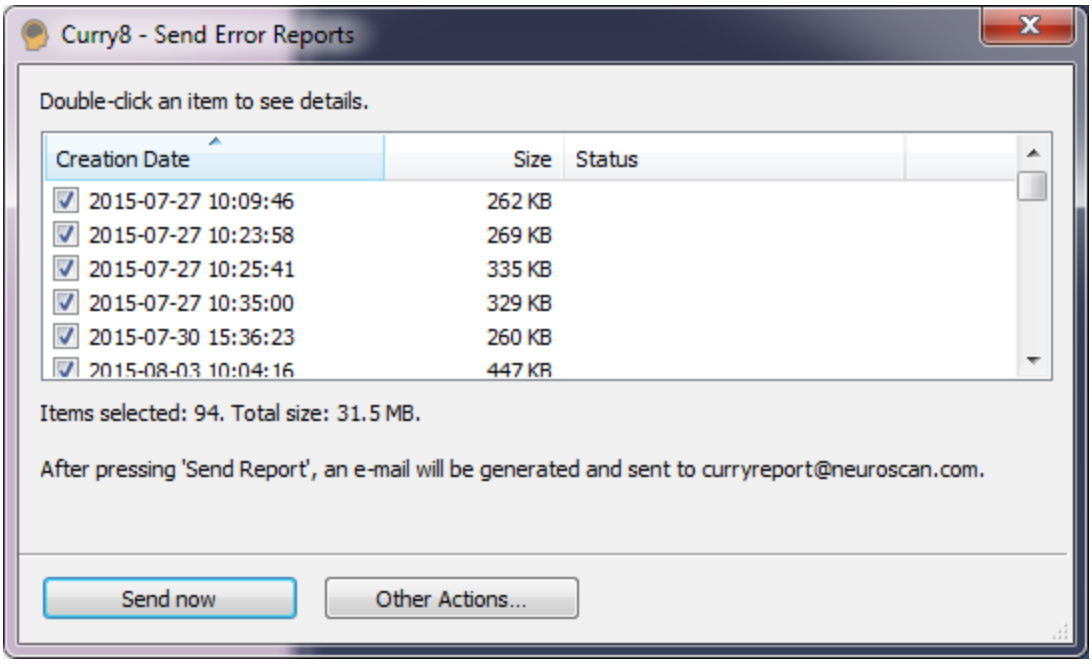
If you click the X to close the window, the report will go into a queue. The next time you start CURRY, you will see a message in the lower right corner. Click on it to send the report(s).



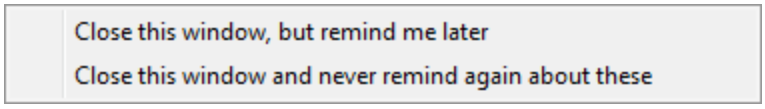
Clicking on it will display the following screen. If you *right click* in the list, you will see options to Select or Deselect all reports, or to Delete selected or All reports.



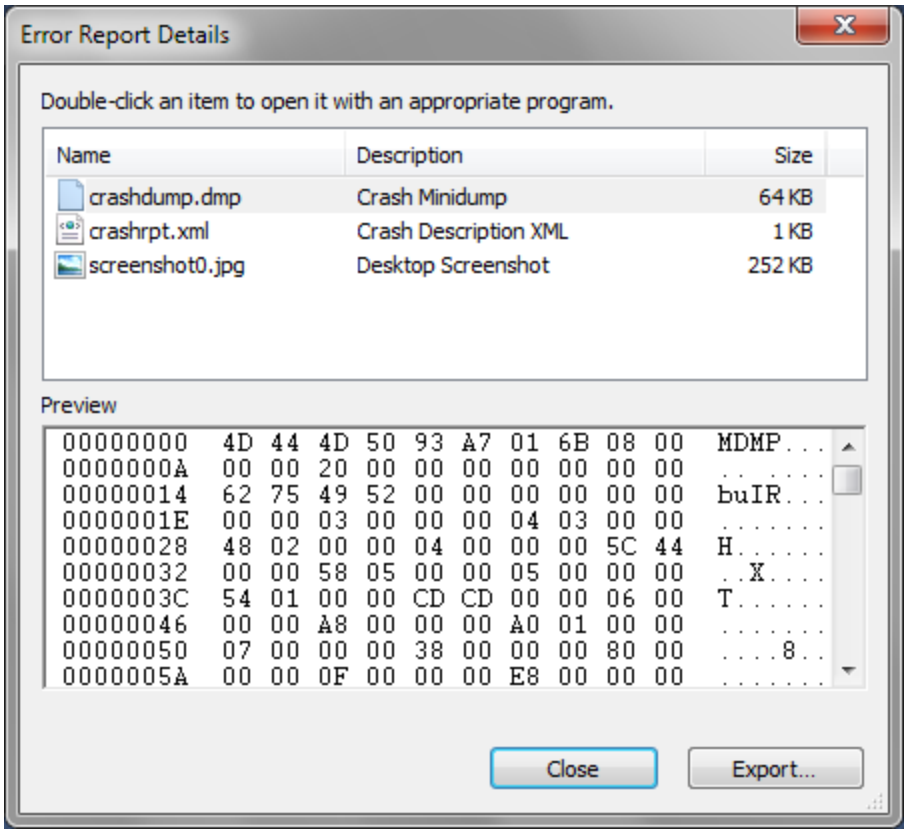
Click **Send now** to send the report(s).



Selecting **Other Actions** gives the options to Close this window, but remind me later, or Close this window and never remind me again.



Double-clicking in the above list displays the following screen. If you *right click* in the list, you will see options to Open, Delete selected files, or Attach selected files. CURRY support will direct you on these steps as needed. If you click **Export**, you can save a zip file that contains the files listed. This is used when you are having problems sending the error report through the normal email or SMTP routes. The zip file can be emailed as an attachment.



For Windows 7 or newer versions, you will find them in the ...*Users**<User Name>**AppData**Roaming**Neuroscan**Curry8**Crash Reports* folder. They may be deleted manually, if desired.

You are encouraged to send the crash reports. Crashes are often computer specific, and we need the information to find solutions that resolve the issues across computers and in some cases, operating systems.

13 Database

The Database structure allows for the easy organization and access to all files (data, parameter, results, configuration) needed for CURRY operation, including *Acquisition*. You do not necessarily have to use a Database. If you want, for example, to take a quick look at a data file, you can just use **File → Open** and select the file you wish to examine. The Database is used for keeping track of all of the files you need for a single subject, a group of subjects, a complete experiment, etc. Databases have a .cdb extension (SQLite, preferred) or an .mdb extension (Microsoft Access).

Within a Database, you may create one or more Groups (or you can not create any Group at all). Each Group typically consists of multiple Subjects. For each Subject, one or more Studies can be created. You may create sub-folders beneath Studies - referred to as Derived Studies - that contain results you wish to keep with that Study. A Data Folder is specified by its type and the name of its associated data file. The files in the Data Folders, under a given Study, are then used together for an analysis (excluding derived folders, which are treated as their own Studies).

Data Folders can contain:
- EEG/MEG data, sensor position, and functional landmark files,
- image data and anatomical landmark files,
- results files,
- parameter files, and
- study logbooks.

Note

Change in file extensions. Beginning in CURRY 8, there are changes to the file formats (extensions) that are used. While the older .mdb format Database files will still be read in CURRY 8, we recommend you use the new (default) .cdb format files for Databases. The .cdb files will not be read by prior versions of CURRY. Data files that are acquired, or otherwise saved, will have .cdt extensions rather than the previous .dat extensions. This is to avoid the confusion with various other files that use .dat. Also, in prior versions of CURRY, two CURRY parameter files were created when functional data were imported - the .dap and .rs3 files. Beginning with CURRY 8, these files are combined into a single .dpa file.

Note

You may load separate MEG/EEG files in the same Study and CURRY will merge them. The files must have the same sampling rate, number of data points and trigger offset. The MEG data files must be loaded first in the Study. If there are two "Other" groups, these will be merged into a single group. For example, if you have MEG, MEG2, MEG3, EEG and Other in the first group, and EEG and Other channels in the second file, these will be merged to create a single display containing MEG, MEG2, MEG3, EEG, EEG2, and all Other channels.

Note

When you first insert a functional data file, CURRY will search for necessary parameters. If the needed parameters are detected, you will see a green check mark . If a question mark is seen, or if there is no check mark, these are indications that you need to go to the **Functional Data Parameter Wizard** to address the missing parameters. This will happen when you attempt to **Open** the Study. You can access the Wizard at other times using the **Data Parameters** button on the Toolbar.

Note

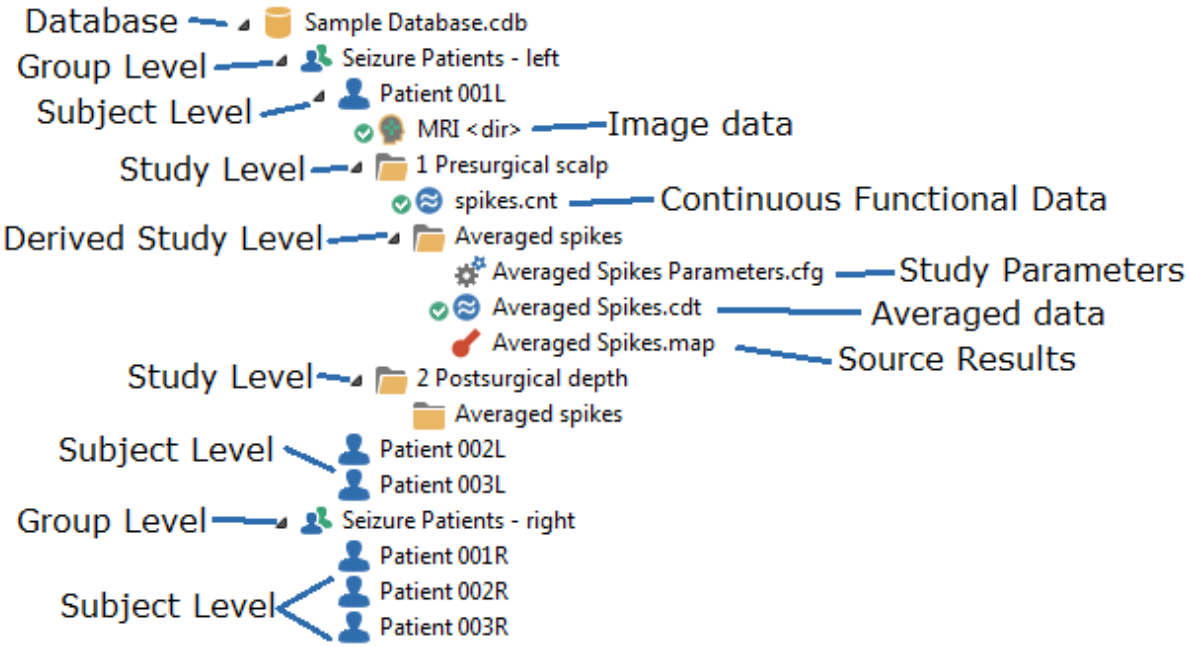
The Database stores only references to data files, i.e., their file names and folder paths, and not the files themselves. These references must therefore be updated whenever the data files are moved. Similarly, if you make a change to a stored data file, all of the places in the Database that point to that file will open the modified file.

The structure of the hierarchy begins with the Database, which subdivides into Groups, Subjects, Studies, Data Folders and Data and Results Files. The Results folder refers to Source Reconstruction results that have been saved. They will appear as (for example):

EpiSpike Dipoles, Scans, and CDR.map;ele;dip;dsc;dsp;cdr;vcd;lfd .

The "name" of the file consists of the basename plus an arbitrary number of extensions, separated by ";".

Other results, such as averaged EP data, are listed in regular folders, typically Derived Studies (which are simply subfolders under Studies).



Creating a Database

In practice, you will likely begin by creating a Database and specifying the files that it includes.

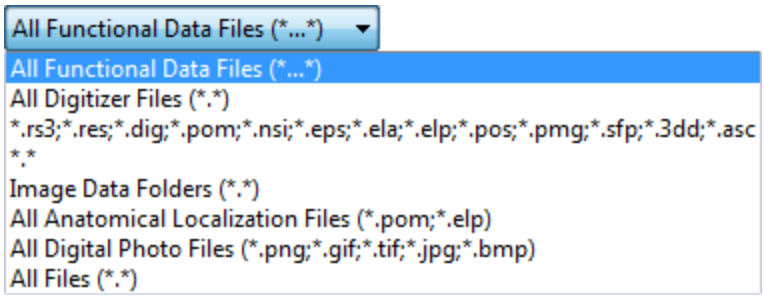
There are six icons at the top of the Database display. These are shortcuts for the more commonly used options.

Add Group . Add a new Group to the Database.

Add Subject . Add a new Subject to the Database, plus an additional "empty" Study.

Add Study . Add a new Study to the selected Subject.

Insert File . Insert file into the selected Study. An Open File window will appear, allowing you to select the file type. You may select multiple files in a single pass using the conventional *Shift+click* and *Ctrl+click* combination key strokes.



You can also *right click* on the Study and select any of the file types shown to insert it.

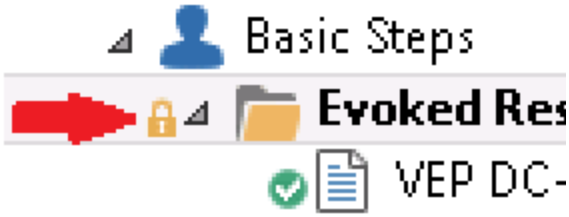
Open or Start Acquisition . One of several ways to open a Study or start an Acquisition. You can also *right click* on the Study and select **Open Study**, or just *double-click* on the data file. If you attempt to open a Study that has no Functional Data in it, you will see the same arrow , but it will instead take you to the Acquisition part of CURRY (assuming you have an acquisition license).

Show Full Path . Displays the full path for the Database and inserted files.

Note
Other symbols may appear, indicating an error reading the Database (verify the path is correct), or that it is a [read only] Database.

Note
You can drag and drop data files, Studies, and Subjects from one location to another in the Database. Dragging and dropping will *move* the file; use *Ctrl+drag* to *copy* the file.

Note
After creating an "in-place" average (In-Place Averaging button), you will see a padlock icon by the open Study.



This means the Study is "locked" for certain functions. When CURRY is displaying the "in place" average, it is in a different state, sort of between Studies, and consequently you cannot insert files or drag and drop files to the Study (similar to it not being possible to Save the Study Parameters).

Please see the *Database* tutorial for more information about creating and using Databases.

Selecting/Importing a Database

Once you have created and stored a Database, you will likely want to access it again. Or, if you have an earlier version of CURRY, you may have Database archives that you wish to Import to CURRY. Follow these steps to retrieve an existing or exported Database.

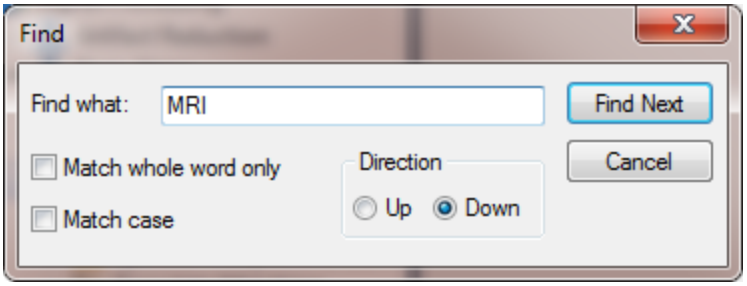
The .mdb Database format used in CURRY 8 is backward-compatible with CURRY 5, 6, and 7. The .cdb Database format is preferred in CURRY 8; CURRY 7 was modified to read them also. Locate and retrieve the .cdb Database file using the Open file utility.

If you wish to open a Database exported from a previous version of CURRY (.dba extension), or re-import an exported Database, you must first have a Database already open. This can be an existing Database, to which the imported Database will be added, or a new Database you are creating. Go to **Database → Import**, and select the desired .dba file using the Open file utility. The new Database will be added to the previously open one.

Searching for Subjects

The Database can be searched for key words in the data filenames, subject names, and study names.

Click **Database → Search**. Enter the text to search. You can have the Search conducted to **Match whole words only** that you enter, or to **Match case**. You can direct the search **Up** or **Down** from the current highlighted position. The found item will be highlighted.



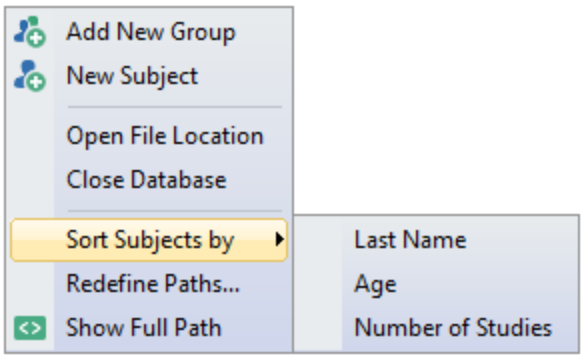
Deleting

Groups, **Subjects**, **Studies**, and **Data files** can be deleted from a Database by *right clicking* on the respective file name, and clicking **Delete Group**, **Delete Subject**, **Delete Study**, or **Remove File from Study**, or, it is much faster to use the *Delete* key (you may then delete multiple items simultaneously). If the Subject or Study is not empty, you will see a confirmation message asking if you wish to delete the Subject/Study anyway. Deleted entries and all entries that are hierarchically below them will disappear after clicking **OK** to the message.

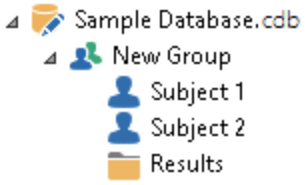
Database, Context Menus

The options associated with the Database are as follows.

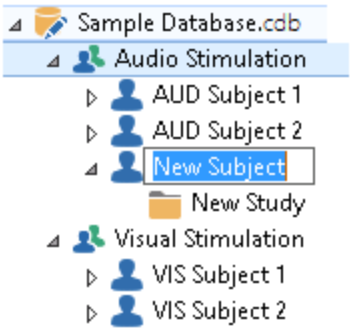
Database. Clicking the *right mouse* button on the Database line shows the displayed option list.

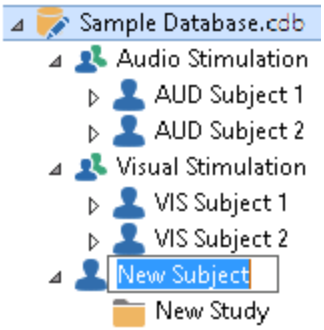


Add New Group  . Select this option to add a new Group. CURRY anticipates that you will wish to also have Subject and Results folders, and includes them for you. To rename the Group, highlight it and press the *F2* key, or *right click* on it and select **Rename**.



Add New Subject  . Select this option to add a new Subject. Subjects can be added directly under the Database, or under an Group, depending on what was highlighted when you selected the option.





A  will appear, with the option to rename it. You can rename it at any time by highlighting it and pressing the *F2* key (or by selecting **Rename** from the context menu).

Open File Location. Opens the location if the Database file in Windows Explorer.

Close Database. Selecting this option will close the Database.

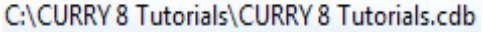
Sort Subjects by. Subjects may be listed, or sorted, in several ways.

Last Name. Selecting this will list the Subjects alphabetically by the last name.

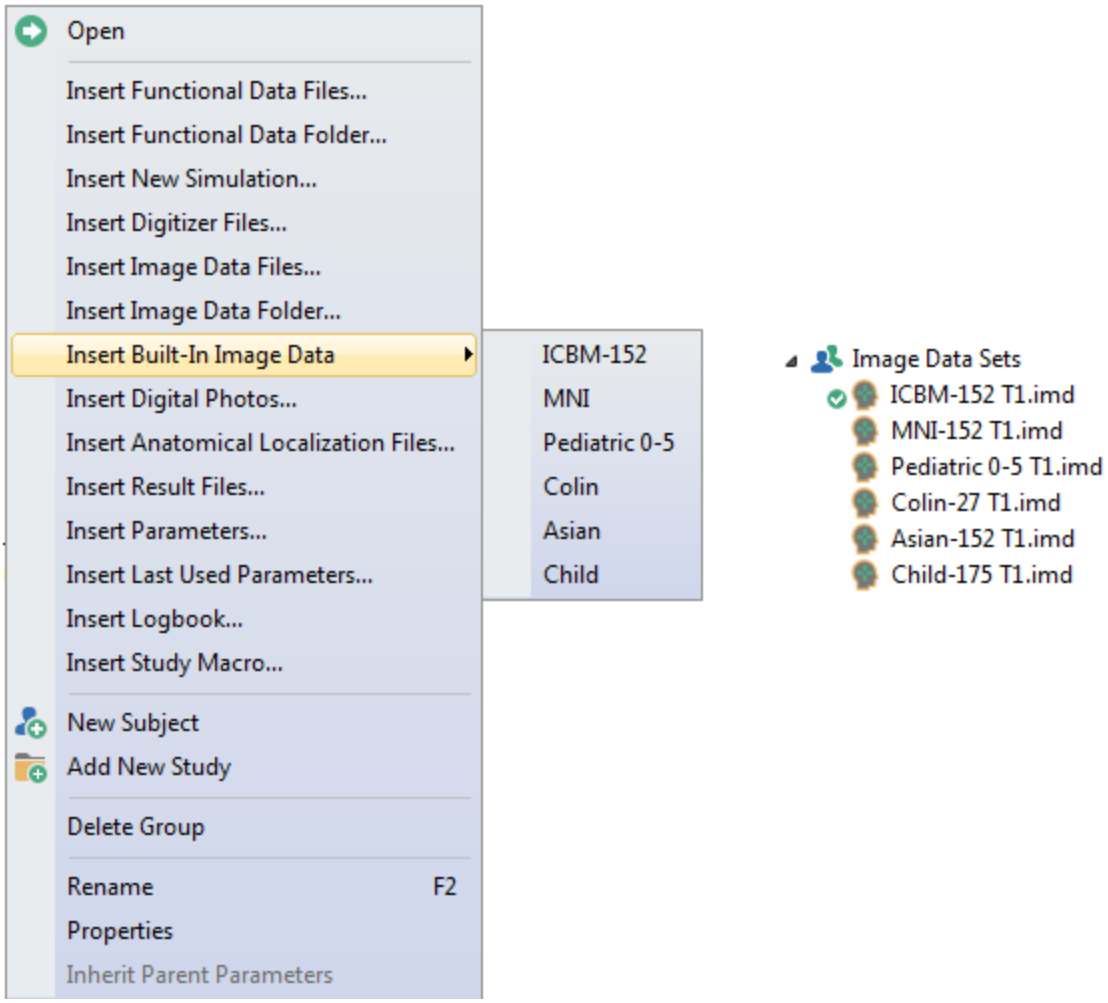
Age. Selecting this will list the Subjects numerically by age.

Number of Studies. Selecting this option will reorder the Subjects based on the numbers of Studies under each Subject, from the fewest to the most.

Redefine Paths. Occasionally you may have need to move your data files from one location to another. If you have created a Database, each of the entries will use the path and file name to all of the files (including, for example, parameter and results files). After you move the files from their current location, the Database may not find them, and you will see red X's in the Database. **Redefine Paths** is a Search and Replace feature that will update the paths to the new locations. Please see the description in the **Database** section above.

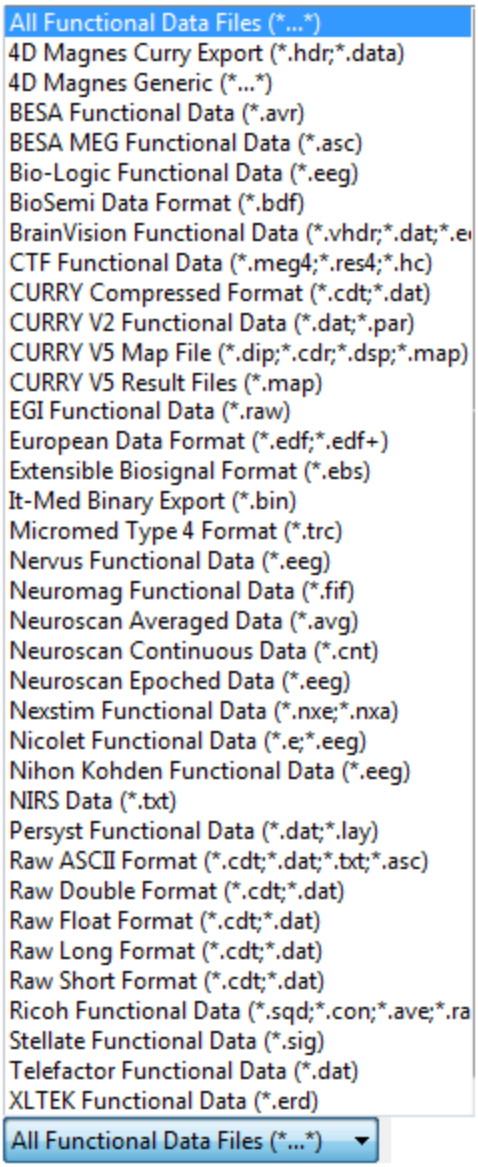
Show Full Path  . When selected, the complete path to all files will be displayed  . Otherwise, only the file names will appear.

Groups. Click the *right mouse* button on a Group to see the following menu. They will appear in the Database as shown.



Open  . Click this option to load the data files in the selected folder into the functional layer (or "working area") of the CURRY program for analysis. You can also *double-click* the data file or Study, or highlight the desired **Study** and click the  icon at the top of the display, or click the  icon when it appears as you position the mouse over the Study.

Insert Functional Data Files. Select this option to insert a Functional Data file into the Database. An Open file utility will appear to select the file. The file will be placed automatically in the Functional Data folder. Click on the "Files of type" drop-down list to see all of the file types that may be inserted. (With Nicolet files, you must have the Nicolet software installed in order to view the data files).

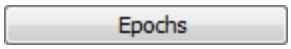


Insert Functional Data Folder. Some EEG formats (such as the Compumedics clinical EEG software, ProFusion, format) have their data in a folder structure. In CURRY7 an arbitrary file would be selected in such a folder (such as the .sdy file in a Profusion folder), but internally it was the folder that was used instead of the selected file. It is necessary in CURRY 8 (and in newer versions of Windows) to use the folder structure.

Using Multiple Averaged Data Files. You can insert any number of compatible .avg files (same channel labels, same AD rate, and same Start point) in the Functional Data folder. When you click **Open Study**, the **Functional Data Parameters Wizard** will appear for the first file having missing parameters. Those parameters will be used for all of the other files in the Study. After exiting the Wizard, the first of the files will be displayed as usual in the Functional Data display. Drag the sliding bar beneath the Functional Data display  , or click one of the arrow buttons , to

see the additional data files, in order. If there are differing numbers of channels across the files, CURRY will deal with this by creating parameter files for each new file with a different number of channels that is encountered.

Settings are applied across the data files. For example, the Timerange you set for one file will be the same for the other file(s). If you compute a *Rotating* dipole for one file, you can see the results for the other file(s) by dragging the sliding bar. You cannot perform independent parallel processing of the files using this method. That is, you cannot obtain results for one file, then slide the bar to see the next file and apply new parameters, while retaining the previous file's results (load the data files into two or more Studies and use them simultaneously, or use **Keep Results**  , to perform sequential processing of the files and compare results). You can, however, average the files (using 

in the 

panel under 

), and then perform any desired operations on the averaged data file.

If you put several files into the same study they will appear as epochs if they are short (less than or equal to 10s) and have the same length (number of samples). The number of channels (electrodes) and sampling rate have to be the same. If you put longer data segments (> 10s) into the same study, they will be concatenated (joined into a single file). In this case the segments can have different lengths (number of samples), and the Wizard will appear as needed. The concatenated data can be split into equal epochs by the back-to-back settings (**Epochs / Averaging**).

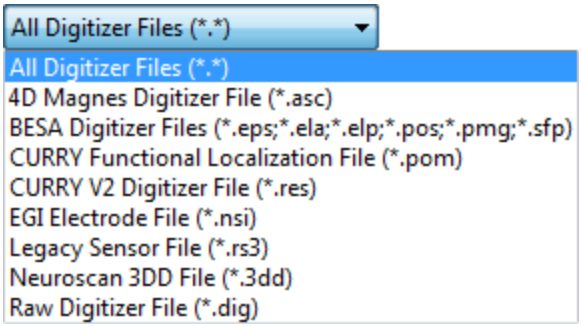
Averaging Multiple MRI Data Sets
You can average multiple MRI data sets in order to get an averaged MRI. The steps are described in the *Averaging MRI Data Files* tutorial, in the CURRY 8 Installation and Tutorials manual. Briefly, for each MRI data set you must first select **Talairach (R,A,S)** under **Coordinates**. Then, under **Image Data**, save each file using the **(*img,imd)** format, with the **Talairach** option enabled on the Save As dialog. Save the files to a common folder, with no additional MRI files. Load these in the Database. Create a new derived folder in the Database to contain the results. *Right click* on that folder and select **Insert Image Data Folder**, and then select the MRI folder containing the files to be averaged. Open that study to see the averaged files.

Using Multiple Continuous Data Files
If you load multiple like continuous data files (same channel labels, AD rate, number of channels) in the same Study, the files will be concatenated together (connected). A "un**x**" event will be place at the point the files are joined, and you will see "file start" at the top of the data display. Subsequent analyses (e.g., artifact reduction) will treat it as a single data file.

When creating epochs from the continuous data files, CURRY does not automatically exclude epochs that contain the un**x** events. You should exclude these epochs manually, as they do not contain valid data.

Insert New Simulation. This option allows you to create simulated data. Technically, it creates an empty .dat file and initializes the wizard with some default values for number of channels, sampling rate, etc., which you may modify. Please see the *Dipole Simulation* tutorial for an illustration.

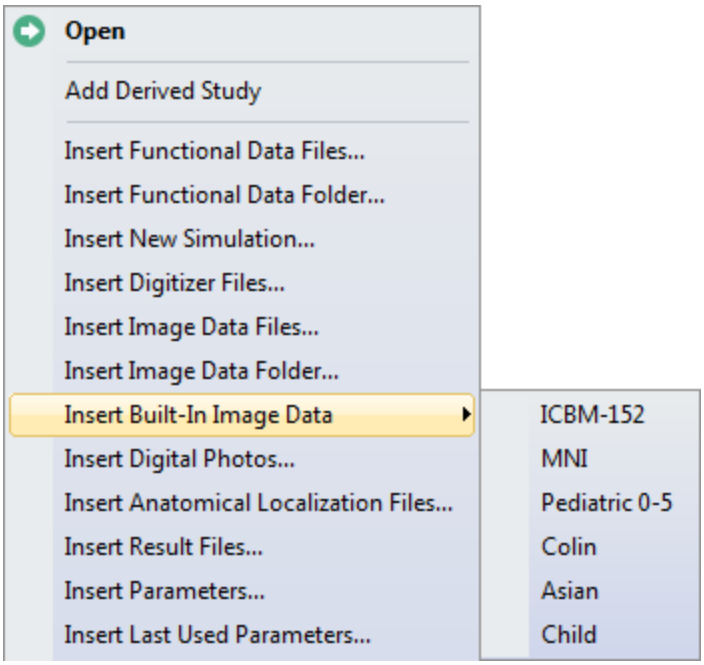
Insert Digitizer File. Select this option to insert a ”digitizer" file into the Database. A digitizer file is, for example, the .3dd file containing the electrode positions and functional landmark locations. Other sensor/landmark files can be loaded as well. An Open file utility will appear to select the file. The "Files of type" list shows the types of digitizer files that may be inserted. The file will be placed automatically in the Functional Data folder. This option is no longer necessary, as the same file may be selected from within the Wizard; however, it remains a functional carry-over from prior versions.



Insert Image Data File. Select this option to insert from one to five Image Data files into the Database (each should be a single file containing all the image slices). An Open file utility will appear to select the file. The file will be placed automatically in the Image Data folder.

Insert Image Data Folder. Select this option to insert an Image Data folder into the Database (a single folder containing all of the image slice files). An Open file utility will appear to select the folder. The folder will be placed automatically in the Image Data folder.

Insert Built-in Image Data. Insert one of the supplied Image Data sets.



ICBM-152. This is one of several templates based on the MNI 152 Database. Details are: 1×1x1mm template that includes T1w, T2w, PDw modalities, and tissue probabilities maps. Intensity inhomogeneity was performed using N3 version 1.10.1. Also included brain mask, eye mask and face mask.

MNI. This is the average of 152 T1 weighted stereotaxic volumes from the Montreal Neurological Institute (MNI).

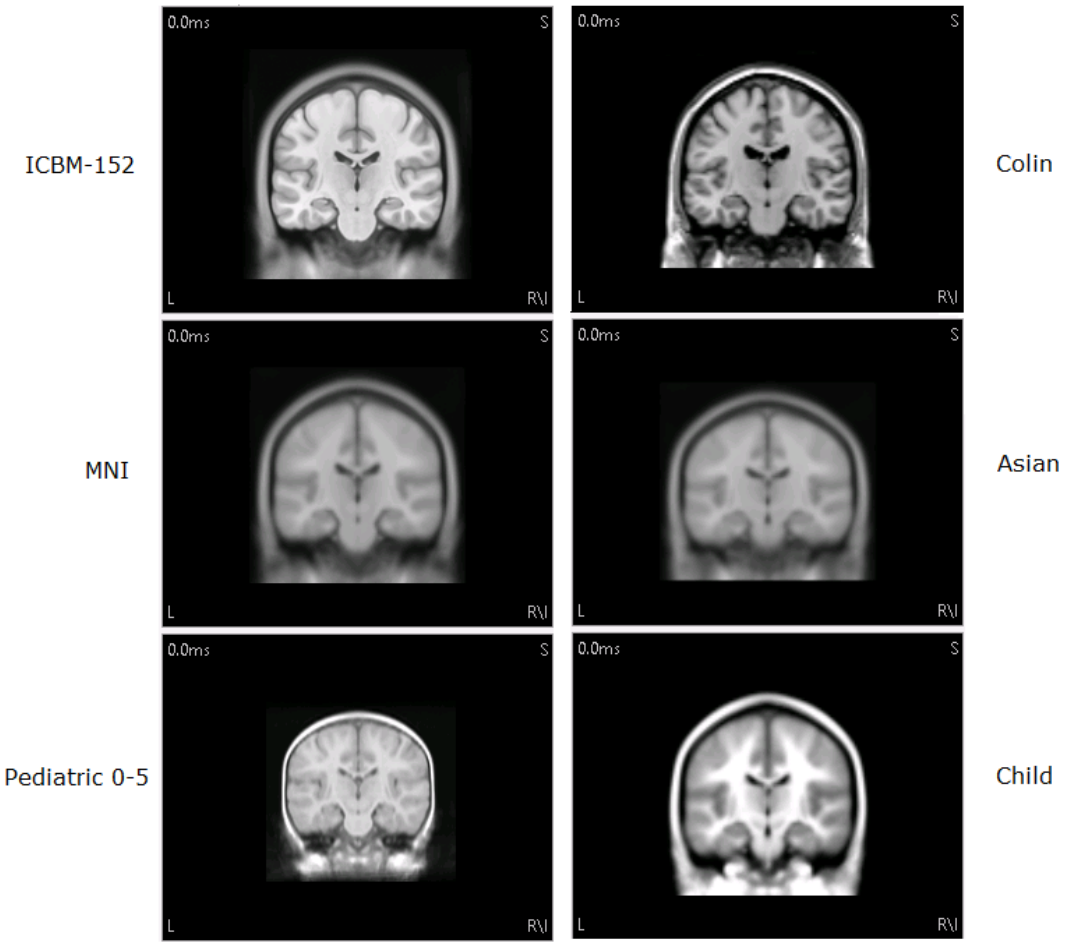
Pediatric 0-5. This is an unbiased magnetic resonance imaging template brain volume for pediatric data from birth to 4.5y age range. These volumes were created using 317 scans from 108 children.

Colin. This is the average of 27 T1 weighted scans from the same male subject. This data set has a very high SNR (signal to noise ratio), resulting in very clear structure definition.

Asian. The Asian MRI is a scaled version of the ICBM-152 dataset (also known as MNI brain). Scaling was performed based on average Talairach dimensions that have been determined based on MRI scans from 62 healthy Chinese subjects. MRI scans were performed by Dr. Wen-Jui Kuo at the Laboratory of Cognitive Neural Science, Yang-Ming University, Taipei, Taiwan. Due to the Talairach-based, piecewise linear scaling used, the Asian MRI in CURRY is fully compatible with the built-in anatomical and functional atlas.

Child. The child average is based on 175 T1 weighted scans from healthy children, ages 4-18.

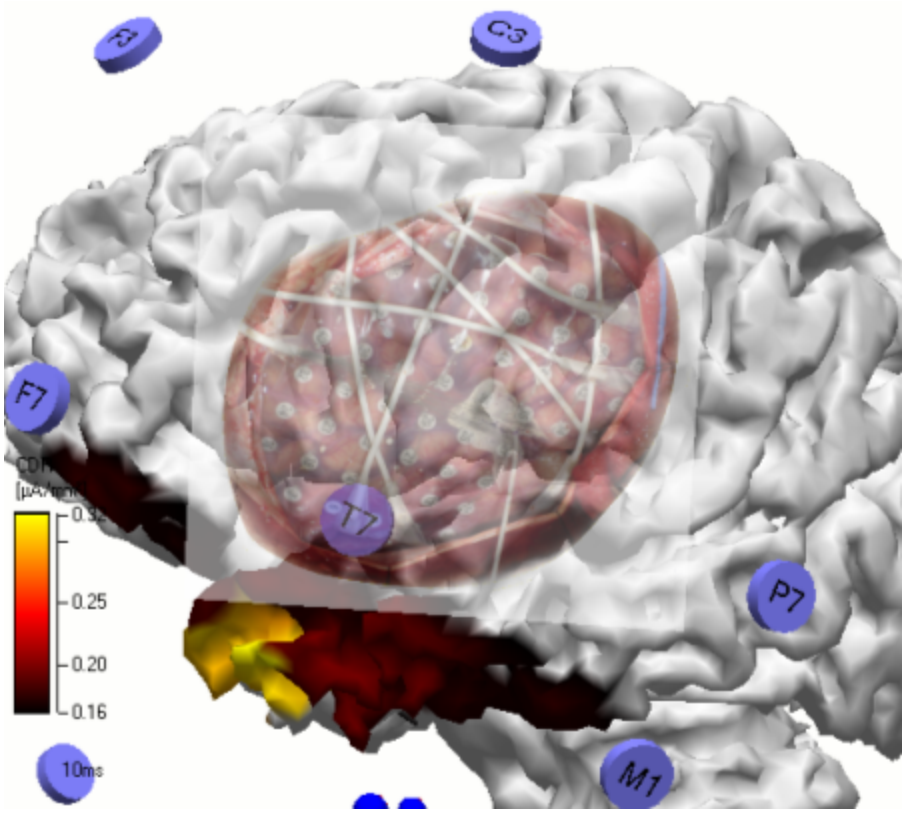
Here are coronal views of the six data sets.



To find out more about the datasets, please see the McConnell Brain Imaging Center (McGill) web site *http://www.bic.mni.mcgill.ca/ServicesAtlases/HomePage*.

Note
You may control which built-in MRI to use with the **Global Parameters**.

Insert Digital Photo. Use this option to select a graphics file that can be used in the 3D View, such as in the following display, where a real-life 2D image of a cortical grid is superimposed on the segmented cortex.



Insert Anatomical Localization File. Use this option to insert an anatomical localization file, if you have one, or it may be inserted from within the Wizard instead. The anatomical locations contain only the landmarks. This is just needed in case you do not have PAN landmarks in your digitizer (*.3dd) file (which rarely occurs), or you want to overrule the PAN transformation (which also rarely occurs).

Insert Result File. If you have saved source reconstruction results, using **Source Results → Save Results As**, you can insert that file(s) into the Database at various levels using **Insert Result File**. To load the file (make the results visible), you need to right click on the results file and select **Load** (or **Load All Results** if you want to load all results files you have inserted).

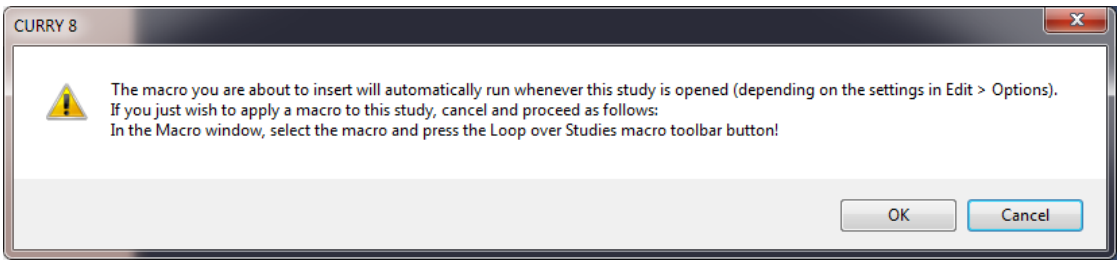
Insert Parameters. This option allows you to select and insert previously created Study Parameter files (.cfg). Please see the **Global, Study and Other Parameters** section above.

Insert Last Used Parameters. This option allows you to select and insert previously created Last Used Parameter files (.cfg). Please see the **Global, Study and Other Parameters** section above.

Insert Logbook. The Logbook is a text file containing the history of operations you have performed. Please see the **History Options** section for more details.

Insert Macro. Use this option to select a Macro that will run automatically whenever the study is opened. Clicking it displays the confirmation dialog. Click OK

to select the Macro that you wish to run automatically whenever the Study is opened.



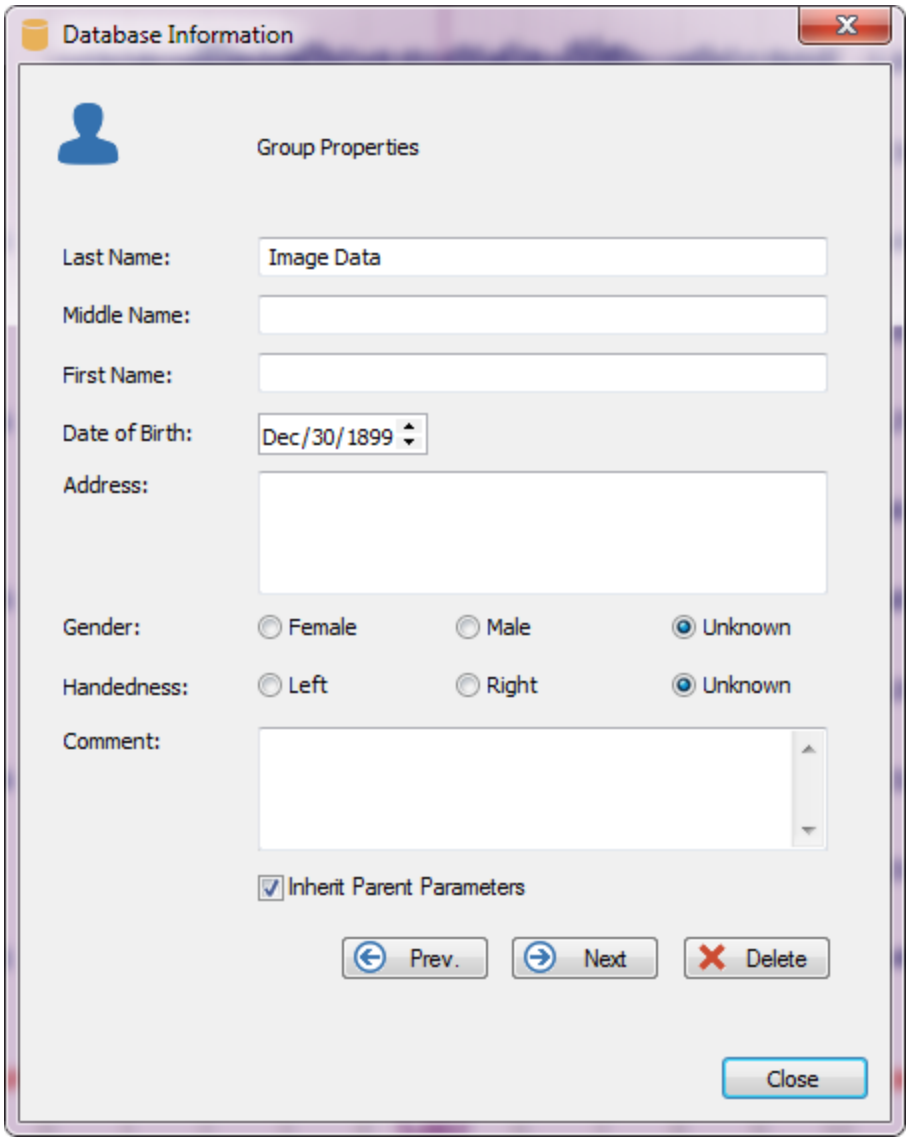
Add New Subject  . Adds a new Subject under the Group.

Add New Study  . Adds a new Study under the Group, bypassing the Subject level.

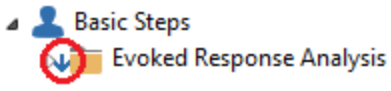
Delete Group. Deletes the highlighted Group.

Rename (*F2*). Allows you to rename the highlighted Group.

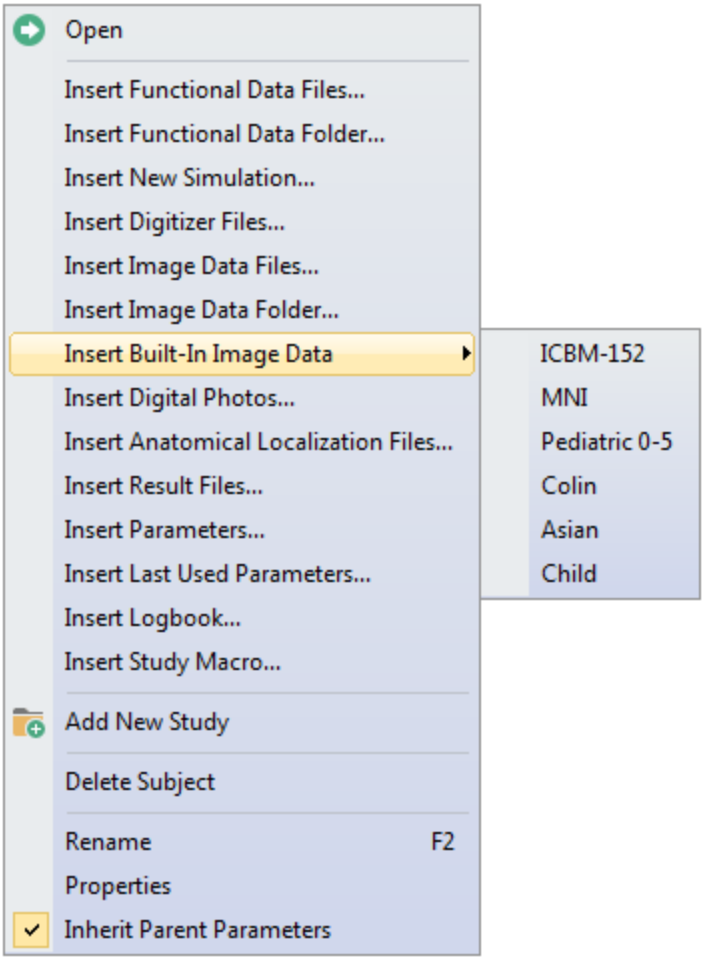
Properties. Selecting Properties will display the information dialog for Groups. The same screen is seen when you select **Database → Show Form**, with the Group highlighted. Here you can add information about the experiment.



Inherit Parent Parameters. At the Subject and Study levels, you have the additional option to "inherit the parent parameters" or not. *Right click* on a Subject or Study and select **Inherit Parent Parameters**. Small down arrows will appear to indicate the parameters from the parent file can flow into the child file. The default setting for Subjects is enabled; for Studies the default setting is disabled.



Subjects. Click the *right mouse* button on a Subject line to see the displayed menu. Most of the options are the same as those for Groups (see above). The differences are listed below.

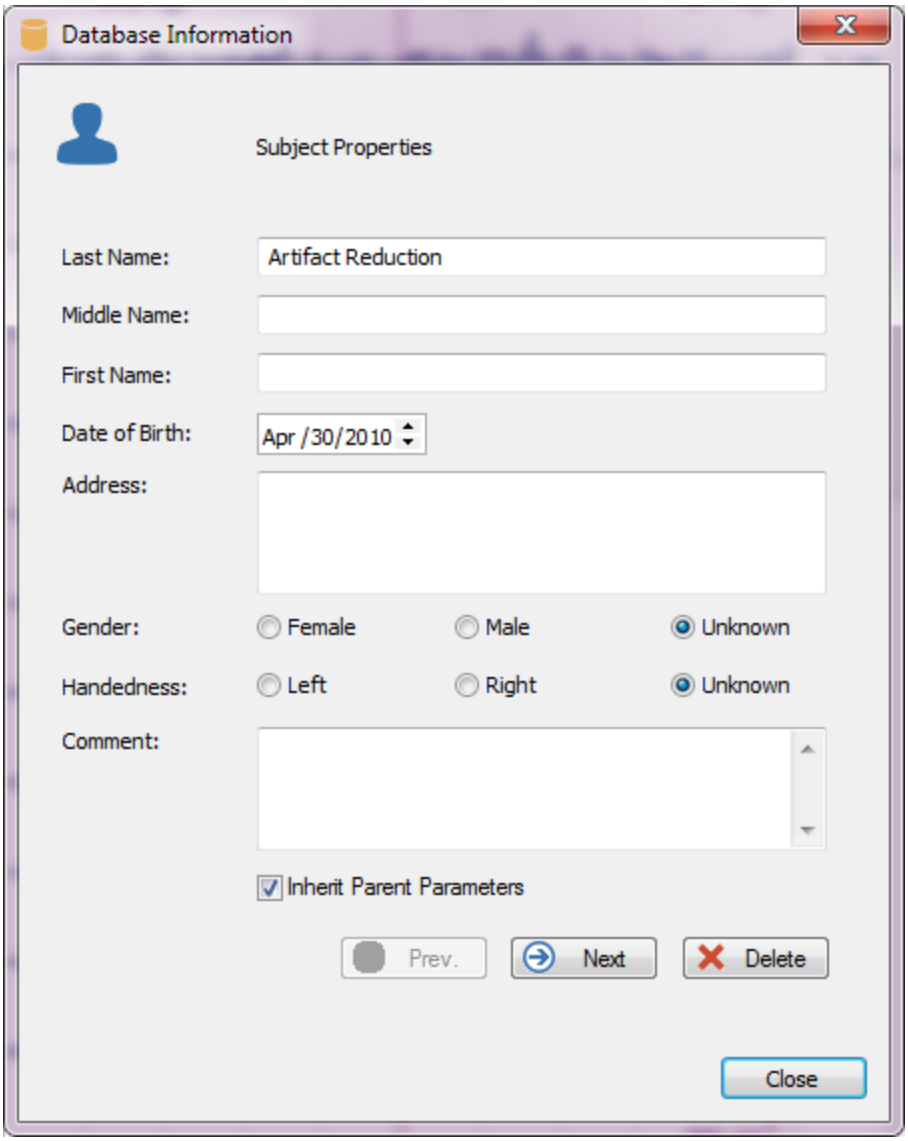


Add New Study  . Select this option to add a new Study. A 

will appear under the Subject.

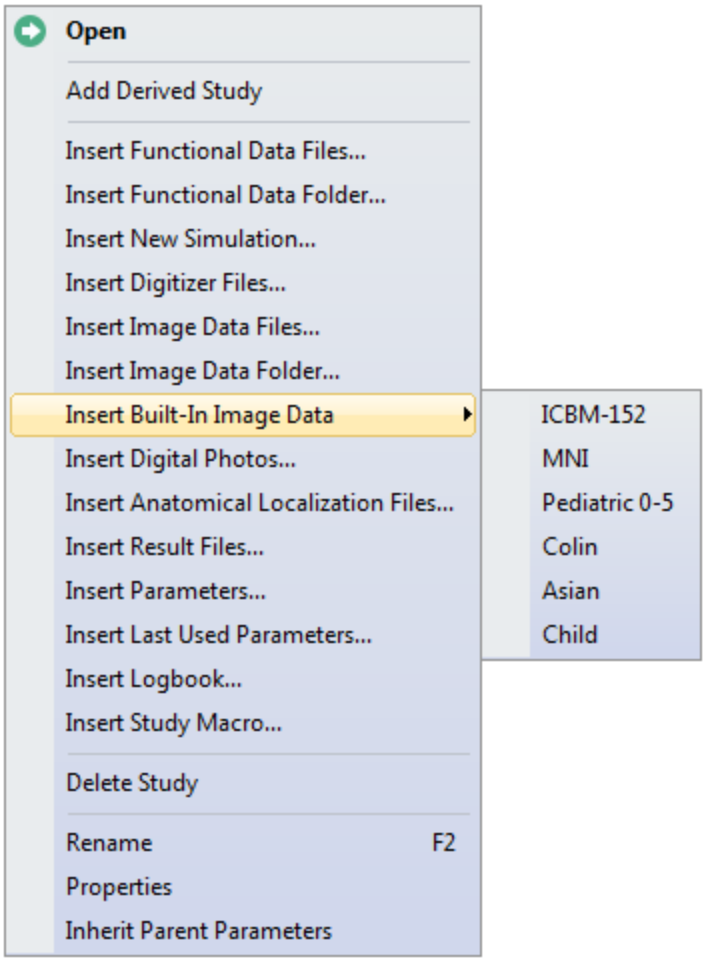
Delete Subject. To delete a Subject, *right click* on the Subject and select this option.

Properties. Selecting Properties will display the information dialog screen for Subjects. This is the same screen as seen when you select **Database → Show Form** with the Subject highlighted.



Inherit Parent Parameters. When enabled, this option will allow the current Subject to inherit Study Parameters from the parent folder above it (see the **Global, Study and Other Parameters** section above).

Studies. Click the *right mouse* button on a Study line to see the displayed menu list. Most of these are the same options described above under Groups. The new ones are described below.

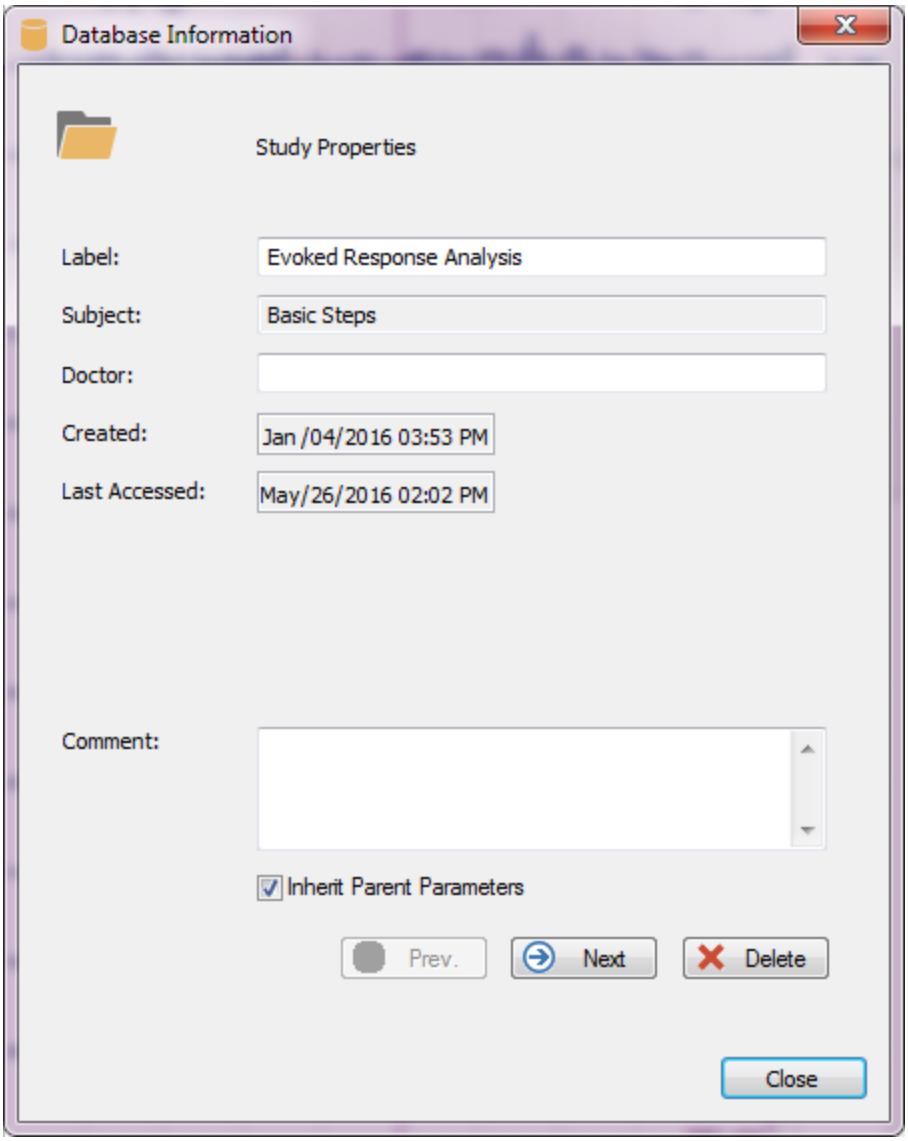


Add Derived Study. Select this option to add a derived Study. A 

will appear under the Study.

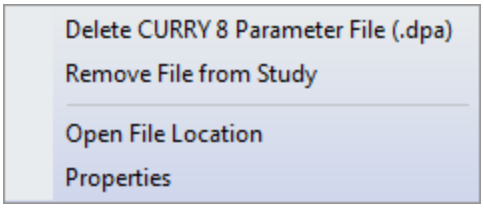
Delete Study. To delete a Study, *right click* on the Study and select this option. The Study is then removed from the Database (and *not* deleted from the hard drive).

Properties. Selecting Properties will display the information dialog for Studies. This is the same screen as seen when you select **Database → Show Form** with the Study highlighted.



Inherit Parent Parameters. When enabled, this option will allow the current Study to inherit Study Parameters from the parent folder above it (see the **Global, Study and Other Parameters** section above). This feature is enabled for Groups and Subjects, and disabled for Studies by default.

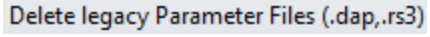
Data Files. Click the *right mouse* on an individual data file to see the displayed menu list. The options on the list will vary somewhat depending upon the type of data file selected.



Delete CURRY 8 Parameter Files (.dpa). This option deletes the parameter file that is created when you import the file via the **Functional Data Import Wizard**. If you delete this file, the Wizard will appear again when you open the Study (providing there really is missing information).

Note

Previous versions of CURRY created the .dap and .rs3 files to contain the various parameters. Beginning in CURRY 8, these files are replaced with the single, simplified .dpa file, although previously created .dap and .rs3 files are still read. In that case, you will see the CURRY 7 message:

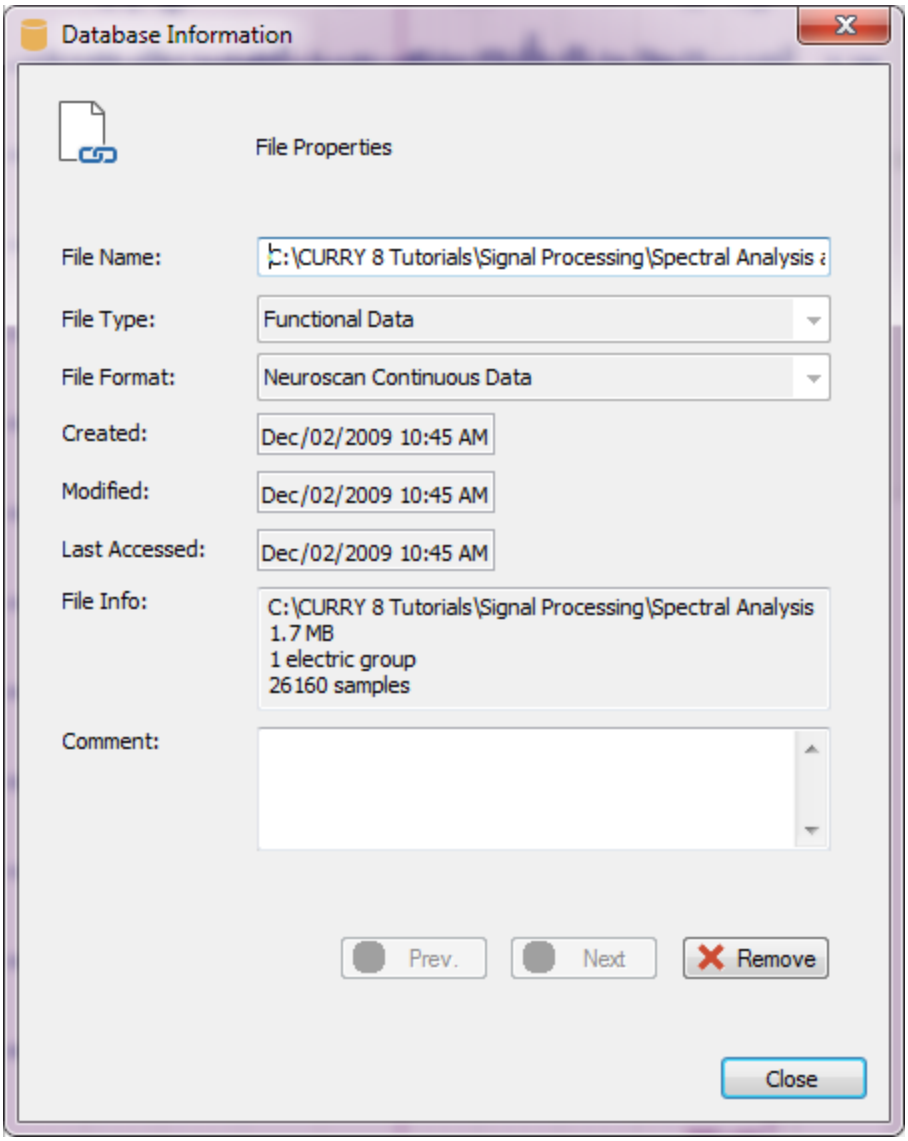


.

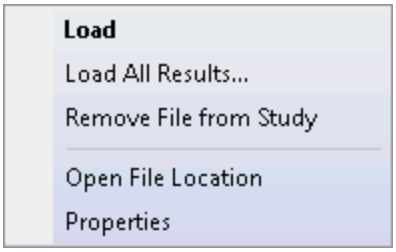
Remove File from Study. This removes the file from the Study. *It does not remove it from the hard drive*.

Open File Location. This opens Windows Explorer to the folder containing the data file.

Properties. Selecting Properties will display the information dialog for data files. This is the same screen as seen when you select **Database** → **Show Form** with the data file is highlighted.



Source Results File. The **Source Results** folder contains a list of saved Source Results files (.map, .ele, .dip, etc. extensions) that can be loaded into the current study. *Right clicking* on a saved results file displays the following list.



Load. This option is used to load a selected result file that has been previously saved.

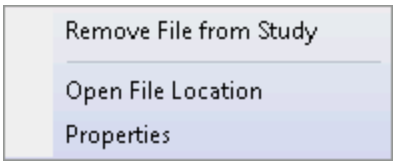
Load All Results. This option loads all saved results.

Remove File from Study. To remove a results file, *right click* on the file and select this option. (This does not delete the file itself).

Open File Location. This option opens the Windows Explorer program. This is a convenience for locating files, renaming them, changing their properties, etc.

Properties. Selecting Properties will display the information dialog described above, when you select **Database** → **Show Form**, with the results are highlighted.

Study Parameter Files (.cfg configuration files). Selecting this option displays the following list.

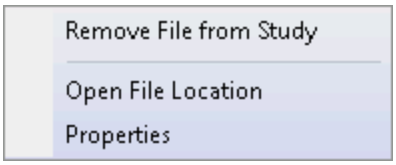


Remove File from Study. To remove a configuration file, *right click* on the file and select this option. (This does not delete the file from memory).

Open File Location. This option opens the Windows Explorer program to the folder containing the .cfg file.

Properties. Selecting Properties will display the information dialog described above, when you select **Database** → **Show Form**, with the configuration file highlighted.

Macro Files (.mac files). Selecting this option displays the following list.



Open in Editor. This opens the .mac file in a text editor (Notepad), where the contents can be modified and saved.

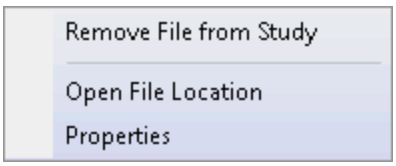
```
Mainframe.MacroParameterDialog = Event List
FunctionalData.DataReferenceChannels = <None>|<None>
FunctionalData.DataDeselChannels = A2;X1;X2;H+;H-;V-;EKG-
FunctionalData.ThresholdChannels = EKG+|V+|<Off>|<Off>|<Off>
FunctionalData.GroupLabel1 = tones
FunctionalData.GroupLabel2 = pictures
FunctionalData.ProcessDataMode =  8
FunctionalData.StartSample =  16396
FunctionalData.ActualSample =  4604
```

Remove File from Study. To remove a configuration file, *right click* on the file and select this option. (This does not delete the file from memory).

Open File Location. This option opens the Windows Explorer program to the folder containing the .mac file.

Properties. Selecting Properties will display the information dialog described above, when you select **Database** → **Show Form**, with the configuration file highlighted.

Logbook Files (.txt files). Selecting this option displays the following list.



Open in Editor. This opens the .txt file in a text editor (Notepad), where the contents can be modified and saved.

```
Study accessed 7/25/2012 1:06:46 PM

PCA components for 199 samples [SNR]:  2.7,  1.1,  0.
PCA components for 199 samples [%]: 44.1,  17.3,  11.
```

Remove File from Study. To remove a configuration file, *right click* on the file and select this option. (This does not delete the file from memory).

Open File Location. This option opens the Windows Explorer program to the folder containing the .txt file.

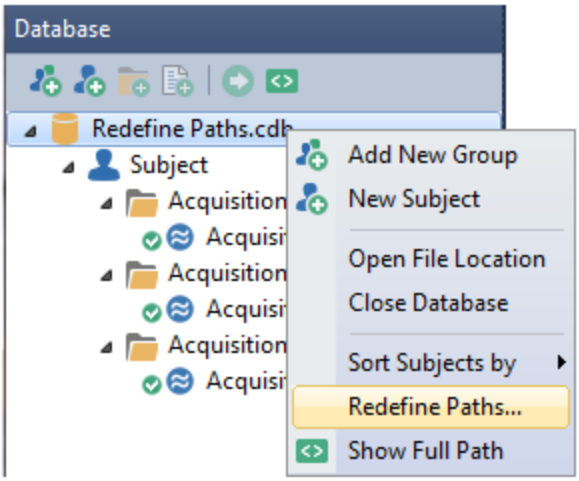
Properties. Selecting Properties will display the information dialog described above, when you select **Database** → **Show Form**, with the configuration file highlighted.

13.1 Multiple User Access of the Database

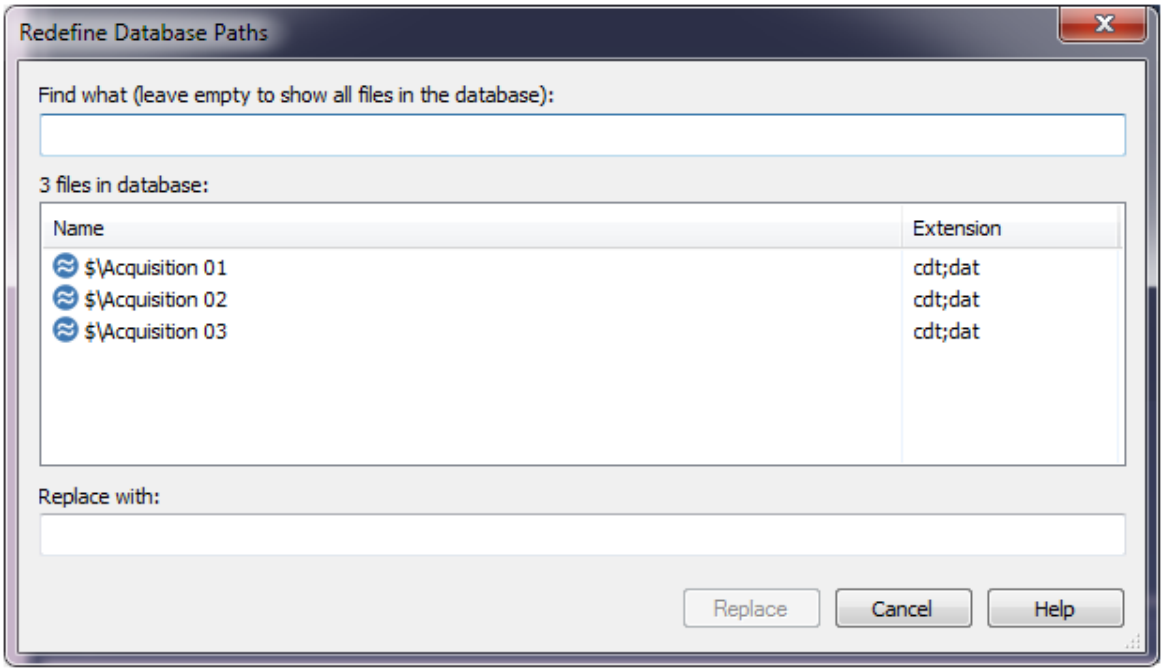
In some situations, it may become advantageous for you to relocate your data files and the Database to a server that can be accessed by multiple users. This is possible, however, CURRY was not designed to be fully compatible for *concurrent* multi-user scenarios, and there are some caveats you need to know and manage yourself.

Is it possible to move the data and Database to a server, so the recording system and CURRY "readers" always see the same files?

If you have placed the files in the same folder (or below) as the Database file (.mdb or .cdb), the files will be referenced relative to the .mdb or .cdb file and you can simply copy the Database file together with the data files to a different location. You can quickly check how the files are referenced by *right clicking* onto the Database and selecting **Redefine Paths**.



Relative paths start with "$". Absolute paths will most likely not work after copying the data and Database (unless they are stored under the same drive letter and folder as before) and may have to be redefined.

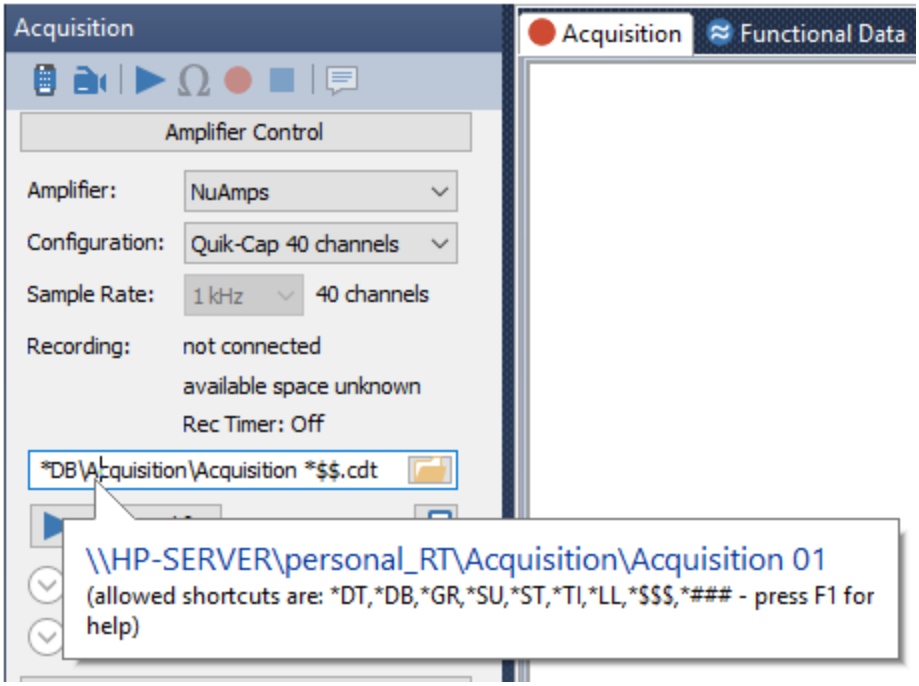


It is possible to work on the same Database from multiple work stations at the same time, but be aware that changes in the Database are not visible instantly on every work station. Changes from other workstations are visible after restarting CURRY or reopening the Database. And since the actual data files are accessed through the file system, CURRY cannot prevent overwriting the same file from different work stations, so this is something you have to be careful with, as well.

Should you record to a central Database and data folder?

If you want to access the Database and data remotely, you have to make sure that only relative paths are used for all files. You can access your Database either by directly referencing your shared network folder, or by mapping the network folder to a drive letter in Windows.

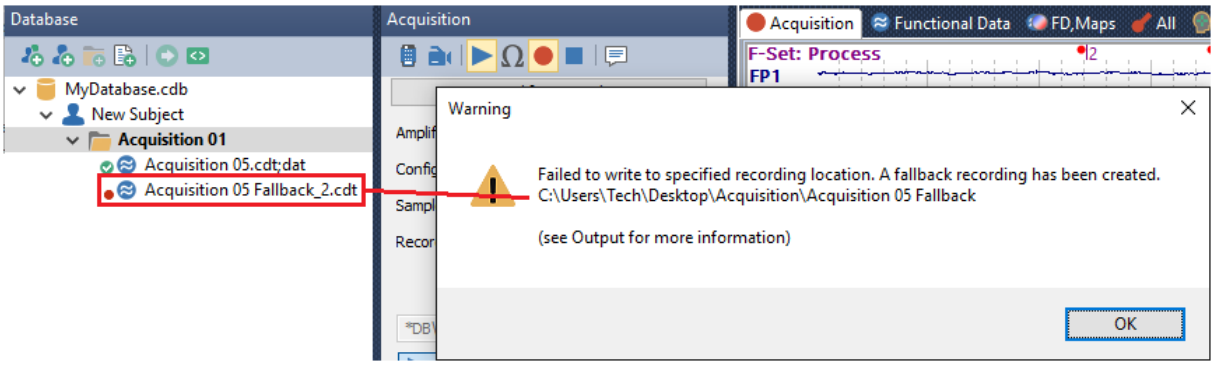
For your recordings it works best if you specify the recording path to start with the path your Database is in (use *DB as shortcut).



Go to **File → Parameters → Save Global Parameters** to permanently use this recording path. Use the **Save Global Parameters** option with care, and make sure no other CURRY instance is running while saving (to prevent inconsistencies).

What will happen to the recording if the network connection fails?

Should the network connection fail during recording, CURRY will automatically create a fallback recording on the local desktop.



Once this happens, CURRY will continue recording to the fallback location until a new acquisition is started and the network folder is accessible again.

After you finished recording, you have to manually copy the fallback recordings to your desired network folder. Insert the original recording and the fallback recording into the same study to concatenate them.

Will the montages and configurations made on the recordings system automatically be seen on the readers?

To achieve this, you have to configure CURRY to use a common folder (which is also placed on your network drive) for its user specific settings. Modify the *Settings folder.txt* file (shown below) to your needs and copy it into the CURRY installation folder (typically *C:\Program Files\Neuroscan\Curry 8*) of all CURRY installations that you want to use the same settings. As mentioned before, CURRY does not prevent you from overwriting the same montage or configuration when it is accessed by multiple clients simultaneously.

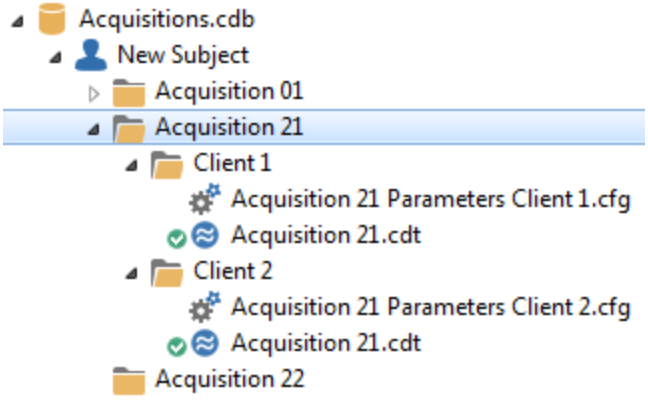
CURRY also stores some last used session parameters to a file that is used by all clients. The client that closes CURRY last will be the one whose parameters will be used for the next instance of CURRY that is started. This mainly affects settings made in the **Edit → Options** dialog, the expand state of the Advanced buttons, the last used Database, some Macro replay settings and some acquisition settings. While this may be a source of problems, you will likely not notice anything.

Can a client reader connect to an ongoing recording?

No. A file that is being recorded cannot be opened by another client. (The NetStreaming functionality makes it possible to receive the same data that the acquisition machine is seeing).

If two clients open the same recording, what happens if they make different changes and save at different times?

Two clients can open the same recording, but only one client should make changes with the intention to save them at a time, especially if "saving" means overwriting the existing data file or event table. It is possible for both clients to work on different Parameter files that use the same data file. For example, with a Database setup like this, each client can freely work with their own set of parameters, but use the same data file.



Settings folder.txt

```
\\hp-server\personal_RT\CurrySettings\
#
# if the first line of this file contains the full path of an existing folder,
# this folder will be used for storing and accessing defaults and settings,
# instead of e.g. C:\Users\Tech\AppData\Roaming\Neuroscan\Curry 8\
# example: C:\Settings\
```

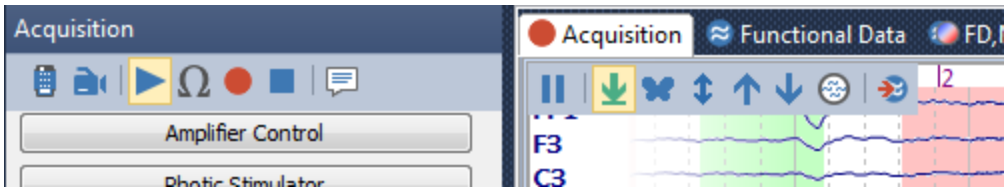
14 Acquisition

The Acquisition module of CURRY is used to acquire data from many of the amplifier systems produced by Compumedics Neuroscan, including *SynAmps RT*, *NuAmps*, *Neuvo*, and *Grael*. A *Simulator* option allows you to replay existing data files for demonstration and testing purposes.

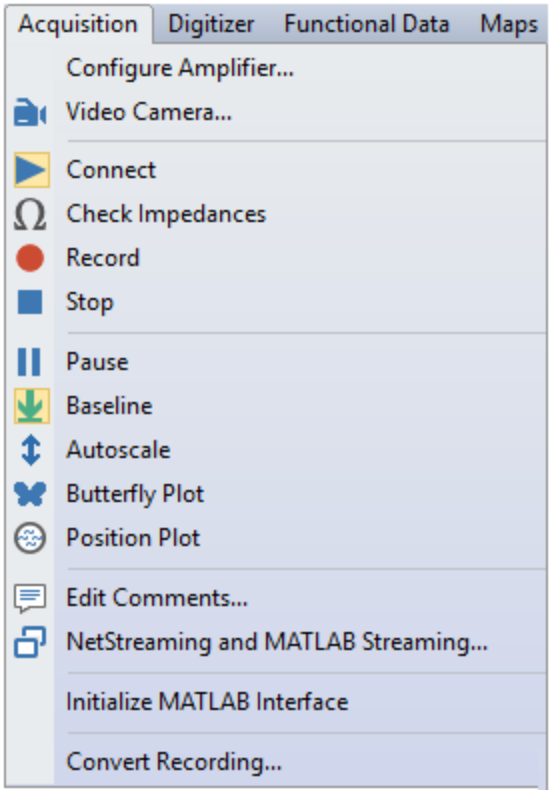
DO NOT CONNECT OR DISCONNECT THE USB CABLE TO THE AMPLIFIERS WHEN THEY ARE ON (the system may crash). Rebooting will be necessary.

IMPORTANT REMINDER
Before you start recording data for a project, *always* run a few pilot subjects first, and go through the *entire* analysis sequence to ensure that everything will work as you intend. Every so often we hear from a user that they have collected all of their data, and then they find some fatal flaw that prevents them from doing the analysis they had intended. I.e., the entire data set is not useable. Detecting the problem early on would have avoided it, and running pilot data all the way through is the best way to detect any problems.

The relevant parts of CURRY are accessed via the icons on the Acquire Toolbar  . (The Acquisition data display shows more icons for continuous  and averaged  data displays).



These are the acquisition options listed on the Main Menu Bar. All may be accessed from the Toolbar icons.



Configure Amplifier. Accesses the amplifier configuration dialogs (see **Configuration Options** below).

Video Camera. This option will show or hide the video camera window, and has the same function as clicking the Video icon on the Acquisition toolbar.

Connect. Connect to the selected amplifier.

Check Impedances. Click this option to view the impedance display.

Care

Impedance tests should only be performed with surface EEG, and never if you are recording from cortical grid or depth EEG electrodes. There is an option in the Configure Amplifiers section to disable

*impedance tests (**Allow Impedance Test**), which is intended for use with grid and depth recordings.*

Record . Click the Record button to start saving the data to the hard drive.

Stop . Disconnect from the amplifier (or stop Impedance or stop Recording, and then disconnect).

Pause . Pause display.

Restart Average . Restarts the online average.

Select Average . Used with online averages to select another average to Overlay or take the Difference. (See **Select Average**).

Baseline . Centers traces in their display space (removes DC offsets from the display). Data are not affected.

Autoscale . Autoscales the display of all traces (data are not affected).

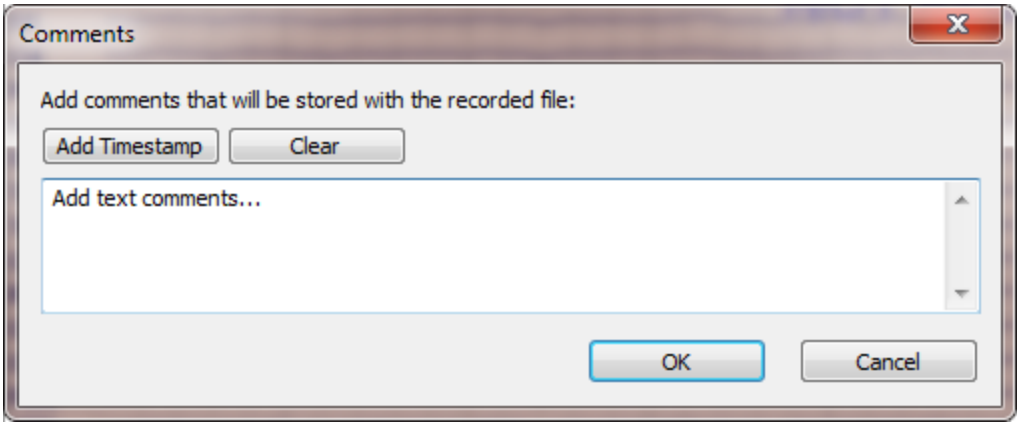
Scale Waveforms Up or Down . Rescales the waveforms (display only).

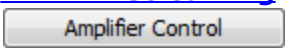
Butterfly Plot . Superimposes all channels.

Position Plot . Displays channels in separate windows about the head.

Send Page to Functional Data . Sends the displayed page to Functional Data for further online processing.

Edit Comments. This allows you to add text comments that will be saved with the file. You can include a Timestamp if desired. When you open the file offline and go to **Functional Data** → **Show Information**, you will see the comments there.

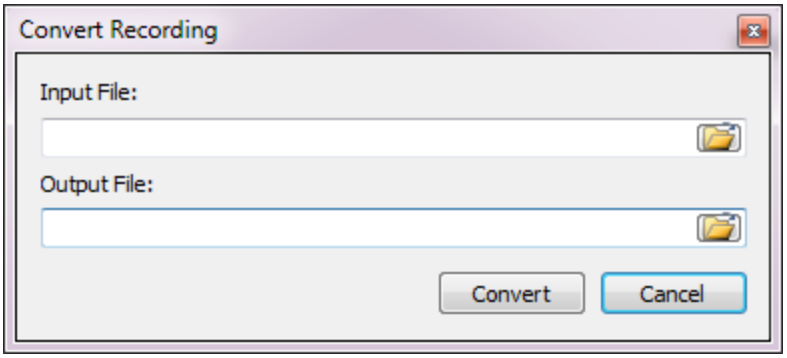


NetStreaming and MATLAB Streaming. This is a shortcut to the **NetStreaming and MATLAB Streaming** dialog, also accessed from the  icon in the 

panel.

Initialize MATLAB Interface. This option can be used to start and initialize MATLAB manually if you plan to use it during acquisition. Otherwise, MATLAB will be initialized when it is needed, which might interrupt acquisition since it can take quite a while. This is especially the case with NuAmps where there is a danger of a buffer overrun. The option can also be used for troubleshooting to check whether the MATLAB interface is working correctly.

Convert Recording. This option was added to the Acquisition part of CURRY so that those with Acquisition Only licenses may export files to other formats (this was formerly available offline only and required an additional license). To convert a file, just follow the directions.

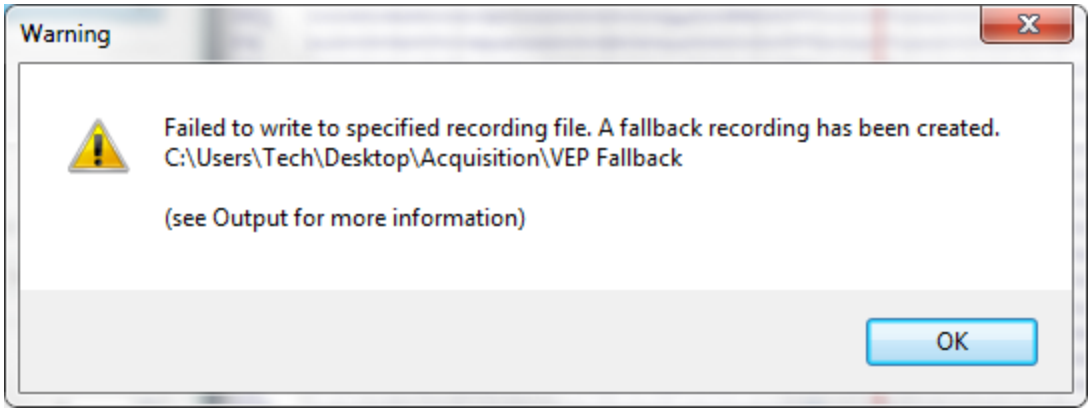


Crash Protection
The *continuous data* in the .cdt file is protected from program crashing up to the last block that was written. You will lose only about 0.1 seconds of data prior to the crash. Concerning *events* that are recorded to the .ceo file, you can lose up to one minute, in the worst case scenario. However, the .cdt file contains the raw trigger channel as a data channel, so you can always restore events that came in through the trigger channel in the last minute. Only events that were not created from the trigger channel (annotations, template or artifact events) can be partly lost after a crash (up to one minute in the worst case).

Average files are written every 10th time an average changes. Once a file is written, it cannot get lost during a crash. So, in case of a crash, the last valid average file will be missing up to 10 epochs. In the rare case of a crash WHILE the average file is being written, you will find a file with the name "<your average filename>_copy" which is the last valid .avg file. The same is true for the event file (.ceo) when the computer crashes while writing this file.

Lost Connection Fallback Folder
If writing the data to disk fails (for example due to FAT limits, or when the connection to external drives or network drives is lost), CURRY will automatically try to create a "fallback" recording in the default folder (the Acquire folder on the desktop) and continue the recording to that location.

If this happens, you will see a message such as the following (note the "Fallback" file in the Database):

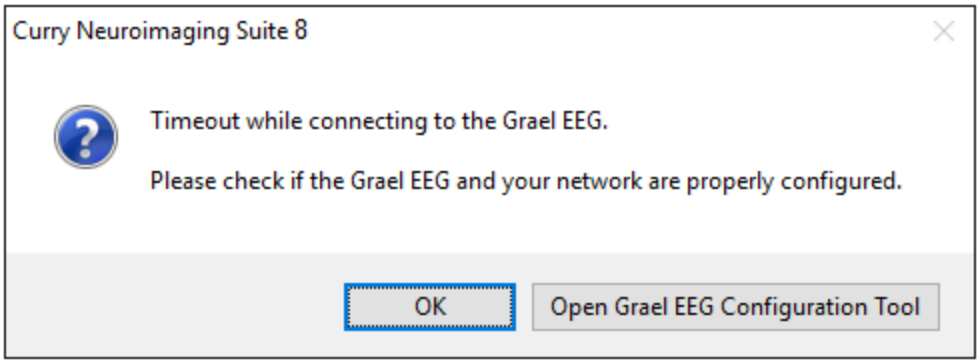


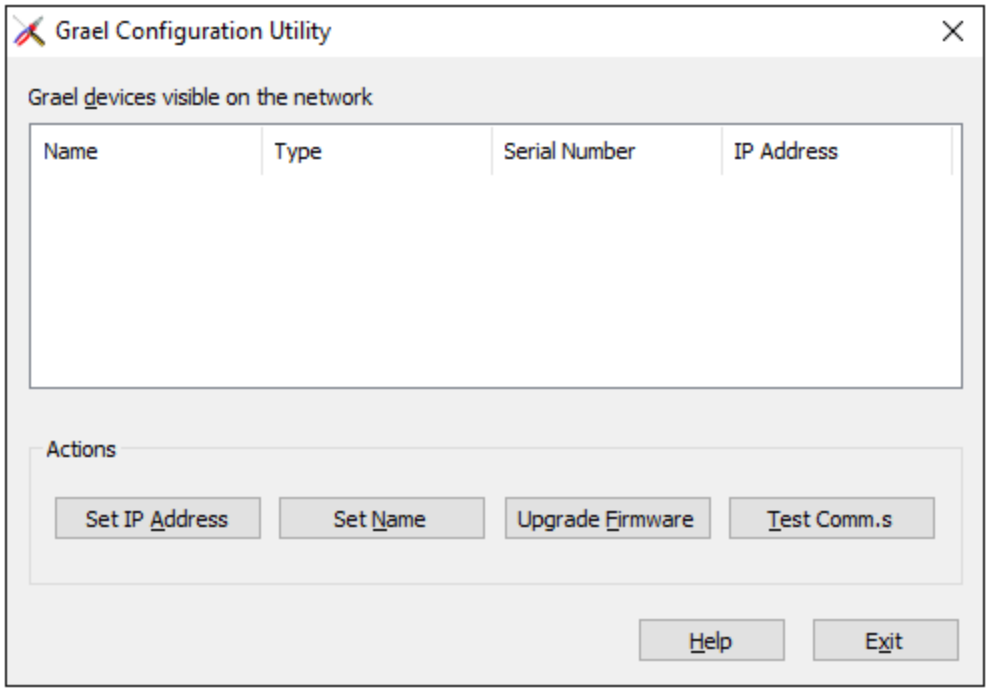
If the Fallback recording fails, the recording will stop.

Once you have begun recording to the fallback destination, you cannot go back to the original destination in the same session. You have to disconnect and connect again.

Place the original and fallback files in the same Study, and they will be concatenated when you open the Study.

Timeout Messages
Occasionally you may see an error message about CURRY timing out while trying to connect to your amplifier. These messages will be amplifier specific, such as in the case of Grael, shown below, where CURRY will try to help you solve the issue. In some cases, you will see a **Help** button (see Grael example below) that will open the amplifier manual.





Special limitations with the Grael trigger module. If you are using the trigger unit with the Grael PSG or EEG amplifier, you should be aware of the following limitations:

1. Triggers are only registered when acquiring data with the fastest sampling rate (2048Hz).
2. Only stimulus events from 1-64 are registered; no response events are recognized.
3. The maximum trigger frequency is 40 triggers per second.
4. The "Record Event Duration" option does not work with the Grael.

Special limitations with the CURRY Express version. If you have an "Express" version of CURRY, the following limitations apply:

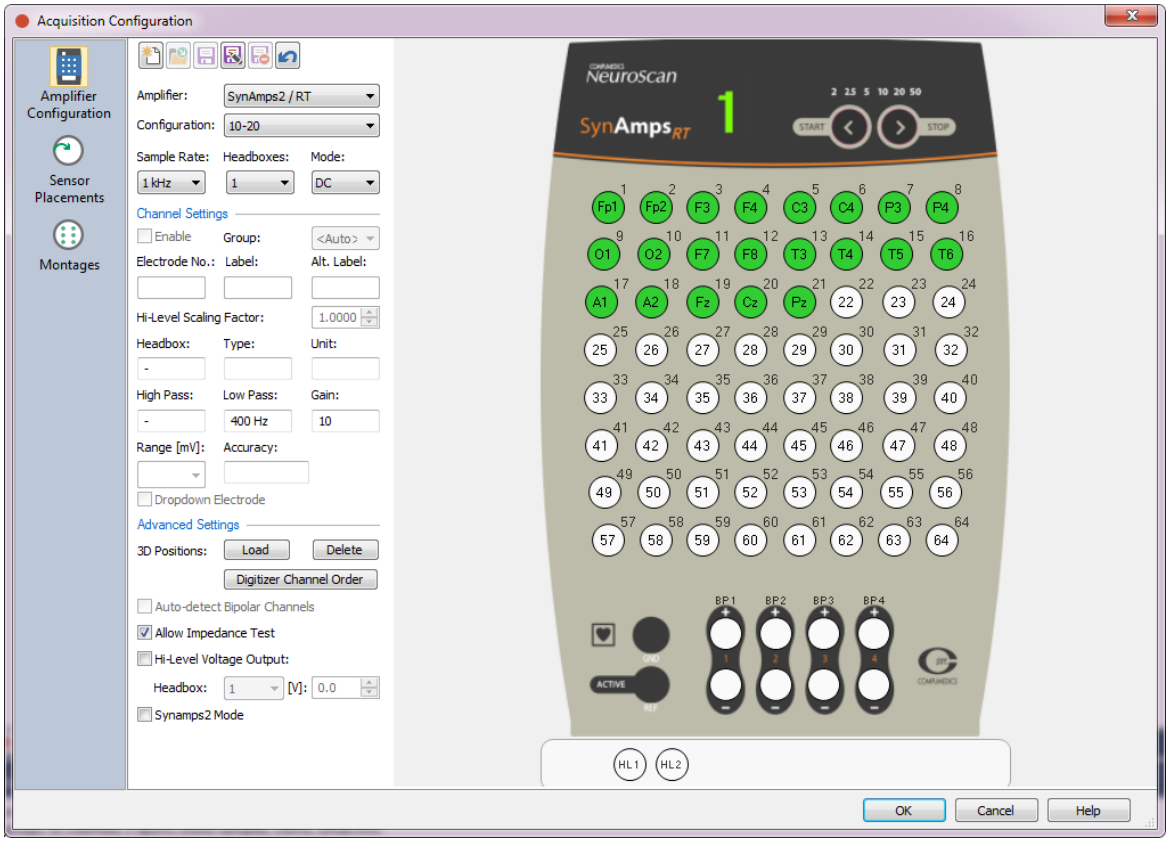
1. Functional Data is limited to opening files that could have come from a NuAmps (1000 Hz and max 41 channels) or Grael (max 2048Hz and max 60 channels).
2. Supported amplifiers: NuAmps, Grael EEG, Grael PSG, Simulator (same restrictions as Functional Data).
3. No photic stimulator support.
4. It is not possible to combine the Express version with the Video module.

14.1 Configuration Options

These are the options that are accessed from the **Acquisition Configuration** icon on the Acquisition Toolbar.

The settings are used to configure the amplifiers for acquiring data, placement of the sensors, and montages.

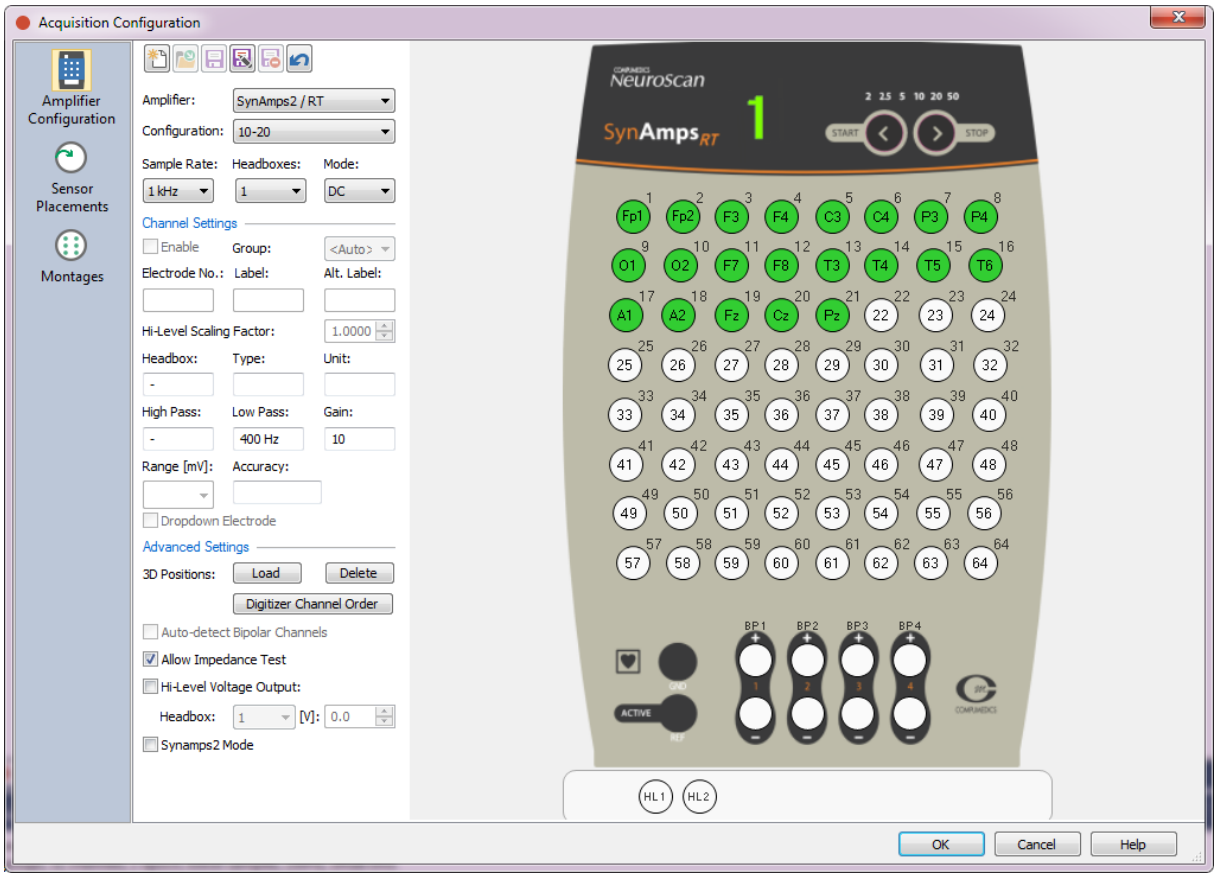
Clicking the button displays the following screen. The three buttons on the left access the amplifier configuration, sensor placement, and montage configuration screens.



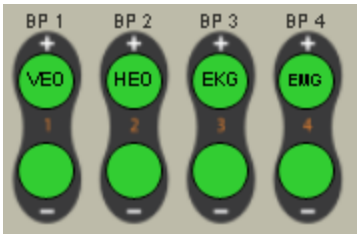
14.1.1 Configure Amplifiers

These options are used to configure the amplifiers for acquisition. You will see a different figure depending upon the amplifier you have; however, the functions of the settings are similar across amplifiers.

With *SynAmps2/RT* and *Neuvo*, there are 70 channels per headbox: 64 referential channels, 4 bipolar channels, and 2 High Level Input (HLI) channels. The 8x8 grid shows the 64 referential channels, with the channel order dictated by the wiring in the cap.

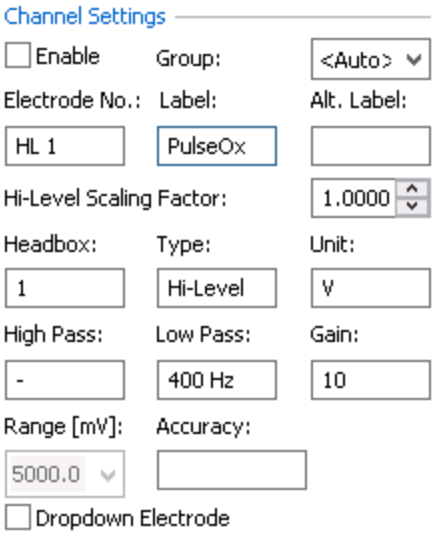


The **Bipolar** channels are seen below the 8x8 grid.



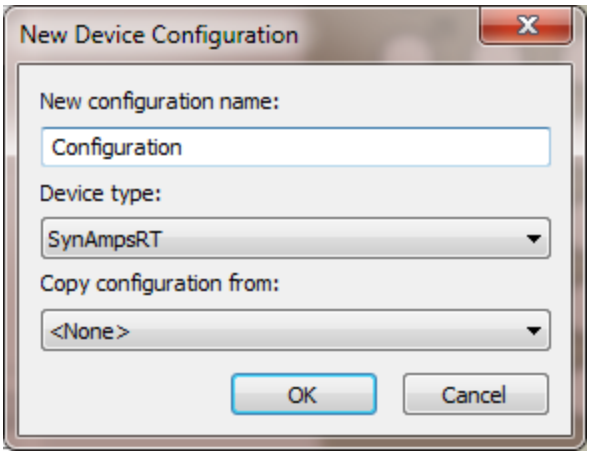
The **HLI** channels are seen at the bottom.

Click on one to see the Channel Settings. HLIs are typically used to input the analog voltage outputs from peripheral devices, such as a pulse oximeter (Pulseometer). There are the only safe inputs to use for connecting to other devices. HLIs can receive voltages from -5.0 to 5.0V. Please see the *SynAmps RT User Guide* for additional information, including a pinout of the connector.



Toolbar Icons  . These icons are present in all of the Configuration dialogs. They will change somewhat in content across the three configuration screens, but the functions remain the same.

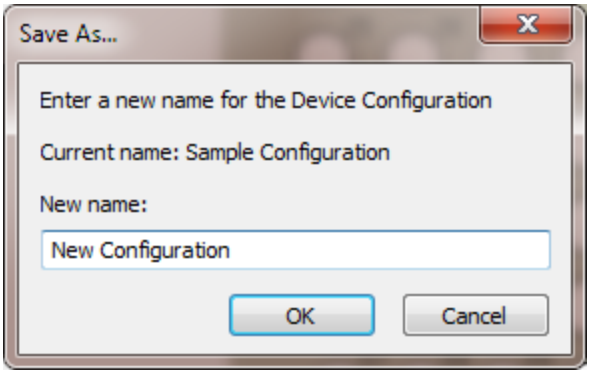
 **New Configuration**. Click this option to create a new configuration file. The following dialog will appear, where you can name the new file. Select the Type of amplifier from the drop-down list. Use **Copy configuration from** to use configuration information from an existing file. The file will be called *SynAmps RT - New Configuration.xml*, in this example. Please see the **Target Folders for Windows 7** section. The amplifier type is added automatically, and you will only see .xml files for the type of amplifier you select later on (for simplification).



 **Open File**. This is used with the Montage Editor only.

 **Save**. Click this option to save any changes to the currently selected configuration file.

 **Save As**. Click this option to save the configuration file with a different file name (or overwrite an existing file).



 **Delete**. Deletes the current configuration file (confirmation dialog will be seen).

 **Undo**. Click to undo all changes made to the current device configuration since it was last saved.

Amplifier Settings

Amplifier. Select the amplifier that you are using.

Configuration. These are a list of configuration files that were either supplied or which you have modified and saved, filtered for the type of amplifier you selected. They are analogous to the "setup files" used in the Scan software (although not interchangeable with them). Note that the initial option in the list is **<Load Configuration File>**. An Open File dialog appears, allowing you to select configuration files from other locations than the default folder (see the **Target Folders for Windows 7** section).

Sample Rate. Select a Sample Rate from the drop-down list. Sample rates vary considerably across amplifiers.

Headboxes. The Headbox field shows on which headbox the selected channel is located. It is informational only.

DC Mode / AC Mode. With some of our amplifiers you have the option to record in DC or AC Mode. In DC Mode, there is no high pass filtering. Because there is no HP filtering, artifacts will not ring the HP filter, and recordings will thus not be affected by the ringing. At the same time, with no HP filtering there will very likely be some degree of DC offset and drifting across the recording. These can easily be corrected offline. AC Mode uses a HP filter, and therefore you will not see the offset or drifting, but you may see ringing.

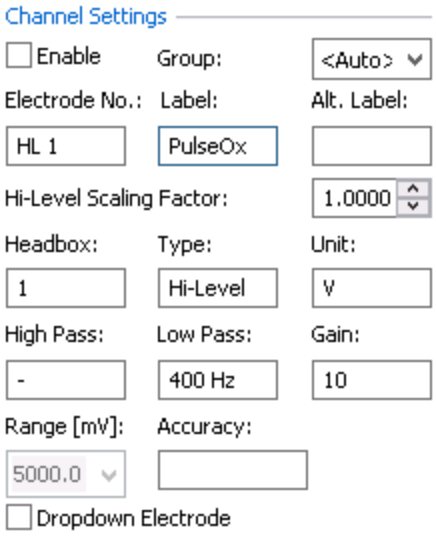
In general, we recommend recording in DC mode in most cases. This results in a more accurate reflection of what the recordings actually contain. For MagLink recordings, it is essential that you record in DC Mode. In recordings where there are stimulus artifacts, such as SEPs and TMS, you should also record in DC Mode. If you are investigating DC potentials specifically, then obviously you will want to record in DC Mode. If you are interested in long latency cognitive ERPs, we also recommend DC Mode, where you can apply minimal HP filtering offline if needed.

If you are not recording in the magnet, and there are no stimulus related artifacts, and if you are sure you will never be interested in the slow potentials that may be contained in your recordings, then you can use AC Mode. The one other advantage of AC Mode is that the dynamic range of the amplifier is greatly reduced, thus resulting in highly precise amplitude measurement.

See the relevant amplifier manual for additional considerations with DC amplifiers.

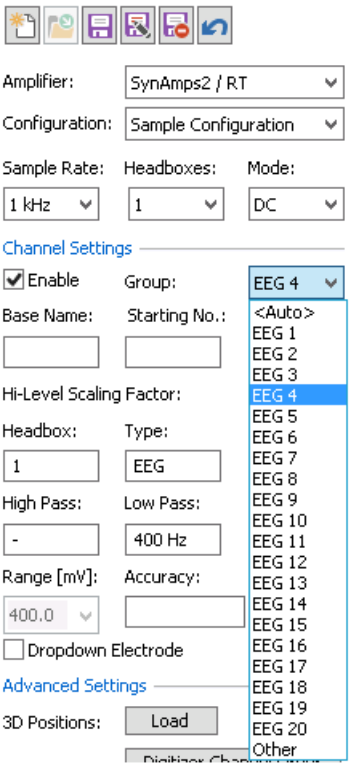
Channel Settings

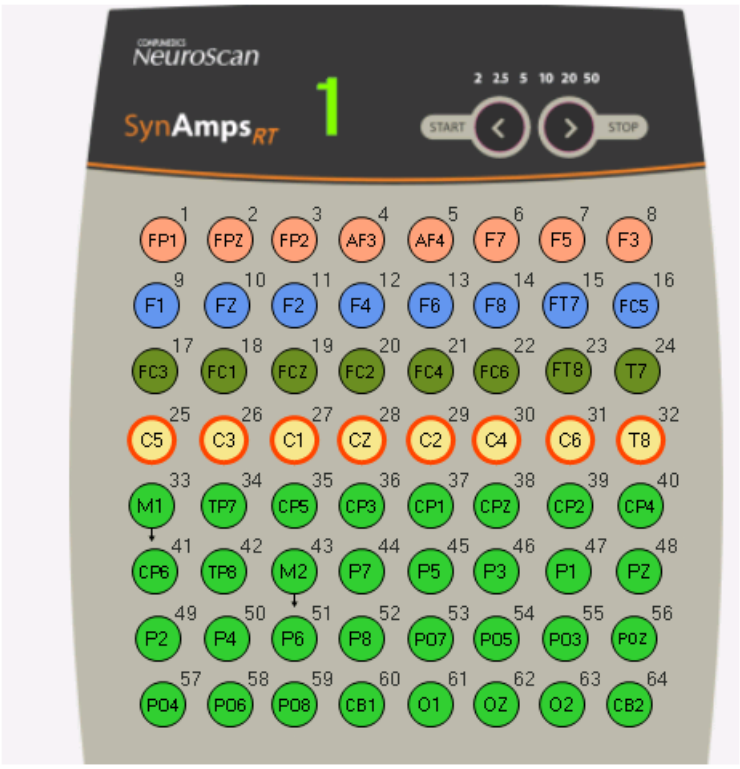
Not all fields will be active, depending on which amplifier you are using.



Enable. The Enable option lets you disable single or groups of electrodes you do not wish to include. Enabled channels are colored green.

Group. This option permits you to assign groups of electrodes to separate EEG groups, or as **Other** channels. This is especially useful when you have depth electrode recordings and you wish to group the electrodes separately. Use **Auto** to have CURRY choose the group for you.

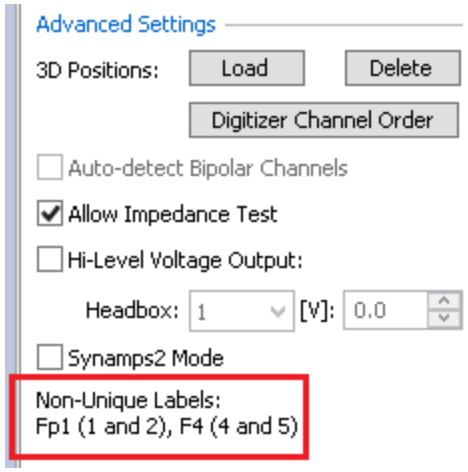




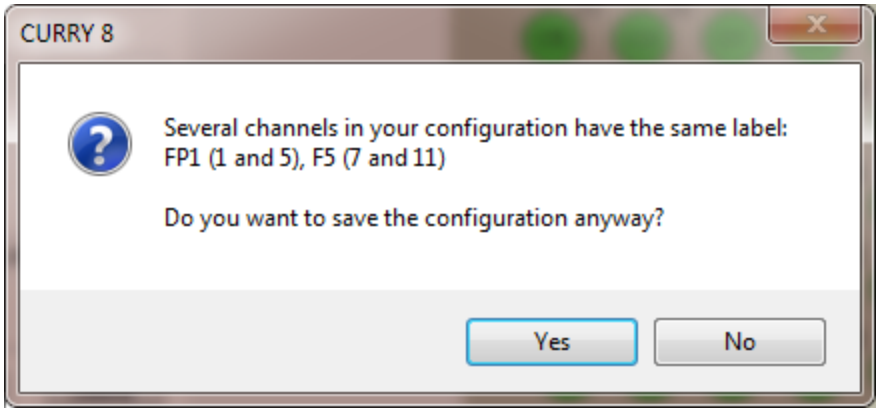
Electrode Number. Click on an electrode in the display to see the electrode settings for it. The Electrode number is the number of the physical channel for that electrode.

Label. This is the electrode label. Electrode labels should be unique, but CURRY will allow non-unique labels as described below. This applies to the Label and Alternate Label fields.

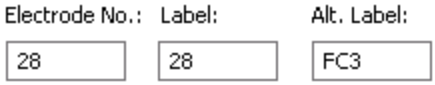
If you need to enter non-unique, or "already used" labels in order to redefine the labels in a different way, CURRY will let you do it, and you will see a message at the bottom of the display telling you that you have repeated labels.



When you try to save the new configuration, you will see a confirmation screen. It is recommended that you avoid duplicate labels.



Alternate Label. This option is used primarily in cases where you have numbered electrodes. The alternate sensor label will be used in the displays.



Hi-Level Scaling Factor. Use this field to rescale the Hi-Level input voltages. Start with a level of 1.0 and see if the scaling for the HLI channel(s) is reasonable. If the channels are appearing with very high amplitudes in the data display, reduce the scaling factor.

Headbox. The headbox field is informational only. If you have multiple headboxes, this field shows you which headbox the selected channel is on.

Type. This field displays the type of channel: EEG, Bipolar, Hi-Level, etc.

Unit. Displays the voltage unit for the selected channel.

High Pass. This is the High Pass filter (0.05Hz) that is applied during acquisition (and is nonexistent in DC mode).

Low Pass. A Low Pass filter is applied during acquisition to avoid aliasing. The LP filter is generally an order 2 Butterworth IIR filter at 40% of the AD Rate, but may vary across amplifiers and AD Rates.

Gain. This is the amplifier Gain, and will vary across amplifiers and DC versus AC Modes (where present). For example, the Gain of a *SynAmps RT* in DC Mode is 10 (and thus the Range is at least +/-200mVs).

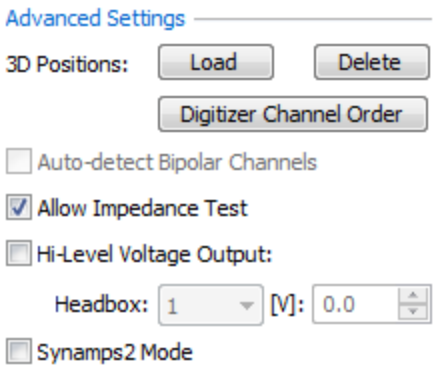
Range [mV]. This is the dynamic range of each of the amplifiers. Voltages outside of the dynamic range will not be recorded (amplifier saturation). The values are presented for informational purposes. With *SynAmps* amplifiers, note the reduction in the Range when in **AC Mode** (as displayed above). In actuality, the true dynamic range is broader than the value displayed, which is a conservative estimate of the true mathematical range. The true mathematical range will rarely if ever be met in real life testing, due to variances in AD converters, noise, etc. The

displayed range, therefore, is at least the value displayed, and may be somewhat larger. The Range varies across types of amplifiers.

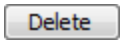
Accuracy. Accuracy refers to the precision of voltage measurement. An Accuracy of 3nV/LSB (Least Significant Bit) means that voltages will be measured to the nearest 3nV. This value represents the ideal degree of Accuracy. In real life this value is seldom if ever met due to the variances in AC converters, noise, etc. The real world accuracy value will be somewhat greater (less accurate) than the value displayed. The Accuracy varies across types of amplifiers.

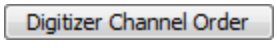
Dropdown Electrode. Since dropdown electrodes do not have a fixed position on the cap, their placement is unknown. The digitizer module requires known positions when interpolation is used. By designating the dropdown electrodes as such, they will be excluded from the interpolation. When you highlight an electrode and then enable the Dropdown Electrode option, you will see a small tail (arrow) below the electrode. The configurations that we supply will have these marked already. This designation is only needed when you are digitizing the electrode positions and have interpolation enabled.

Advanced Settings

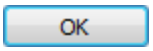


3D Positions. If you have 3D positions in the form of a .pom file, these can be loaded 

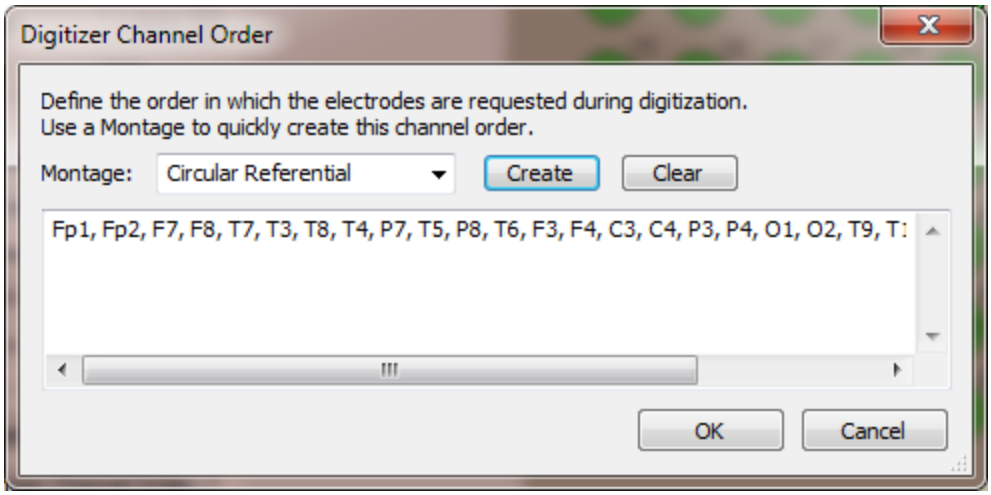
and saved with the configuration file. Remove the positions with 

. Be careful that you do not save the positions from one subject and then use them with a different subject. Label matching is used to recognize the positions. If there are missing or mismatched labels, you will see a message to that effect. You can create the order in which the channels are to be digitized by clicking the 

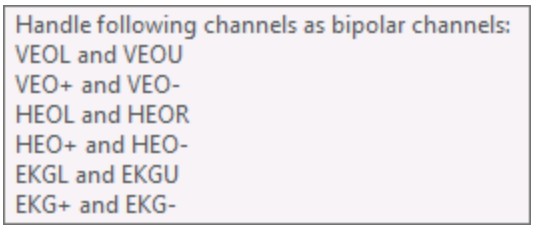
button. Select a montage that you wish to use, and click the 

button, or type in the labels manually. Click 

when you have the desired order.



Auto-detect bipolar channels. This option is active for NuAmps amplifiers only. When enabled, the channels having labels displayed in the Tooltip will be treated as bipolar channels. For example, channels carrying the names of HEOR and HEOL will be seen as "HEOR-L".

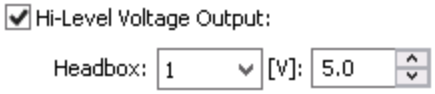


Allow Impedance Test. Impedance testing is enabled by default. *If you are recording from ECoG grids, strips or depth electrodes, you should not perform impedance tests*. This option will prevent impedance testing.

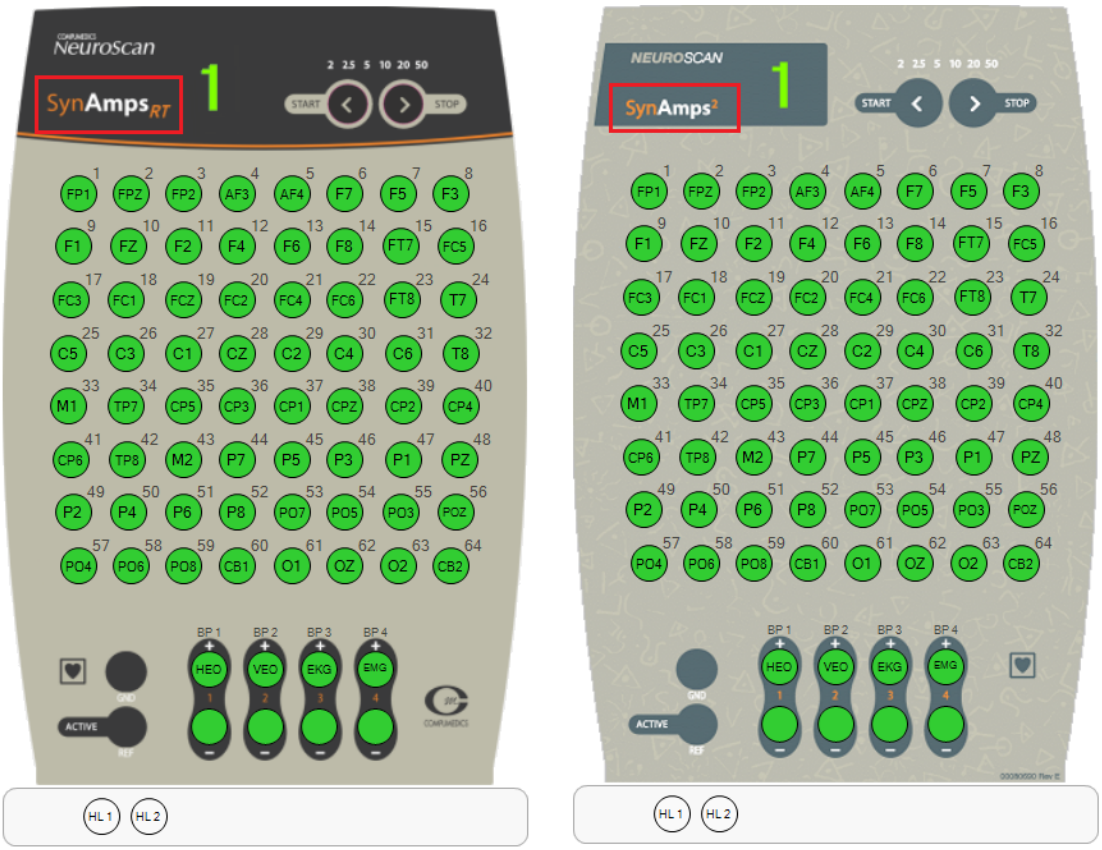
Care

It is strongly recommended that you do not perform impedance tests if you are recording from an ECoG grid, strip, or depth electrodes.

Hi-Level Voltage Output [Headbox] [V]. Certain devices are powered via the SynAmps System Unit. Specify the headbox you are using (if more than one), and enter the voltage in the **Voltage** field. Entering a value of 5 means that +/-5V will be used. The Voltage Output is set per headbox, not per HLI channel. (See the *SynAmps User Guide* for a pinout of the Redel connector).

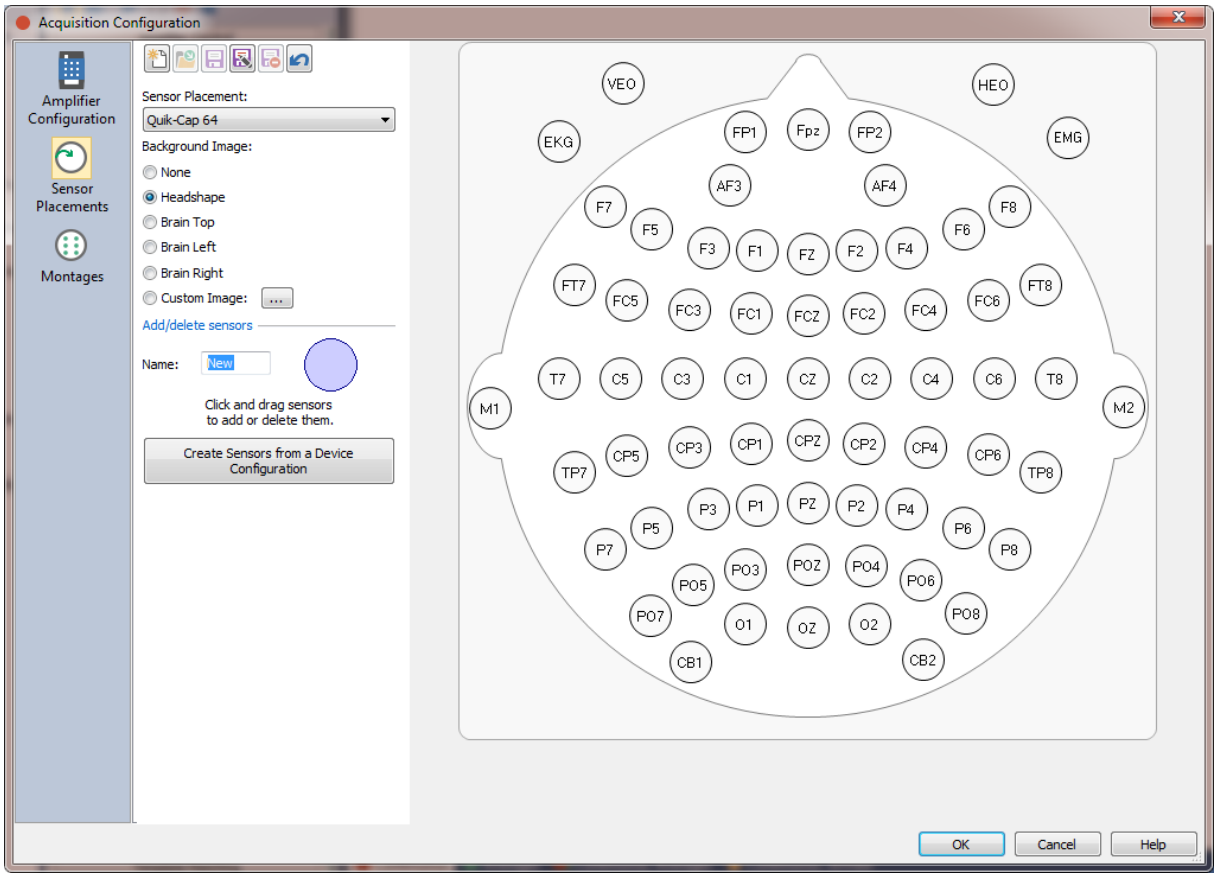


SynAmps2 / NeuvoRT Modes. At the bottom of Acquisition Configuration window, you may see an option for the **SynAmps2** or **NeuvoRT Mode**. This lets you select the display that matches your amplifier. For example, if you see the SynAmps RT headbox, and you have a SynAmps2, enable the **SynAmps2 Mode** option to see that headbox.



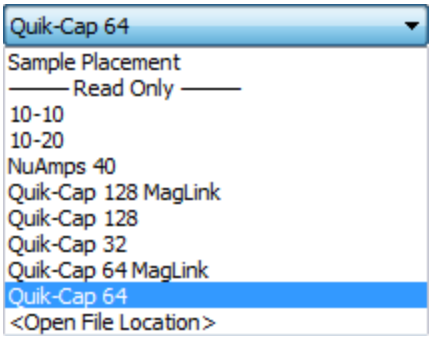
14.1.2 Configure sensor placement

This screen is used to position electrodes and add/remove electrodes (or other sensors). The placements are used by the montages; you need a placement to be able to create a montage.

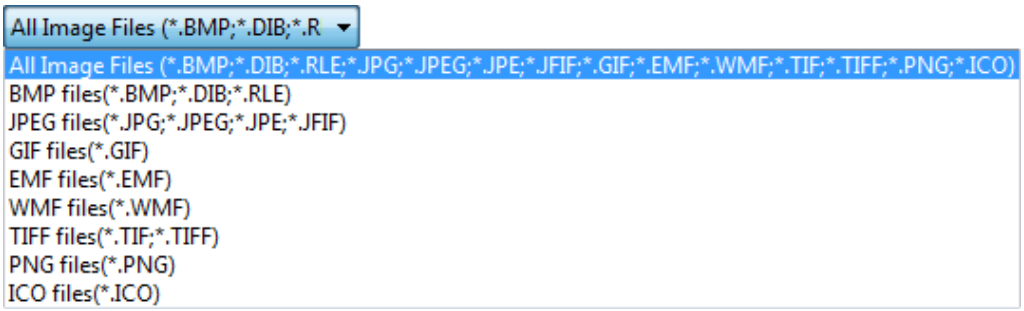


Settings

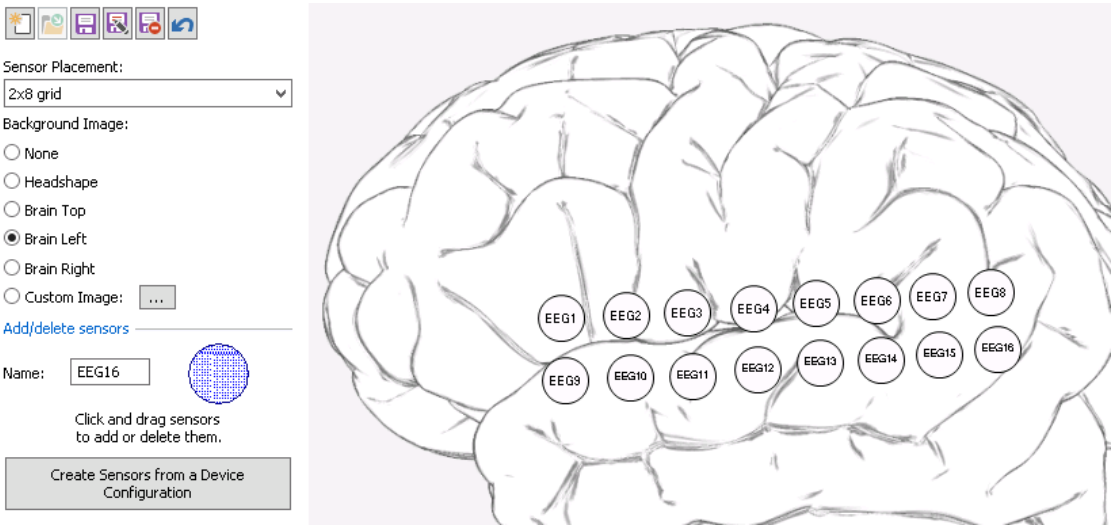
Sensor Placement. When creating a sensor placement scheme, it is often convenient to start with one of the supplied configurations. These include placement schemes that correspond to our current caps, plus more generic 10-10 and 10-20 configurations. Select one that is closest to your needs and make modifications to it. When you save the new file, it will be included in the list (above the *Read Only* line).



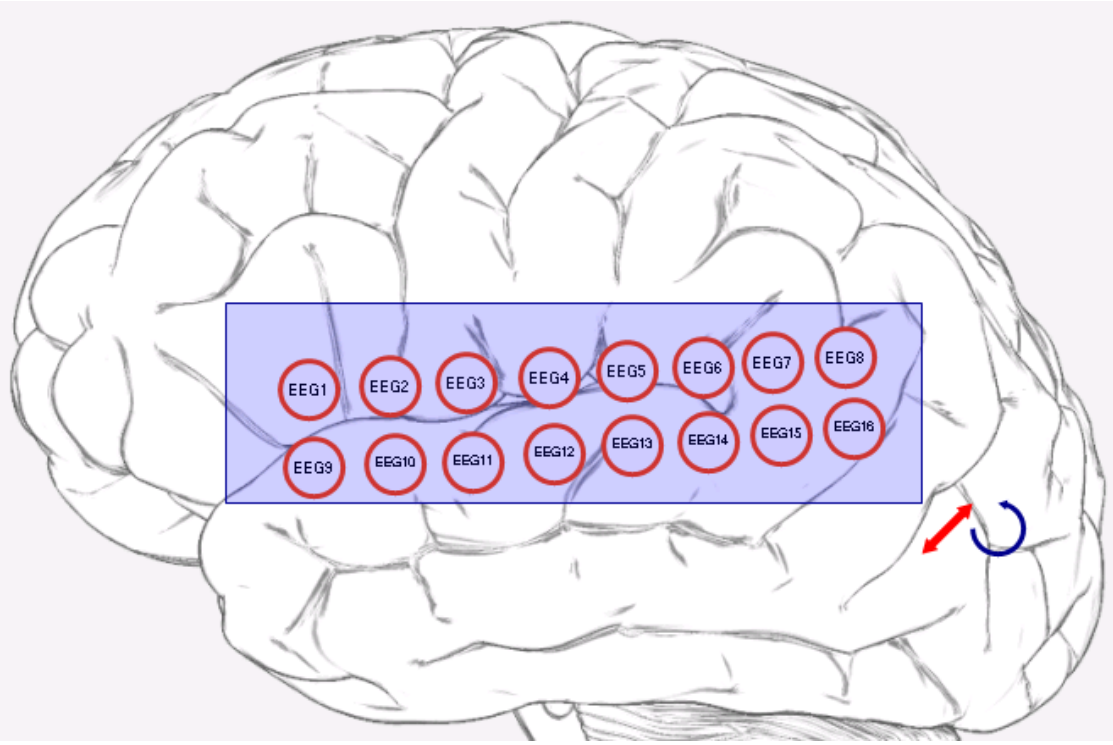
You may elect to have no background image None, the generic head shape Headshape, Top, Left or Right Brain views, Brain Top, or a custom image Custom Image: in any of the following types.



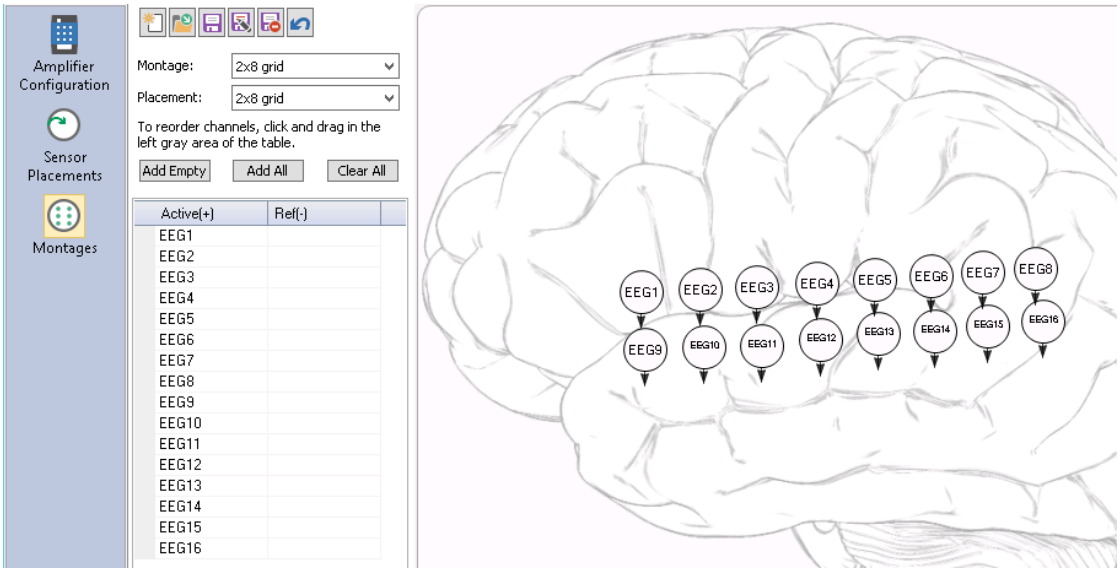
The "Brain Views" are included for you to make ECoG grid/strip placements that can be used with Position Plots during acquisition (only). For example, say you are creating a 2x8 grid. Click and drag the electrodes to the purple spot to Delete them; enter a label and drag the purple spot to the desired location to Add them. In this case the labels are EEG1 to EEG16, to match the data channel labels, and they were positioned on the Brain Left vie..



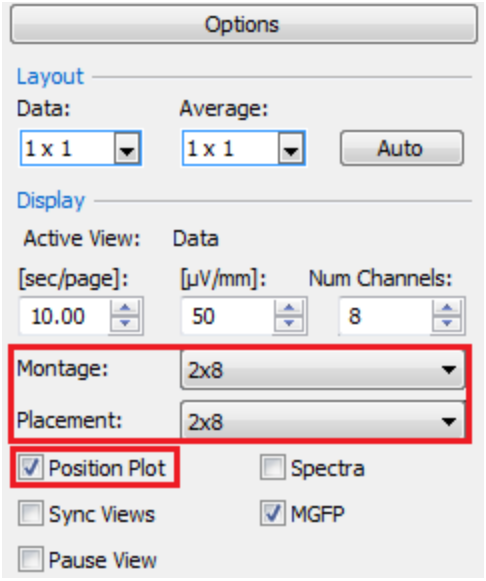
If you drag a box around the electrodes, you can then reposition the entire grid just by dragging it, or else use the two tools that appear to stretch or shrink the display, or to rotate it.

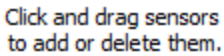


Create a Montage, as described in the **Configure montages** section (*double-click* on the electrodes in the desired order).



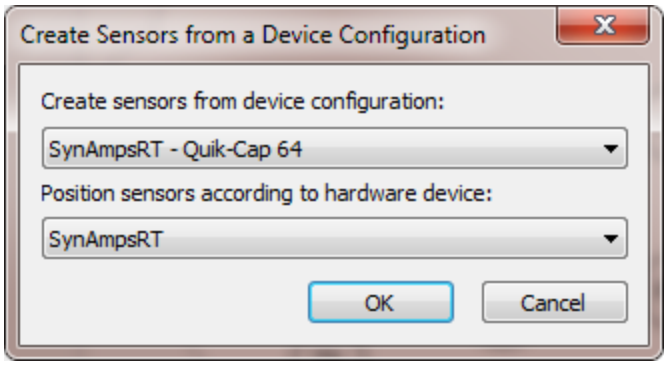
During acquisition, select the Montage and sensor Placement files (in the **Options** panel), and enable **Position Plot** to see the electrode displays in the same positions.



Add/delete sensors. To add a new electrode, enter the label in the **Name** field, and then drag the purple circle to the desired location. To delete an electrode, drag it to the indicated area below the name field 

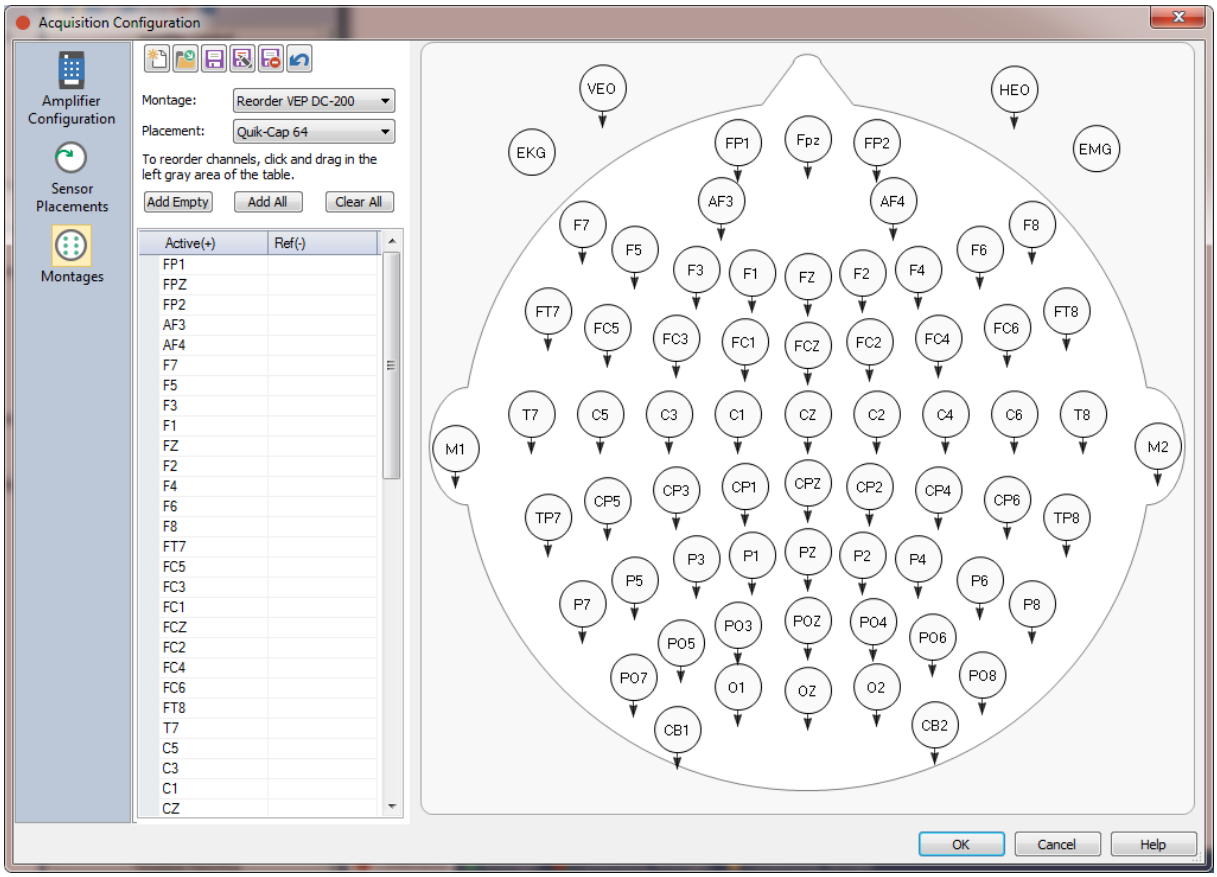
.

Create Sensors from a Device Configuration. Select this option if you want to start with an existing configuration file. Select the file from the drop-down list, and select the type of amplifier you have. If you create positions from an existing configuration file, the electrodes are added to the existing placement (already existing electrodes will not exist twice). You can, however, start from an empty display. You can also drag a rectangle around all electrodes to mark them and then press *Del* to remove them all. Then you can create new positions from scratch.



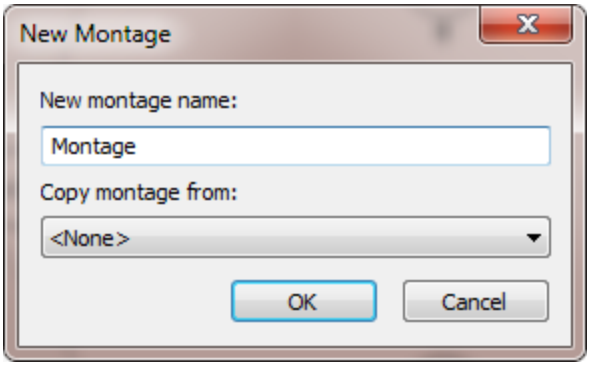
14.1.3 Configure montages

Use these options to configure your own montages and to reorder the channels. See the *Montages* section in the **Options** parameters for more information.



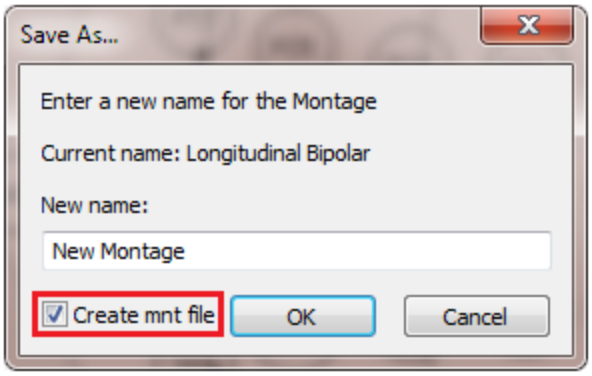
The row of buttons at the top are the same as those used with **Configure Amplifiers**  .

For example, click the **Create a new montage** button  to see the following dialog. Enter a montage file name. If you are starting with a copy of an existing montage file, select it from the list.



Click the **Import a montage file**  button to open an existing .xml or .mnt file.

The next two buttons are the standard **Save** and **Save As** buttons  . In the Save As dialog, you have the option to **Create mnt file**. Mnt files are easier to edit manually (in a text editor). Use the **Import a montage file**  button to open the edited file.



The last two are the **Delete the active montage** and **Undo all changes made to the current montage since it was last saved** buttons  .

Montage Settings

Montage. The drop-down list displays the montage files (.xml) that have been supplied or created. Please see the **Target Folders for Windows 7** section.

Placement. The drop-down list displays the electrode placement files (.xml) that have been supplied or created. Please see the **Target Folders for Windows 7** section.

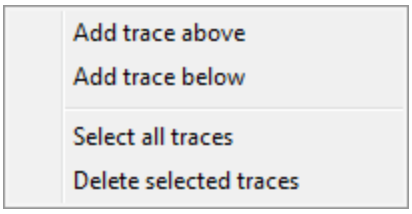
Add Empty adds a blank line between groups of sensors. When you apply the Montage and then select the Butterfly Plot, the channels will be grouped before and after the spaces (you will see multiple Butterfly Plots). **Add All** adds all sensors to the list (so they can be reordered by dragging and dropping). **Clear All** removes all entries from the list.

Matrix (When creating a montage to reorder the channels, there will be no Ref(-) electrode).

Active (+). Displays the active electrode (+).

Reference (-). Displays the reference electrode (-).

Context menu options
Right click in the electrode list to see the following options.



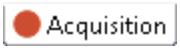
Add trace above. Adds an empty line above the selected line.

Add trace below. Adds an empty line below the selected line.

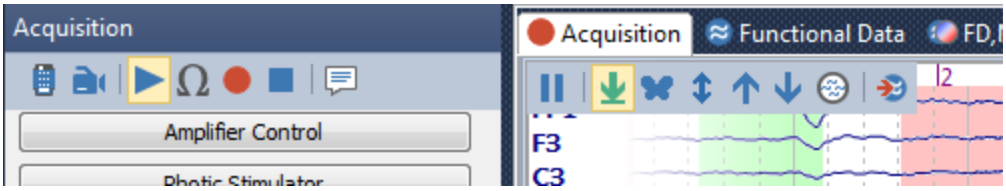
Select all traces. Highlights (selects) all lines in the list (you may use *Ctrl+left click* to select individual lines).

Delete selected traces. Deletes selected lines in the list.

14.2 Acquire Parameter Dialogs

The Acquire Parameter Dialogs are used to set up acquisition options. These are seen when you click 

in the lower left hand row of tabs.



Acquisition Toolbar Icons  . These options are found at the top of the Acquisition parameter panel. Toolbars are also found at the top of the continuous  and average  data displays.

Configure Amplifier  . Accesses the amplifier configuration dialogs (see **Configuration Options** below).

Video Camera  . Show or hide the video camera display.

Connect  . Connect to the selected amplifier.

Check Impedances  . Click this option to view the impedance display. If you perform an impedance test while recording the EEG data, the results will be stored and seen in the **Show Information** field, under **Functional Data** (offline). From there they may be copied/pasted elsewhere.

 **Care**

*Impedance tests should only be performed with surface EEG, and never if you are recording from cortical grid or depth EEG electrodes. There is an option in the Configure Amplifiers section to disable impedance tests (**Allow Impedance Test**), which is intended for use with grid and depth recordings.*

Record  . Click the Record button to start saving the data to the hard drive.

Stop  . Disconnect from the amplifier (or stop Impedance, stop Digitizer, or stop Recording, and then disconnect).

Edit Comments  . Add text comments that will be stored with the data file.

The next icons are found by positioning the mouse in the upper left corner of the acquisition data display for continuous and averaged data.

Select Average  . Used with online averages to select another average to Overlay or take the Difference. (See **Select Average**).

Pause  . Pause display. In the average data display, this option has the same effect as the **Enable** option in the **Averages** table.

Restart  . This option occurs only in the averages display toolbar. Clicking it restarts the selected average. It has the same effect as clicking the **Restart** button in the **Averages** table.

Baseline correction  . Centers traces in their display space (removes DC offsets from the display). Data are not affected.

Butterfly Plot  . Superimposes all channels.

Autoscale  . Autoscales the display of all traces (data are not affected).

Increase Display Scale  . This affects the display only and not the saved or processed data.

Decrease Display Scale  . This affects the display only and not the saved or processed data.

Position Plot  . Displays channels in separate windows about the head.

Send Page to Functional Data  . Sends the displayed page to Functional Data for further online processing.

It is important to understand that the parameters you set in these panels can be saved as Study Parameters. Click the **Save Study Parameters** icon  on the Toolbar. A Save As dialog will appear with a default name based on the date and time - you can use your own naming system as well (.cfg file). If you have already saved the Study Parameters, clicking the icon will update the existing file (you will not see anything happen).

Saving the Study Parameters takes a "snapshot" of all possible settings. Use care when saving them to be sure you do not save any undesired parameter settings.

The Study Parameter file you save can be applied to future recordings. Before opening the Study that you will be using for acquisition, *right click* on the Study and select the .cfg file you have created. This will save you from having to reselect parameter settings.

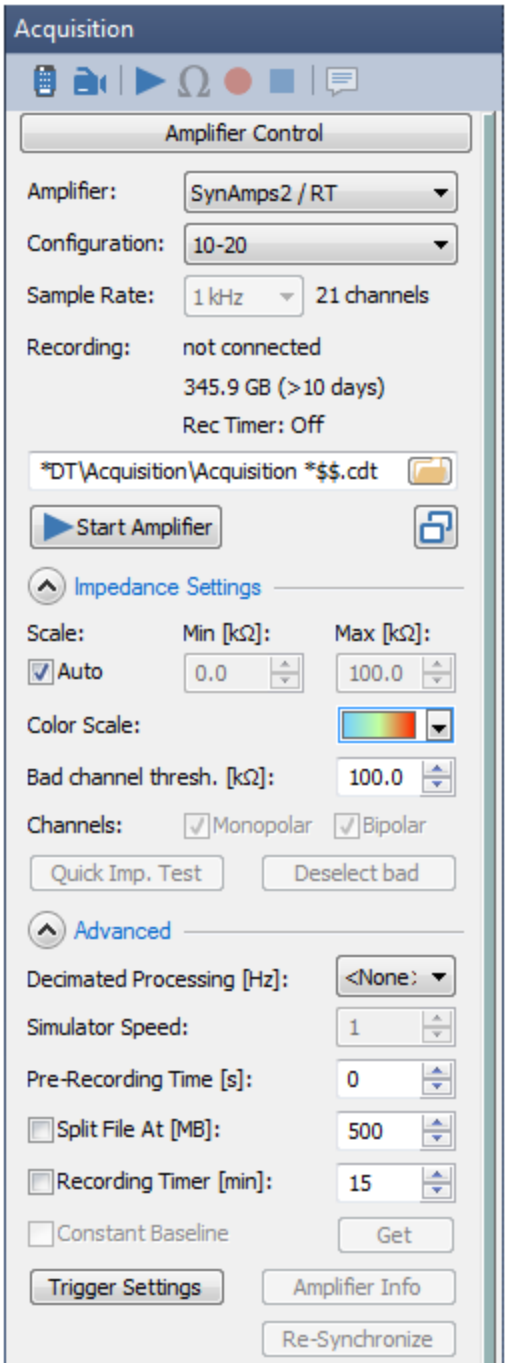
The Study Parameters can also be used in offline data analysis. The Study Parameters file contains independent settings for online and offline parameters. Therefore, a single parameter file can be used both online and offline. It may be less confusing in the long run, however, to have separate online and offline parameter files.

Online Data Processing Sequence
A simplified online data processing sequence uses the following order:

- Interpolate channels
- Baseline correction
- Rereference
- apply LDR
- get MGFP of unfiltered data
- perform threshold detection and artifact reduction of all phases for *unfiltered* data
- filter data
- project PCA components loaded from file
- run Matlab script
- get MGFP of filtered data
- template matching
- perform threshold detection and artifact reduction of all phases for *filtered* data

14.2.1 Amplifier Control

These parameters are used to select the type of amplifiers, communication with the amplifiers, acquisition options, and file recording information.



At the top of the **Acquisition** parameter panel are several icons  .

Configure Amplifier  . Accesses the amplifier configuration dialogs (see **Configuration Options** below).

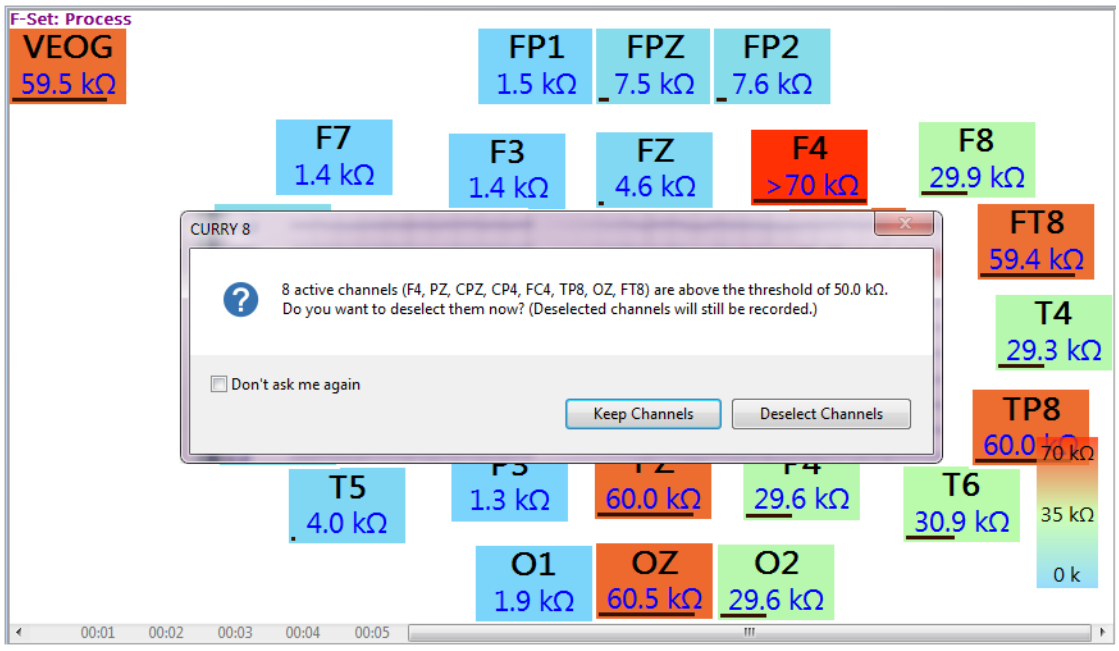
Video Camera  . This option will show or hide the video camera window.

Connect . Click to connect to the amplifier and begin viewing the channels. This is the same as the Start Amplifier button under **Amplifier Control**. If the Simulator has been selected, click to access the file to replay. Click a second time to disconnect (same as the button).

Impedance . Click to perform an Impedance test. Click a second time to stop impedance testing (same as the button). Use the *mouse wheel* to vary the Range scale. If the impedances for any channels are above the threshold you set, you will see a message, when you exit the Impedance test, asking if you want to designate them as **deselected** channels (the data will still be recorded). The same message will appear when you press the Deselect bad button (under **Amplifier Control**) or when you click the **Quick Impedance Test** button (and there are impedances exceeding the Threshold).

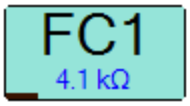
If you perform an impedance test while recording the data, there will be "garbage" displayed on the screen during that section. This section will be designated automatically as a Bad Block.

The figure below shows a *SynAmps* 64 channel cap configuration. The dialog is basically the same as the Position Plot, so you can do anything to the individual windows that you can do in the regular Position Plot. The upper half shows the "+", the lower half the "-" channel.



The black bars below each window show the impedance level graphically, using the selected Range, from left to right. If you enlarge the windows (using the context menu option Enlarge Window Size And Optimize Layout), you will see the impedance levels as text. You can also manually increase the size of the displays (dragging a corner

while holding down the Alt key will resize all displays). Then select Optimize Position Plot Layout from the context menu to position the displays without any overlap.



Care

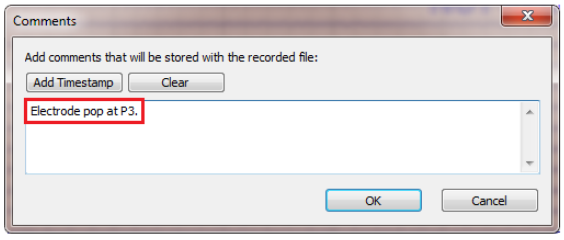
It is strongly recommended that you do not perform impedance tests if you are recording from an ECoG grid or depth electrodes. There is an option in the Configure Amplifiers section to disable impedance tests, which is intended for use with ECoG and depth recordings.

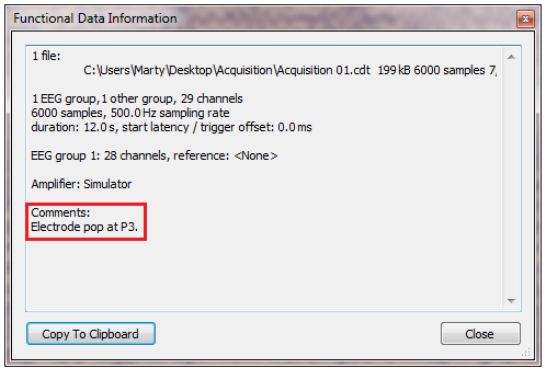
If you perform an impedance test while recording the EEG data, the results will be stored and seen in the **Show Information** field, under **Functional Data** (offline). From there they may be copied/pasted elsewhere.

Record. Click to begin recording the data to the hard drive. The "NOT RECORDING" message will disappear. Click again to stop data storage, yet leave the display running. Click a 3rd time to resume recording to the same data file. (To record to a new data file, you must first disconnect and reconnect to the amplifiers).

Stop. Press this button to disconnect from the amplifiers, or stop the current process (impedance, recording). When you click Disconnect *while recording*, the recording will be stopped/paused. When you click Disconnect when *not recording*, the amplifier will actually disconnect.

Add Comments. Clicking this button allows you to enter comments during acquisition. Click **Add Timestamp** to include the date and time. The comments are saved in the .dpa parameter file. The comments are seen when you go to **Functional Data** → **Show Information**.





Amplifier Control

Amplifier. Select your amplifier from the drop-down list, or select the **Simulator**. The **Simulator** may be used to replay existing data files. When you click the

button, you will be prompted to select a data file. You may select continuous, epoched or averaged data files - each will keep playing over and over (epochs will be concatenated). You can replay MEG data through the Simulator, although all channels will be converted to "Other" channels (you will see a message to that effect). Use can still use these for voltage threshold artifact detection, and you may still create averages from the MEG data.

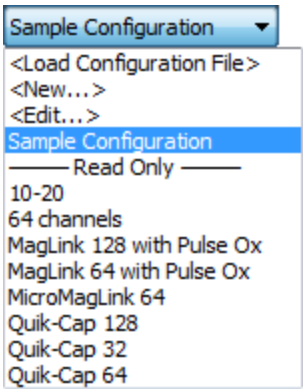
Some of the amplifiers from Compumedics (*Grael, E-Series*, *Neuvo*, *SynAmps Wireless*, *Siesta*, etc.) can be configured over a network using NetBeacon. If you are connecting to the amplifiers over a network in those instances, select the **<Search Network Amps>** option. You will see the amplifiers listed by number, and you should choose the one you wish to use.

When you click **<Search Network Amps>**, the *NetBeaconService.exe* program is started in the background (you won't see anything happen). However, your firewall may detect it and display a message similar to the following.

If that happens, just click the **Allow access** button.

When a network amplifier is found, you will be asked if you want the software to automatically look for network amplifiers in the future, so you never has to press **<Search Network Amps>** again.

Configuration (current file). Select one of the existing Configuration files (.xml) from the drop-down list. Files above the Read Only line are ones you have created; files below it are supplied from Neuroscan and are Read Only. Select **<Load Configuration File>** if you have stored your file in a different location (please see the **Target Folders for Windows 7** section). Click **<Edit>** to go to the **Amplifier Configuration** screen.



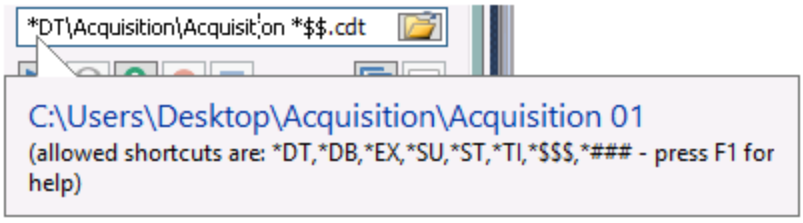
Sample Rate. The current AD Rate is displayed. The AD Rate is applied to all channels for most of the amplifiers (exceptions are possible with some of the clinical amplifiers). For user created configurations, the rate is not only displayed, but also changeable.

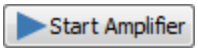
Recording. This field is used to select the target folder and assign a file name for the file you are recording.

The available space on the hard drive is displayed. The recording will automatically stop when the hard drive is about to get full. A warning will appear when the disk space is below 4GB or 10% (whichever value is smaller). The recording will be stopped when the disk space is lower than 2GB or 5%.

To calculate file size, use the following formula: (Number of channels) * (Sample rate) * 15 / 65536 = MB per minute. If the amplifier has an explicit trigger channel, use (Number of channels + 1).

If you click in the path/file name field (or position the mouse over it), you will see a Tooltip that helps explain the automated path and file name feature. In the example below, *DT\ is a substitution for the path to the Desktop. Additional shortcuts are seen in the Tooltip, including automatic numbering conventions (*$$$ and *###). "Acquisition\", after *DT\, creates (or adds to) a folder on the Desktop called Acquisition. *Acquisition *$$.cdt* is the actual data file name. The *$$ starts numbering at 01, or the first available number after that, and increments with each file that is recorded. The automated naming convention is described more thoroughly in the **Macro** section below, where automated naming conventions are important if you want to run a macro without user intervention. If you do not want to use the automated options, just click on the Browse button, then select a folder and enter a file name in the traditional Windows manner. To save the path for use in all acquisitions, save it with the Global Parameters (or Study Parameters).



Start Amplifier 

. This is the same as the **Connect** button  . Click to connect to the amplifier and begin viewing the channels. If the Simulator has been selected, click to access the file to replay. Click a second time to disconnect (same as the  button).

Configure as NetStreaming Server or Client  . It is possible to send the data you are acquiring to another computer on the network, or to MATLAB. Please see the **Configure as NetStreaming Server or Client** section for details.

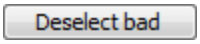
Impedance Settings

Scale

Auto. The display will be scaled to the largest and smallest impedances. Disable it to enter the values of your choice.

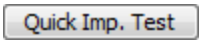
Min[kΩ], Max[kΩ]. These fields set the range of the impedance display.

Color Scale. Select a color scheme for the corresponding impedance values.

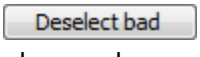
Bad Channel Threshold[kΩ]. Enter an upper Threshold for impedance values. Channels having values that exceed the threshold will be designated as deselected channels when you click the 

button (and acknowledge the confirmation screen).

Channels. If there are large DC offsets in the recording, the impedances from the bipolar channels can affect those in the EEG channels (monopolar). If you encounter this, test the impedances for bipolar and monopolar channels separately. Otherwise, measure both at the same time (default). Note also that the impedance update rate increases greatly when you only measure impedances on the monopolar channels. Therefore, while working on the impedances on the monopolar channels, it is suggested to switch off the bipolar channels to get a much faster update rate.

Quick Impedance Test 

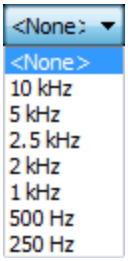
. The Quick Impedance Test obtains the impedance values (acquisition will be suspended for 1-2 secs), and saves them in the .dap file. A check for bad electrodes is also made.

Deselect bad 

. When you click this button, you will see the same message shown above, if there are channels that have impedances greater than the Threshold. These can be designated as deselected channels or not.

Advanced Settings

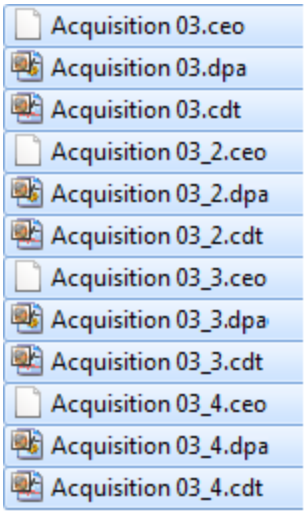
Decimate for Processing [Hz]. This option applies to online processing only. If you are sampling at high rates, yet the online processing you are doing can be done at lower sampling rates (to reduce data processing demand), you can select a lower sampling rate. This does not affect the continuous file that is being recorded. It will affect the online averages that you are creating (with the decimated data).



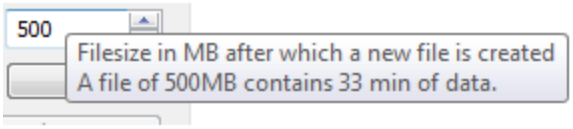
Simulator Speed. This controls the speed of the replay of files when the Simulator option has been selected. This is recommended only with fast computers. Depending on the filtering/averaging/cleaning methods running, a high number in this value can be very CPU consuming.

Pre-Recording Time [s]. The program will also save the number of seconds you enter (assuming they are all in the buffer) prior to the point where you start saving the continuous data. The buffer is approximately 200MB. The Pre-Recording Time will not be included in the video recording, only the data file.

Split File At [MB]. When making long recordings, it is sometimes desirable to make multiple smaller continuous files rather than one single file. Enable this option and set the number of desired MB. The files will be named with a numerical suffix. The event and parameter files are created automatically for each file. To load them like a single file, place them in the same study, in the correct order. If you recorded the file using the Database (not an Unfiled Study), the files will appear in the same Study, in the proper order, automatically.



A Tooltip will display the duration of the file in minutes.



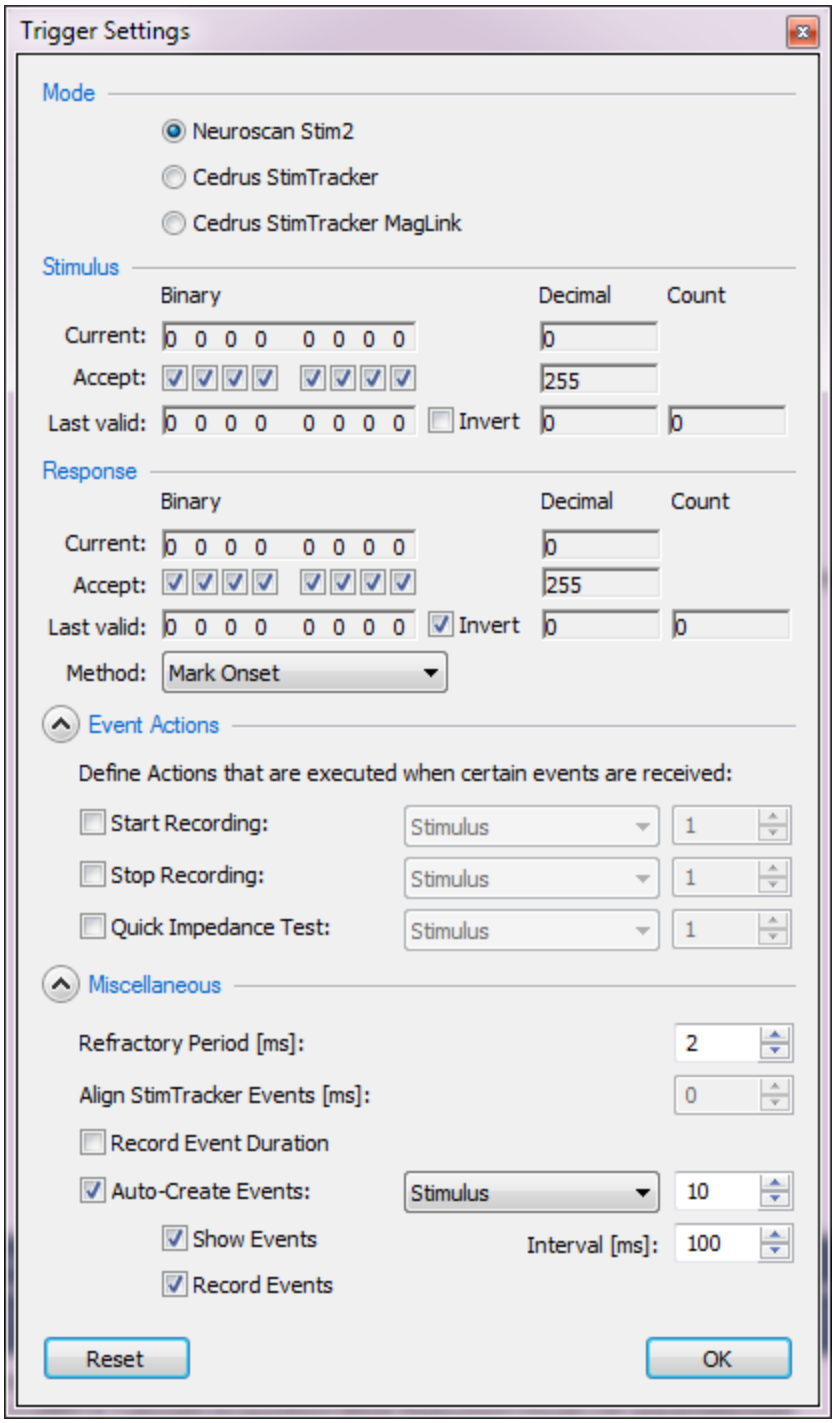
Recording Timer [min]. This option allows you to automatically stop a recording after a fixed amount of time (minutes).

Constant Baseline Correction. When you press the Get button, a DC drift/offset correction will be performed. This is a momentary correction, that is, it corrects for the immediate offsets, and may need to be repeated as the recording continues. Unlike the **Baseline** correction options in the **Filter Parameters** panel, which affect the display only, the Constant Baseline Correction will be saved with the data file. Since the correction will create an abrupt voltage transition in the continuous recording, a small Bad Block will be inserted whenever you press the Get button. This will prevent the acceptance of invalid epochs during averaging. Generally, you will not need to use the Constant Baseline Correction. If you do use it, you should do so sparingly, especially while stimuli are being presented, since the coincident epochs will be invalidated (you cannot create epochs that contain bad blocks). Normally, the Baseline correction under Filter Parameters will be sufficient online, and offline you can use the **Constant** correction (**Baseline / Bad Blocks**) to remove the offset. If you are having severe DC drifting/offset issues, this is likely due to subject preparation issues, such as using mixed metals across the electrodes, or a different conductant at the reference or ground electrode than the EEG sites. It is better to resolve the recording issues at the source, rather than with periodic baseline correction.

Trigger Settings

These options provide additional controls for handling variations from the expected TTL pulses used for transmitting trigger information. The options used primarily for troubleshooting purposes when you are encountering difficulties with triggers. See **Appendix A** for more details regarding the use of these options. Clicking the button displays the Trigger Settings dialog, which reads the states of the trigger input board on the amplifier. You must be connected to an amplifier or the Simulator for the fields to show anything.

The display is divided into **Mode**, **Stimulus** and **Response**, **Actions**, and **Miscellaneous** sections. Events are seen in **Binary** and **Decimal**. The **Accept** fields let you block the input from selected bits (normally all are enabled). The **Last** fields display the most recently received stimulus and response events. The **Count** fields display how many stimuli and responses have been registered. The **Invert** fields let you switch the logic for Stimulus and Response bits, if needed. Normally, for STIM2 systems, the stimulus events are not inverted, and the responses events are inverted. If you are using the Neuvo amplifiers and system unit, however, the stimulus bits must be **Inverted**. If you are using the Cedrus StimTracker, the **Invert** option for **Responses** will be deselected.



General Options

Mode. If you are using STIM2 or any other presentation system where its trigger events are emulating STIM2, select that option. If you are using the Cedrus StimTracker system, select that option. If you have a MagLink or MicroMaglink system with a StimTracker, select that option.

Stimulus and Response

When using the StimTracker system, the distinction between stimulus and response events becomes blurred. Briefly, the Cedrus Response Pad pulses are seen as stimuli in the Stimulus section, rather than in the Response section (stimulus events codes of 248-255, corresponding to buttons 1-8, are sent from STIM and converted automatically into r1-r8 events). Response bits 0-3 are generally not used; they come from the TTL Input connector on the back of the StimTracker. Response bits 4-7 carry the TTLs from StimTracker for the microphone, auditory stimuli, and 1 or 2 light sensors. The TTL pulse from the MRI Trigger Interface uses the Photocell2 connector (in place of a second light sensor), and is converted by CURRY into r5 events. Please see **Appendix A** for more information.

Note also that the **Method** options will let you add triggers at the **Onset**, **Offset**, or **Onset and Offset** of the StimTracker events.

A summary of the events for STIM2 with a StimTracker, with a **SynAmps2** or **RT**, is shown below.

StimTracker Signal	See by Neuroscan as	
Event marker bit 7	Trigger bit 7	128
Event marker bit 6	Trigger bit 6	64
Event marker bit 5	Trigger bit 5	32
Event marker bit 4	Trigger bit 4	16
Event marker bit 3	Trigger bit 3	8
Event marker bit 2	Trigger bit 2	4
Event marker bit 1	Trigger bit 1	2
Event marker bit 0	Trigger bit 0	1
Lightsensor 1	Response bit 7	pho1
Lightsensor 2 /MRI scanner	Response bit 6	pho2 /r5
Microphone	Response bit 5	mic1
Audio L+R	Response bit 4	aud1
TTL input, line 4	Response bit 3	r8
TTL input, line 3	Response bit 2	r4
TTL input, line 2	Response bit 1	r2
TTL input, line 1	Response bit 0	r1

Cedrus Response Pad buttons 1-8 use Stimulus events 248-255 and the corresponding Trigger bits 0-7. CURRY converts stimulus events 248-255 to response events r1-r8. The 248-255 stimulus events in SCAN are converted to response events using a batch file, such as stim2resp.tcl.

The TTL inputs 1-4 refer to the TTL Input jack on the back of the StimTracker, which is not used in the typical configuration.

With **NuAmps**, trigger events are affected somewhat differently, due to the special parallel-to-serial adapter cable. The following table summarizes the events with NuAmps. CURRY will make the changes automatically when you select **NuAmps** for the amplifier and the **Cedrus StimTracker** option in the **Acquisition** part of CURRY in the **Amplifier Control** → **Trigger Settings** section.

StimTracker Signal	See by Neuroscan as	
Event marker bit 7	Not recommended for use with NuAmps	
Event marker bit 6	Trigger bit 6	64
Event marker bit 5	Trigger bit 5	32
Event marker bit 4	Trigger bit 4	16
Event marker bit 3	Trigger bit 3	8
Event marker bit 2	Trigger bit 2	4
Event marker bit 1	Trigger bit 1	2
Event marker bit 0	Trigger bit 0	1
Lightsensor 1	Response bit 3	pho1
Lightsensor 2	Response bit 2	pho2
Microphone	Response bit 1	mic1
Audio L+R	Response bit 0	aud1

Cedrus Response Pad buttons 1-8 use Stimulus events 120-127 and the corresponding Trigger bits 0-6. CURRY converts stimulus events 120-127 to response events r1-r8.

There are the special considerations with NuAmps.

- We have seen in some instances where events codes that use Event marker bit 7 are not always reliable. We recommend not using that bit, which means you should only use event codes from 1-127. If you need more than that try them, but be aware that there could be a problem.

- Note that responses are being carried via stimulus bits. CURRY will recognize stimulus bits 120-127 and convert them automatically into r1-r8 events. For this to happen, you need to set the Response Base Word in Stim2 (**Options → Response Device Settings**) to **119**. This means that you should not use 120-127 events as stimulus events - they will be seen as responses.

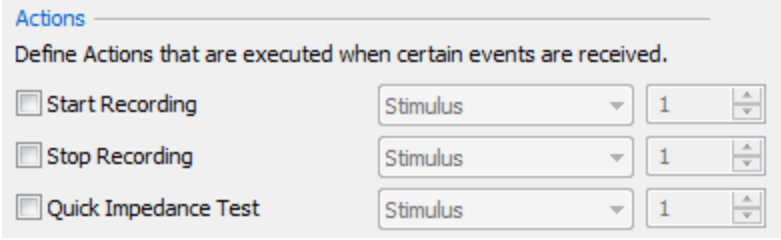
- When you use **Trigger Test** in **Stim2**, you should see events of "255" in CURRY (you will see r8's with SynAmps).

- Response bits 4-7 are not used with NuAmps.

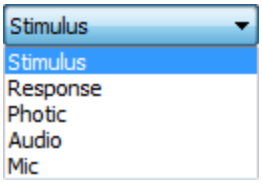
Method. The Method options are used with the response bits only, with either the older Stim2 system (with the Stim Audio System unit), or with the StimTracker. Realize that when using the StimTracker, 4 of the response bits are for the direct measurement of microphone, audio, and photic sensor events.

The options are to create events at the Onset of the event, the Offset, or both Onset and Offset. For example, if you are presenting a checkerboard pattern reversal stimulus, the StimTracker will detect the dark to light change and CURRY will register a pho1 event. This is if you have selected the **Mark Onset** option. To get events for the light to dark changes also, you would need to select the **Mark Onset and Offset** option (or use a second photic sensor). The event for the Offset will be 10x that of the onset event. For this example, that would be pho10 events when the pattern reverses back again. Similarly, with audio stimuli, you would see an aud1 for the onset of the stimuli, and an aud10 for the offset. If you want trigger events only at the end of the stimuli (i.e., when the measured signal drops below the threshold), select **Mark Offset**. These same options will apply to responses with the older Stim2 system (with the Audio System Unit).

Event Actions. You may instruct CURRY to take certain actions when selected events are received; the actions are to Start Recording, Stop Recording, and perform a Quick Impedance Test.



Enable the desired action, select the type of event (Stimulus, Response, Photic, Audio, or Mic), and set the numerical value for the event.



Miscellaneous

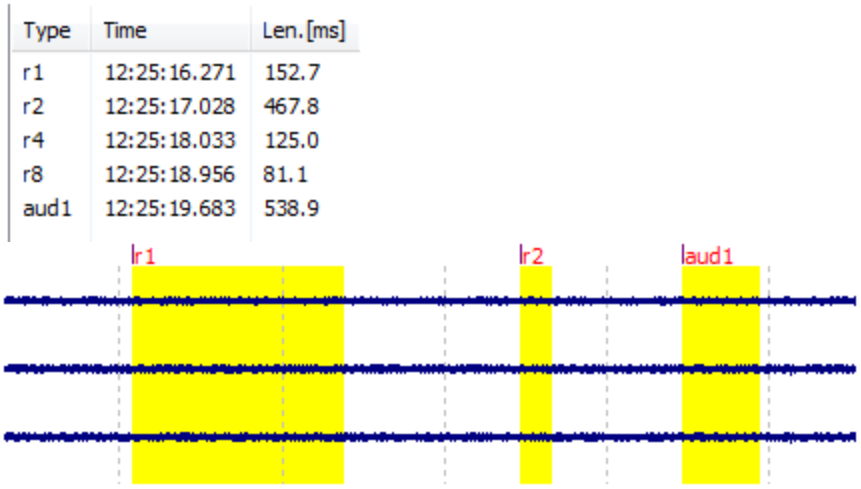
The **Refractory Period [ms]** is used to avoid multiple response events due to "bouncing" bits. The default is set to 2ms, which is sufficient for avoiding the bouncing of the StimTracker response pad. This refractory period works per event. After a Stim2 event there cannot be another Stim2 event within the refractory period, but events of a different type (like a resp1) in that time will pass. This makes sure that, for example, a periodic r5 event is not blocked because it incidentally occurs in the refractory period of an r1 event.

The **Align StimTracker Events [ms]** option is used only when you have a StimTracker system, generating pho1, pho2, aud1, or mic events, which are paired with the stimulus TTL events from STIM2. When enabled, CURRY will replace the stimulus type code latencies with those generated from the StimTracker, which is more precise. The **[ms]** field should be larger than the duration of the greatest difference between the stimulus type codes and the StimTracker event codes. This correction is used online primarily when you are creating online averages. Only the original times of the stimulus and StimTracker type codes are saved with the

continuous data file, meaning that you will need to perform the same correction offline as well. The offline **Align[ms]** option is found in the **Averaging** panel under **Events / Epochs**.

Record Event Duration. If you enable **Record Event Duration**, you will see the length of stimulus and response events. This option is only available for SynAmps2/RT and Neuvo amplifiers (not NuAmps or Grael).

The durations appear in the **Event List** (select **Show Duration** from the event list context menu).

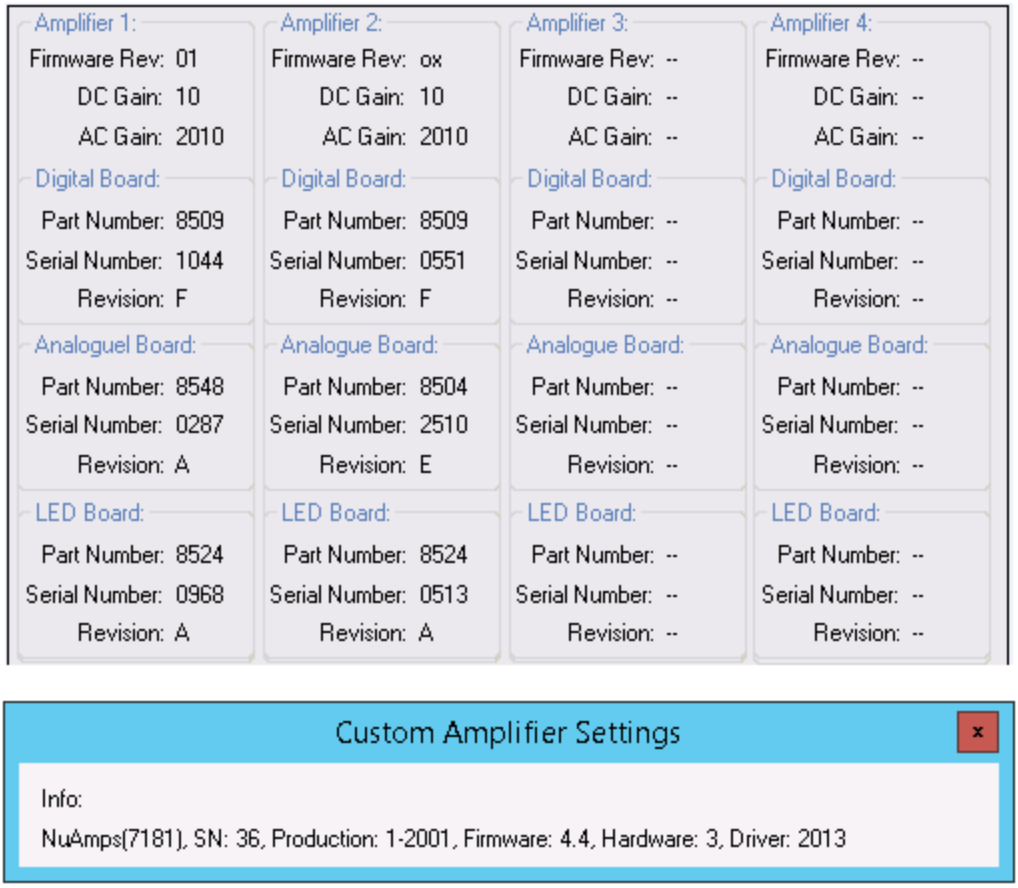


Auto-Create Events. This option is used to insert specified events at specified time intervals in the continuous data file. This allows you to do online back-to-back epoching, as well as other instances where you need events in the file. Note that you also have the option to **Show Events** or not, and to **Record Events** or not.

Reset. Clicking the **Reset** button displays a dialog asking if you want to reset the Trigger Settings to the default values.

Re-Synchronize
This trouble-shooting button is used in rare instances where data channels suddenly change, such that channels that were flat (by design) start showing data, where some channels that had been showing data become flat, or where "garbage" suddenly appears in some channels. Or, impedances may shift from correct channels to incorrect ones. CURRY 8 will automatically detect and correct these occurrences in most cases (by quickly reconnecting to the amplifier). Failing autodetection, you can click the **Re-Synchronize** button to correct the issue. In these rare and unpredictable instances, you will lose about a half second of data after clicking the button. A "Resynch" annotation event is placed in the file when this happens.

Custom Amplifier Settings. This button will become active if you are connected to the amplifiers, depending upon which amplifiers you are using. *E-Series* amplifiers (and the *Simulator*) have no custom settings. If you have *SynAmps2*, *SynAmps RT*, *NuAmps*, or *Neuvo*, you will see information about the headboxes.



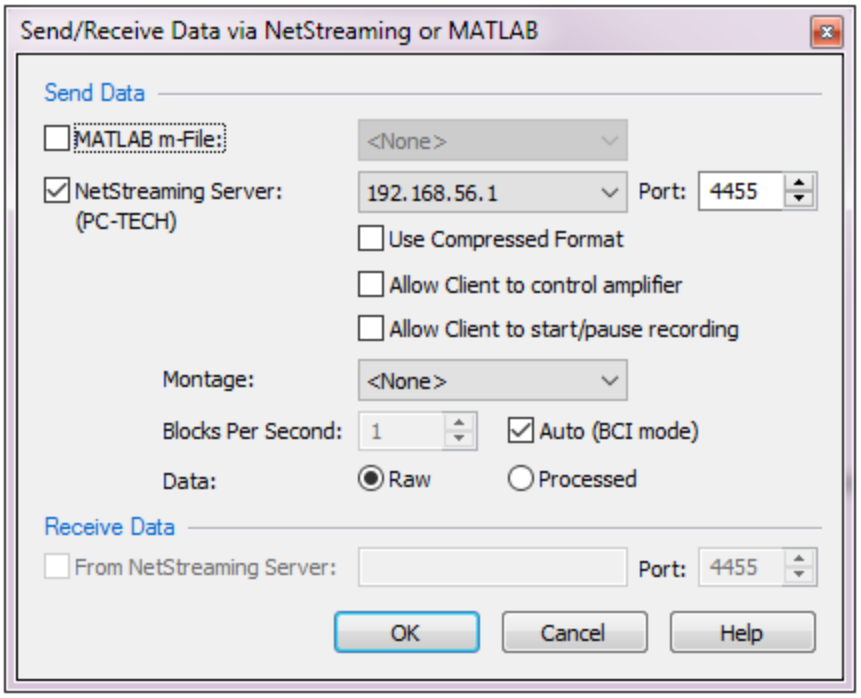
With other amplifiers (*Grail* and *Siesta*), there are options you may select. Please refer to the amplifier manual for details.

14.2.1.1 Configure as NetStreaming Server or Client

There are two ways you may use the NetStreaming option in CURRY - transfer live data to another computer running CURRY (where the sender is the **Server** and the receiver is the **Client**), or transfer live data to MATLAB or other third party applications (or both at the same time).

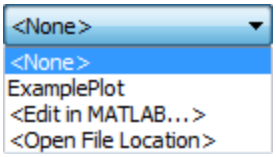
If you have two computers on the network, each will need a CURRY license/dongle (at least for Acquisition).

Click on the  icon to see the NetStreaming dialog.



Send Data

MATLAB m-File. Sending the data stream to MATLAB is generally done for BCI purposes. Select the MATLAB script you are using. In the dropdown list, you will see the list of MATLAB files, as well as the **<Edit in MATLAB>** and **<Open File Location>** options. Sending data to MATLAB is independent of whether this instance of CURRY is also used as a Server or Client. You can send data to MATLAB from either the Client or the Server.



This applies to the MATLAB interfaces in Functional Data and Acquire.

This data get sent from CURRY to MATLAB:

- indat: waveform data
- inlabels: list of channel labels
- insampleratehz: sampling rate of waveform data in Hz
- instartsample: absolute startsample of the current datablock
- inevents: list of events (sample number and event type) within current datablock
- inepochtype: event type of epoch (only used for epoched data)

These variables can be filled in MATLAB to send data back to CURRY:

- outdat: waveform data, must be of the same dimensions (number of channels and samples) as indat
- outevents: list of output events (sample number and event type) within current datablock; events will be merged with the existing event list in

CURRY (only for contiguous data)

More detailed information about the data types can be found in the header of each FD2 example m-file.

During an acquisition, CURRY can stream continuous data to MATLAB in two ways:

1. Via MATLAB's COM interface:

   - MATLAB must be installed on the same computer that CURRY runs on
   - two-way communication is possible: modify data and/or events in MATLAB and send changes back to CURRY Acquisition
   - CURRY comes with demo m-files (contact curry8help@neuroscan.com)

2. Via TCP/IP:

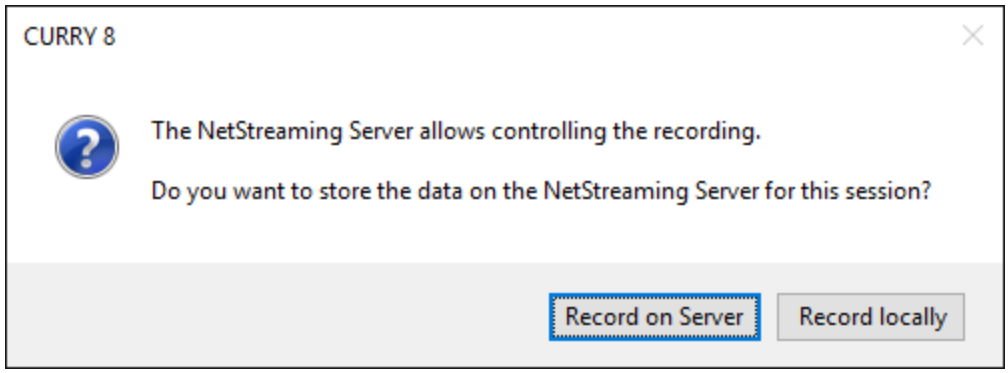
   - data can be streamed to MATLAB or any other custom software over the network
   - data cannot be fed back into CURRY, but recordings can be controlled remotely (start/stop recording or impedance check)
   - CURRY comes with demo projects for MATLAB and C++ (contact curry8help@neuroscan.com)

NetStreaming Server (<name>) / Port. This is the network port that is used for TCP/IP communication from one computer to the other. You may see more than one item listed in the dropdown list; be sure to select the IP address you will be using. The **Port** setting must be known if there are firewall exceptions to be set.

Use Compressed Format. Use the compressed format or not. This has no effect on data quality, only on the packet size that is sent. Compressed is recommended unless the receiving program is something other than CURRY that may not be able to read the compressed format. The non-compressed option uses a raw float format (contact curry8help@neuroscan.com for details).

Allow Client to control amplifier. Enabling this option allows the client computer to control the starting of acquisition, impedance testing, stop recording, and disconnecting the amplifier. Confirmation dialogs will appear on the Server when the Client requests an action, so that the Server has the option to reject the request.

Allow Client to start/pause recording. The Client will have the ability to start/pause the recording to the server or locally to the client computer. The Client has the option see the data being recorded on the server.

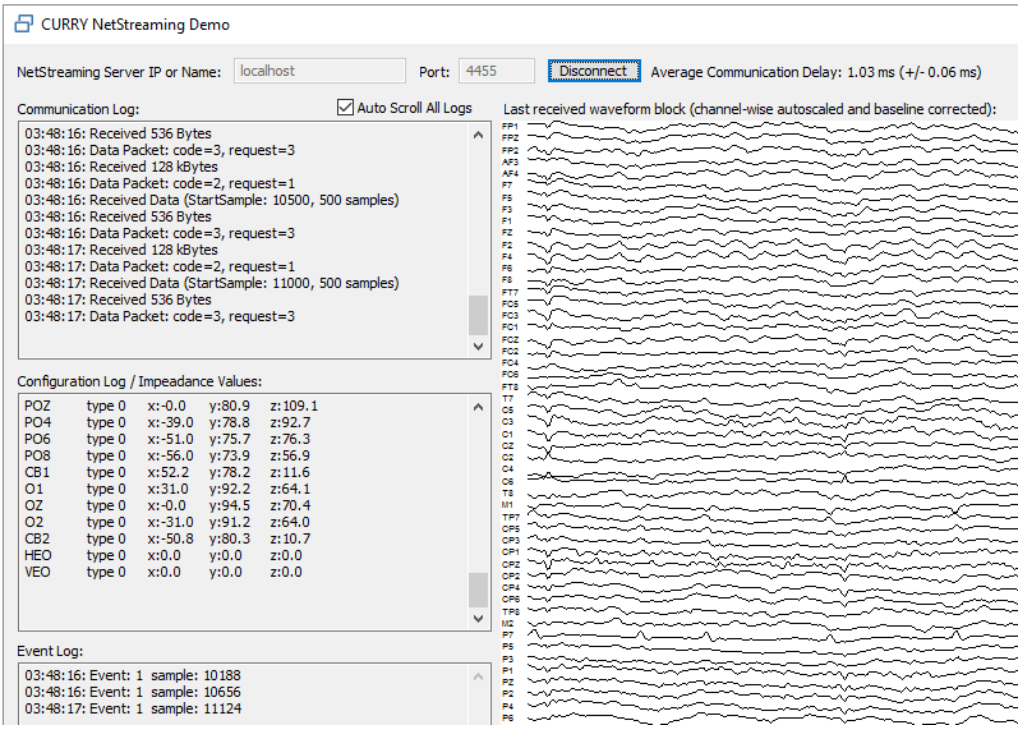


Montage. The data sent out will be using the selected montage. You can use this to, for example, reorder or reduce the number of channels that are sent out. The montage cannot be changed while a streaming session is running. (You can select another montage at any time, but CURRY will notify you that the change will only be effective in the next session.)

Blocks Per Second. Set the number of blocks per second to be sent to the other computer or to MATLAB.

Auto (BCI Mode). The blocks will be sent as quickly as they are received from the amplifier (recommended for BCI applications). This not only determines the blocksize from what the amplifier provides, but also internally uses "zero-delay" sockets and speeds up other internal communication steps, so that the delay due to communication is smaller than before. This mode increases the CPU usage, so if you are not depending on a very low delay, it is better to not use the BCI Mode.

The C++ Netstreaming Demo now also tries to measure the communication delay on connect (look to the right of the Disconnect button):



Data. You may send either the **Raw Data** or the **Processed Data**. Sending the Processed Data may add a delay in the transmission because of the time required for the processing sequences (filtering, artifact reduction, etc.). Artifact Reduction may add a delay and increase the block size of the transmitted data block.

Receive Data

Client Server IP or Name / Port. On the receiving computer, open the same NetView dialog, and enable the **Client Server IP or Name** option only. Enter the same IP address or computer name ("Lazarus" in the above example) that you entered for the Server. The **Port** must be the same as on the Server.

On the Server side, you need only to then click OK. You will see a green circle appear letting you know that it is waiting for the Client to connect (see also the Tooltip associated with the circles).

On the Client side, you will see a blue circle.

When the connection has been accepted, you will see a green disk on the Server side.

When the connection is made, you will see the blue circle change to a blue disk, and you will see the data that the Server is displaying. Once the Client is connected to the Server, you cannot change the Amplifier field.

You will see a red circle when you are set up as a Client, but the Server is not connected yet. This happens, for example, if you were set up as a Client the last time you used CURRY, but have not tried to connect to the Server yet (by pressing the connect button). The Client does not know yet if the Server is available, but is prepared to try.

You may Record data on the Server computer or on the Client computer, or both. The Client is functioning as an independent computer, almost as if it were connected to the amplifiers. You can Pause the display, look back, and select almost any of the regular acquisition options. If you start an Impedance test on the Server side, you will see the results on the Client.

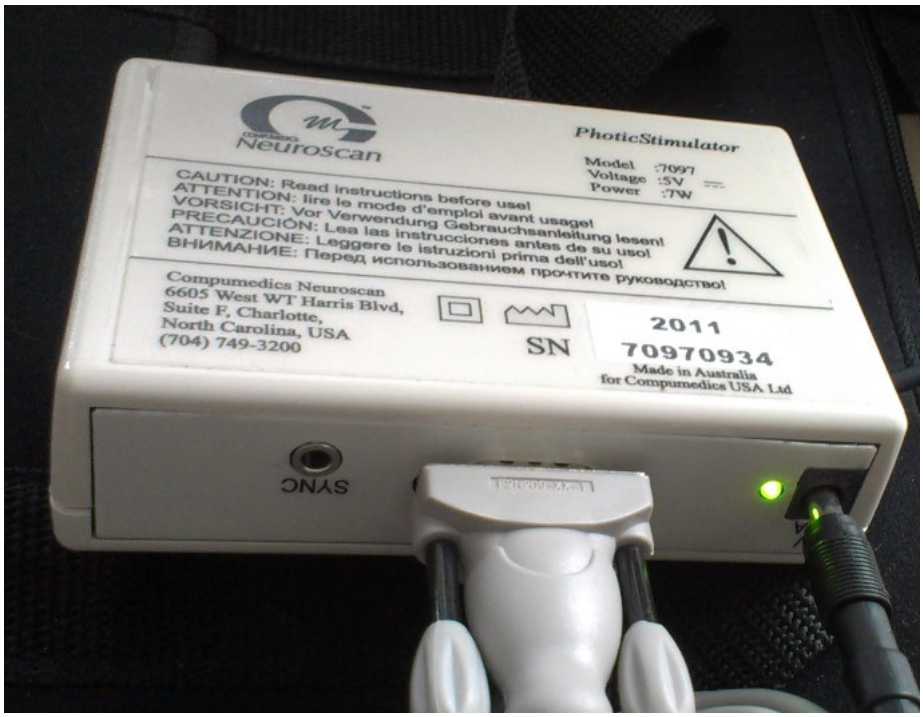
When you stop acquisition on the Server, a message to that effect will be seen on the Client. If the Server reconnects, the Client display will then continue, as long as you have not broken the connection.

The Server or the Client may disconnect at any time by deselecting the Server or Client option in the NetView dialog.

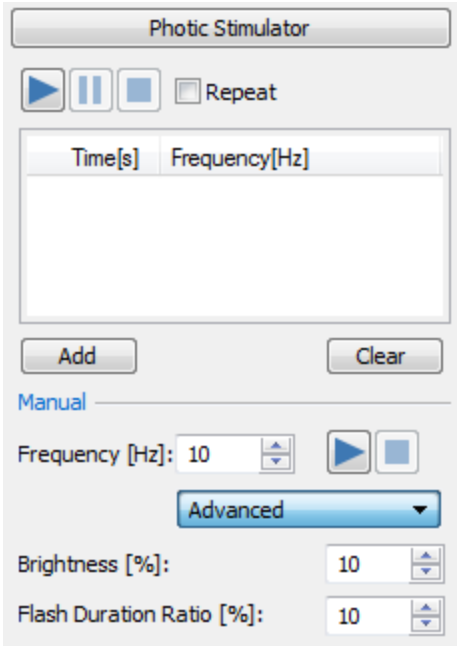
14.2.2 Photic Stimulator

CURRY can interface with the Compumedics Neuroscan Photic Stimulator (Model 7097). From CURRY, you may control the flash rate, intensity, create sequences, and insert pauses.

Installation is straightforward - just connect the cables. A standard serial-to-USB converter is needed to connect to the CURRY computer.



The controls in CURRY are found in the Acquisition panel.



1. To create a sequence of flashes, click the Add button. Enter the **Time** (duration, in seconds) for the first sequence, and enter the desired **Frequency[Hz]**. Click Clear to clear the sequences.

	Time[s]	Frequency[Hz]
	10	7

2. Repeat the process to add more sequences.

3. To add a Pause between flash sequences, enter a **0** for **Frequency**. There will be a pause for the number of seconds you entered for **Time**.

	Time[s]	Frequency[Hz]
	10	7
	5	0
	10	14

4. Click the  button to start the flash sequences. Click  to Pause the sequences. Click  to Stop the sequences at any point. Click  to keep repeating the sequences until you stop them. Stop them using the Stop button, or by unchecking the Repeat option (the current sequence will finish and then the flashes will stop).

Manual
To control the flashes manually, enter the desired **Frequency** under **Manual**, and click the  button to start the flashes. Click  to **Stop** the flashes.

Advanced
The intensity of the strobe is controlled by the **Brightness[%]** field.

The **Flash Duration Ratio[%]** controls the duration of each flash. If set for 100%, there is no "off" time, and the light will be on all the time. If set for 50%, the light will be "on" and "off" for equal amounts of time. The actual duration of the on and off times will depend on the selected frequency. A flash Frequency of 10 Hz has a flash duration of 100 ms. If you set the Flash Duration Ratio to, for example, 10%, then the "on" time will be 10 ms and the "off" will be 90 ms.

14.2.3 Filter Parameters

This dialog contains filtering and other processing parameters.

Display filters can be applied to any or all channels. See the offline **Filter Parameters** section below for more information about filtering.

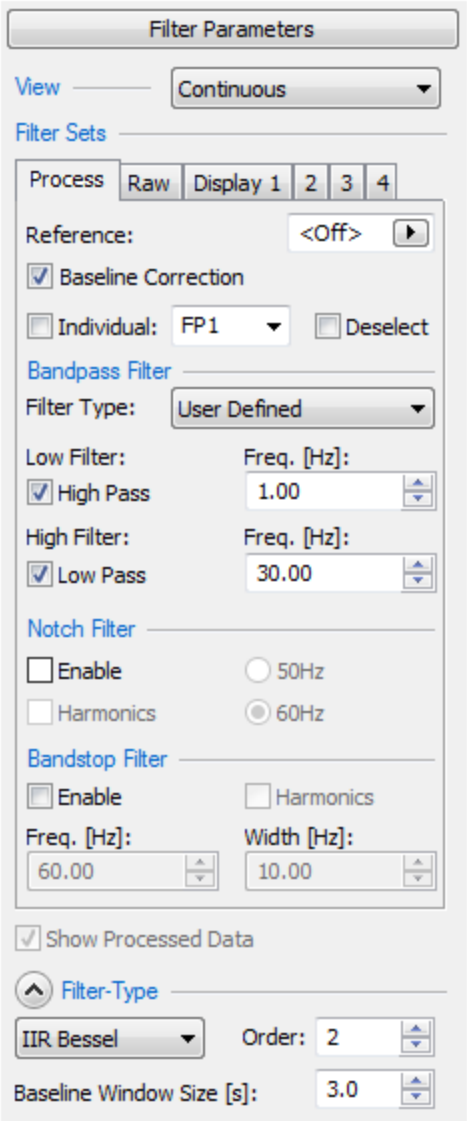
*With continuous data, filtering affects the display of data only. The unfiltered, unprocessed continuous data only are saved. The additional IIR filters that are applied to the online averages can cause latency shifts in the data (one pass filters). The filter settings you use online can be saved with the online acquisition parameters. Offline, you should use the FFT filters (offline **Filter Parameters** panel) for best results.*

Online filters are Bessel or Butterworth IIR (infinite impulse response) filters, with a user-defined order, with slope of 12dB/oct, or 40dB/decade.

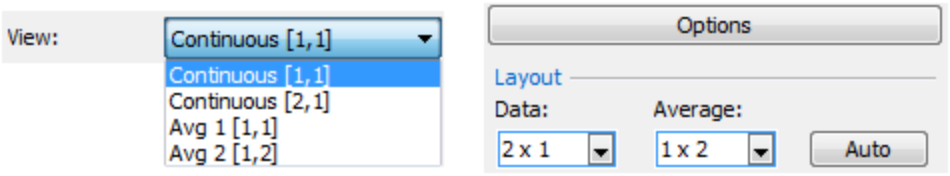
As a general note about sequencing, the order in which operations are applied is:

> Filtering → Artifact Detection/Reduction → Averaging (including Conditions, SNR Rejection, and Voltage Rejection).

The online **Filter Parameters** panel contains the following options and settings.



View. When you are displaying multiple views, as selected with the **Layout** options under **Options**:



the **View** field will let you know which display you are working with (which one has the focus). The numbers in the brackets correspond to the Column and Row of the selected display.

Filter Sets. When you select one of the tabs, you can create an independent set of parameters that may be applied to one or more data displays. The tabs let you program different filter sets, and then apply them just by changing tabs.

Process. Processed data are the data that are sent to Artifact Reduction, and these have typically been Baseline Corrected, Filtered, etc. Since it is the artifact reduced data that are used for the online averages, these parameters are applied to the data going into the online averages. The "Process" parameters do not affect continuous data that are saved - that is always the raw uncorrected data (for continuous data).

Raw. When you select the Raw tab, all of the parameters are grayed out, except for Baseline Correction, which remains an option. Thus, you will be seeing the raw data as coming in from the amplifiers (with or without Baseline Correction).

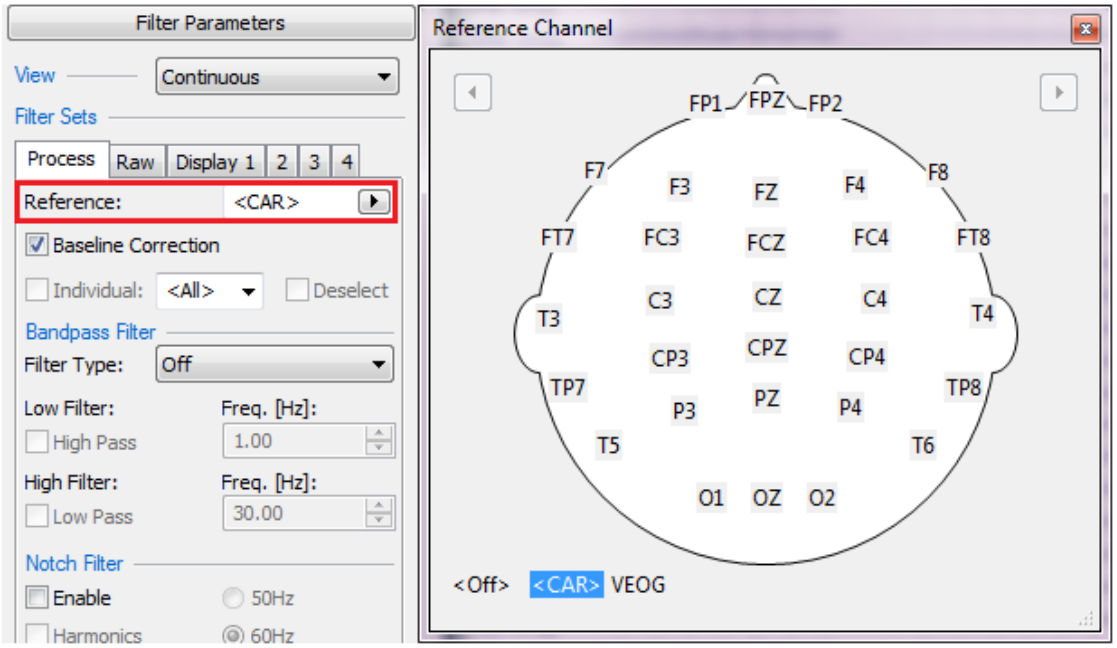
Display 1 - 4. You may create up to four sets of display options. These affect the display only; they do not affect the stored continuous data, or the continuous data that go into artifact reduction. If you apply display filters to online averages, where the continuous data were filtered already, the averages will be filtered a second time with the display filters. The saved average will contain the data as it comes from Artifact Reduction. Additional Display filters in the average views do not affect the stored averages.

Note
Note that you cannot, have, for example, Raw with Baseline Correction and another Raw without Baseline Correction, or Process with filtering and another Process without filtering. Each define a singular set of parameters that is applied whenever either one is selected. You can, of course, view the same raw data with or without baseline correction. You can use just one of the Display sets (with **Show Processed Data** deselected; described just below) in addition to the Raw set.

Note
Use *Ctrl+Alt+P* to select the Process Filter set, *Ctrl+Alt+R* to select the Raw set, and *Ctrl+Alt+1-4* to select the Display sets.

Reference. A new reference can be derived online. Click the button to see the Reference Channel display. Click on an electrode, or use *Ctrl+click* to select up to two electrodes to use for the reference. (CAR is the Common Average Reference). The raw data are saved regardless of the Reference selection (which may be

reselected offline). If you have NuAmps, with nothing elected for the Reference, each channel is referenced to ground (and that is what will be saved).



Baseline Correction. The Baseline option is used to remove DC offsets from the display (the data being recorded are not affected). Baseline Correction will be applied to all channels unless you specifically select the individual channels.

When using the Process Filter Set only, Baseline correction is performed using a rolling average of the N recent seconds. N is determined by the **Baseline Window Size [s]**, found in the **Advanced** section (set to 3 secs by default). If you are recording DC potentials, with Baseline Correction, the rolling average could affect the DC potentials you are recording. Varying the window size can reduce that. All other baseline corrections are static (and display only), and update depending on the window size that is set in each view.

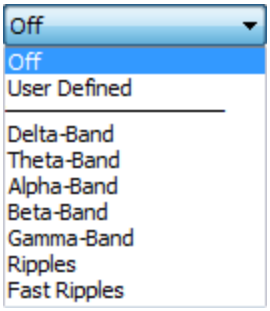
Individual. The filter settings are applied to all channels unless you specify individual channels for different settings. Select a single channel from the drop-down list and then select the desired parameters for that channel. Individually filtered channels are indicated with an asterisk.

Deselect. This is the same as *right clicking* on the channel label and selecting **Deselect Channel**. When Deselected, the channel will be excluded from operations that include multiple channels, such as MGFP, CAR, etc.

Bandpass Filter

Filter Type. Preset bandpass filters for Delta, Theta, Alpha, etc. may be selected from the **Filter Type** drop-down list. **Ripples** and **Fast Ripples** select faster frequency bands to focus on High Frequency Oscillations that have been associated with epilepsy. Ripples sets a bandwidth of 80-200 Hz and Fast Ripples sets a bandwidth of 200-450 Hz (AD rates slower than 1000 Hz will have different upper limits, as the highest low pass filter cannot exceed half the AD Rate). The

User Defined option lets you set the parameters as desired. The parameters are seen in the lower fields, and may be edited as desired.



Low Filter
High Pass. Enter a Frequency value (or use the arrows) to set a High Pass filter (frequencies below this value will be attenuated).

High Filter
Low Pass [Hz]. Enter a value (or use the arrows) to set a Low Pass Frequency (frequencies greater than this value will be attenuated).

Notch Filter. Adds a 50 Hz or 60 Hz Notch filter. The Harmonics setting controls whether harmonics (multiples) of the selected filter frequencies are suppressed.

The check boxes for each filter type allow you to apply only selected filters, without having to turn them off.

Bandstop Filter. A Bandstop filter is the opposite of a Bandpass filter. Rather than passing frequencies between the high and low pass limits, the bandstop filter attenuates frequencies about a selected frequency (similar to a notch filter). The Harmonics setting controls whether harmonics (multiples) of the selected filter frequencies are suppressed.

Freq. [Hz]. Center frequency for the bandstop filter.

Width [Hz]. Width is the interval from the 50% attenuation points about the center frequency.

Show Processed Data. This option is used with Display1-4. It gives you the option for removing the processing steps you have performed (filtering, baseline correction, artifact reduction). The same applies to the average views. Using this checkbox allows you to either view the average build from the raw data, or from the processed data. Only the processed average is saved.

Filter-Type

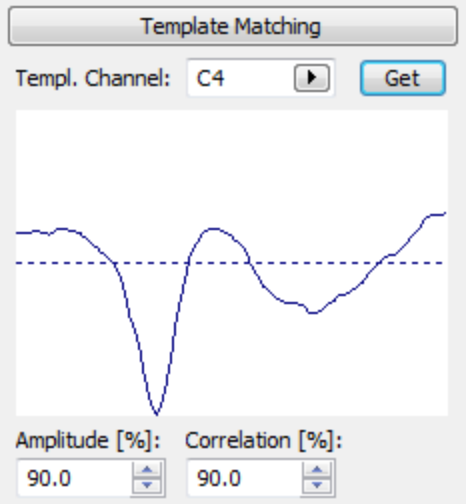
Unlike offline, where you have options for the filter shape, in online filtering, only the IIR filter is possible. You have the choice of using a Bessel or Butterworth filter, with the Order from 1 to 4.

Baseline Window Size[s]. This is used on conjunction with the Baseline Correction when a rolling average is used for determination of the offset to be

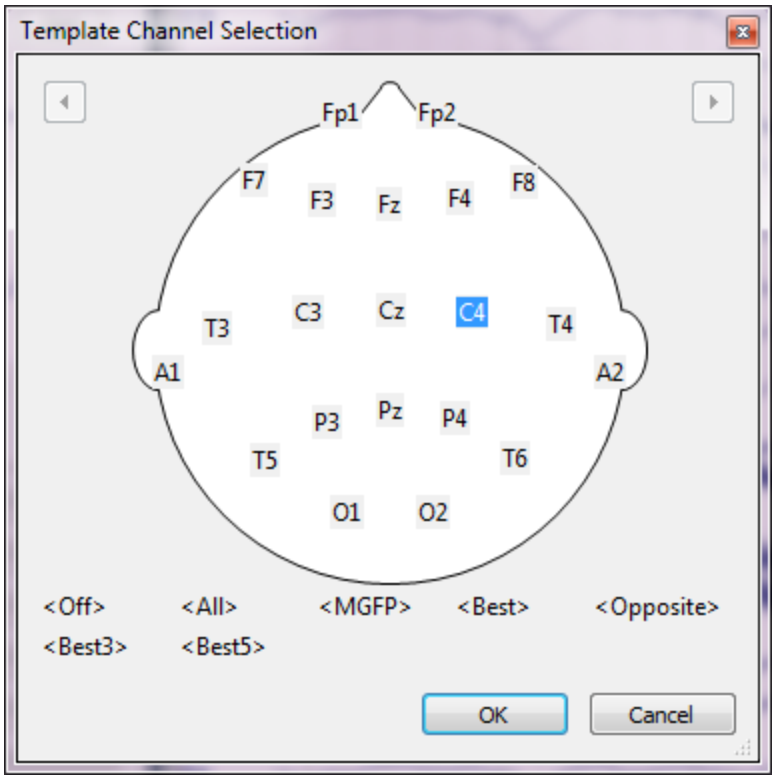
subtracted. If, for example, 3 is selected (default), the previous 3 seconds are used (and constantly updated).

14.2.4 Template Matching

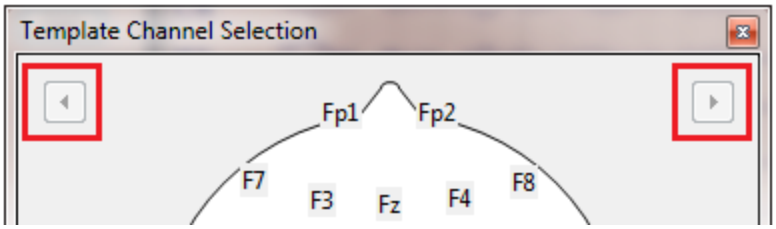
It is possible to use the Template Matching functionality of CURRY online, as well as offline. Online, it can be used to identify, for example, spike activity, and save the detected spike events within the data file. Detected events can be averaged online. Template Matching can also be used to identify artifacts and reduce them in the online display (the uncorrected data only are saved). This provides an alternate method for artifact reduction online (as opposed to using the voltage Threshold method, for example). See the acquisition *Template Matching* tutorial for an example of its use.



Template Channel. Select the channel(s) that you want to use. Note that you may select multiple channels manually, you can use the MGFP channel, the channel with the best SNR, the 3 or 5 channels with the best SNRs, or All channels. **Opposite** selects the same channel as **Best**, and then finds the channel with the largest difference to this signal.



On this and all other similar screens that display the sensor placements, you will see additional left and right arrow buttons if you have additional channel groups (MEG, EEG, etc.). Click an arrow to see the sensor distribution for that device. In some cases, you may have more "Other" channels than will fit in the space allocated for them. In those cases, you will see a small arrow  that will access the additional channels.



Get. With the display paused, set the two outer cursors (use *Shift+left mouse* to position the second cursor, or use *Ctrl+click and drag*) to encompass the waveform of interest. Press the 

button to transfer the latencies to be used. These will be reflected in the waveform display.

Amplitude [%]. CURRY will monitor the file for voltages that are a percentage of the value in the template. **75**% in this field means that CURRY will search (in the designated channel) for voltages that are at least 75% of the voltage in the template. Larger amplitudes are also included, as follows. If you set the Amplitude to 50%, that will include amplitudes from 50% of the template to 1/0.5%, or 200% larger. (All potential matches from 30% Amplitude and 50% Correlation are detected, regardless of the values that are entered. The matches that are

displayed in the Event List are the ones that fit within the parameters that you set).

Correlation [%]. CURRY will perform a correlation between the new region with the same region in the template. If the correlation meets or exceeds the level you set, the new region will be detected as an event (in conjunction with the Amplitude criterion).

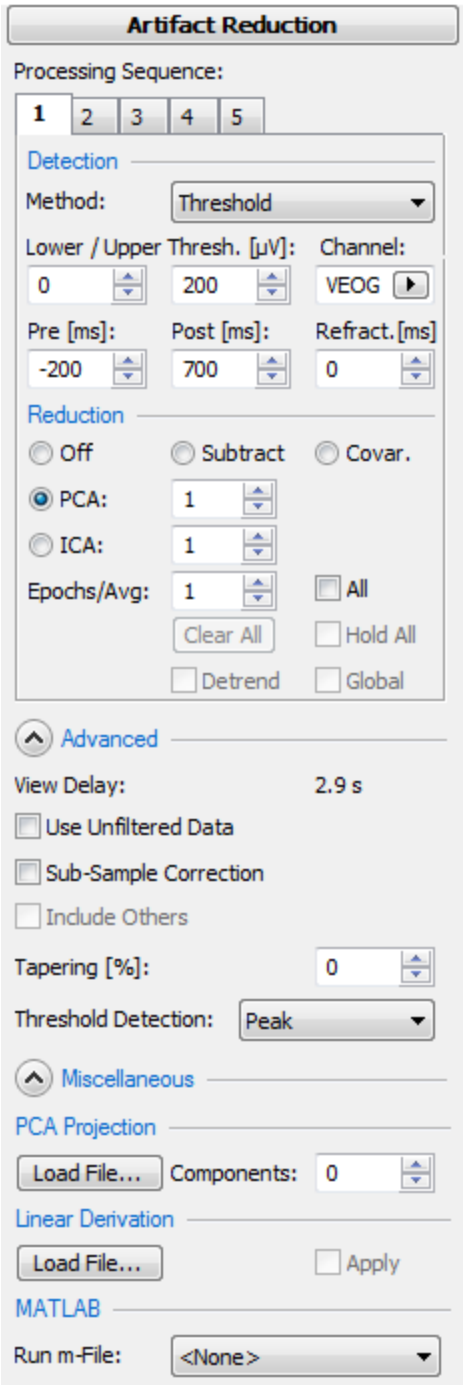
Both criteria must be met for there to be a match.

14.2.5 Artifact Reduction

Online artifact reduction is controlled by these options. You can reduce more than one type of artifact at a time. There are a variety of methods for detecting as well as reducing the artifacts. See the offline **Artifact Reduction** section below for a more complete description of the options.

As a general note about sequencing, the order that operations are applied is as follows:

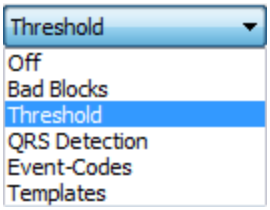
Filtering (by Processed Filter Set) → Artifact Detection/Reduction → Averaging (including Conditions, SNR Rejection, and Voltage Rejection).



Processing Sequence. If you have a file with more than one type of artifact, you may want, for example, to remove the eye blinks first and then remove EKG artifact. Set **Sequence** to **1** and then select the method and enter the parameters. Then select **Sequence 2** and set its type and parameters, and so on.

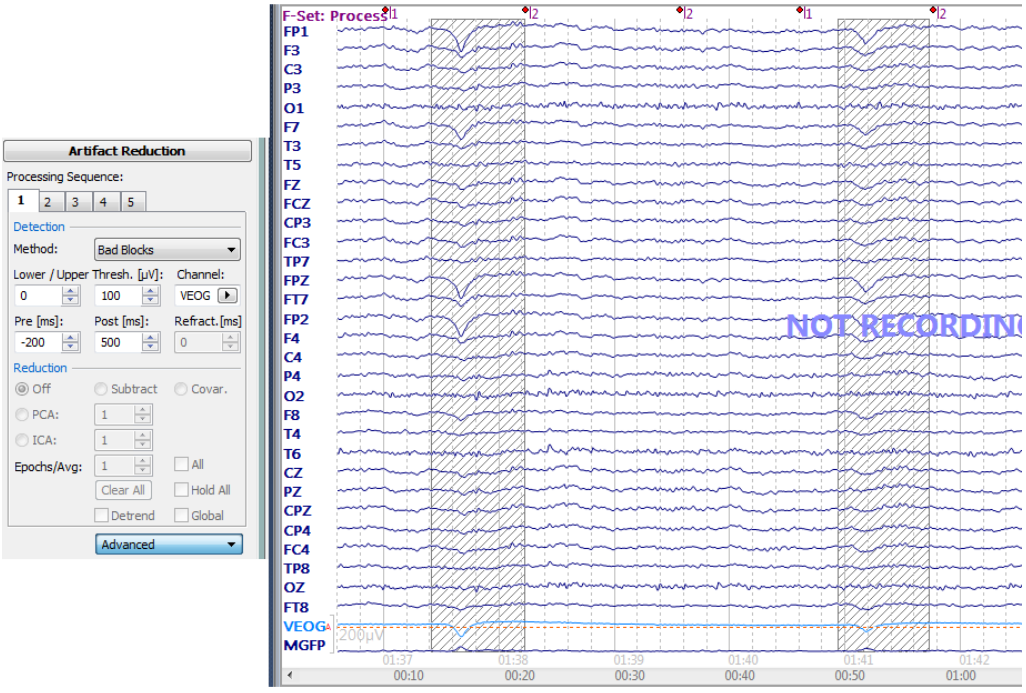
Detection
These options are primarily used to detect artifacts.

Method. Select the artifact reduction method that you wish to use.

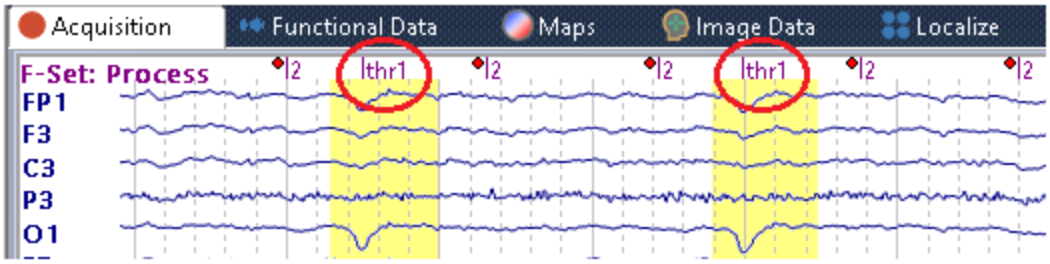


Off. No detection method is selected.

Bad Blocks. Sections of the incoming data file can be detected automatically as Bad Blocks, which will then be excluded from subsequent analyses. In the example below, blinks were detected and marked as bad blocks. Voltages from the selected channel (VEOG) in excess of the thresholds that were set, result in bad sections from -200 to 500 ms (from the peak of the blink). The program will wait 500 ms from the peak before looking for the next blink. Unlike manually selected bad blocks, the automatically selected bad blocks are not saved with the data file, unless you save the Study Parameters. To remove the automatically selected bad blocks, set **Method** to **Off**.



Threshold. Any single channel, including the MGFP channel, or combination of channels will be scanned for voltages in excess of the **Threshold** values entered. The **Pre** and **Post** times define the interval from the point at which the Threshold was detected. The intervals will be shaded in yellow in the data file. The detected artifacts will be seen as "Thr1" (or whatever the Sequence number is) in the continuous data file. See the *Common Artifact Reduction* tutorial for more details.



QRS Detection. This method is designed primarily for reduction of heart beat (pulse) artifact. The QRS complex is detected automatically and QRS1 events (or what the Sequence number is) are seen in the data file.

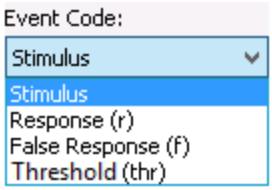
The QRS Detection method uses an automated QRS Detection routine, based on a public domain algorithm for QRS detection (Open Source ECG Analysis Software Documentation; Copyright © 2002 Patrick S. Hamilton).

The algorithm is used for peak detection and trigger placement. With it, there is no need for the Refractory Period or Threshold parameters. You can still define the duration of the artifact, as well as the channel(s) that are to be monitored for detection. (See the offline **Artifact Reduction** section below for more details).

Event-Codes. Rather than using a voltage threshold to detect artifacts, this option uses event codes in the recording. For example, in an SEP recording you might have stimulus artifact occurring at and just after the stimulus type codes. Define the duration of the artifact and use Subtract to replace the artifact with flat lines (**Epochs/Avg** = 1) or by subtracting whatever residual EEG is in the average (**Epochs/Avg** = larger value). Try PCA or ICA Projection to project the artifact from the data.

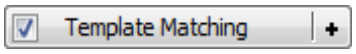
This is also the method used to remove MRI gradient artifact (see the online and offline *MRI Gradient and Ballistocardiogram Reduction* tutorials for details).

In addition to the **Stimulus** and **Response** options, you will also see **False Response** and **Threshold** options.



The **False Response** option applies only when you are replaying a file with the amplifier simulator, where you have already merged the behavioral data file that contains Accuracy information. In that case the "Responses" mean the correct responses, and the False Responses mean the incorrect responses. You may then elect to correct only those intervals where the subject made a correct or incorrect response.

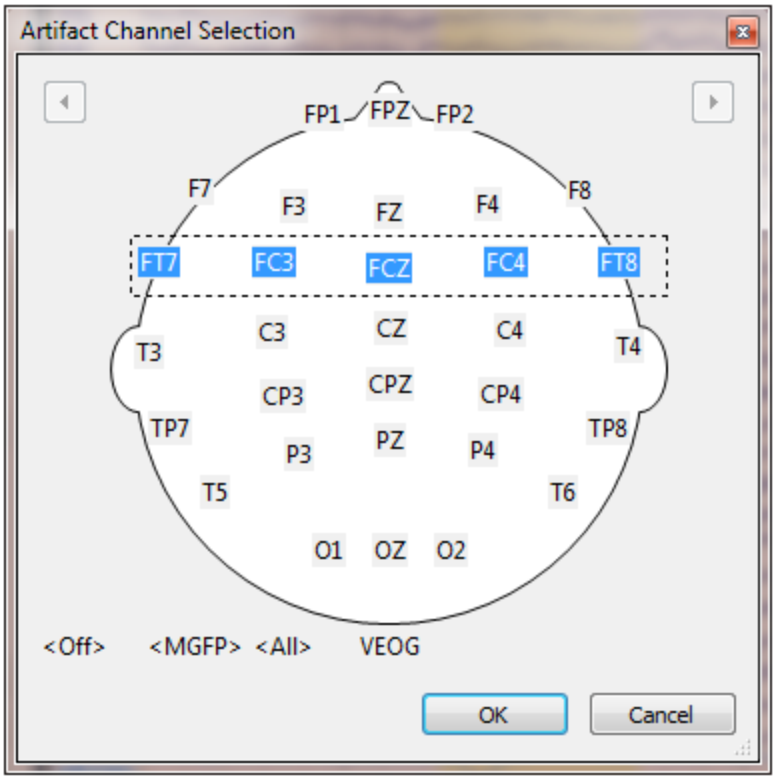
The **Threshold** option allows you to decouple artifact detection with artifact reduction. It is used in a later Processing Sequence, after the artifacts have been detected using **Threshold** for **Method**. For example, say you wanted to compare blink reduction where you use one threshold criterion for Sequence 1 (100μV), a different threshold for Sequence 2 (200μV), and another threshold for Sequence 3 (300μV). For Sequence 4, select **Event-Codes** for the **Method** and **Threshold** for **Event Code**. Use Reduction for the 4th sequence only. Then, if you select Threshold 1, all detected blinks will be corrected. If you select Threshold 2, only those with a threshold at or above 200μV will be corrected. If you select Threshold 3, only those with a threshold at or above 300μV will be corrected.

Templates. If you have set up the 

parameters to find features of interest (e.g., blinks), you can then use the **Templates** option to reduce them (see also the offline **Template Matching** section below). If you are using Templates (in Processing Sequence 2, for example), with gradient reduced data (in Processing Sequence 1), you must enable **Use Unfiltered Data** when reducing the *gradient* artifact, or else no matches to the template will be found in the gradient reduced sections of the file.

Lower/Upper Threshold [μV]. This sets the voltage thresholds (positive or negative values). Values exceeding the thresholds (on the channels you select) will result in detection of the artifact.

Channel. You may select a single channel to be monitored (for the Threshold), a combination of channels, the MGFP channel, or All channels (any one can meet the Threshold criterion). Use *Ctrl+click* to select individual channels, or, you may drag a rectangle around a group of electrodes to select them.



Pre [ms] / Post [ms]. Pre and Post define the start and end latencies for the artifact interval.

Refract [ms]. Defines the minimum time that must elapse from one threshold detection to the next possible one (voltages that would meet the Threshold criterion during the Refractory period will be ignored). The Refractory period must always be at least the sum of the durations of the **Pre [ms]** and **Post [ms]** spans (no additional events can be detected in the artifact interval). A zero in this field (default) also uses the sum of the Pre and Post [ms] spans. Setting **Refract** to **0** lets you reduce the Pre or Post [ms] intervals without also having to reduce the refractory period also. Zero is always the sum of the two intervals.

Reduction. Select the method of artifact reduction you wish to use.

Off. No method is selected.

Subtract. When selected, the "rolling" average artifact - based on the number you selected for **Epochs/Avg** - will be subtracted from the current artifact.

Covariance. When selected, a covariance analysis is performed between the artifact channel and each EEG channel. Linear transmission coefficients (similar to beta weights) are computed, and, based on the weights, a proportion of the voltage is subtracted from each data point in the artifact interval.

PCA Components. A PCA analysis is performed on the averaged artifact. You may then select how many PCA components you wish to remove. Inspect the corrected data as you increase the number of components. Use only the number that results in artifact removal, while minimizing the effects on the remaining data.

ICA Components. An ICA analysis is performed on the averaged artifact. You may then select how many ICA components you wish to remove. Inspect the corrected data as you increase the number of components. Use only the number that results in artifact removal, while minimizing the effects on the remaining data.

Epochs/Avg. This sets the number of artifact epochs to be used in the artifact average. The N most recently detected artifacts will be used (rolling average).

All. If you enable All, then all of the detected artifacts will be used for the artifact average, and the number will increment as more artifacts are detected (accumulating average).

Clear All. This option clears the artifact average (when **All** is enabled), and resets the counter.

Hold All. This option will stop adding new artifacts to the artifact average, and the counter for **All** will stop incrementing. If you deselect Hold All, the new artifacts will be included with the previous ones in the **All** average. Click **Clear All** if you want to restart the average artifact. (You should not enable Hold All when no artifacts have been detected, as this will prevent any correction).

Detrend. Detrend is a rarely needed option for reducing gradient artifact in certain situations (online only). In these cases, the artifact varies in a linear fashion across TR blocks, and therefore the usual average and subtract method is not wholly effective. Detrend computes a weighted average that results in a well corrected file. If the usual correction (try with and without **SSC** first), is not effective, try using Detrend. When using Detrend, the number of **Epochs/Avg** only allows even numbers.

Global. When you enable Global, the correction will be applied to all data points in the file from that point onward, as opposed to only the artifact interval being corrected. The Global option is useful for avoiding the sharp voltage transitions that may occur at the edges of the artifact intervals. It is active only with the Covariance and PCA reduction methods.

Advanced

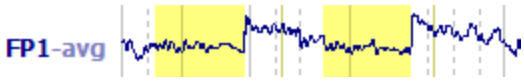
View Delay 0.0s. This field will display the delay that is present between the raw and corrected data, due to the time required to perform the correction.

Use Unfiltered Data. Selecting this option will use the unfiltered data even though you have applied filters to the data. The intended use is for MagLink data files where you typically perform several artifact reductions (gradient, BCG, blink), and you need the unfiltered data for the gradient reduction and filtered data for the other methods.

Sub-Sample Correction. Sub-Sample Correction (SSC) is used for gradient artifact reduction when the routine [subtraction] correction does not produce reliable results due to subsample jitter about the event marks. A cubic spline is used with a correlation correction to adjust the jitter. If there is no jitter in the file, the SSC option will have no effect (and is time consuming), so it should be used only when needed. It can be used with or without clock synchronization, and with any AD rate. **Use Unfiltered Data** should be enabled when using SSC.

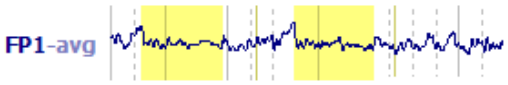
Include Others. Enabling this option will include channels designated as Other channels in the correction when using Subtract or Covariance (not PCA or ICA).

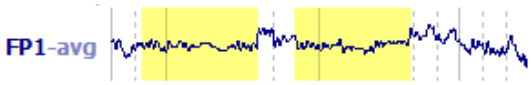
Taper [%]. On occasion, you may see sharp transitions from the artifact corrected areas to the uncorrected areas.



There are several ways to reduce these sharp transitions. One is to apply a taper. Here a 45% taper has been applied.

Other ways are to use a high pass filter (left), and to extend the interval that is being corrected to include more of the artifact (right).

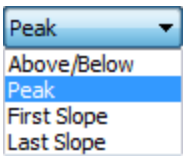




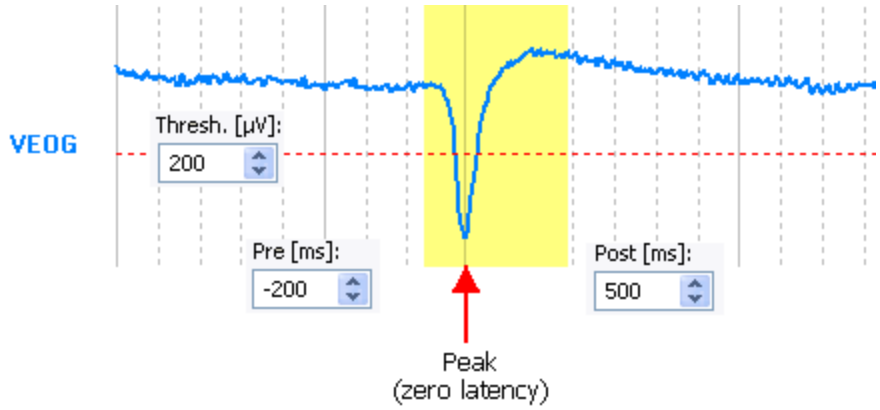
Offline, you can use the **All** and **Global** options.

Threshold Detection: The Threshold Detection options are used to align the peaks of the artifacts (minimize smearing of the average artifact due to latency jitter). They are active only with the **Threshold** method of artifact detection.

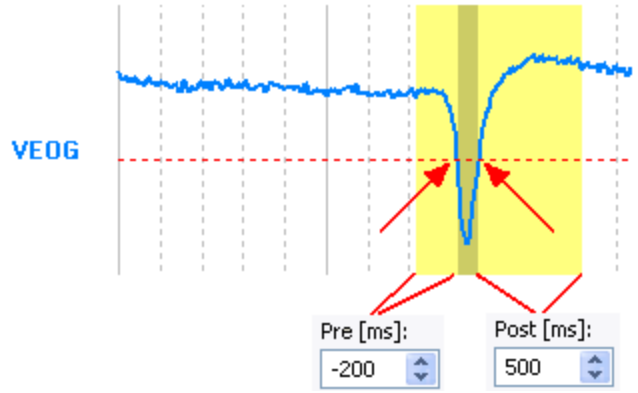
The default setting is **Peak**, and that is generally sufficient in most cases.



In that case, the "peak" is defined as the greatest voltage (positive or negative) between the two Threshold crossings (red dashed line). The **Pre [ms]** and **Post [ms]** intervals are measured from the zero latency point at the peak.



Above/Below. This option uses the intersection with the first Threshold as the end of the **Pre [ms]** interval, and the intersection with the second Threshold crossing as the start of the **Post [ms]** interval. This option is used primarily with MagLink data files, where there may be occasional jitter from the scanner pulses. Note that this is the only option where the width of the complete artifact interval can vary from one instance to the next. This is a problem only if you want to average the artifact events from the Event List - you cannot average epochs having differing widths. (This is not an issue when the artifacts are averaged in the process of Artifact Reduction).



First Slope. The zero latency point is where the first crossing of the Threshold occurs.

Last Slope. The zero latency point will be where the second crossing of the Threshold occurs.

PCA Projection. This option is used to select a .pca file you have created that represents the artifact or other feature(s) that you wish to project from the data. The function online is the same as offline; see the end of the offline **Miscellaneous** section for details.

MATLAB. Online use of MATLAB is very similar to offline; see **Interfacing with MATLAB** (the same FD2 prefix code is used). The only internal difference is that MATLAB will receive short chunks of data (1 sec) instead of the whole page. If this causes your MATLAB filters to ring, you would need to keep the filters initialized or keep temporary data in MATLAB.

Linear Derivation. Linear derivation files (LDR) were created in Scan for a number of purposes. CURRY 8 can create simple LDR files, and it will read and apply certain ones from Scan. For example, if you have created LDR files to reduce artifact using the Ocular Artifact Reduction transform, or from the Spatial Filter transform, those LDR files will work in CURRY 8 as long as the number of channels and the channel order are the same (otherwise you will get a message saying the matrix must be square). The labels are ignored in the LDR file, therefore, if you try to reorder the channels with an LDR file, the channels will change, but the labels will not. If you change the labels in the LDR file for any reason, such as renaming an interpolated channel, the labels will not be changed in CURRY (although the channel will be interpolated). [These restrictions may change in subsequent versions of CURRY].

Click the Load File... button to select an existing LDR file and the **Apply** field to apply it.

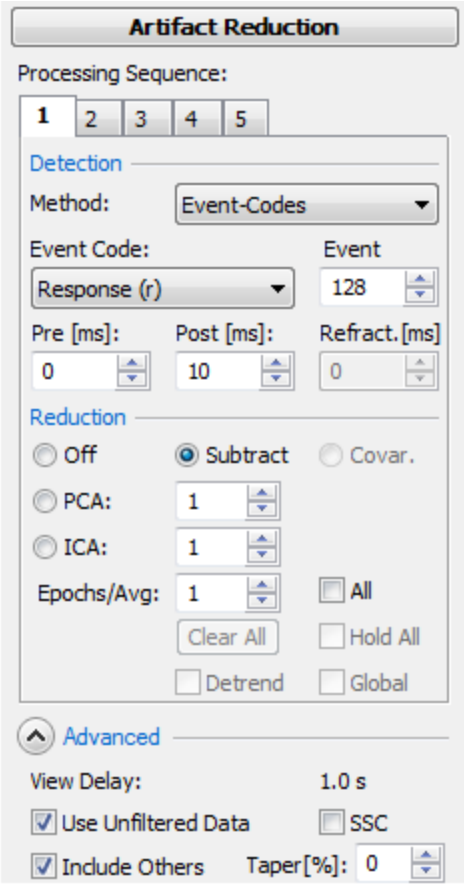
For information about creating linear derivation files, please see the **Creating LDR Files** section below.

Deblocking. In the Scan software there is a "Deblocking" option, used to remove (zero out) stimulus artifact. A TTL pulse from a peripheral device is sent via the SynAmps System Unit to Acquire, where you could specify the duration of the post-stimulus artifact that you wanted to be corrected.

The same capability exists in CURRY 8, but in a slightly different way. Deblocking is still controlled by a TTL signal sent from the peripheral device to the System Unit using the Deblocking Interface cable P/N 00081300 (included with the System Unit package). This cable connects to the Inter-System Unit connector on the back of the System Unit. The duration of the TTL pulse from the peripheral device should be about 1-5ms (depending on the sampling rate). The Deblocking pulse must return to the original response bit resting state (5V) between pulses. In other words, CURRY 8 expects negative logic (at least for the current version), and the events will be registered when the TTL pulse goes

to 0V. (You may invert the logic for the deblocking TTLs, although this will invert the logic for all TTLs).

The deblocking events are interpreted as "r128" events, and can be treated as any other event type in the software. To correct the artifacts, use Artifact Reduction, as shown below.



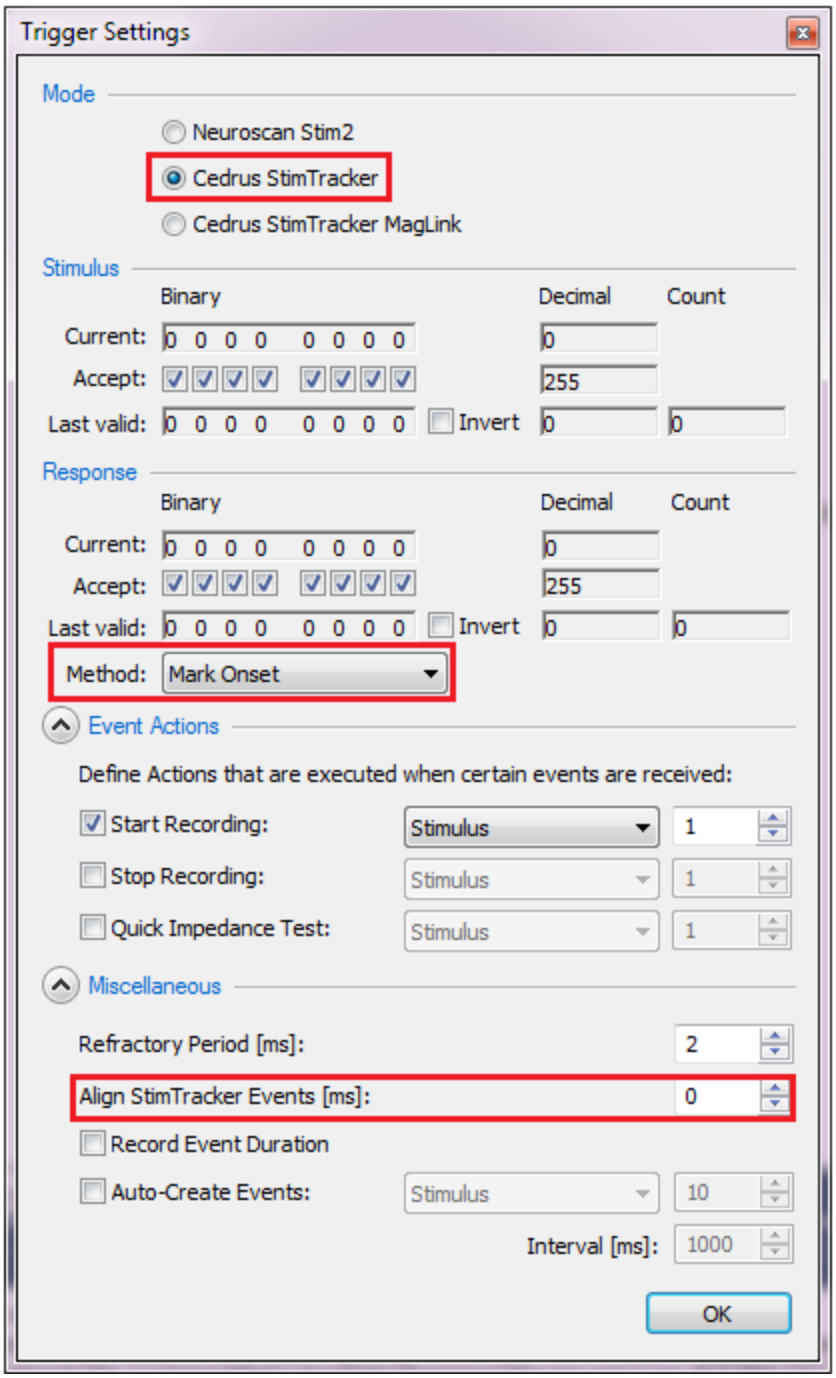
In this case, where **Epochs/Avg** is set to **1**, the 0 to 10 ms intervals after the r128 will become flat lines. You could also increase the numbers of Epochs/Avg, and/or try using PCA instead of Subtract, to see if the correction improves.

14.2.6 Averages

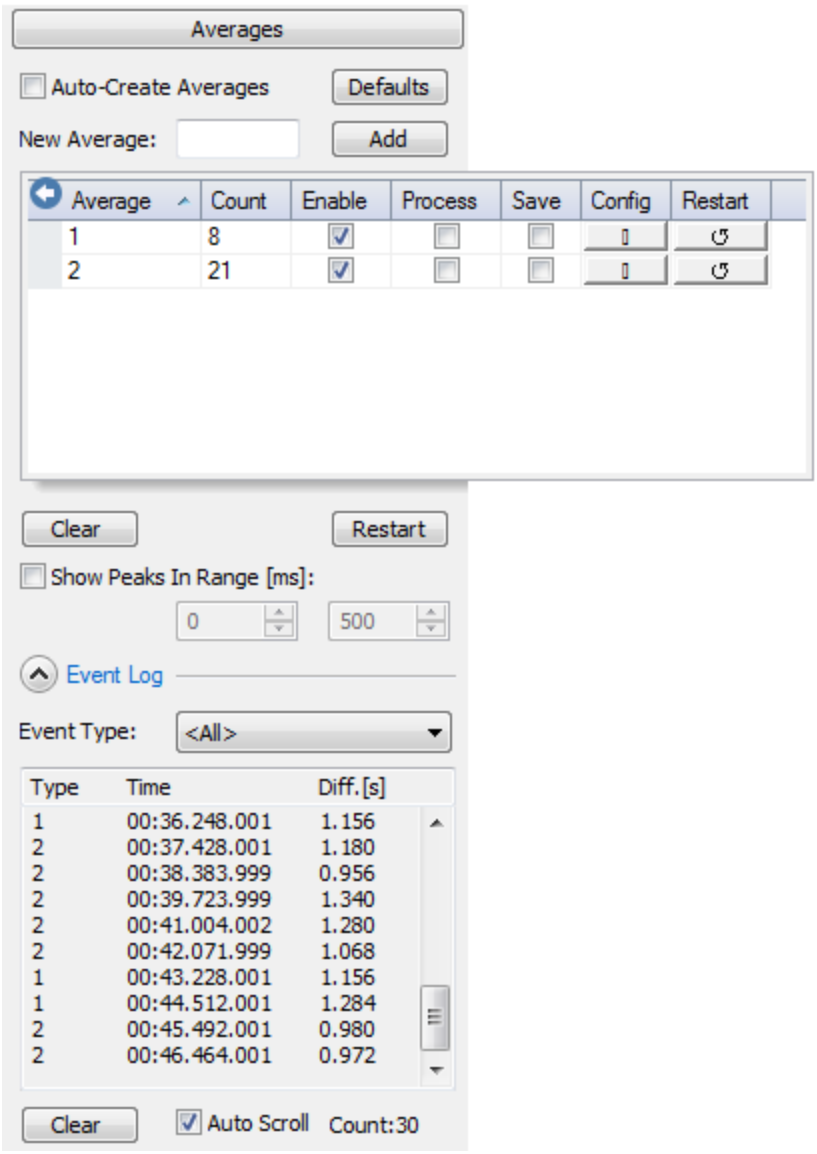
When you acquire data with events (stimulus and response events from Stim2 or other systems), or when you replay (Simulator) an existing file with events, you may create online averages of the events. The averages can be as simple as all events of a specified type, or a series of types, or more complex with conditional logic applied.

If you are using StimTracker, be sure to select the **Cedrus StimTracker** (or the **Cedrus StimTracker MagLink**) option in the **Trigger Settings** dialog under **Amplifier Control**. The **Method** options will let you add triggers at the **Onset**, **Offset**, or **Onset and Offset** of the StimTracker events. The **Align StimTracker Events [ms]** field lets you correct the timing of audio and visual events using the StimTracker events (see

the **Amplifier Control** section for more information, as well as the **Events / Epochs** section).



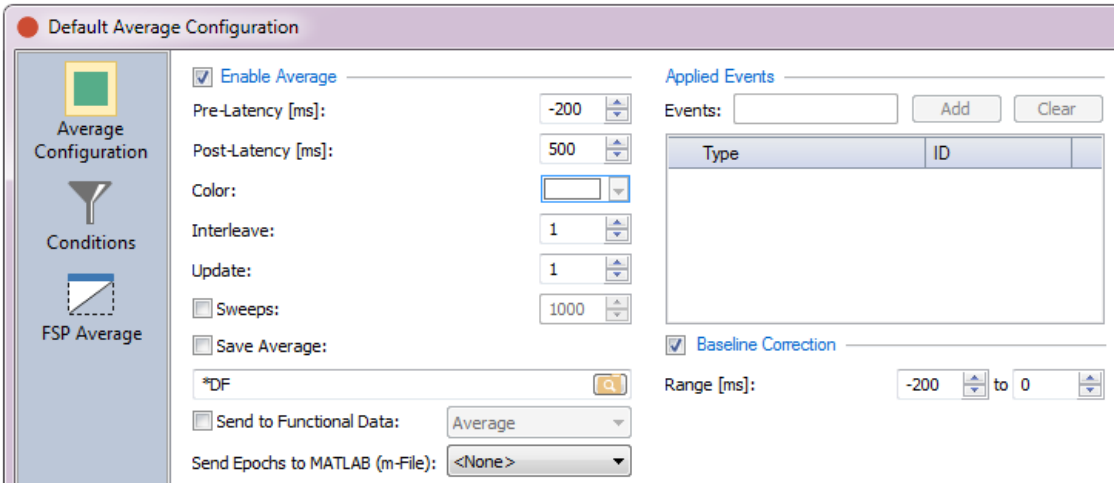
CURRY can display up to 12 online averages at a time. Up to 100 can be recorded.



Auto-Create Averages. When this option is enabled, online averages with the **Enable** field enabled will be created and displayed for all events that are encountered. When disabled, no new averages will be created automatically. Only those averages listed will be displayed (all existing averages will still be updated).

Defaults. Clicking the Defaults button displays the Average Configuration dialog. These are the default settings that will be used in subsequent screens (where they can also be changed, as needed, for individual online averages). If you set the default parameters as desired and then save the Study Parameters, the defaults will be applied in future acquisitions where you apply the same configuration file.

Average Configuration



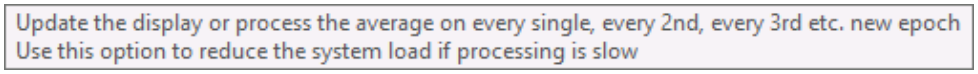
Enable Average. Enable this field if you wish to create online averages. All parameters you set here are applied to all averages that you create from this point. Existing averages will not change when you change the defaults.

Pre-Latency [ms] and **Post-Latency [ms]**. Enter the pre- and post-latency times for the epoch interval. These create the span of the online averages. The settings you enter here are applied to all online averages. If you wish to use different intervals for different averages, you can set them individually in the **Config** section for each event type.

Color. The Color option is not used in the Default configuration. It is used when you are configuring each online average. This sets the color of the box appearing in the bar at the top of the online averages. The color helps to differentiate one average from another. Color is also used to color the epochs in the ongoing data.

Interleave. This option is used to limit the epochs that are being used in the online average. When set to 1, all epochs are included in the average. When set to 2, every other epoch is included. When set to 3, every third epoch is included, and so on. This is the same as the Interleave option offline.

Update. Update is used to determine how often the average display is updated and saved to disk. In contrast to **Interleave**, all epochs are included in the average, but the display is updated only every 3rd, 5th, etc. epoch. This is used to reduce the load on the system when stimuli are being sent at fast rates (more than two per second).

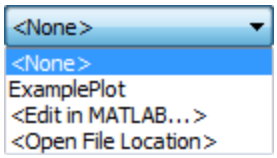


Sweeps. This sets the maximum number of accepted sweeps; averaging will stop when this number is reached.

Save Average. Enable this option to save the online averages. The averages will be saved in the target folder. The same path substitution convention that is used for saving the continuous data, in the Amplifier Control panel above, is used for the path here (see the **Amplifier Control** section for more details). In this example, *DT is the path to the Desktop, and \Acquisition is a folder on the Desktop.

Send to Functional Data. When enabled, the average is sent automatically to the Functional Data display every time a new epoch is added (depending on the Interleave setting). If you are looking, for example, at a dipole during a certain Timerange you can watch it stabilize as the online average builds.

Send Epochs to MATLAB (m-File). Use this option to send epochs to MATLAB and back before adding them to the average.



Applied Events
These fields are not active in the Default configuration.

Baseline Correction. When enabled, the DC offset will be removed based on computations from the interval set below (typically the prestimulus interval).

Range [ms]. Start and end of the baseline correction interval.

Conditions. If there are Default Conditions settings that you want to apply to all online averages, they may be set here. Otherwise, they can be set for each online average individually. Details of Conditions are described just below.

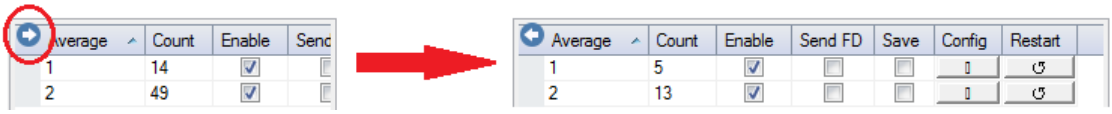
FSP Average. If there are Default settings that you wish to use for online Fsp averages, they may be set here. Otherwise, they can be set for each online average individually. Details of FSP Averages are described just below.

New Average. Generally, you will know in advance which online averages you will want to create. Enter the event type and click the Add button to add the event to the list. Each line will result in an online average. You can enter single events or groups of events (1-5, 10, 15-20, or r1-5). Stimulus events use the numbers only; response events must have an "r" before the number, just as they are seen in the continuous data display.

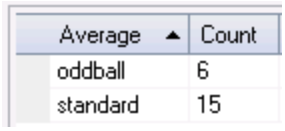
If you do not enter any type codes, and if you have **Auto-Create Average** enabled, each type code that is encountered will generate an online average.

Stim2 sends stimulus type codes from 1-255, and that is the limit CURRY will recognize when other systems are used.

File Info and Options. This displays a list of events that will be used to create online averages. To remove a line in the list, highlight it and click the *Del* button on the keyboard. Note that if you position the mouse just to the left of "Average", you will see a button used to expand the display.



Average. These are the averages that will be created. You can use text strings in place of the type codes, if desired.



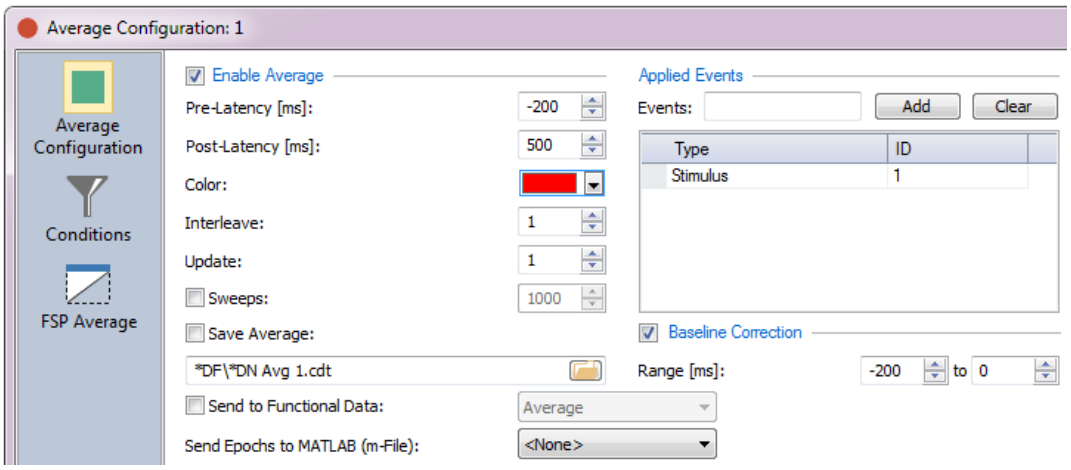
Count. The Count fields display the number of accepted epochs that have been encountered.

Enable. When enabled, the average will be created and displayed. This option allows you to configure online averages without displaying them, unless desired. This can also be used to pause averaging when you know that the subject is not paying attention during stimulation.

Send FD. When **Send FD** is enabled, the Average is sent automatically to the Functional Data display every time a new epoch is added. If you are looking, for example, at a dipole during a certain Timerange you can watch it change as the online average builds.

Save. Selected averages will be saved in the target folder.

Config. It is possible to create conditions for including selected events by clicking the **Config** button >>. The display is applicable for each row of events. (*Double-clicking* on the event row will also open the window).

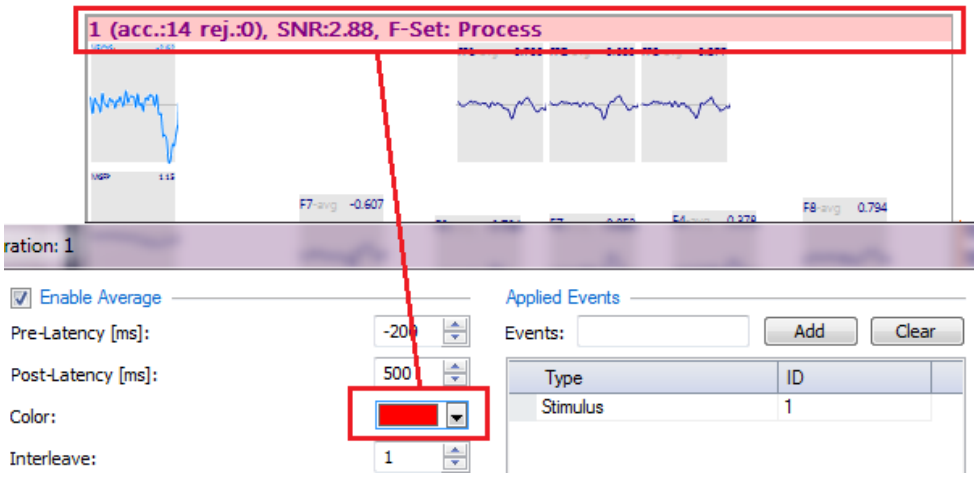


Average Configuration. These parameter settings are used to configure the epochs and averages.

Enable Average. This is a copy of the Enable option seen on the previous screen.

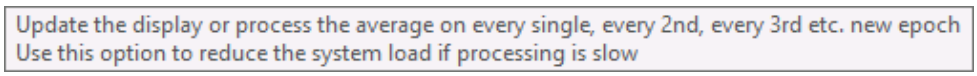
Pre-Latency [ms] / Post-Latency [ms]. These are used to set the epoch intervals for different online averages. They will be the same as the Default settings you entered in the Defaults dialog, but may be changed to override the defaults.

Color. This sets the color of the event bars that appear in the ongoing data, as well as the bar appearing in the top of the online averages. The color helps to differentiate one average from another.



Interleave. This option is used to limit the epochs that are being used in the online average. When set to 1, all epochs are included in the average. When set to 2, every other epoch is included. When set to 3, every third epoch is included, and so on. This is the same as the Interleave option offline.

Update. Update is used to determine how often the average display is updated and saved to disk. In contrast to **Interleave**, all epochs are included in the average, but the display is updated only every 3rd, 5th, etc. epoch. This is used to reduce the load on the system when stimuli are being sent at fast rates (more than two per second).

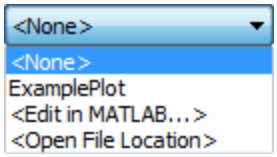


Sweeps. This sets the maximum number of accepted sweeps; averaging will stop when this number is reached.

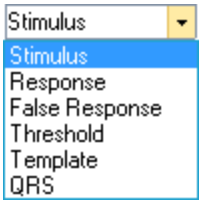
Save Average. When enabled, the online average will be saved to the folder you designate, using the file name you select. The same path substitution convention that is used elsewhere in CURRY - saving the continuous data file, default average files, macros - is used here (see the **Amplifier Control** section above for a description). A Tooltip will provide a list of allowed substitutions. You can also click on the Browse button and select a path and file name in the usual Windows manner.

Send to Functional Data. When enabled, the average, or single epochs, is sent automatically to the Functional Data display every time a new epoch is added. If you are looking, for example, at a dipole during a certain Timerange you can watch it change as the online average builds. This is the same as the **Send FD** option on the previous screen.

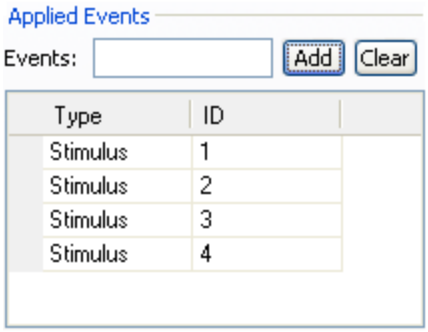
Send Epochs to MATLAB (m-File). Use this option to send epochs to MATLAB and back before they are added to the average.



Applied Events. These are the events (types) that will be used in the remaining configuration. You can use any or all of the event types in the recording. Threshold and QRS come from **Artifact Reduction**; Template comes from **Template Matching**. In other words, here you may add additional events that you wish to include in the average.



Initially, you will see the event(s) corresponding to the line from which you clicked the **Config** button. For example, if you entered stimulus types 1-4, you would see:



You can add more events by entering them in the field and clicking the Add button. Clicking the Add button even when the event field is empty will also generate a new line that then can be altered. To delete events, click to the left of the Type field for the specific event to highlight the line, and then click the *Del* button on the keyboard. Click Clear to remove them all.

Baseline Correction. When enabled, the DC offset will be removed based on computations from the interval set below (typically the prestimulus interval). The baseline correction is performed on every epoch, and therefore affects the outcome of Voltage Rejection (thresholds can be affected).

Range [ms]. Start and end of the baseline correction interval.

Conditions. This section is used to construct a conditional statement that determines which epochs *will be added to* (not excluded from) the online average for the event code on the row where you clicked >>. While the program is focusing on the specific events you have selected in that row, it is also monitoring all events, in a two-step process. An example of this is shown below.

Conditions. The conditional statement may exist on a single line, or it may be connected to additional lines using the "and/or" operators. To remove a line in the list, highlight it and click the *Del* button on the keyboard. The explanation of the conditional statement is best conveyed using some examples (see also the **Averaging** section below).

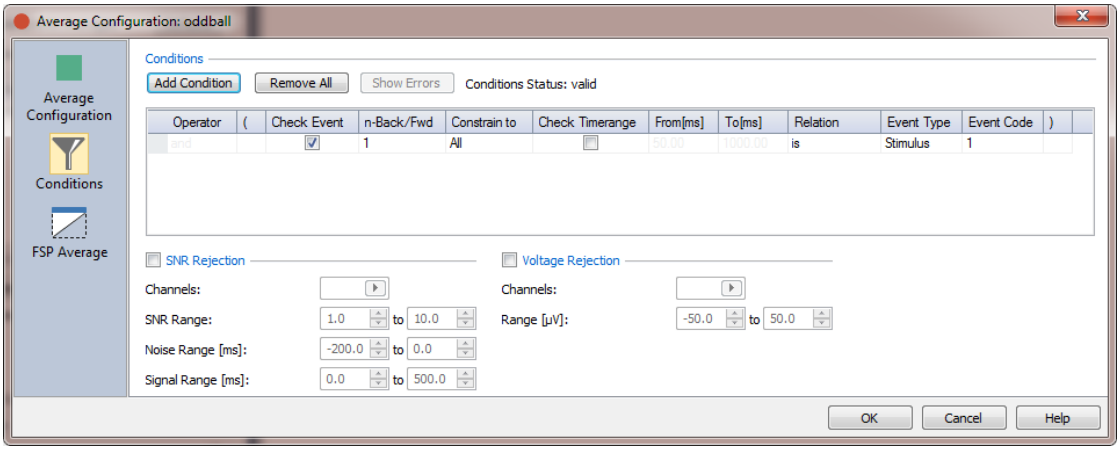
When set to Stimuli, or Responses, only stimulus or response events of the type specified in the Event Type field will be used. If All is selected, any event will be used.

For example, there are the following events in a sequence:

S1 r1 S1

The program is currently focusing on the second S1, and 1 is in the Event Type field. n-Back/Fwd is set for -1 (the previous event). If

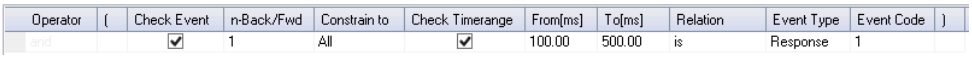
Constrain to is set to **Stimuli**, only the stimulus 1 events are recognized, and the previous event will be the prior S1 event. If Constrain to **All** is selected, the r1 event will be recognized as the previous event.



Note. In the **Event Type** column you will see a listing for **False Responses**. This applies only when you are replaying a file with the amplifier simulator, and you have already merged the behavioral data file that contains Accuracy information. In that case the "Responses" mean the correct responses, and the False Responses mean the incorrect responses. You may then elect to include only those epochs where the subject made a correct response. You can also do this offline; see the Condition section under **Averaging**.

Example 1. You do not wish to use any conditional statements, but you do wish to use **Voltage Rejection** and/or **SNR Rejection**. In this case, simply ignore the conditional fields and do not click the Add Condition button. Make any other selections as desired. These will be applied to the events for the line you selected when you clicked >>.

Example 2. Let's say you have Stimulus events with Type 1 Response events following them, and you wish to include sweeps only when the responses fall within a certain range after the stimuli (too early indicates impulse responding, and too late might indicate distraction). Click the Add Condition button and enter the parameters as shown.



If there is a Response event of Type 1 within the Timerange from 100 to 500 ms after the stimulus, then add that epoch to the online average.

The row containing the **Config** button that you pressed is the Stimulus type that will be used.

Let's say also that there could be multiple Response Types, and you wish to include those sweeps that contain either Type 1 or Type 2 responses. That requires a second line with the **Or** operator in between.

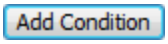
Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	Event Code	)
and		☑	1	All	☑	100.00	500.00	is	Response	1	
or		☑	1	All	☑	100.00	500.00	is	Response	2	

Example 3. Let's say that you only want to include the selected events that ARE NOT preceded by a Type 2 Stimulus event. This implies of course that there are more than one stimulus event Type. Say there are Type 1 and Type 2 stimulus events. To be more precise, we do not want to include a Type 2 event that is preceded by another Type 2 event (as when there may be two or more "oddball" stimuli in a row in a P300 paradigm). In the initial Event Configuration screen we would have set up online averages for Type 1 and Type 2 (we want to see both). Click the **Config** button for the Type 2 average to set up the conditional statement. This is an example where CURRY focuses on the Type 2's and applies the conditional statement to them, yet it also is aware of all the events such that Type 1's are registered also. If the program acted only on the Type 2's, then every Type 2 would be preceded by a Type 2, and all epochs but the first one would be rejected.

The statement reads, if the previous event (whenever it occurred) is not a Stimulus Type 2 event, then add the current event (Type 2, from the row in which the **Config** button was pressed) into the online average. In this case, we did not define a Timerange, so that will be ignored.

Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	Event Code	)
and		☑	-1	All	☐	100.00	500.00	is not	Stimulus	2	

Example 4. Getting a little more complicated, let's say the selected events are Stimulus Type 1's. You wish to include them in the online average only if the **next event** is a **Stimulus Type 2**, **or** a **Stimulus Type 3**, **and** only if there is a **Response** event after the **Stimulus Type 3's**, which is **greater than** a **Response Type 2**.

First, click 

three times and enter the following parameters:

Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	Event Code	)
and		☑	1	All	☐	100.00	500.00	is	Stimulus	2	
or		☑	1	All	☐	50.00	1000.00	is	Stimulus	3	
and		☑	2	All	☐	50.00	1000.00	is greater than	Response	2	

The first line basically says: "If the next event is a stimulus type 2 event,".

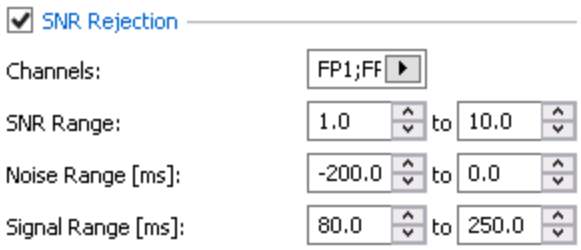
The second line says: "Or, if the next event is a stimulus type 3 event,".

The third line says: "And, if there is a response event greater than Type 2 after the event after the current event".

For the selected event that you started with, only those epochs that meet the conditions will be included in the online average.

Please see also the **Averaging** section for additional information.

SNR Rejection. SNR, or Signal-to-Noise, rejection uses the ratio of Signal to Noise as criteria for accepting/rejecting sweeps for the online averages. This can be used in place of, or in addition to voltage threshold criteria. The **Noise Range** is typically the pre-stimulus interval, or whatever Timerange does not contain the signal of interest. The **Signal Range** is the Timerange that contains the main part of the evoked responses.



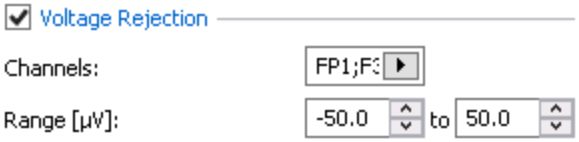
Channels. Select the channel(s) that you wish to include in the SNR analyses.

The **SNR Range** is the range of SNR values that will be accepted. If the SNR is too low, that means either the signal is low or the noise is high, and in either case you may not want to include the sweep. If the SNR is too high, that can result from an artifact in the Signal Timerange, and you would want to exclude these. In the beginning, it may be difficult to set the SNRs accurately. With experience, it will be come more apparent what values you should use with your particular recordings. Also, you can do the analyses offline, where you can see graphically what reasonable SNR cutoffs would be, and this will help in subsequent online recordings.

Noise Range[ms]. This is typically the interval that does not contain the signal, such as, most commonly, the pre-stimulus interval. This interval is used to give the noise estimate.

Signal Range[ms]. This is the interval that contains the signal of interest, i.e., the interval with the highest voltage in the ERPs, and not necessarily the interval that contains the entire span of the ERPs.

Voltage rejection. Select one or more channels to be monitored. When the detected voltage exceeds the Min or Max thresholds, that sweep will not be added to the online average.



Channels. Select one or more channels to be monitored.

Range[µV]. Enter minimum and maximum values that, when exceeded, will result in that epoch being excluded from the average.

As a general note about sequencing, the order that operations are applied is as follows:

Filtering → Artifact Detection/Reduction → Averaging (including Conditions, SNR Rejection, and Voltage Rejection).

 **FSP Average**. If the brain potential you are interested in has a particularly low signal-to-noise ratio (SNR), then you will need to collect a large number of sweeps. For example, extraction of the auditory brainstem response (ABR) usually requires thousands of sweeps. This situation presents two related problems: (1) the SNR can vary considerably between recording sessions, so that the same number of sweeps may yield averages of different quality; and (2) the SNR can vary considerably within a recording session so that a "bad" block of sweeps can potentially degrade the average which is building.

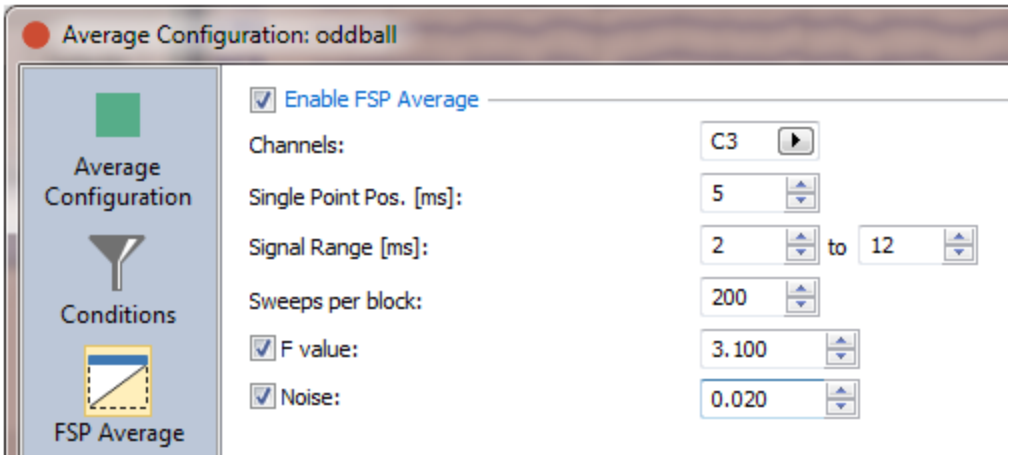
The first problem (between-session SNR variability) could be handled by collecting sweeps until a prespecified SNR in the average is achieved — if there were a way of estimating the SNR as the average is building. A statistical approach to solving this problem was detailed by Elberling and Don (1984) who proposed use of the Fsp ("single point F") statistic. Please refer to the above mentioned article for complete details. Briefly stated, the Fsp is essentially a ratio of two variances: the estimated variance of the signal between two time points, divided by the estimated variance of the noise at a single point. If certain assumptions and approximations are made, the sampling distribution of the Fsp statistic can be computed. For each target SNR that one wishes to achieve in an average, there is a critical Fsp value such that one can state with confidence p that the actual SNR equals or exceeds the target value. This critical Fsp value can be used as a stopping criterion for averaging. All averages obtained in this way — though they be constructed from differing numbers of sweeps — will have about the same quality of SNR.

The Fsp statistic is computed for blocks of sweeps.

Perhaps of greater significance for offline analysis is a solution to the second problem of within-session variability of the background noise. If the total number of collected sweeps is divided into several blocks, a single point estimate of the background noise (i.e., variance about the mean) can be computed for each block. By "single point" it is meant that a fixed point in time for each sweep is chosen for this computation (or Timerange). There

may be considerable variability in the background noise estimates for the different blocks of sweeps. Ordinary averaging would give each block an equal weight. Intuitively, however, one would prefer to assign a higher weight to blocks of sweeps with lower background noise. This intuition is fulfilled by a Bayesian weighting scheme: The total average is constructed by weighting each block average by its reciprocal single point variance, divided by the sum of all block reciprocal sp-variances (Elberling & Wahlgreen, 1985).

Thus, the Fsp average is a Bayesian weighted average with computation of the Fsp statistic for each block, and for each electrode.



Channels. Select the channel(s) that will be used for the Fsp computations.

Single Point Position [ms]. The point position value determines the location (in milliseconds) within the sample interval (Signal Range) of the single-point estimate of the background noise. Under normal circumstances, this value would be placed within the bounds of the Signal Range.

Signal Range [ms]. The Signal Range encompasses the interval containing the signal of interest. For ABRs, this is typically about 2-12ms. It should be at least 10 ms to capture a complete cycle of an ABR component.

Sweeps per block. The Sweeps per Block value determines the number of sweeps that is collected for the ongoing within-block average. For the ABR a value of 250 sweeps is typical.

F value. It is possible to terminate data acquisition when the current Fsp value equals or exceeds a specified F value. A typical value for this field for the ABR is 3.1.

Noise. Data acquisition can also be terminated if the background noise is lower than a specified value. A typical value for this field is 0.02µV.

If you have both **F Value** and **Noise** enabled, acquisition will continue until both criteria are met.

Elberling, C. and Don, M. 1984. Quality estimation of averaged auditory brainstem responses. *Scand Audiol*, **13**, 187.
Elberling, C. and Wahlgreen, O. Estimation of auditory brainstem response, ABR, by means of Bayesian inference. *Scand Audiol*, **14**, 89.
Elberling, C. and Don, M. 1987. Detection functions for the human auditory brainstem response. *Scand Audiol*, **16**, 89-92.

Restart. Restarts the online average for the specific event type.

Clear 

. Clears all of the list of all of the averages.

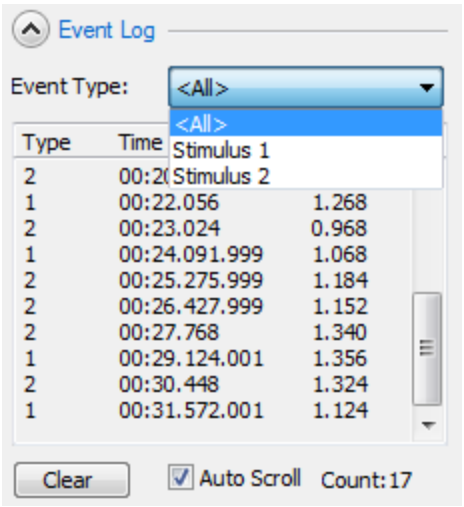
Restart 

. Restarts averaging for all online averages.

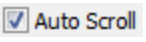
Show Peaks in Range [ms]. This is an online peak detection feature. The Maximum and Minimum voltages in the selected Timerange will be displayed with blue and red plus signs for each channel.

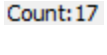
Event Log
The Event Log options let you view the real-time events in a list, along with the time they occur plus the difference in seconds between events.

Event Type. This option lets you filter the events in order to see just a single one, if desired (such as, the MRI scanner events for timing purposes).



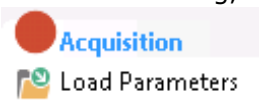
Clear the 

button to clear the list and the **Count** field. The 

feature will automatically scroll the list when enabled. When disabled, you can move manually through the list. The 

field shows how many events have been detected.

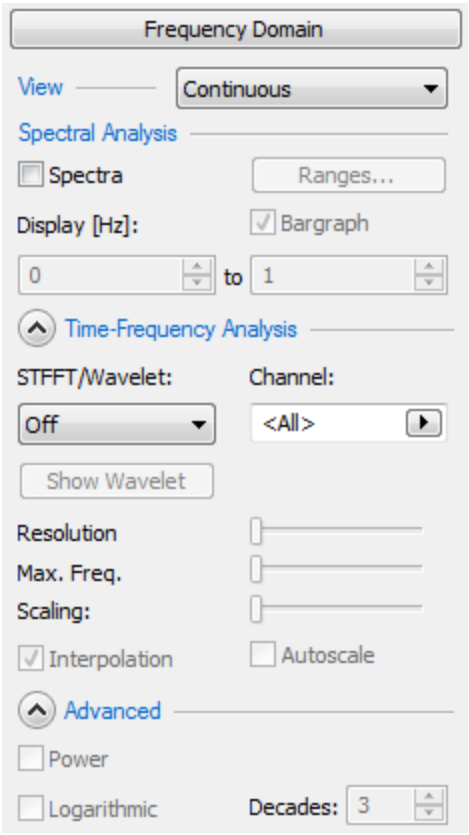
When you are through setting the parameters, and you wish to use them again in the future, click the **Save Study Parameters** icon  on the Toolbar. Before you open

an empty Study for the next recording, *right click* on the Study and select **Insert Parameters**, or use 

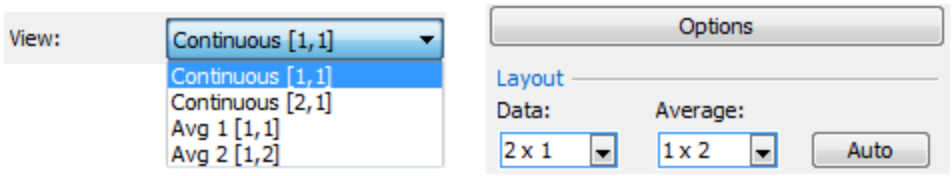
from the **Workflow**. Then select the .cfg file you have created.

14.2.7 Frequency Domain

These settings allow you to perform online frequency domain analyses (FFT power spectra and wavelets).



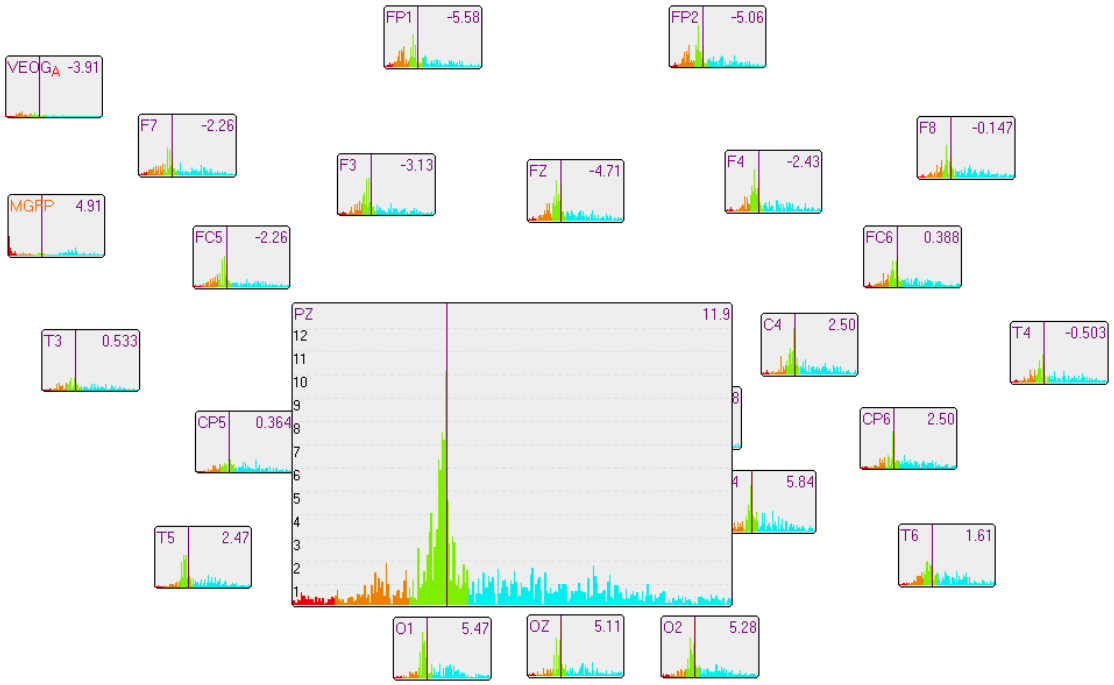
View. When you are displaying multiple views, as selected with the **Layout** options under **Options**:



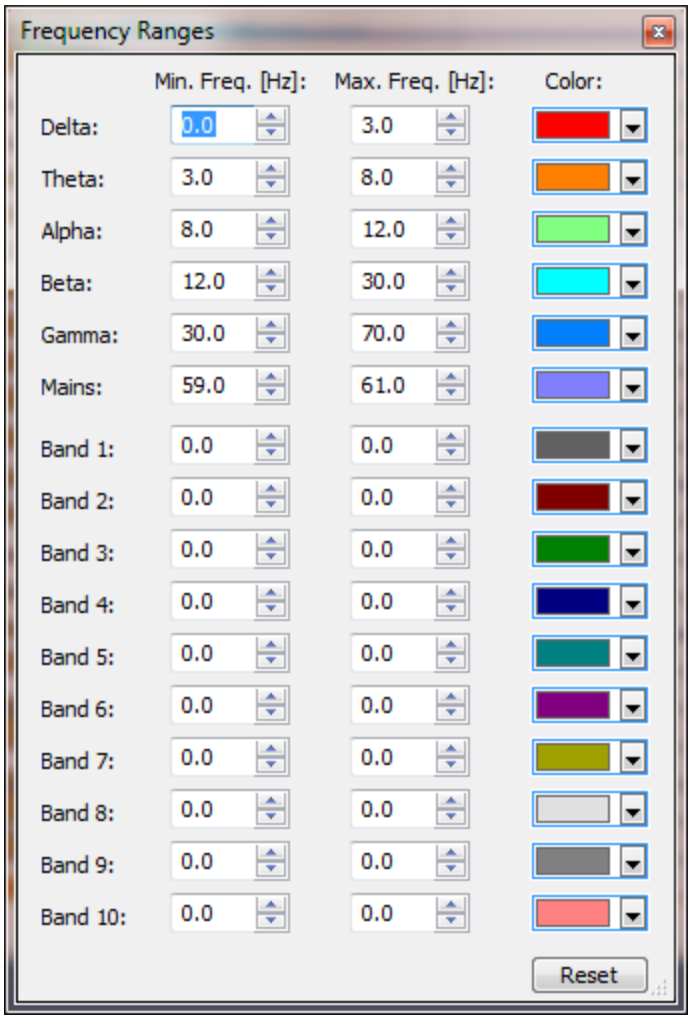
the View field will let you know which display you are working with (which one has the focus). The numbers in the brackets correspond to the Column and Row of the selected display.

Spectral Analysis

Spectra. An FFT spectral analysis is computed *over the data that are displayed* (the Timerange is ignored), plus enough extra samples at the beginning and end of the file in order to achieve a number of samples that is a power of 2. Change the number of seconds that are displayed to focus in or spread out the section that is displayed. Once the power spectrum is computed, you can select the **Frequency Range** of interest. The **Position Plot** option was selected below.

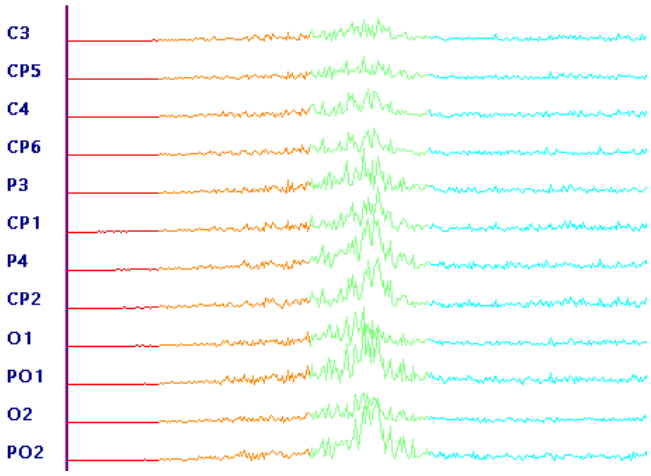


Ranges. This option allows you to redefine the Frequency ranges and colors (you cannot create overlapping bands).

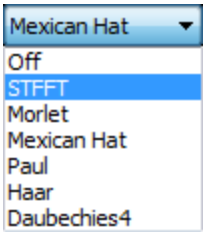


Display [Hz]. Select the frequency range you wish to display.

Bargraph. This allows you to view the FFT data in bar graph display (left). When disabled, data are displayed in a line graph (right).



Time-Frequency Analysis
STFFT/Wavelets. Short Time FFT (**STFFT**) and Wavelets can be computed online. For a more complete discussion, see the offline **Frequency Domain** section.



Channel. Select a single, combination, or all channels to include.

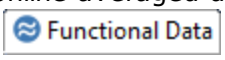
Resolution. Selects the temporal/frequency resolution. There is always a tradeoff between frequency and time. Dragging the cursor to the left gives better frequency resolution, with wider time intervals. Dragging to the right gives better time resolution, with broader frequency intervals.

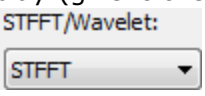
Max. Frequency. Moving the control will increase or decrease the maximum frequency that is displayed (the maximum frequency is displayed in the upper left corner). The absolute maximum is determined by the sampling theorem (sampling frequency/2).

Scaling. This controls the sensitivity of the color scale.

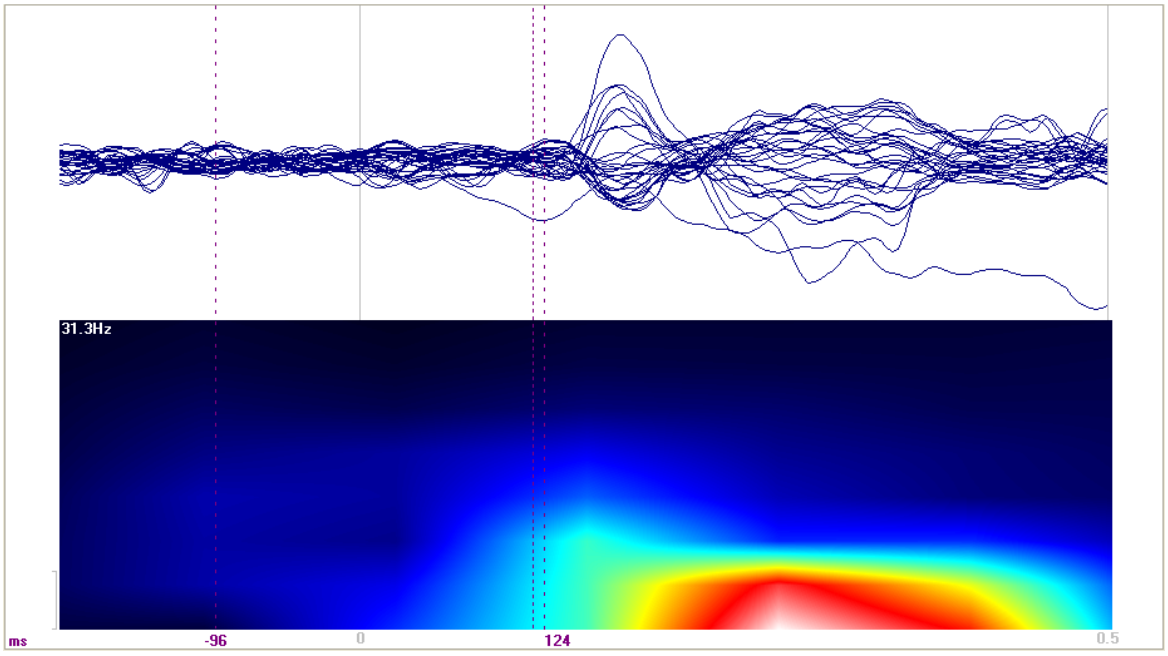
Linear Interpolation. With Linear Interpolation removed, the results for individual blocks may be seen.

Autoscale. Autoscale will scale the display to whatever data are seen. In some cases, that may include large artifacts, which will cause the scaling to be inappropriate. In that case, uncheck Autoscale and a fixed scaling will be used.

If you want to see the STFFT or wavelets with online averaged data, select the average display (give it the focus) and click the 

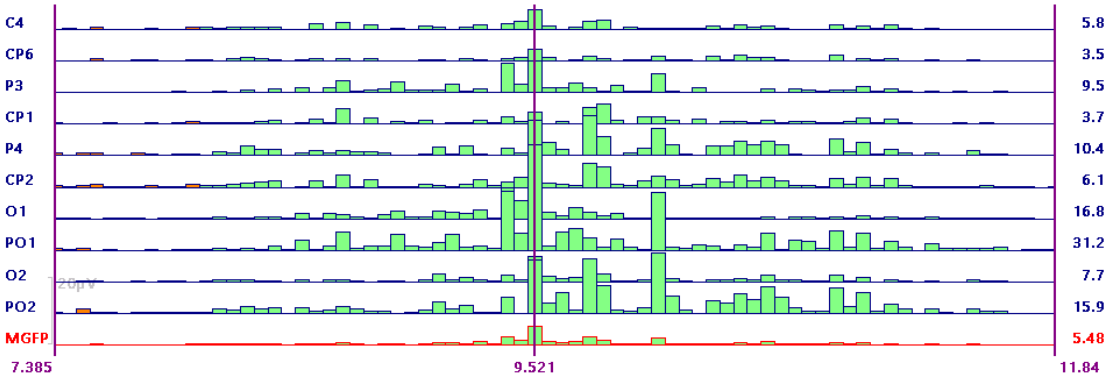
display. Then select the 

or Wavelet option.

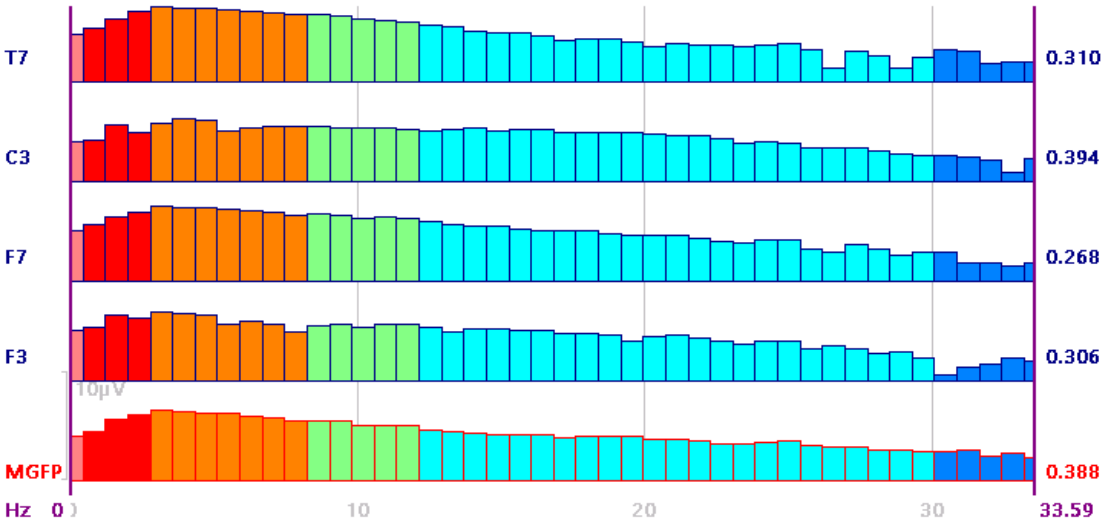


Settings

Power. Enable this option to see microvolts squared (power). The Power option increases voltage greater than 1.0 and decreases voltages less than 1.0.



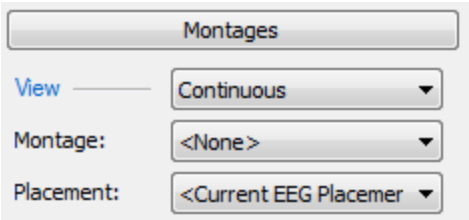
Logarithmic. Enabling this option will display the **Spectra** data with a logarithmic scale. The adjacent field is the number of **Decades**. The greater the decade value, the better the lower power frequencies will be visualized.



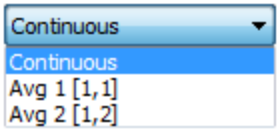
14.2.8 Montages

Montages may be applied online as well as offline. Montages affect the display only. For example, if you select a bipolar montage and then perform Artifact Reduction, the data that are used are the channels before you selected the montage. If you select a montage and then average the sweeps, you will see the selected montage, but when you remove it, the original channels will be there. Mapping uses the original data, not the montage data.

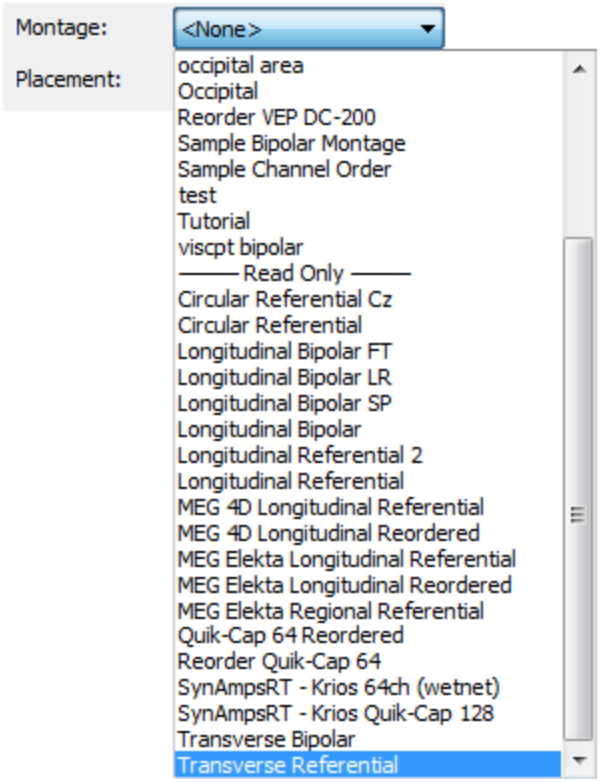
For details about creating montages, please see the offline **Montages** section below.



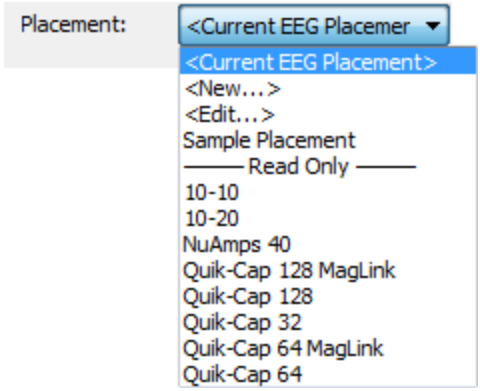
Montages may be applied to **Continuous** or **Average** data displays. If you have more than one continuous or average file displayed, you will see options for selecting each one.



Select a montage from the drop-down list. Files above the *Read Only* line are user created; files in the *Read Only* section are supplied montages. Montages that do not contain any channels of the current device group are sorted out and placed in the *Invalid For This Group* section (so you can see directly which files can be meaningfully applied to a group). Click **<Edit...>** to access the Montage Editor to create or edit montages (see **Configure montages** above). Click **<Reorder>** to access the Montage Editor in a form prepared for creating a montage to reorder the channels.

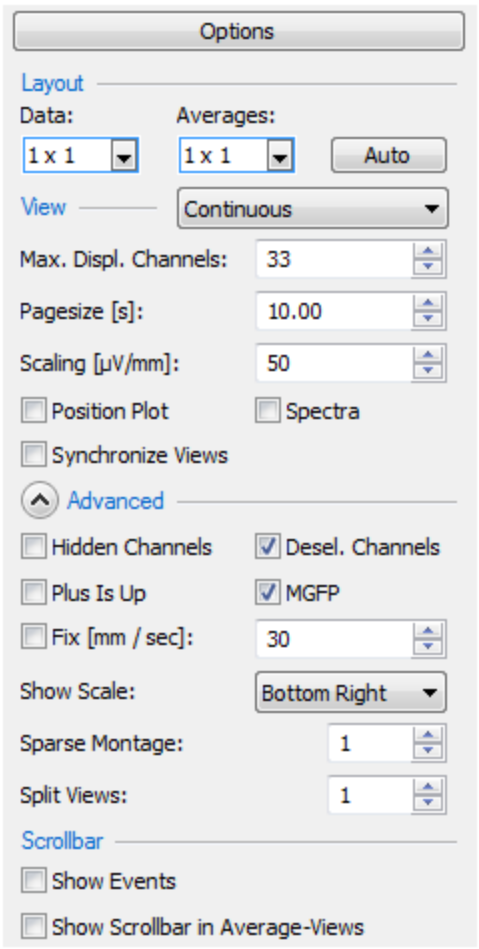


Placement. Placements refer to the positions of the displays in **Position Plots**. Create a new one or use one of the supplied placements.



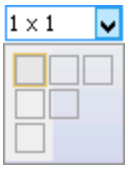
14.2.9 Options

These fields contain display options.

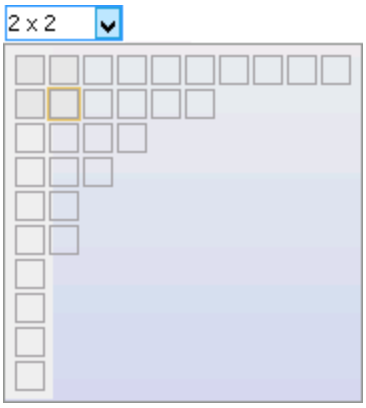


Layout

Data. Select the number and positions of the views you want to use with continuous data. The selection below will result in two views of the incoming data, one above the other.

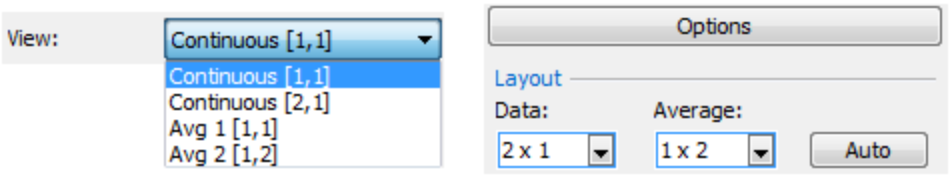


Average. Select the number and positions of the views you want to use with average data. The selection below will result in four views of online averages, in a 2x2 grid.



Auto. When selected, the layout will be set automatically to show all existing averages that are defined in the event table under **Averages**.

View. When you are displaying multiple views, as selected with the **Layout** options under **Options**:



the View field will let you know which display you are working with (which one has the focus). The numbers in the brackets correspond to the Column and Row of the selected display.

Max. Displ. Channels. Decrease the number to see fewer channels in the display. A scrollbar will appear on the right allowing you to scroll down to the other channels. You can also position the cursor in the data display and use *Shift+mouse wheel* to change the number of channel displayed.

Pagesize [s]. This sets the number of seconds that are displayed on the screen.

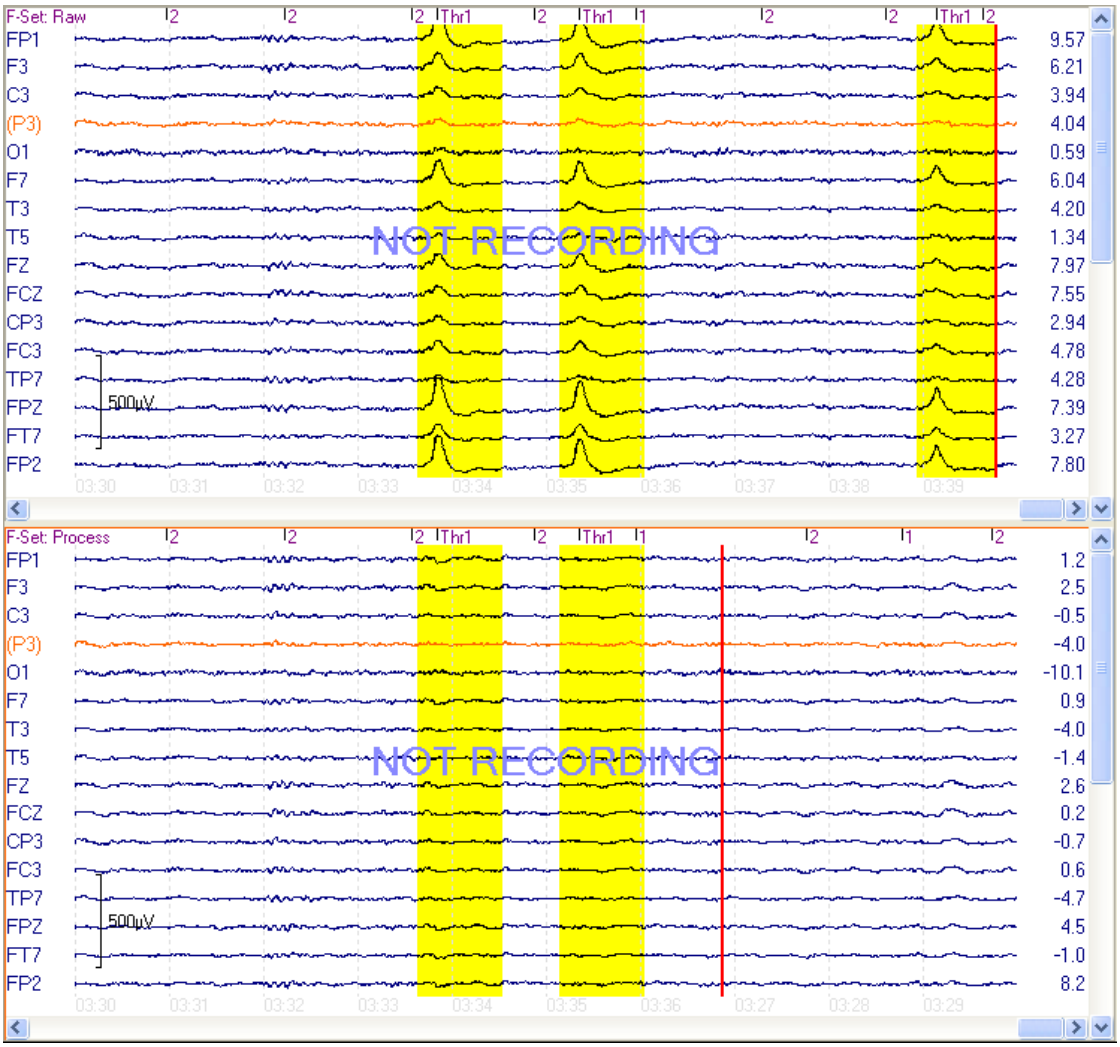
Scaling [μv/mm]. Display scale. The number of microvolts per millimeter is set (or displayed).

Position Plot. The display having the focus will be changed to the Position Plot, where each channel is displayed in its own window.

Spectra. This option enables the display of the FFT power spectra. See the Frequency Domain section for more information.

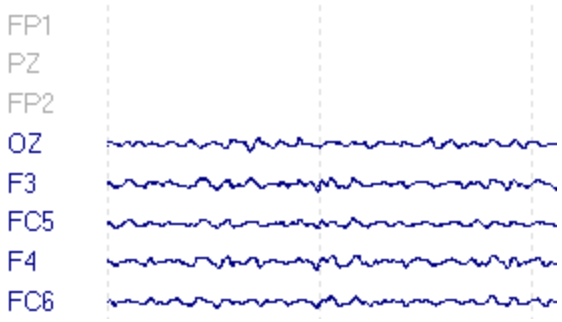
Synchronize Views. When viewing multiple displays, such as, several online averages, the cursor movements and other selections that affect one view will be applied to all other views, when this option is enabled. The selected filter sets for continuous views are not affected by the synch option. Disable it to affect each view independently.

The figure below shows Synched views where Artifact Reduction for blinks is in progress. There will be a delay between the cursor in the Raw view (top) versus the Process view (bottom), as there is a necessary delay for artifact reduction to be performed. Note that while the cursor positions differ, the data being displayed are aligned in time.



Advanced

Hidden Channels. If you have used the Hide Channels option above to remove selected channels from the data display, you can enable the Hidden option to see the labels of those channels. Then you may unhide them as desired.



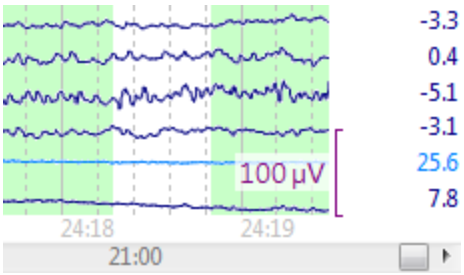
Deselected Channels. Set channels as deselected channels. Deselected channels are excluded from subsequent analyses.

Plus is Up. Polarity toggle. Enable to display traces with positive voltages going up.

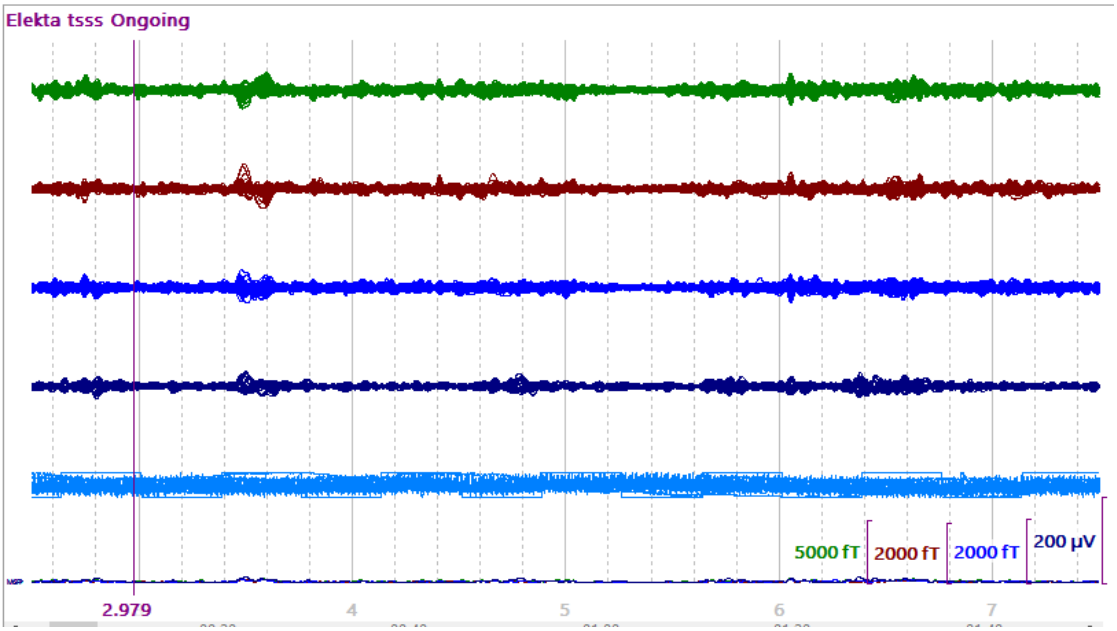
MGFP. When enabled, the Mean Global Field Power will be displayed in red below the data (a composite value reflecting the variability across channels).

Fix [mm / sec]. This shows the number of millimeters that are displayed per second on the screen display. Enable it if you want the mm/sec setting to stay fixed.

Show Scale. This option lets you position the Scale Tool in different corners of the display, or off.

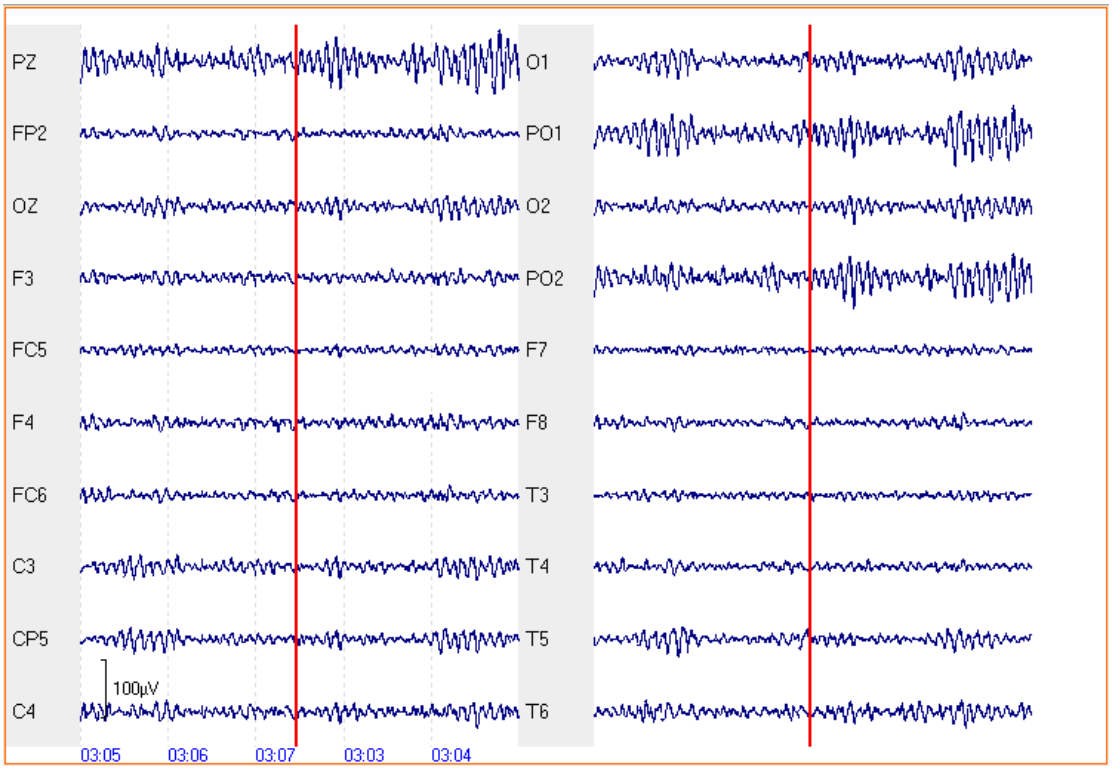


If you have multiple Device Groups (as with MEG data), the Scale Tool color will match the group color.



Sparse Montage. **Sparse Montage** is used in conjunction with **Max. Displayed Channels**. If you have, for example, 64 channels, and you want to view a subset of 16, set Sparse to 4 (64 / 16 = 4). Every 4th channel will be displayed.

Split Views. Split views display the same data channels in side-by-side displays. In the figure below, 20 channels were displayed in the initial window. Setting Split View to **2** displays the channels side-by-side.



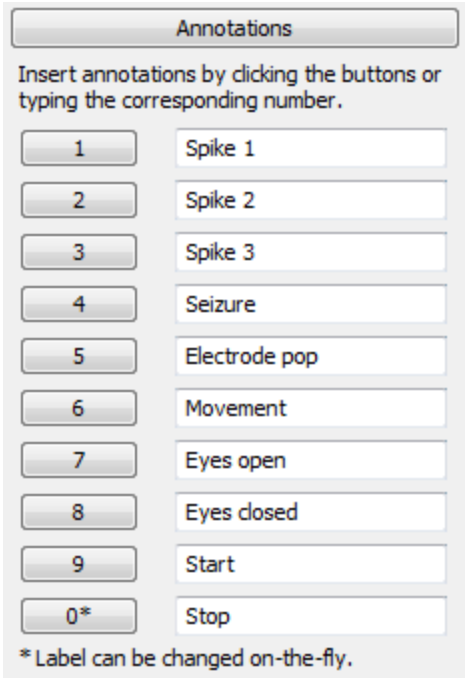
Scrollbar

Show events. Toggles the display of the event lines below the data display (not the events themselves).

Show Scrollbar in Average-Views. This option allows you to zoom into sections of the average data display. Once enabled, press the *Ctrl* key while positioning the mouse over the scrollbar. Small arrows will appear on each end. Drag an end to reduce the section of the data that are displayed.

14.2.10 Annotations

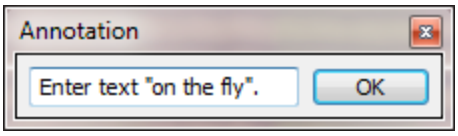
These fields are used to add text comments to the continuous data file during acquisition.



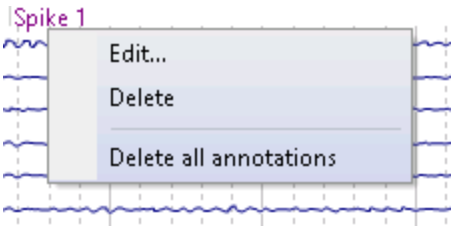
The entries shown above are from the Global Parameters. You can change the text and save the changes as Global Parameters, Study Parameters, or Last Used Parameters.

To add the text to a continuous file during acquisition, either click the desired button or the corresponding key from the keyboard. If the buttons are not active, click in the Data Display to activate them.

The "0" option is a special case. Here you can enter any text you want, "on the fly", and it will be displayed in the recording. When the data display has the focus, click the 0* button or the *0* key. Type in the desired text and click **OK**. The text event will be added *at the point you clicked the* 0* *button or pressed the 0 key*.

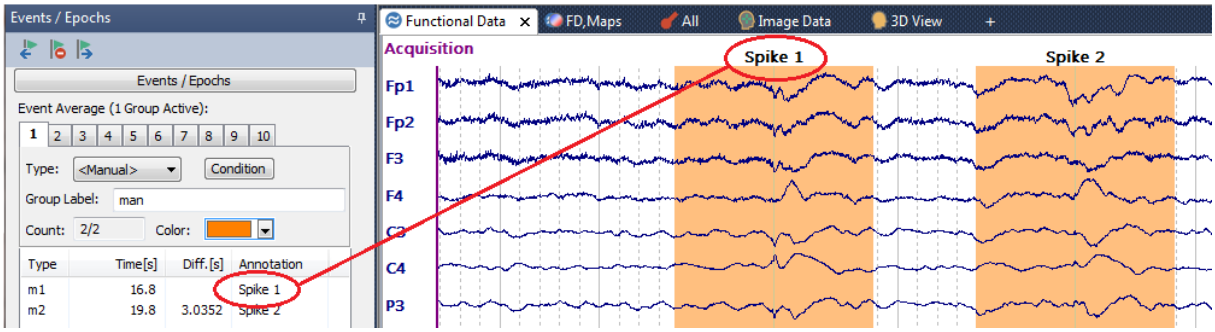


Right click on an annotation you have entered in the file to see additional options. You can **Edit** the annotation, **Delete it**, or **Delete all annotations**.



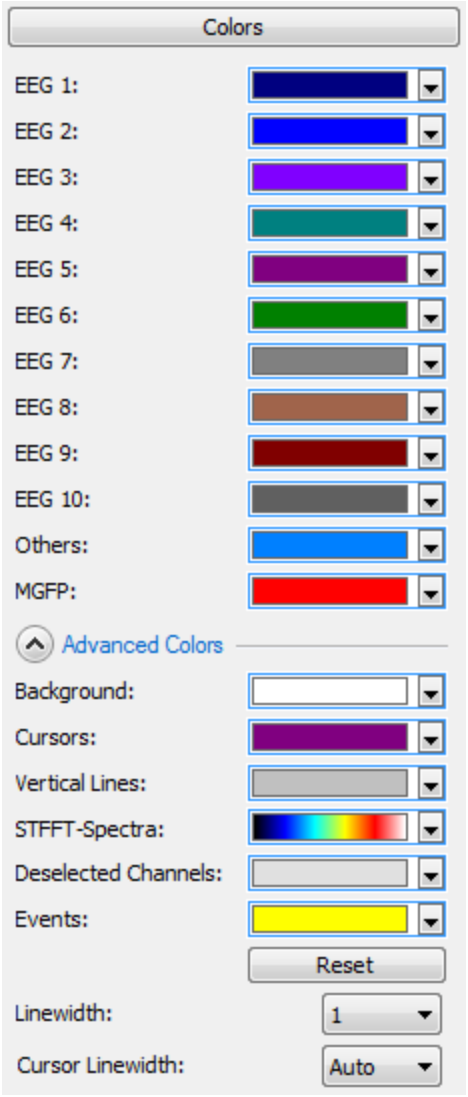
If you Pause the data display, you may grab-and-drag an annotation to a different location.

Offline, the annotations appear in the continuous data file. In the Event List, they appear as **m1** through **m0** event types, and are treated as any other events.



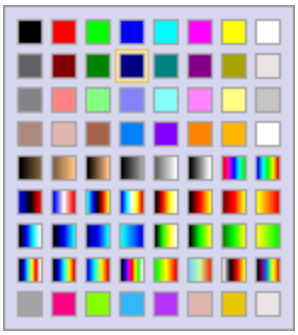
14.2.11 Colors

These fields are used to set the colors of the various components in the acquisition display.



The Colors panel allows you to select the color of the elements indicated, including up to 10 EEG Groups, the events in the file, deselected channels and epochs, the Mean Global Field Power waveform (**MGFP**), the cursors, vertical lines, and the background of the display. "Others" determines the color for the "other" channels. The **Covariances** (seen in Noise Estimation) and the colors seen in the **STFFT-Spectra** displays are not used here (they are set in the Colors panel for Functional Data). Click the Reset button to return the colors to their default settings. The **Linewidth** and **Cursor-Linewidth** options are used to vary the width of the waveforms and vertical cursors (1, 2, or 3 pixels). If you select **Auto**, CURRY will adapt the line width to the number of channels that are displayed - the fewer the channels, the bolder the lines.

When you click on one of the drop-down arrows, you will see a palette of colors from which to choose. Note that some are solid colors (top four rows), while others will apply a color spectrum. The new color will be applied when you select it. Not all colors are available with each object. See also **Edit → Options → Colors** for creating customized colors.



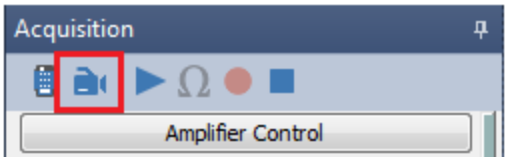
14.2.12 Video

Using Digital Video

Assuming you have a "V" license, you may record a digital video of the subject or patient, and replay it synchronized with the data file (see also the **Video** tutorial in the *CURRY 8 Installation and Tutorials* manual). The "V" license is not needed to replay previously recorded video files.

Clicking the **Show video window** icon will let you record a digital video movie along with your data file, or replay the video offline.

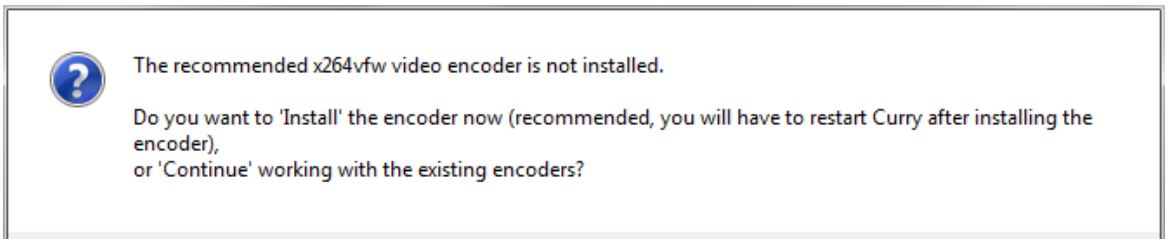
The Show Video icon is found at the top of the Acquisition panel.



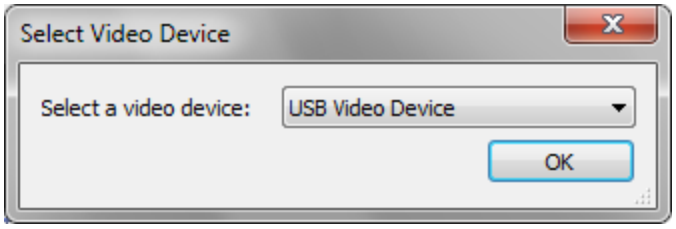
Typically, these are used in clinical recordings to correlate patient behavior with seizure activity in the EEG, but it can also be helpful in research recordings for monitoring various types of artifact. If you have more than one continuous data file with video in the same folder, the video files will be concatenated along with the data files.

To use this feature, you should first install your camera and verify that it is functional with its own software. Then start CURRY and go to the acquisition module . Click the **Show video window** icon .

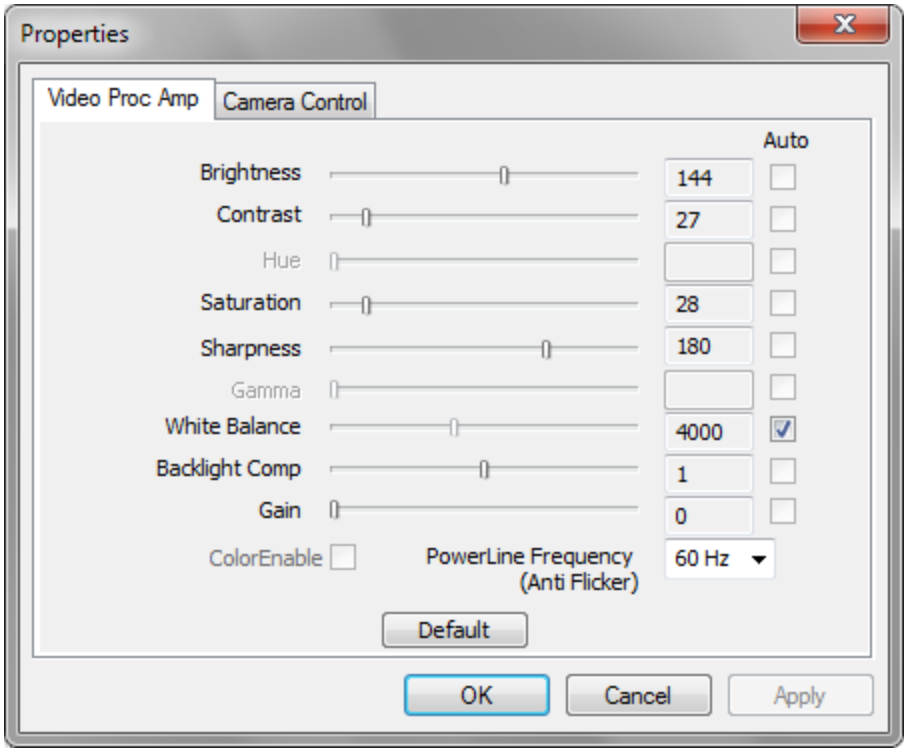
You may see the following message appear. Click **Install**, and follow the installation instructions. You will need to restart CURRY.



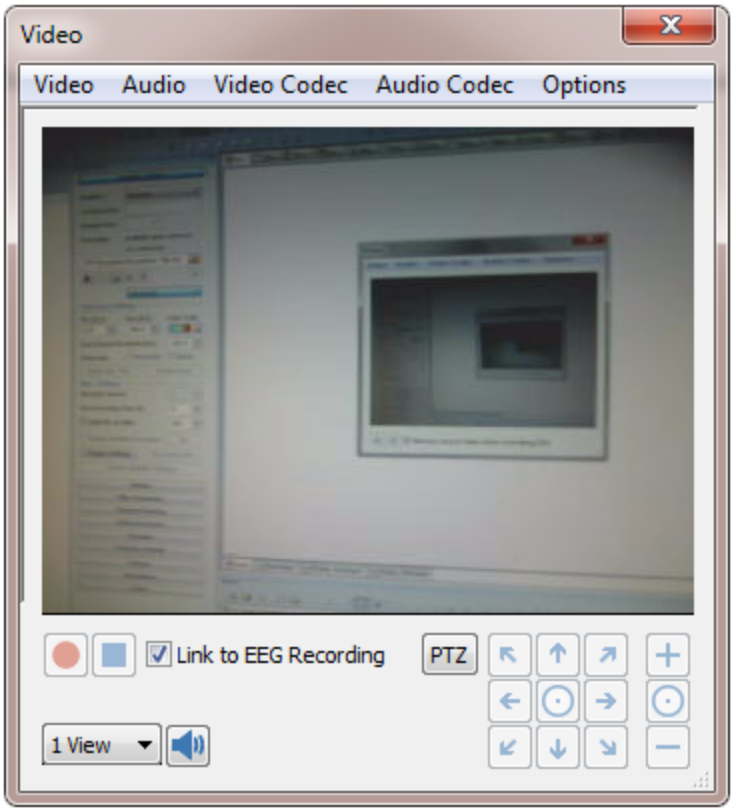
When you click the Video icon again, you will see the following screen appear. The list may have a single option or several options, depending on what has been installed on your computer. Select the one that corresponds to the camera that you are using.



After clicking OK, you will see the **Properties** dialog for your camera. This will vary from camera to camera. Make any selections as desired. (To access the Properties dialog again, either reselect the video device from the **Video** option in the **Video** window (with the camera view), or else select **Options** → **Video Filter**).

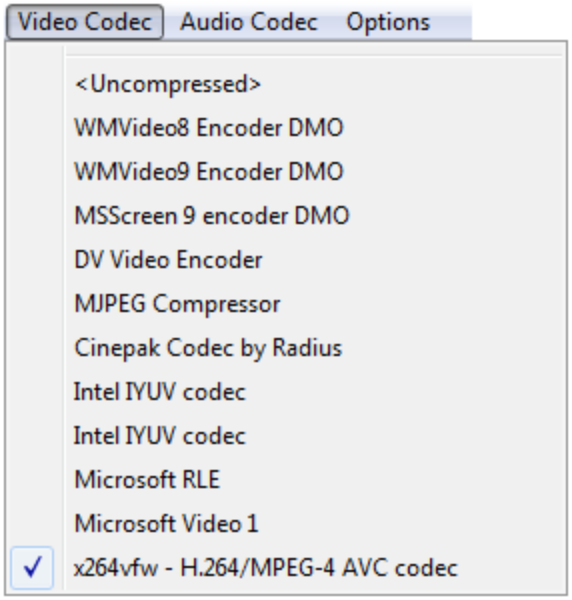


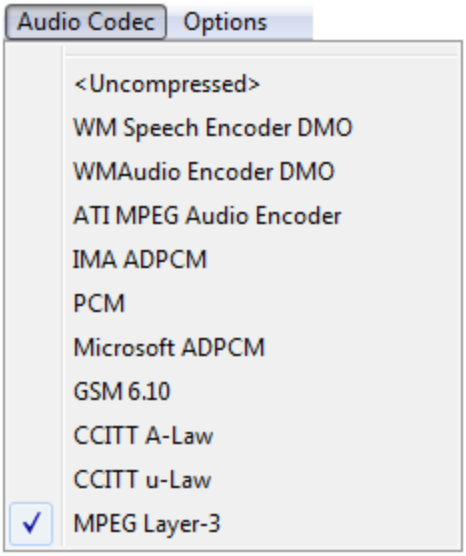
After clicking **OK**, you should see the **Video** dialog appear with the view from the camera.



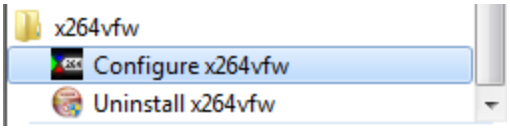
What you see under **Video**, **Audio**, **Video Codec**, and **Audio Codec** will depend on your camera and the files that were installed with it, as well as other hardware you have installed. (Codecs are programs that encode a data stream or signal for transmission, storage or encryption, or decode it for playback or editing). The **x264vfw** video codec will be installed automatically, as we have found this to be the best codec regardless of the speed of your computer.

CURRY will automatically select **x264vfw - H.264** for the **Video Codec**, and **MPEG Layer-3** (MP3) for the **Audio Codec**.

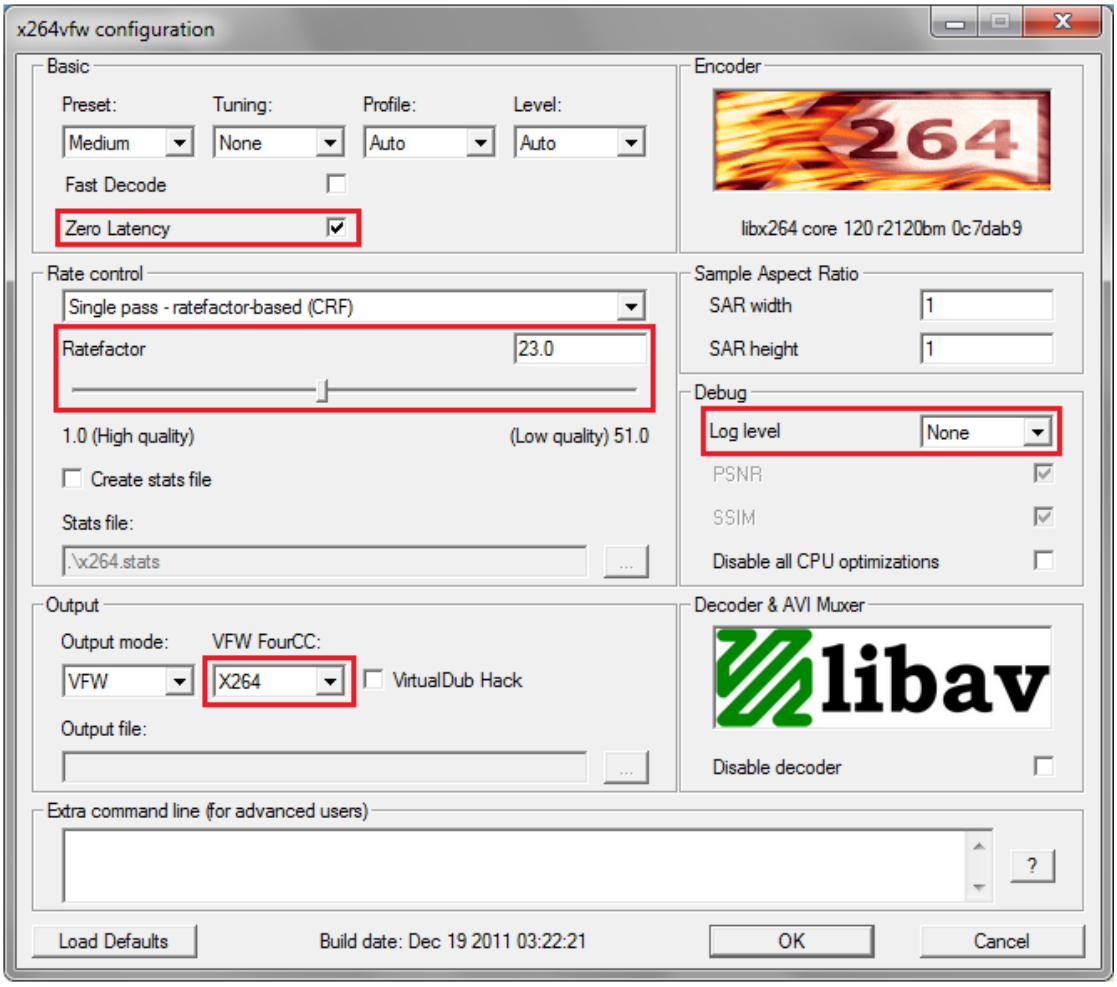




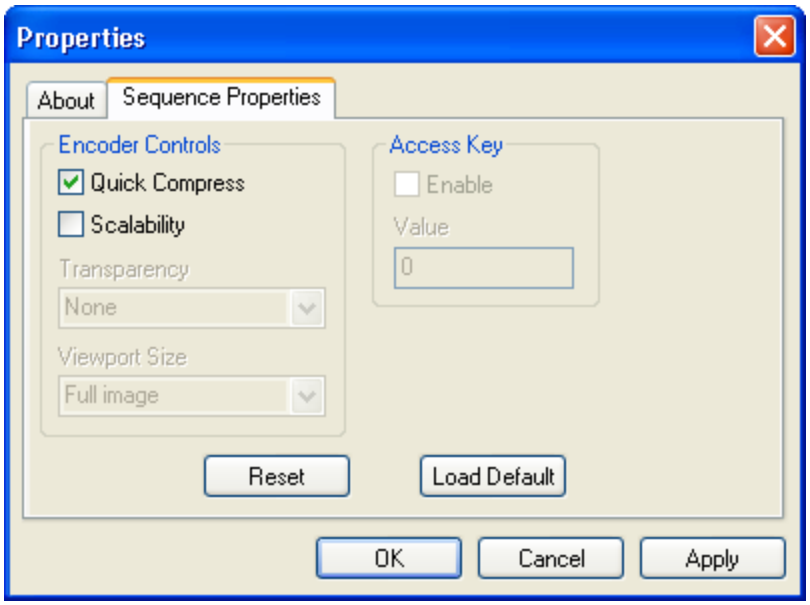
If you want to modify the parameters for this codec, go to **Start** → **All Programs** → **x264vfw** and run the **Configure x264vfw** program.



Enable **Zero Latency** to ensure that audio and video will be in synch. You may wish to vary the **Ratefactor** (from **High quality** to **Low quality**). Low quality leads to better performance on slow computers. When your video preview window shows a large lag during recording, or the system becomes unresponsive, you should reduce the quality. Verify that **X264** has been selected under **Output**, and that the **Log level** is set to **None**. It is recommended that you not change the other settings unless you are sure of the effect they will have.

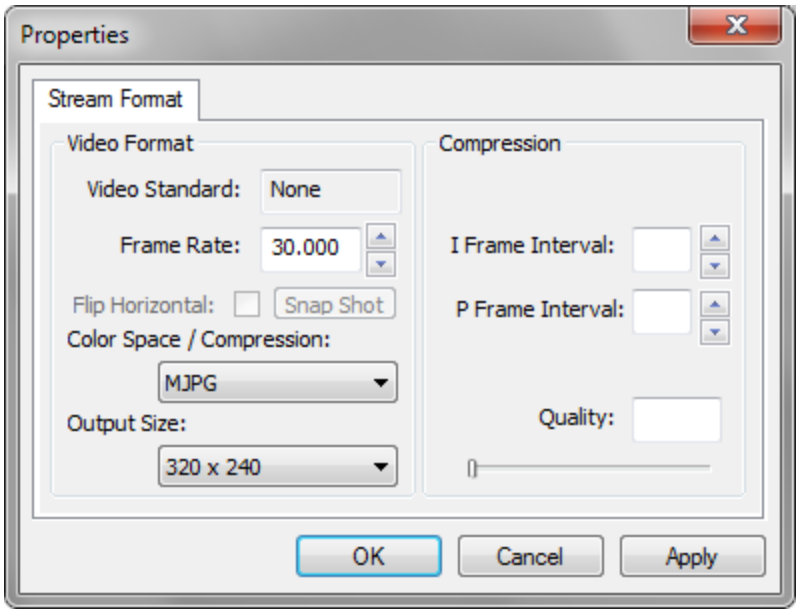


If instead of the x264vfw codec you select the **Indeo** compression filter, click on it in the **Video Codec** list, and select the **Sequence Properties** tab. Make sure **Quick Compress** is enabled (otherwise the encoding might consume too much performance).



If you record Audio, you will hear the audio track when you replay the file.

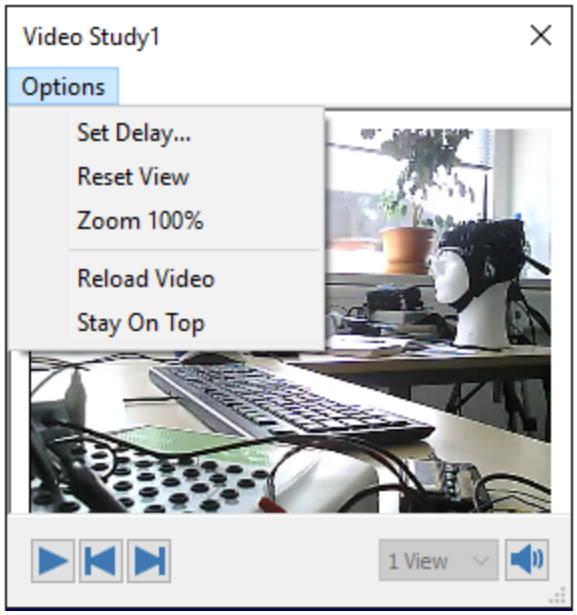
Options. The Options dialog contains one option that is especially important: **Video Settings**. Clicking it displays the **Properties** dialog, and what you see will vary from camera to camera. Depending on the camera you have, you may find that many if not all options will function. On the other hand, we have seen that with some less expensive cameras, you may not be able to record the video if you use higher Output Sizes unless you switch to a different Color Space/Compression option. Changing that can reduce the Frame Rate, which will result in a jerky recording. We suggest that you try different settings to find the ones that work best with your camera. In testing, be sure to test wile recording, as simply viewing may be fine, but then the display freezes when you start to record. It is not possible to save all possible settings for all possible cameras. In some cases, it will be necessary to reselect the options you want to use each time you restart acquisition.



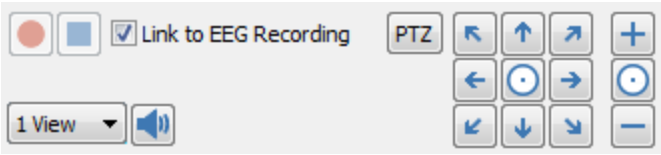
The other options are as shown. Most are self-explanatory. The **Video Filter** shows the Properties screen, which will vary across cameras. Similarly, the Audio Filter option will display the Properties if an audio device has been detected.

Reload Video is used on those rare occasions when the video replay window becomes black, or shows any other kind of strange behavior (such as a flickering loop of the same two images / video frame does not update).

Stay On Top forces the video window to stay on top of all other windows. By default, the dialog is set so that it stays on top, but that property does not always "stick" and so the window can become hidden behind CURRY. If this happens, select **Stay On Top**.

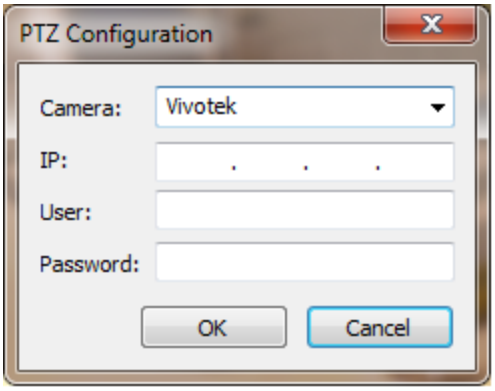


At the bottom of the display, if you enable the **Link to EEG Recording** option, the video will be begin recording when you begin recording the EEG data (and stop when you stop recording the EEG).



If the option is disabled, you will see the **Record** and **Stop** buttons, allowing you to start and stop the recording manually.

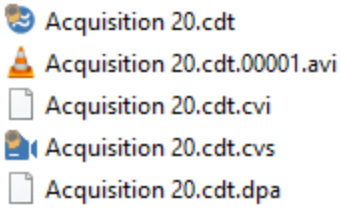
The Pan Tilt Zoom PTZ options include the standard remote directional controls for your network camera. As of this writing, these options may only work with Vivotek network cameras. The IP address, User name, and Password are the same as you entered in the [Vivotek] Video Capture Filter. They need only to be entered again here.



You can use the *mouse wheel* to zoom in and out, and you can click and drag to adjust the visible section. *Right click* in the display and select **Reset View** to restore the original display. Click **Zoom 100%** after zooming in and/or enlarging the display to restore the original view.

You can configure up to three Views with the single camera. Zoom in on one, drag the view to a different perspective on another, and so on. The Mute button lets you turn on and off the audio.

When you start recording the EEG, the video will start recording also. When you make a recording, you will see, in addition to the data, event, and parameter files, the video synchronization, index, and .avi files that are created. You may see more than one .avi file.



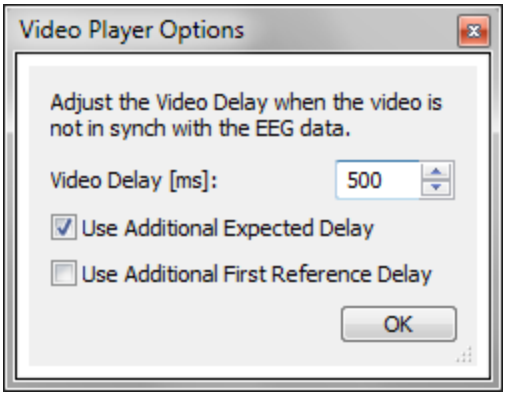
Please note that the file extensions for CURRY 8 have changed from CURRY 7. The previous ".syn" files are now called ".cvs" (Curry Video Synch). The previous "...Videoindex.xml" files are now called ".cvi" (Curry Video Index). (CURRY 8 still can read videos created with the old naming scheme from CURRY 7)

The number of .avi files depends on several points. The video files cannot be much larger than 200MB (for crash safety). Video files are split when you pause and resume a recording. Video files are split when the software detects a synchronization error in the "video rendering and encoding pipeline". The .cvs file contains the synchronization information; the .cvi file contains the times of all video files that belong to a recording. If you move the files to a different folder, be sure to move all of them.

When you replay the EEG file in the offline part of CURRY, you may click the **Show video window** icon again to see the Video window. Click the **Play Video** button to start the synchronized replay of the video with the data file. Click the **Pause Video** button to pause the replay. Use the **Previous** and **Next Frame** buttons to step through the replay. You may also drag the slider at the bottom of the data display, and the video will track with it.

There is typically a delay between what is seen in the data, and what is seen in the video. This will vary from camera to camera. The best way to determine the correction factor is by filming the amplifier and connecting the cables to an input. Then look for the movement in the video and look at the artifact in the EEG data. It is also possible to connect a photic cell to an EEG channel and film a light source flashing at the photic cell.

If there is a difference, *right click* in the video display and select **Set Delay**.



Once you determine the delay, enter that value (in ms). It should remain constant. If, however, you make changes in the camera Properties (described above), or switch cameras, the delay may need to be determined again.

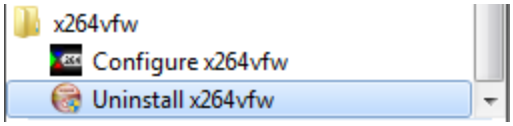
The "Reference Delay" is the delay between the moment the camera started to record video and the moment the first video block was received from the software. This delay also includes the time the codec needs to process the video stream. The **Use Additional First Reference Delay** checkbox is active by default. This is a static delay, just like the delay time you can set yourself.

The "Expected Delay" is not activated by default. It is a dynamic delay. It uses information from the .syn file about time differences between the actual time code that is received and the time code that is expected to be received. The **Use Additional Expected Delay** checkbox should be turned on when the synchronization during replay gets lost over time, or when the delay changes over time. The video can also get out of sync over time when the performance of the computer is to low to encode the video. You would then need to lower the resolution or the quality of the video compression.

The **Reset View** option (or *double-clicking*) seen in the context menu will return the video display to the default setting (after, for example, using the *mouse wheel* to zoom in or out, or dragging the display within the window).

Depending on the driver being used, some settings are stored in the registry. CURRY 8 saves the last used video settings (including the resolution and device codec) in the *SessionDefaults.cfg* file.

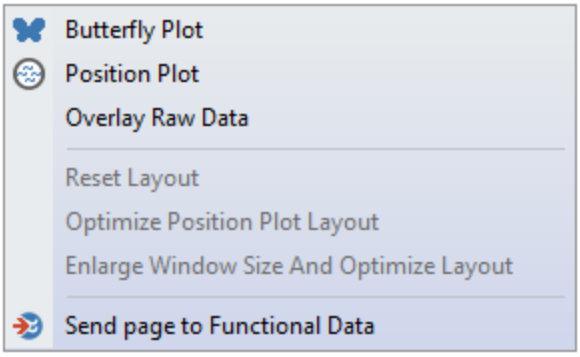
Technical Notes
1. Uninstall the x264vfw codec by running the Uninstall program from the Start menu.

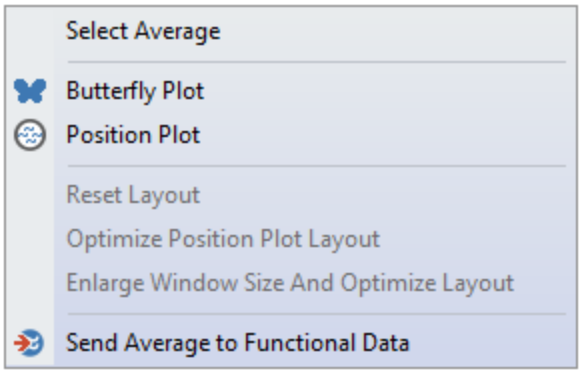


2. If you need to start the video installation process over from the beginning, go to Edit → Options → Acquisition and click the Reset Video Settings button.
3. The program that actually installs the x264vfw codec is x264vfw_35_2120bm_31356.exe, and may be found in the *...\Program Files\Neuroscan\CURRY 8\Video\Codecs* folder.

14.2.13 Context Menu Options

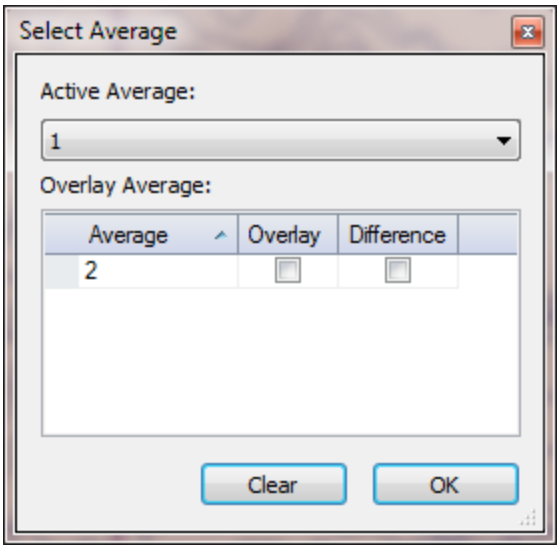
Additional options are available when you click the *right mouse* button in the continuous data or average data displays.





Select Average. This allows you to select the average that you want to display, and to overlay one online average file with another. The Active Average field shows the average that is currently being displayed. To change it, select a different one from the drop-down list. The option may also be accessed from the Toolbar icon  in the average data display**.**

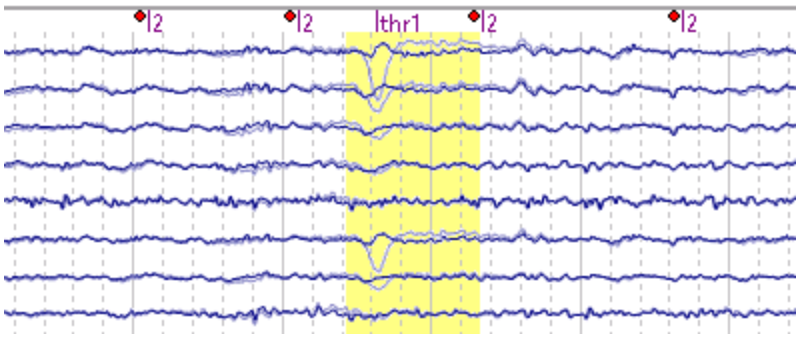
To compare averages, select the type from the Average list. You may **Overlay** the waveforms and/or show the **Difference** between them.



Butterfly Plot. A Butterfly Plot superimposes all of the channels.

Position Plot View. EEG channels are displayed in individual windows in their approximate positions on the head. Deselect to show continuous view.

Overlay Raw Data. Enable the option with continuous data to see the raw as well as the corrected/filtered EEG.



Reset Layout. Returns the Position Plot layout to the original positions (removes Rotation, Mirroring, moving, and resizing).

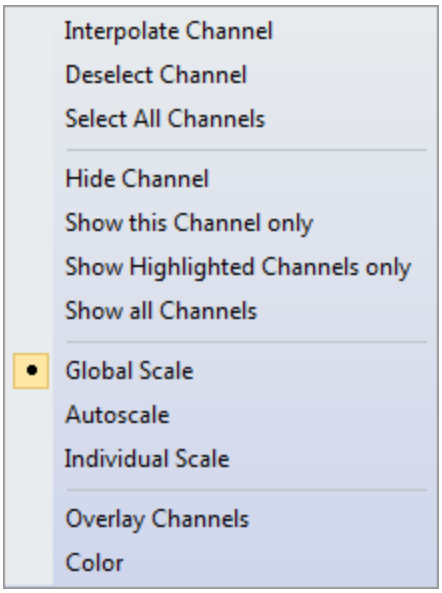
Optimize Position Plot Layout. If the Position Plot appears with overlapping channels (as may happen when positions in 3DD files are used), click this option to separate them.

Enlarge Window Size and Optimize Layout. Designed primarily for use during impedance testing, this option will enlarge the windows, making it easier to read the information, and yet avoid overlapping with other windows. It may be used at other times when you wish to enlarge all of the electrode windows.

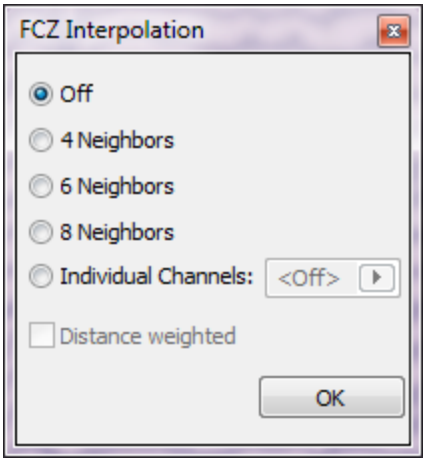
Send Page to Functional Data. Select this option to transfer the current display page to the Functional Data (where you may perform additional analyses, such as source reconstruction).

Send Average to Functional Data. Select this option to transfer the current online average to the Functional Data (where you may perform additional analyses, such as source reconstruction). If you have selected **Send to Functional Data: Average** in the **Averages** panel, you will see the Functional Data (and also the source reconstruction) update with each new accepted sweep.

Clicking the *right mouse* button on an *electrode label* displays the following list of options.



Interpolate Channel. This option is to reconstitute a bad channel based on the average of the N channels neighboring it (it should be used only as a last resort when you absolutely have to have data for that channel). Selecting the option displays the following dialog (with the selected channel showing in the Title Bar).



Deselect Channel. Changes the channel color (as set in **Colors**). The data are recorded but excluded from online analyses.

Select All Channels. All deselected channels will become selected channels.

Hide Channel. The label remains and the channel disappears (but is still recorded).

Show this Channel only. Only the selected channel is displayed, and highlighted. Data that are being recorded are unaffected.

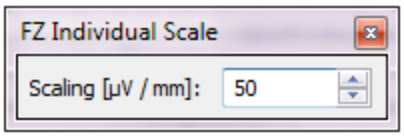
Show Highlighted Channels Only. Use *Ctrl+click* to highlight selected channels, then select this option to display only those channels. Use **Show All Channels** to undo.

Show All Channels. Displays all hidden channels.

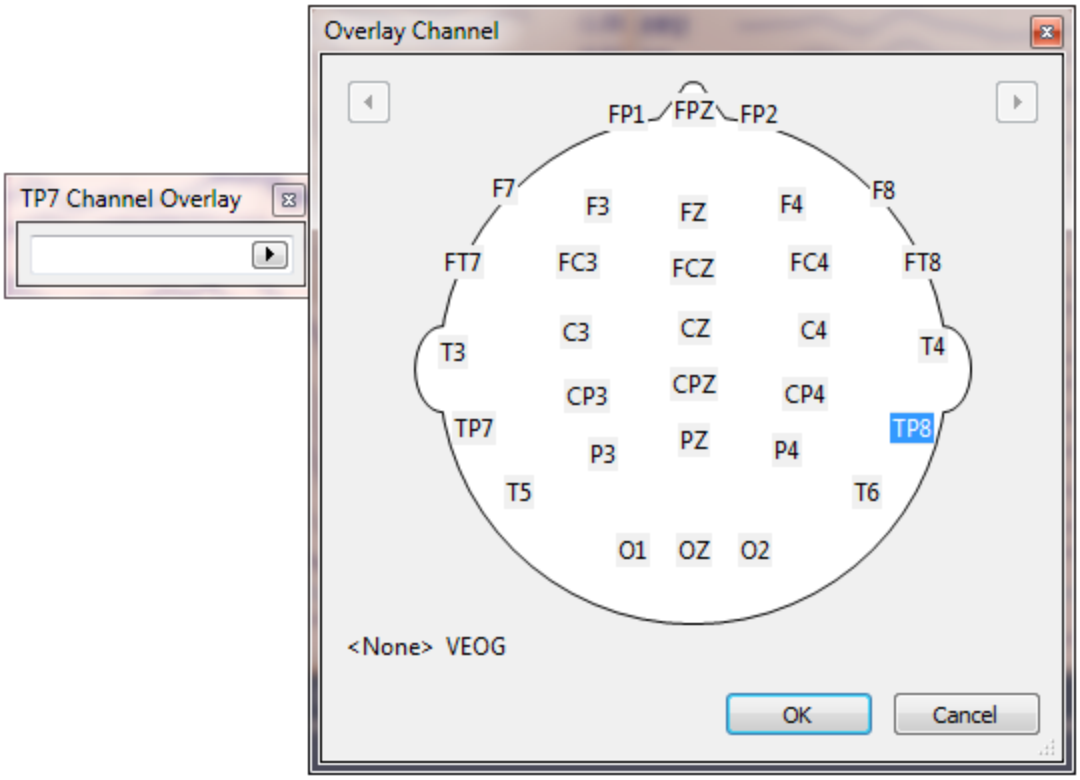
Global Scale. Scales all channels except Other channels (e.g., when rotating the *mouse wheel*).

Autoscale. Autoscales the display of the selected channel. Data that are being recorded are unaffected.

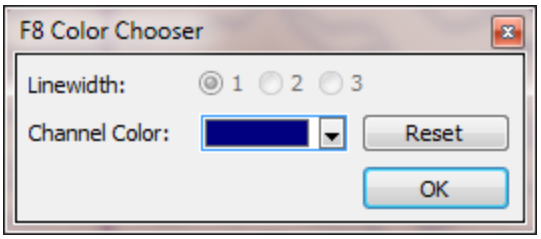
Individual Scale. Lets you scale the channel individually.



Overlay Channels. The Channel Selector display will appear where you may select one or more channels to be overlain on the selected one.



Color. Change the color of the selected channel from the color options.



15 Digitizer

CURRY 8 supports the Polhemus FasTrak, FasTrak 3 and Patriot devices, as well as the NDI Polaris device for digitizing electrode and fiducial positions. The FasTrak models are recommended over the Patriot model, because the Patriot, with its single receiver (plus stylus) is more prone to error if the subject is less than very compliant (more head movements and possible movement of the cap or receiver cable). You will need a "D" license to access this part of CURRY.

For directions on the use of the digitizer to record sensor and landmark positions, please see the **Digitization of Sensor and Landmark Positions** tutorial in addition to the information presented below.

Hardware installation directions for the FasTrak and Polaris systems are shown just below.

The digitizer panel parameters and operation are presented just after that.

15.1 Hardware Installation - FasTrak/Patriot

Hardware Installation - FasTrak/Patriot

Described below are the specific interface concerns related to CURRY 8. The user is referred to the accompanying Polhemus manual for all other hardware concerns. Familiarization with this manual and the operation of the device is required before proceeding with the steps listed below.

The installation of the Patriot is the same as is described for the FasTrak below, with the exception that there is only a single reference coil with the Patriot.

CAUTION - All Polhemus devices are sensitive to electrostatic discharge (ESD). Be sure to take precautions when following the instructions listed below. Power should not be applied to the device until so instructed.

1. Attach the communication cable. There are two types of communication cables: a USB cable and an RS-232 (serial port) cable. The USB connection is faster and is recommended over the serial port connection. The serial option is included should there be unexpected problems with the USB connection.

Connect the USB cable to the computer and to the digitizer.

2. Attach the transmitter. The transmitter is a plastic cube, roughly 2" on all sides, with a long cable and connector attached. With the power off, plug in and firmly screw the transmitter cable into the connector labeled **Transmitter**. The transmitter should be attached to the head of an aluminum tripod, supplied with the system.

3. Attach the stylus. The digitizing stylus is a pen-like device with a long cable and connector attached. Plug in and firmly screw the stylus cable into the connector labeled **Receiver ONE.** The stylus must at all times occupy the first receiver position. Other positions will result in erroneous data.

4. Attach the power cable. An external transformer is provided with the FasTrak. Make sure the power switch on the back panel is set to the **Off** position. For both devices remove the power cable from the transformer and plug the circular DIN type connector into the connector labeled **POWER** on the back of the device. Now plug the power cable into the back of the transformer and the other end into the wall socket.

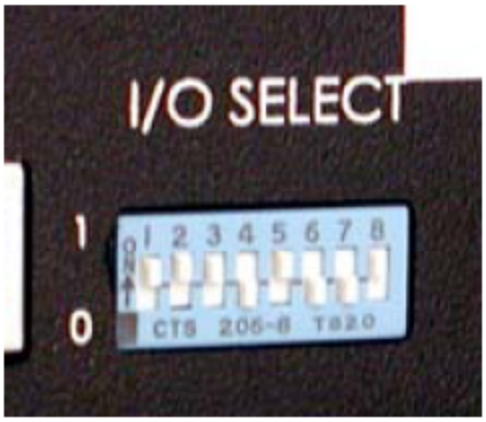
CAUTION - Never plug the DIN connector into the device with power applied to the transformer. Damage to the device may occur!

5. Attach the 3 additional receivers. Attach the three additional receivers. These receivers are used to form a reference plane on the head or object to be digitized. If the device was purchased directly from Compumedics Neuroscan, the cables typically will be tied together to form a harness. Plug these connectors in **TWO**, **THREE,** and **FOUR**. The switches on the front of the unit should all be On.

You can use either one or three receivers - if you use two, the second one is ignored. If you use no receivers, you will need to immobilize the head, using, for example, a bite bar.

6. Check the serial communication switches on the digitizer. The digitizer should be set for the 115200 Baud rate (factory settings), 8 bits, 1 stop bit, no parity. The appropriate switch settings can be found in the user manual of the device. If you purchased the digitizer from Compumedics Neuroscan, the switches have likely been preset; however, it is a good idea to check them to make sure.

Looking at the back of the digitizer unit, find the bank of 8 dip switches. The default settings are 11101001, where 1 is up (on), and these are the correct settings for use with CURRY 8.



The first 3 set the Baud Rate. For 115200, they should all be on. The complete list of settings is as follows.

Baud Rate	1	2	3	
1200	0	0	0	
2400	1	0	0	
4800	0	1	0	
9600	1	1	0	
19200	0	0	1	
38400	1	0	1	
57600	0	1	1	
115200	1	1	1	(factory setting)

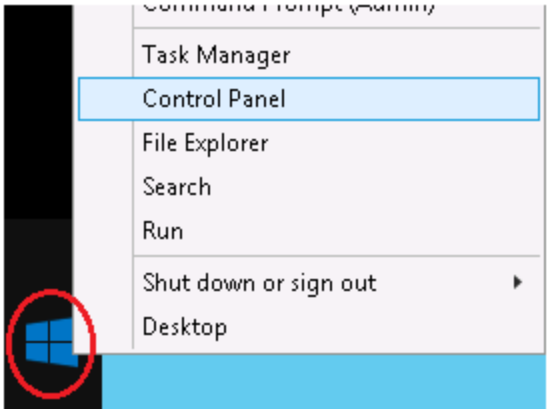
For reference, the 8 switches are as shown.

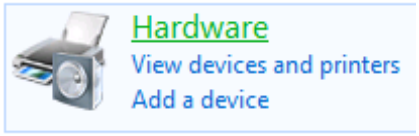
Switch Position	Function
1	Baud rate select
2	Baud rate select
3	Baud rate select
4	Not used
5	Character width: "0" = 7 bits, "1" = 8 bits
6	Parity select
7	Parity select
8	I/O Select -- **UP** for **RS-232**

If you have been using 3DSpaceDx from the Scan software, you probably were using a Baud Rate of 57600 (where the first 3 switches are 011). We recommend changing it to 115200 for CURRY 8. You will also need to make a change to the Baud Rate (Bits per second) in the Device Manager, as described below.

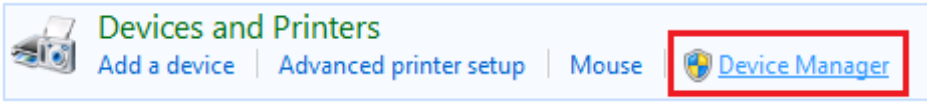
Note
The Baud Rate is set in two places, and both must be set the same: the switches on the back of the digitizer, and the COM port settings in the Device Manager. If you change the Baud Rate in one place, you must also change it in the other one as well.

Check the serial communication parameters on the host computer. It may be necessary to configure the serial port to handle the 115200 Baud Rate. To check or change the Baud Rate, *right click* on the **Windows** button and select the **Control Panel**.



Click on 

and the select the **Device Manager**



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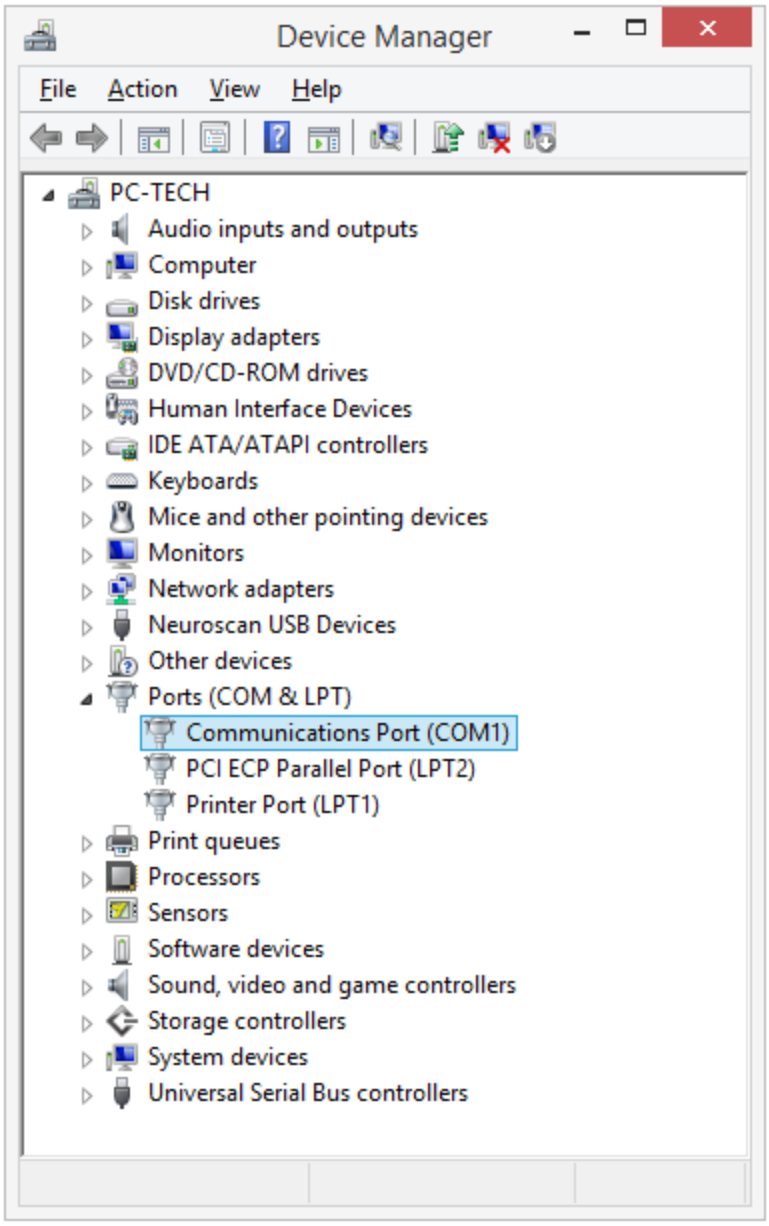
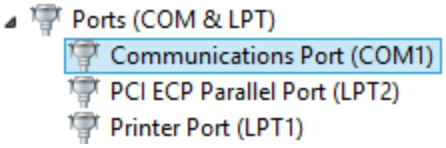
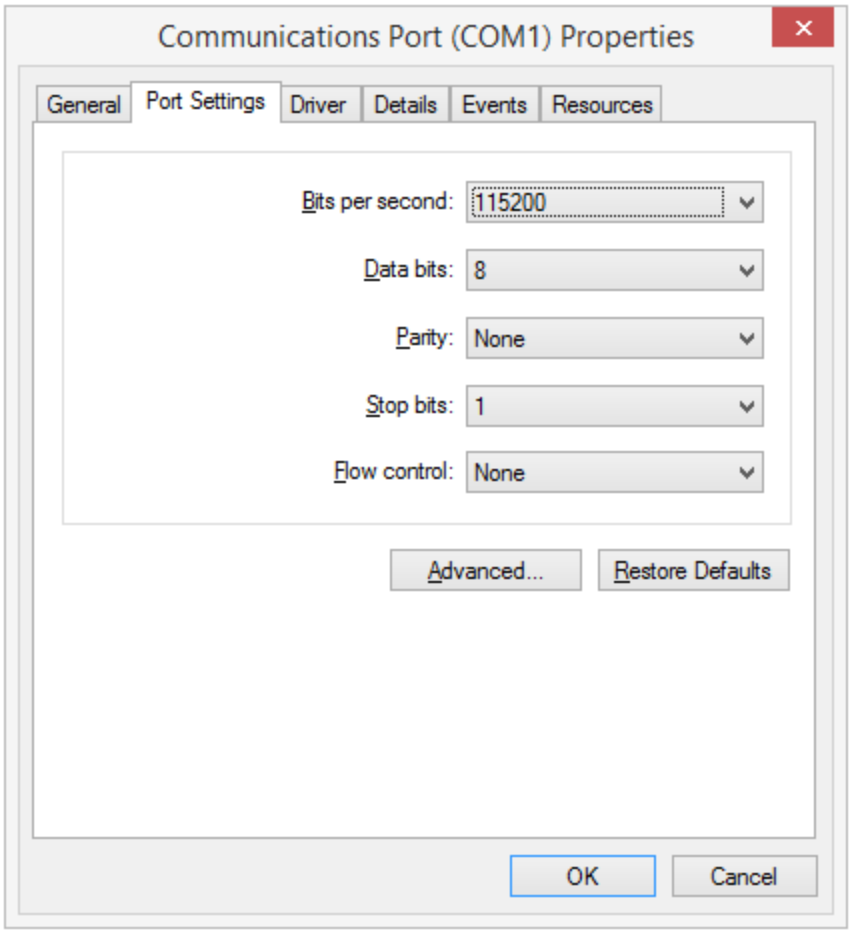
A list of the installed devices will appear. In this case, there is a USB-to-serial adapter, which still shows up in the same field as if there was a serial port.



Expand the Ports  Ports (COM & LPT) device tree. Note which COM port is being used, as you will need to enter this in CURRY 8.

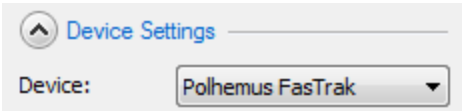


Double click on Communications Port and the **Properties** page will appear. Set the **Bits per second** field (the Baud Rate) to 115200.



Click OK and exit out from the Control Panel. The host computer is now configured for 115200 baud transmission rates.

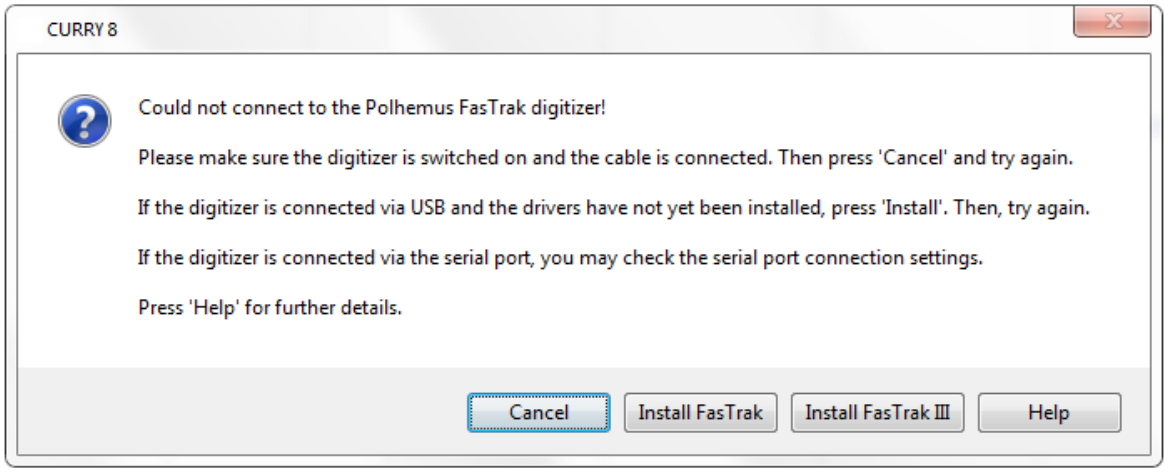
7. Select the device in CURRY 8. The USB or serial port settings are autodetected.



Care

When you have everything set correctly, turn on the digitizer. *Remember, do NOT make any connections to the digitizer, or make any switch changes, while the digitizer is ON.*

8. Install the current USB drivers. In most instances you will be using the USB method for communication. The first time you attempt to connect to the digitizer, you will see the following message. This will appear if the digitizer is not turned on, if the cable is not connected, or if the needed USB drivers have not been installed. Assuming the digitizer is on and connected correctly, you need only to click the **Install** button to install the USB drivers. (The same message will appear with the Patriot).



The current USB drivers are now installed.

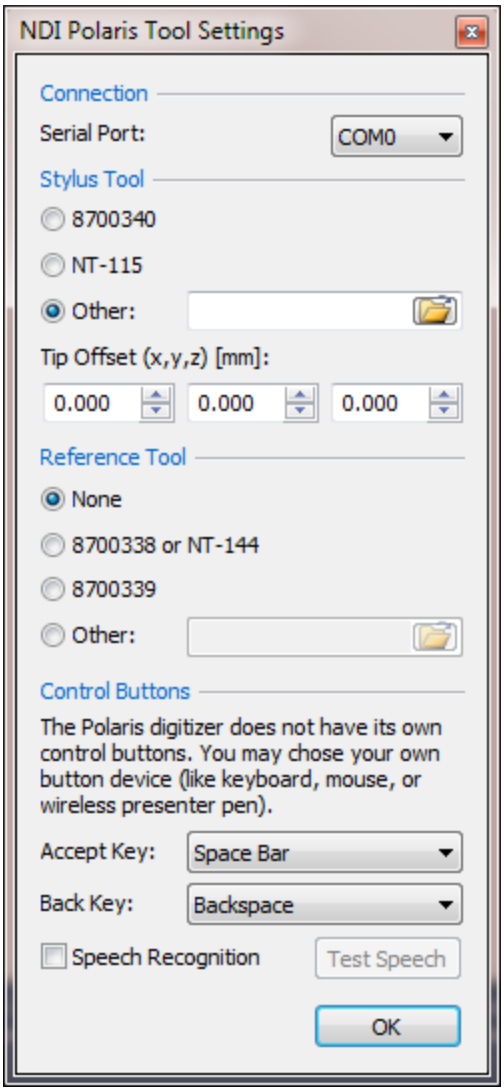
15.2 Hardware Installation - NDI Polaris

Hardware Installation - POLARIS

Described here are the specific interface options related to CURRY 8. The user is referred to the Polaris User Guide for the installation and all other hardware concerns. Familiarization with that manual is required before operating the device.

You will need to note which COM port is being used, so that you can enter it in the CURRY software.

Polaris Settings. If you are using the NDI Polaris Vicra device, the **Polaris Settings** button will become active. Clicking it displays the following screen.

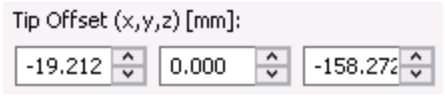


Connection. Select the COM port that you are using.

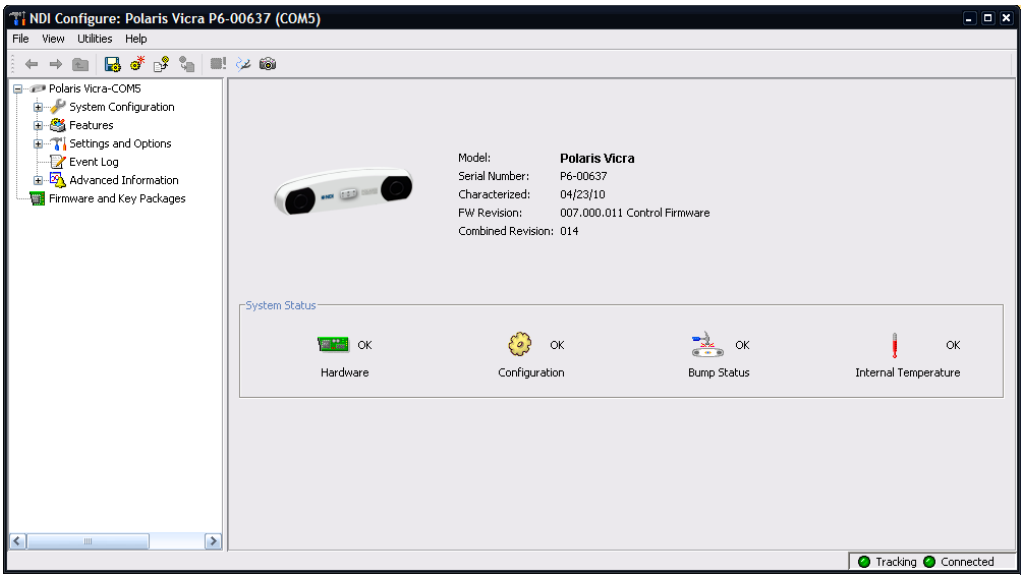
Stylus Tool. The common stylus tool is numbered **8700340**. If you are using a different Stylus tool than the one we provide, you will need to load the .rom file for that tool (created with the Vicra software). The .rom files that Curry uses are installed to the folder *\Acquisition\NDI Vicra Tool Definitions;* you would need to browse for wherever your .rom file has been saved. The NT-115 from ANT can be used as a stylus.

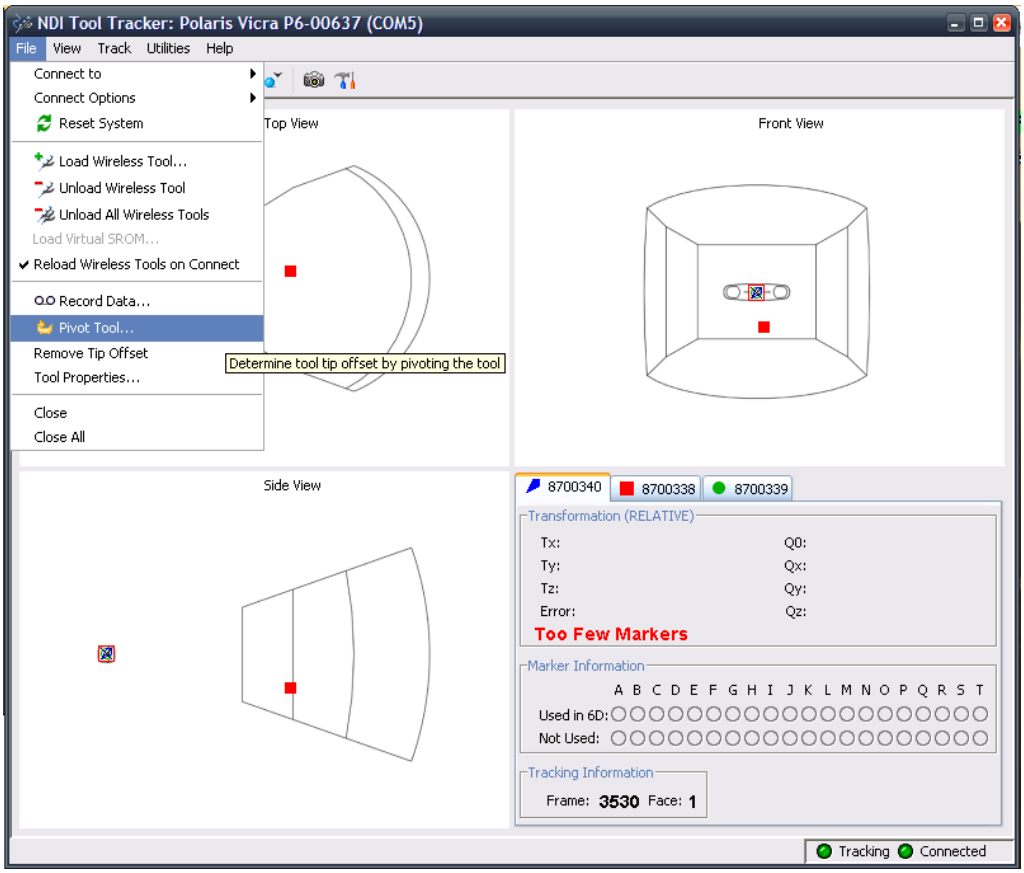
Reference Tool. The common Reference Tool is numbered either **8700338** or **8700339**. If you are using a different Reference tool than the one we provide, you will need to load the .rom file for that tool (created with the Vicra software). The .rom files that Curry uses are installed to the folder *\Acquisition\NDI Vicra Tool Definitions;* you would need to browse for wherever your .rom file has been saved. Select **None** if you are not using a Reference Tool. In that case, the head movement is not tracked, and you would have to make sure that the head is not moving during digitization (such as using a bite bar). The NT-144, from ANT, is the same as the 8700338 Reference Tool.

Tip Offset (x,y,z) [mm]. The default tip offset was determined with the evaluation Stylus that was used during development.



It was measured with the **Pivot Tool** option in the NDI Tool Tracker software (included with the NDI CD). The offset in Curry is an average of 10 measurements.





NDI calls this procedure "Pivoting". It should be performed periodically in case the tool shape changes over time.

Control Buttons. Since the stylus does not have its own control buttons, you can use either the keyboard or Speech Recognition to tell the program to **Accept** a measurement or go **Back** to a previous position. Select the keys you wish to use from the drop down lists.

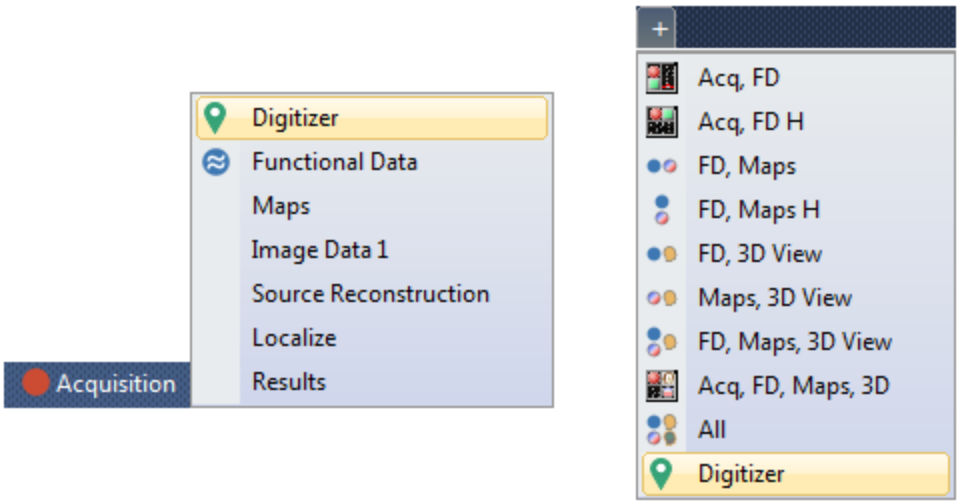
If you wish to use **Speech Recognition**, enable the option and click the **Test Speech** button. There are various words that will be recognized for the Accept, Stop, Previous, and Next commands. For example, speaking "Go" or "Accept" will be recognized as Accept. The last valid command is displayed. When you use speech, you should make sure you are in a quiet environment. Try not to say anything other than the allowed commands to reduce the danger of false recognitions.

15.3 Hardware Installation - NDI Krios

Please refer to the Krios manual for hardware installation directions, as well as instructions for its operation.

15.4 Digitizer Parameters and Operation

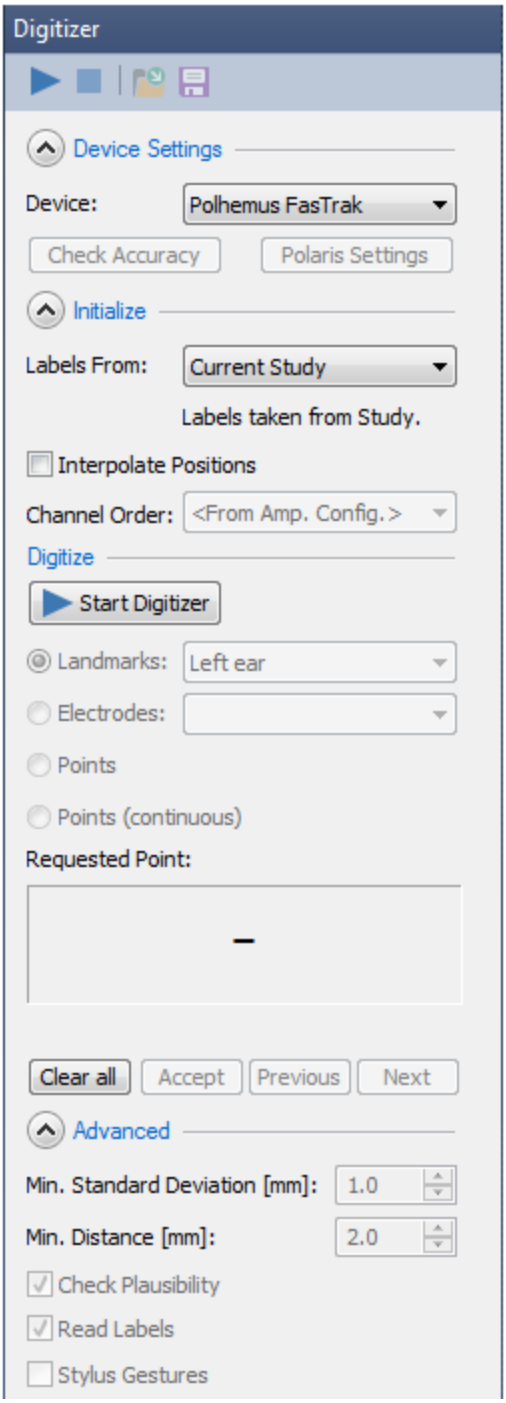
Digitization may be accessed via several routes. The most common is to simply click the New icon on the main Toolbar. This will take you into the Acquisition part of CURRY. You will see the **Digitizer** tab Digitizer at the bottom of the parameter panels. You can also access it by selecting Digitizer from the list of display tabs. That will open the Digitizer parameter as well.



You can also open a Study with a data file in it. You will see the same tabs for accessing Digitization. This method is useful if you will be using the electrode order in the open data file (described more below).

Lastly, if you have a D license only, you will see the Digitizer part when you open CURRY.

The controls for digitization are found in the **Digitizer** parameter panel.

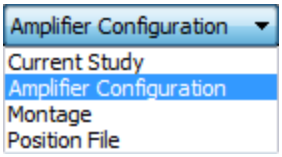


Toolbar Icons
At the top of the Digitize panel are four control icons.

The four buttons are to **Connect to** the digitizer  , **Disconnect from** the digitizer  , **Load** previous digitizer files  , and **Save** the results to a new file  (.pom extension).

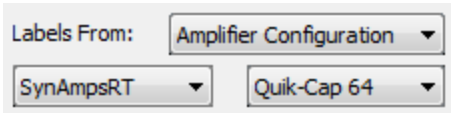
Digitizer panel
Initialize. The top part of the panel initializes the digitizer.

Labels From. The first step is to select the channels to be digitized. There are several ways you may do this.



Current Study. If you have a Study open that contains a data file that has the electrodes you want (this can be an Functional Data File, a running Acquisition or locations in the Localize list), in the order they should be, use this option.

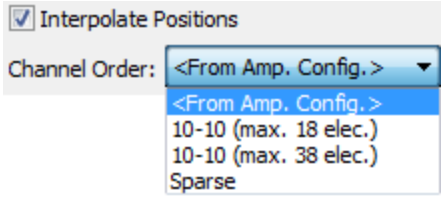
Amplifier / Configuration. If you do not want to use an existing Study, you may instead select the Amplifier you are using and the Configuration file you are using. You will then be guided to digitize the electrodes in that configuration and in that order.



Montage. You may also select a Montage file instead of the other options.

Position File. Similarly, you may select an existing .pom file that contains the electrode positions. The labels will be used to guide you through digitization.

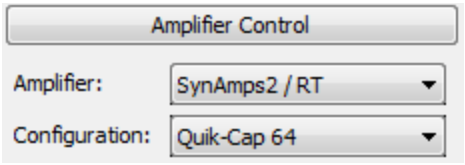
Interpolate Positions/Channel Order. CURRY has several options that will allow you to digitize various subsets of electrodes instead of all of them, and then perform an interpolation to estimate the position of the omitted ones. The different options let you select which subset of electrodes to digitize, or you may select your own.



The three landmarks will be digitized first, as usual. Then CURRY will guide you through the electrodes to be digitized. After the 5th one has been digitized, the interpolation will begin, and you will see the general head shape change in the **3D View** as more electrodes are digitized, and the interpolation becomes more accurate.

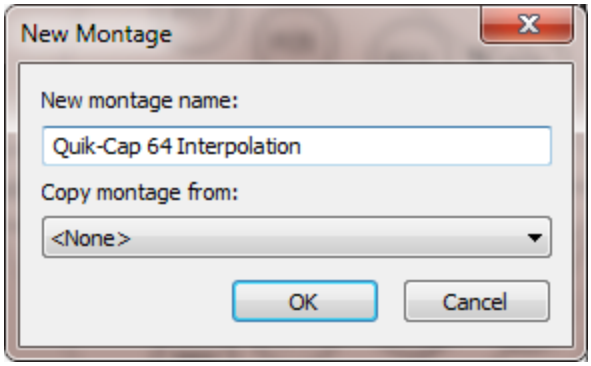
From Configuration (default). The other methods described below use lists of electrodes that are defined within the CURRY program. In the **From Amplifier Configuration** option, you take your existing Configuration file and modify it to include the list of electrodes to be used for digitization, or you may use one of the lists we provide for most of the caps. If you want to create your own, the basic steps are as follows.

1. Go into **Acquisition** by clicking the  icon. In this example, we are using a SynAmps RT and the Quik-Cap 64 Configuration file. Select your **Amplifier** and **Configuration** in the **Amplifier Control** panel, if needed.

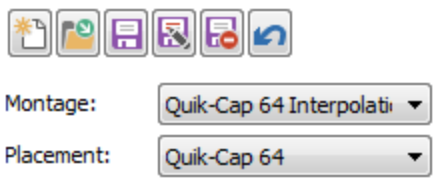


2. Click the **Acquisition Configuration** icon  and go to Montages 

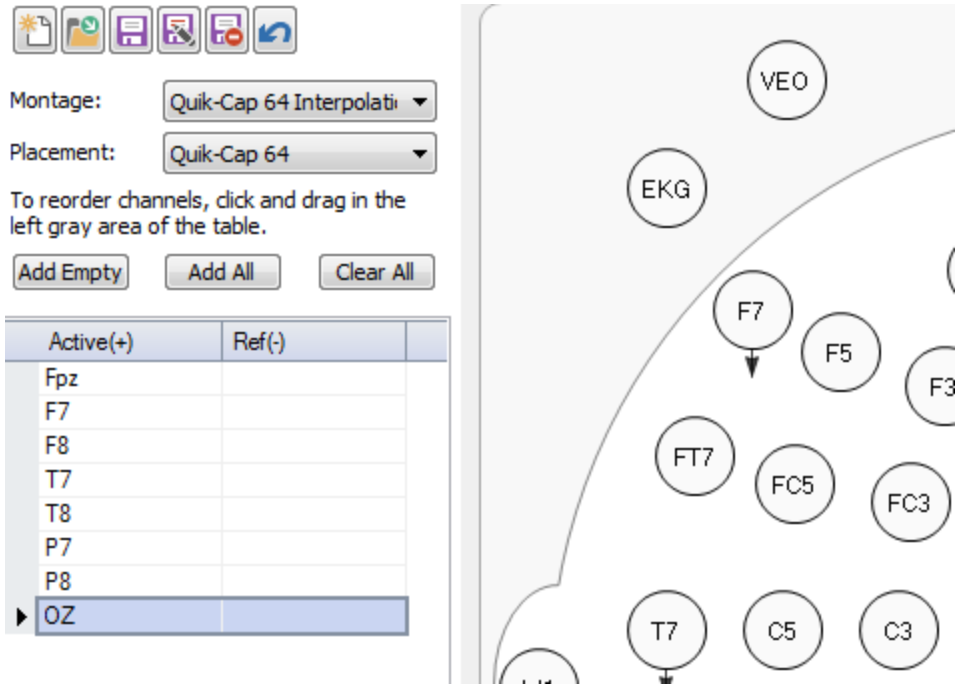
. Click on the **New Montage** icon  and enter a file name - *Quik-Cap 64 Interpolation*, for example.



3. After clicking **OK**, select the Placement file - in this case, Quik-Cap 64. This now displays all of the electrodes.



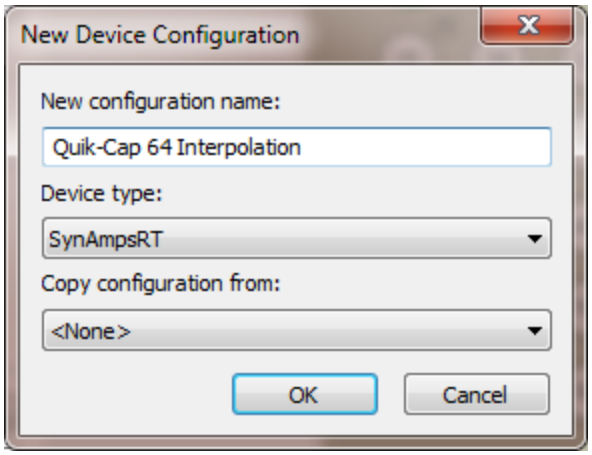
4. *Double-click* on the electrodes you want to digitize, in the order you want. You will see a down arrow for each selected electrode. (You will likely use more electrodes than are shown here).



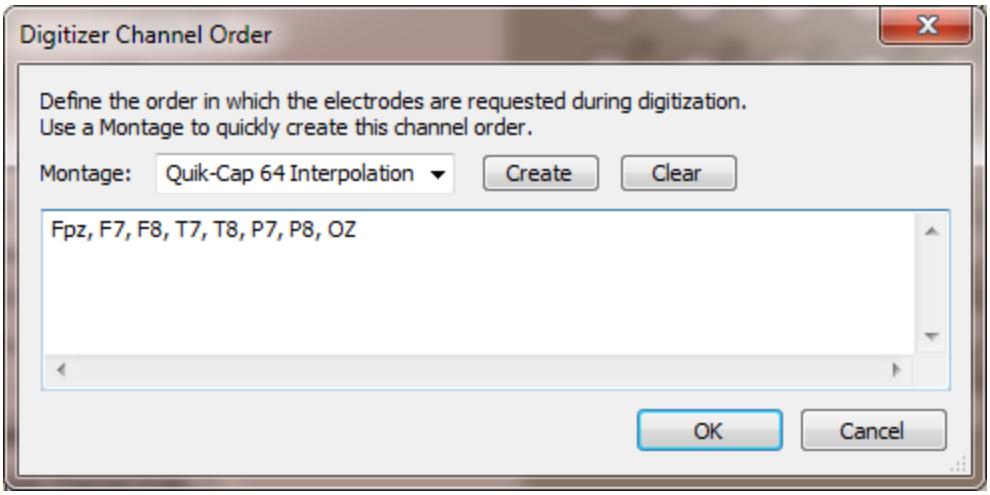
5. Save  the completed Montage file.

6. Now go to the **Amplifier Configuration** section 

. Click the **New Configuration** icon  and enter a file name - *Quik-Cap 64 Interpolation*. This is the configuration file; we already created the montage file (the file locations are different so you may use the same file name, if desired). Click OK.

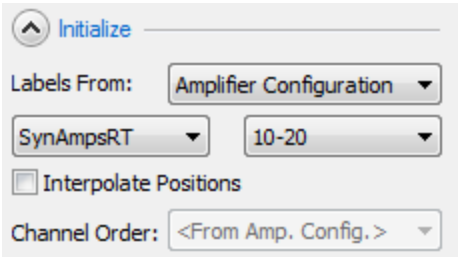


7. Go down to the **Advanced Settings** and click the Digitizer Channel Order button. This displays the **Digitizer Channel Order** dialog. In the **Montage** field, select the montage file we created above. Then click the Create button. You will now see the list of electrode labels we created. If need be, you may modify this list by just typing into it. Note that these are the electrode labels. With some files you may see numbers, but they are still the channel labels. Click **OK** when finished. Click **OK** again to leave the configuration dialog.



If you were using one of the supplied lists, you would simply select that here.

8. Select the new Configuration file that now contains the list of electrodes to be digitized in the **Digitizer** panel.



9. After you digitize the Landmarks, you will be guided [auditorily] through the list of electrodes you created.

Should you realize that you need to add a few more electrodes, you may select them from the **Electrodes** drop down list or from the 2D position plot (by *double-clicking* on the electrode you want to digitize).

When you stop, the 3D View display of the positions will be the ones that are used.

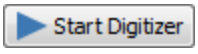
Note
If the digitizer list does not contain any matches to the Configuration file, such as, when there is no list of electrodes in the configuration file, it will be the same as if the Interpolation were set to Off. Similarly, the "10-20" options do not work as well with the 128 channel caps, as there may be few channels that match.

10-20 (max. 18 electrodes). Assuming you have selected a Configuration file (under **Amplifier Control**) that has conventional electrode labels, this option will select the 10-20 labels from that file for digitization (FP1, FP2, etc.). This gives a good selection of sites from around the head. The remaining electrode positions will be interpolated. For example, with a 64 channel cap, you will need to digitize only a maximum of 18 of the 10-20 electrodes, plus the landmarks.

10-20 (max. 38 electrodes). This is similar to the previous option, except that it contains more positions. For example, with a 64 channel cap, you will now be asked to digitize a maximum of 38 electrodes.

Sparse. The Sparse mode will ask for differing numbers of electrodes depending on the initial number of electrodes. You will be asked for every 5th, or every 3rd, or every 2nd electrode. This is done in rounds, where the first round asks for every 5th electrode, and the second round will ask for every 3rd electrode, i.e., the electrodes in between the "5th" electrodes. Stop when you have enough positions.

Digitize. These options control digitization.

Start Digitizer 

. This has the same function as the **Connect** icon 
.

Landmarks. The Left Preauricular, Nasion and right Preauricular landmarks are listed. After the landmarks have been digitized, the **Electrodes** field will be active.

Electrodes. The electrodes, from the configuration file, are listed. The program will cycle through these in the order shown; you may select an individual electrode from the list, as desired. You can also use the Previous and Next buttons.

Points. This functions the same way as when measuring electrodes (single points are measured). This is used in situations where you do not have a configuration file, but you still want to measure positions on a cap or some other object.

Points (continuous). This [seldom used] option allows you to digitize the subject's head shape. If you have the subject's MRI data, you can segment the skin surface (as part of the BEM Model, for example), and this can be used in place of digitizing the head shape. If you use the MNI average MR data set, you can segment the skin surface from that, and use it instead of digitizing the head shape. If you do not have the subject's MRI data, and you want the actual subject's head shape, you can obtain it with the this option.

The **Requested Point** counter will keep a running count of the number of digitized points. If you make any serious mistakes during digitization and wish to start over, click the Clear all button.

When you are ready to begin digitizing the head shape, place the tip of the stylus at a point on the head. The idea is to digitize all surfaces from the neck up. If you divide the head into regions, it is easier to keep track of what you have and have not sampled. Keep the stylus tip in contact with the surface being sampled. Digitization will occur as long as you hold the stylus button down. Release the button BEFORE you remove the stylus from the head, and press the button AFTER you make new contact with the head, in order to avoid spurious points being digitized. Don't move the stylus too fast. You should see the points appearing in the 3D View display (or in Localize set for the 3D View) along with your actual movements about the head. If you move the stylus faster than the data transfer can manage, you will lose points and have to make more passes over the same area.

If you have any spuriously digitized points, you may remove them as you would any points in the **Localize** display (e.g., *right click* and select **Delete Entry**).

Requested Point. This field displays the current landmark or electrode being digitized, or else gives a running total of points being digitized.

Clear all. Clears all digitized points.

Accept / Previous / Next. **Accept** has the same function as clicking the stylus with the FasTrak, or accepting a position measurement with the Vicra. **Previous** and **Next** move to the previous or next landmark or electrode in the **Landmarks** or **Electrodes** lists.

Advanced

Minimum Standard Deviation [mm]. When a point is digitized, not just a single point is measured, but rather a series of points during the approximate half second during which the measurement is made. If the stylus happens to move during that sampling

interval, there will be distributions of the measured XYZ points, which are reflected in the color scale. The color scale will change accordingly when you change the Minimum SD (the scale will be twice the value you enter to show the bad values). If the SD color is in the orange/red range, you may want to redigitize that electrode.

Minimum Distance [mm]. This option is used with the **Headshape** option. The stylus must move at least the **Minimum Distance** for the points to be registered. This avoids registering multiple points if the stylus position is paused during digitization.

Check Plausibility. When enabled, the program will check the plausibility of the electrode you are digitizing against the idealized positions (label-matching). If the position is 40-80mm off, you will hear a warning signal and see a Warning in the Output section. If it is more than 80mm off, you will hear a voice message to that effect. If desired, you should go back and redigitize that position (move the stylus away - see **Stylus Gestures** just below).

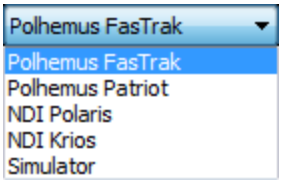
Read labels. If you do not want the program to announce the labels as they are digitized, you can turn the voice off. You will still hear the beep sounds for the good and bad electrodes.

Stylus Gestures. When enabled, you may move the stylus away from the head (at least 30cm), and click the button to return to the previous electrode to remeasure it. This is one method for backing up when you have a bad electrode measurement.

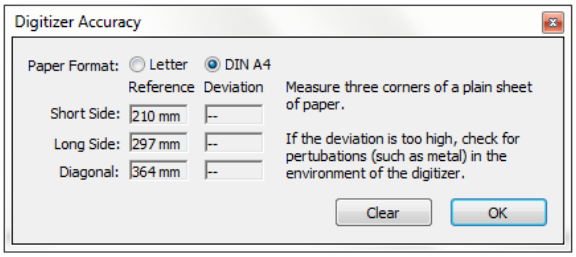
Device Settings

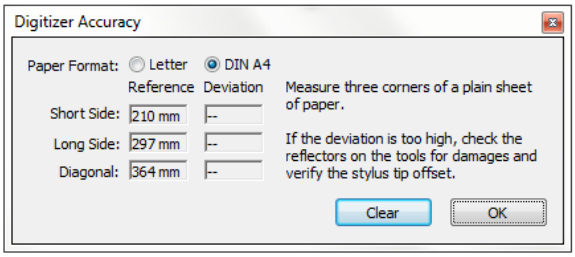
Device. Digitization will use the Polhemus FasTrak, FasTrak 3, Patriot, or the NDI Polaris systems. If you have a FasTrak 3, use the same FasTrak option. Operation of the CURRY software with a Krios is demonstrated afterward. A Simulator mode is included for demonstration purposes.

The only difference between the FasTrak and the Patriot is that instead of three reference coils with the FasTrak, the Patriot only has one. This means that attaching it to the head is a bit more critical, as you have to make sure that the reference coil is really tight and does not rotate relative to the head at all.

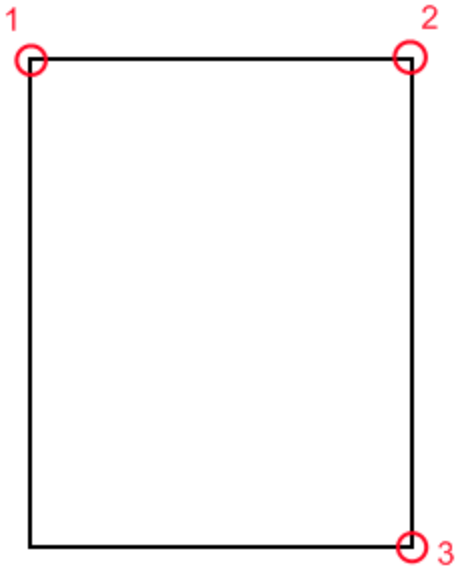


Check Accuracy. This option is used to check the accuracy of the digitizer, especially in the environment in which it is located. Clicking it displays the following dialog (FasTrak on the left, Vicra on the right).

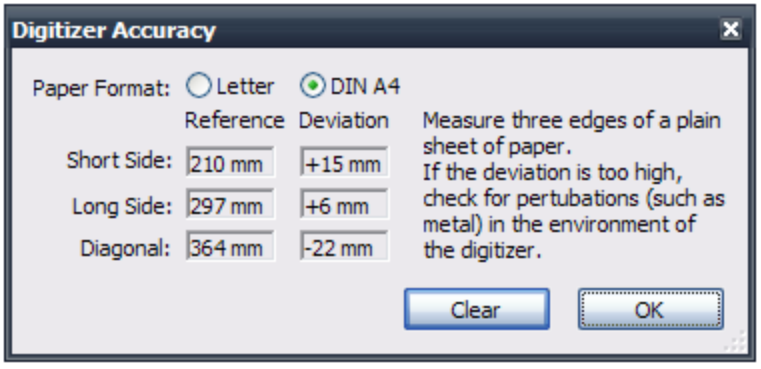




Lay a sheet of standard paper (letter size or A4) on a plain surface close to the Polhemus receiver (or in the field of view of the Vicra camera). Select the format of the paper. Then measure any three corners (the order does not matter) and look at the Deviations.



In this example (with a FasTrak), there was metal in the immediate environment and so the Deviations are large.



Best results with the FasTrak will be obtained when you minimize the nearby metal, such as by positioning the digitizer in the middle of the room, on a wooden or plastic table. For the Vicra, verify that the tooltip offset is correct (Pivoting), or if the reflecting marbles are damaged.

Click the Clear button to clear the Deviation fields.

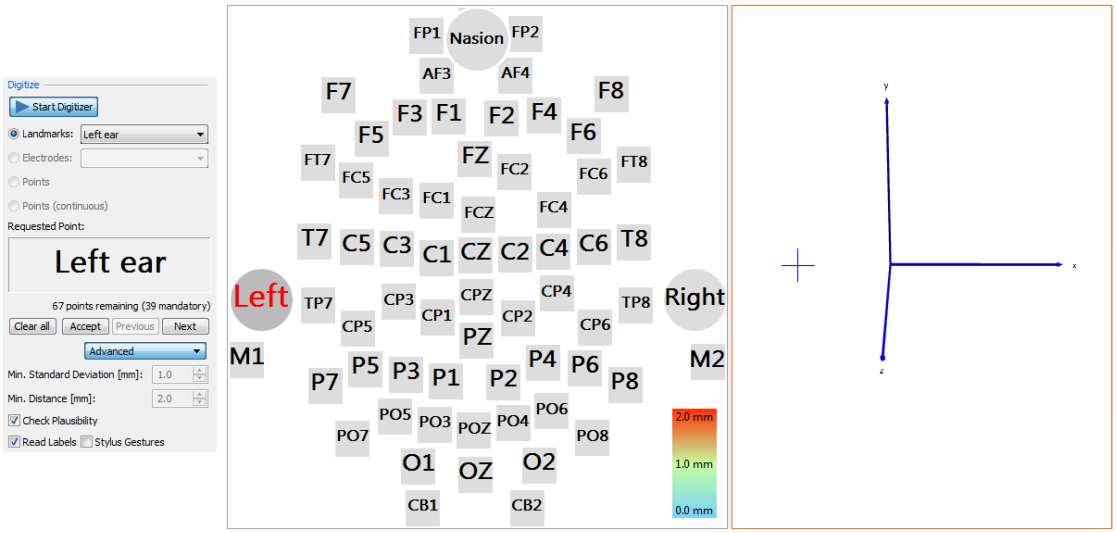
15.4.1 Operation (except Krios)

The actual operation of the digitizer is fairly straightforward. Please refer to the **Digitization of Sensor and Landmark Positions** tutorial for a more complete example. Briefly, the steps are as shown below (assuming you have the digitizer in position on the subject, etc.).

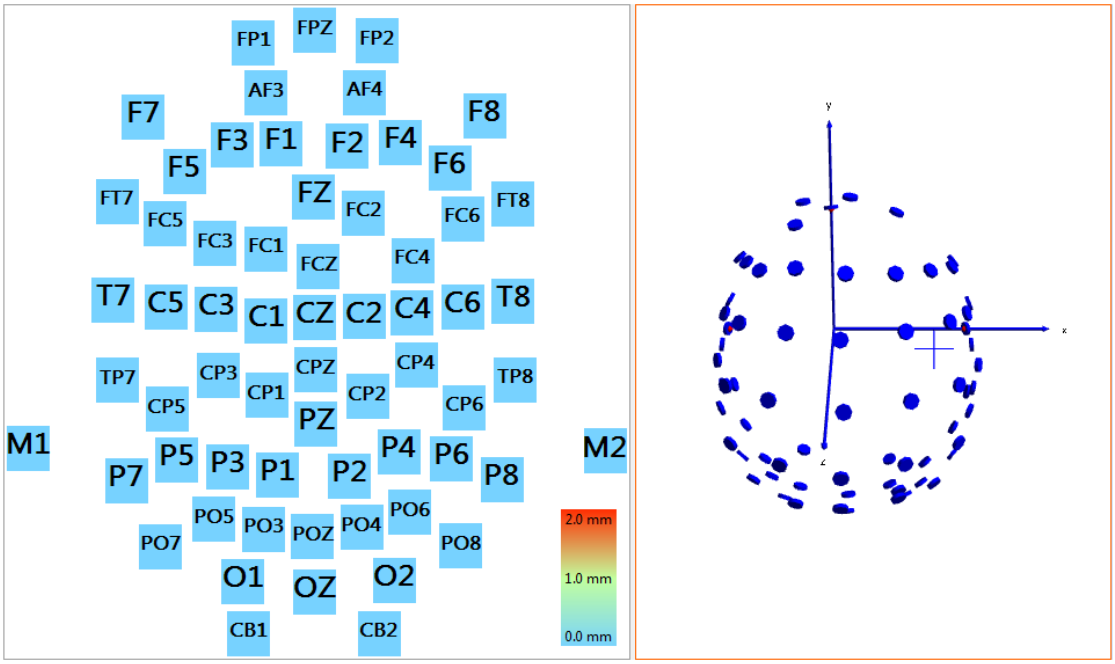
1. Decide which of the options you will use for the list of electrodes to be digitized and select the desired option.

2. Decide whether you will use Interpolation, and if so, which method you want to use.

3. When you are ready, click the **Connect** icon . The display will be similar to that shown below. The current electrode will flash in red on the 2D Position Plot. You will see a + sign in the 3D View, showing the position of the stylus.



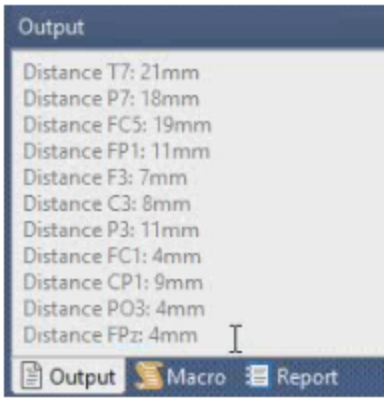
4. Click the stylus button, or the Accept button, to record the position. The next electrode, or landmark in this case, will flash. Continue in this manner until all position have been digitized.



Saving the positions

If you are acquiring EEG data in the same study before or after digitizing, the positions will be automatically stored with the recording. If you are digitizing without recording EEG data you have to manually save your positions using  . Curry will recognize that the digitized positions were stored, and will remind you to save the positions explicitly when you close the study if the positions were not already saved.

As you digitize the electrodes, you will also see a list of Distances in the **Output** (only if you have Interpolation and Debugging enabled). These are the distances between the measured point and the previously interpolated position. As the process continues, these differences should become smaller and more stable.



15.4.2 Operation (Krios)

Operation (Krios)
In the initial version of CURRY 8, the Krios will not be directly supported. You will need to install the Krios driver and Krios software from NDI.

The CURRY program uses an "algorithm" to perform several operations that create the interface between the Krios device and the CURRY software. Most simply said, the algorithm (which is assigned to the "Assign Labels" button or clicking **Button #1** on the Krios) performs the following:

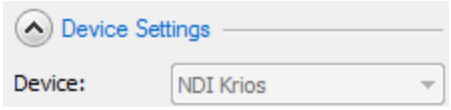
- assigns labels (from the Template) to the Krios measured point cloud
- reorders the points to match the amplifier channel order
- detects Landmarks and the Reference electrode (optional)
- performs a PAN transformation based on the Landmarks (if they exist)
- interpolates missing points (optional)
- deletes unneeded points (optional)

The cap has to be prepared with reflective stickers on each electrode. The Krios works better when there is a denser distribution of stickers. That is why it is always recommended put a sticker on Ground and Reference. The Ground position is not used, but having it helps with fitting the measured sites to the template. The Reference position is also not part of the template that is later used in CURRY, but CURRY can detect and use the Reference position, if there is one.

Using CURRY with the Krios
At this point it is assumed that you have installed the NDLink and NDI Toolbox software (if not, see the next section below).

(Contact curry8help@neuroscan.com for a video that explains the operation of the Krios in more detail).

1. Go to the Acquisition part of CURRY, and select 

. Select the **NDI Krios** device 

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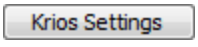
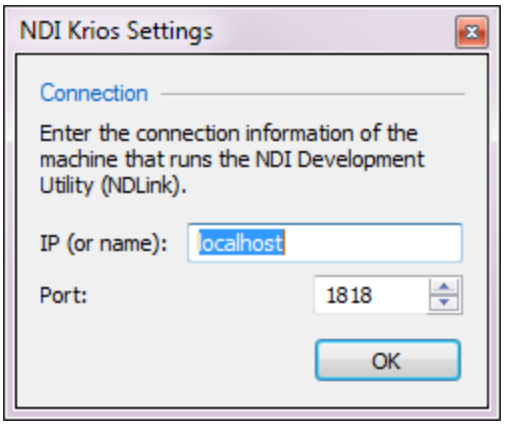
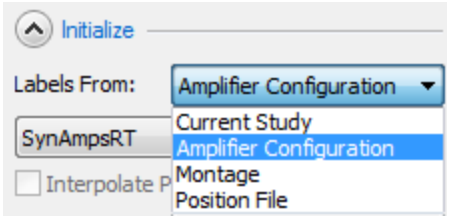
   If you are running the NDLink Tool on the same computer as CURRY, you will not need to access the 

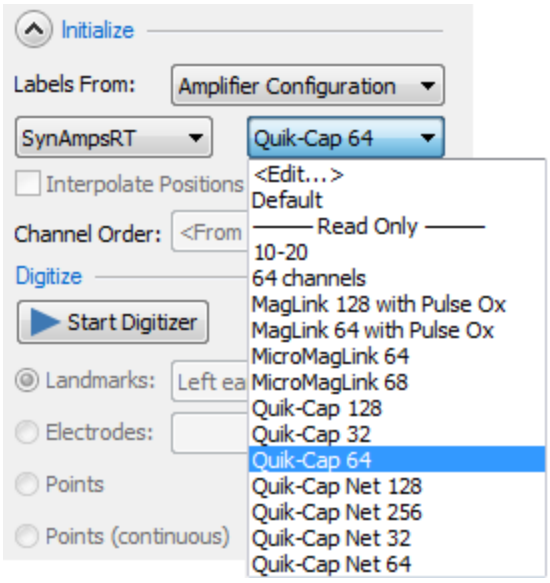
button. This is all set up as the default. If you run the Tool on another computer, you will need to change the IP address to the computer where the NDLink Tool is running.



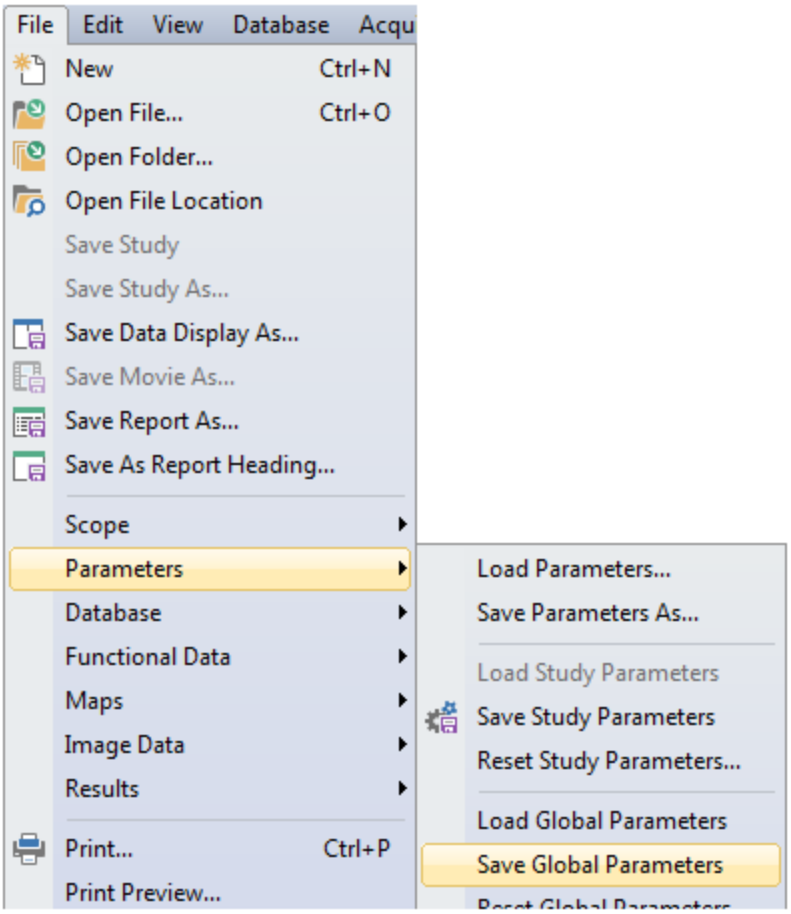
2. Select the **Amplifier Configuration** you want to use. If you are using a running acquisition, you may select **Current Study**. The other options present different ways for selecting the template that you wish to use. This is where the labels to initialize the digitizer will come from.

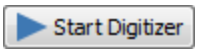


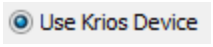
3. Select the amplifiers you are using, and the select the configuration you want to use.



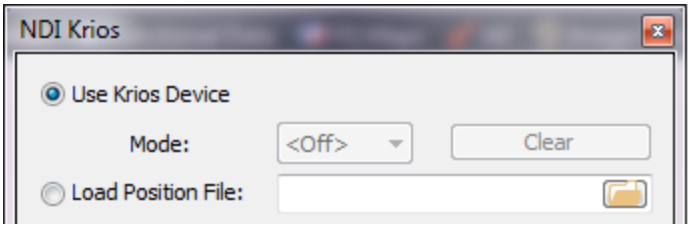
4. Before starting digitization, it is a good idea to save the current settings as **Global Parameters**.



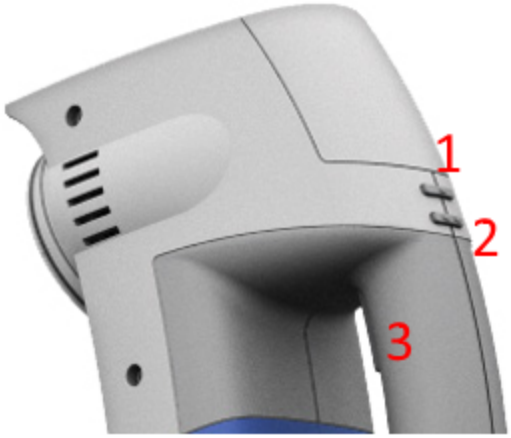
Click the 

button to select the file that you have created with the Krios software. The NDI Krios dialog will appear. If all is set up properly, the 

button will be selected (and you will hear a confirmatory beep).



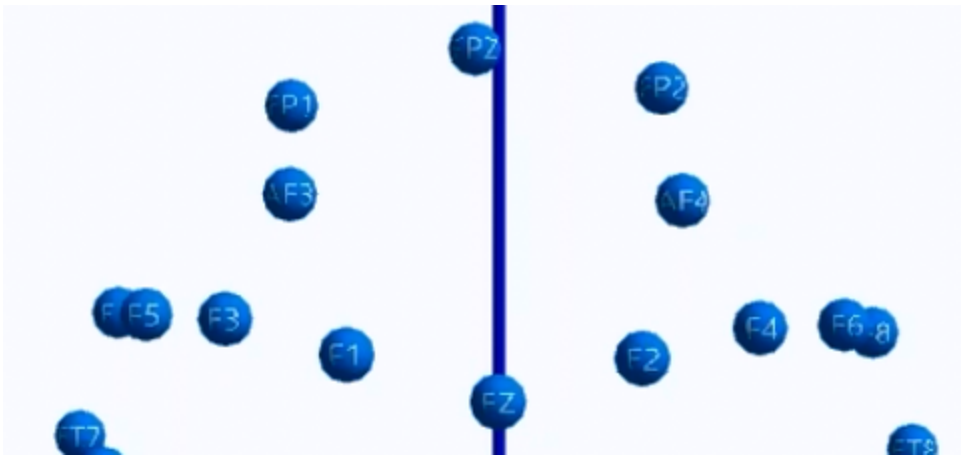
Set the **Mode** to **Capture** either by selecting it from the list, or by double-tapping the big button (#3) on the Krios device.



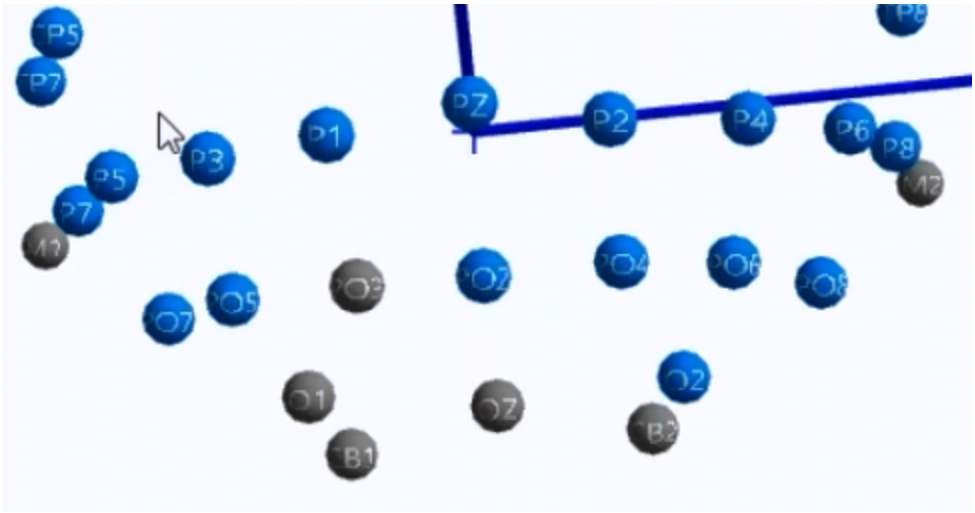
5. In the **3D View**, you will see the points as they are digitized, as you move the device about the head. The blue spheres are the digitized electrodes (Rigid Body points), and the yellow ones are the stray markers that are detected, but not yet added to the Rigid Body.

If you look closely at the Krios device itself, you will see an LED light. When the device is locked on to the Rigid Body (it is following the 3D View), the light will be blue and pulsating slightly. If the light turns red, this means that the device is too close, too far, or not seeing any points. You will hear audio feedback when the points are being detected, as well as seeing them in the **3D View**.

6.When you are done, press Button 1, and this will switch the **Mode** from **Capture** to **Off**, and also perform Label Matching for the positions that have been measured.

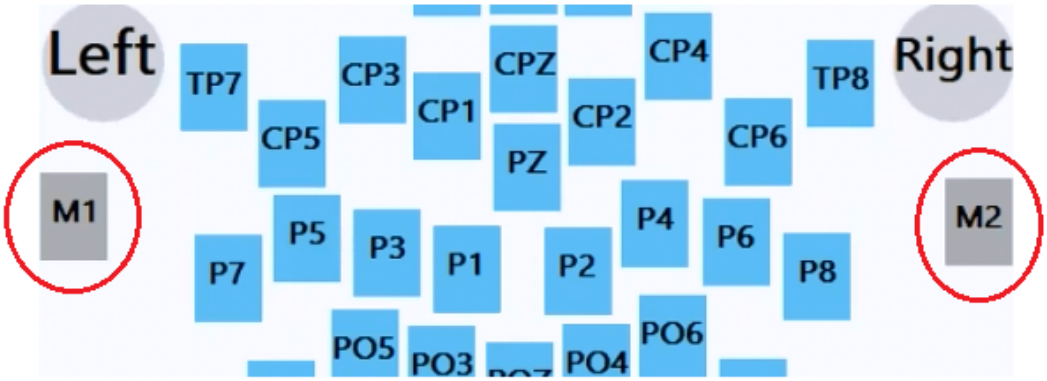


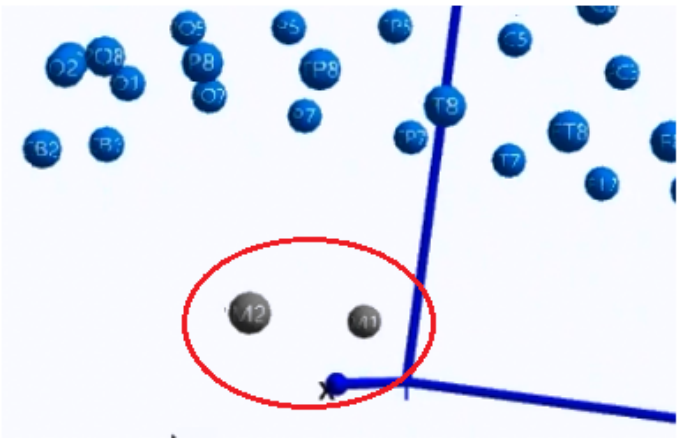
7. If you have unmeasured points, these will appear as dark points. They have been interpolated, based on the positions that have already been measured, but not measured themselves.



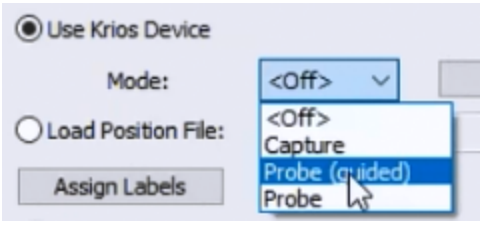
To measure them, double-tap the big button on the Krios device and continue digitizing the electrode positions. When you have them all, again click Button 1 and Label Matching will occur.

8. After all of the regular positions have been digitized, note that M1 and M2 will remain (as they are drop-down electrodes that have no reflective markers and may be obstructed by hair, etc.). The Landmarks also have not been measured (Left, Nasion, Right).

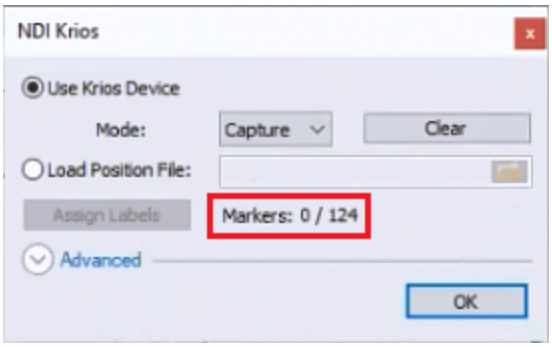




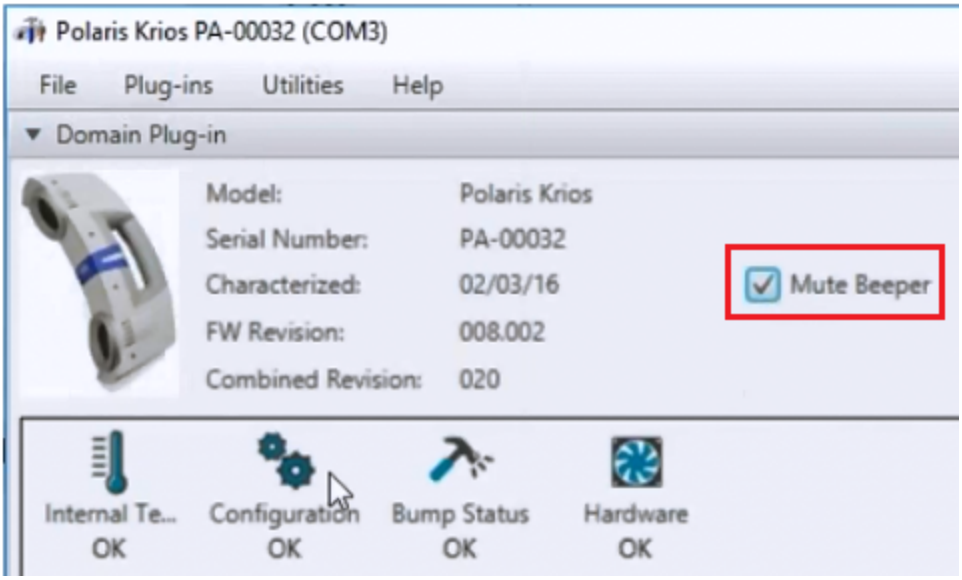
In this case the Probe tool is used to measure their positions. This is selected either by selecting **Probe (guided)** manually, or by double-clicking the big button on the device once to enter **Capture Mode**, and a second time to enter **Probe (guided) Mode**.



As you digitize the points, you will see the counter increment. These are the number of reflective markers that are included with the cap you are using. This is not the number of EEG electrodes, as it will include the Ground electrode but not, for example, the mastoids. So the number will be close to the number of EEG channels, but not necessarily the same. This information is contained in the amplifier configuration files supplied by us. When other caps are used, that information is not known, and so you will see an estimate of the number of markers, such as 0/~124. If you create your own configuration file, from one of our supplied files, and you turn off N channels, you will still see the original number of reflective markers, whether they are being used or not. Once all of the markers have been measures, you can move on to the next step.



Incidentally, should you hear an annoying beeping coming from the Krios device, you can turn it off by enable the **Mute Beeper** option in the NDLink Tool dialog.

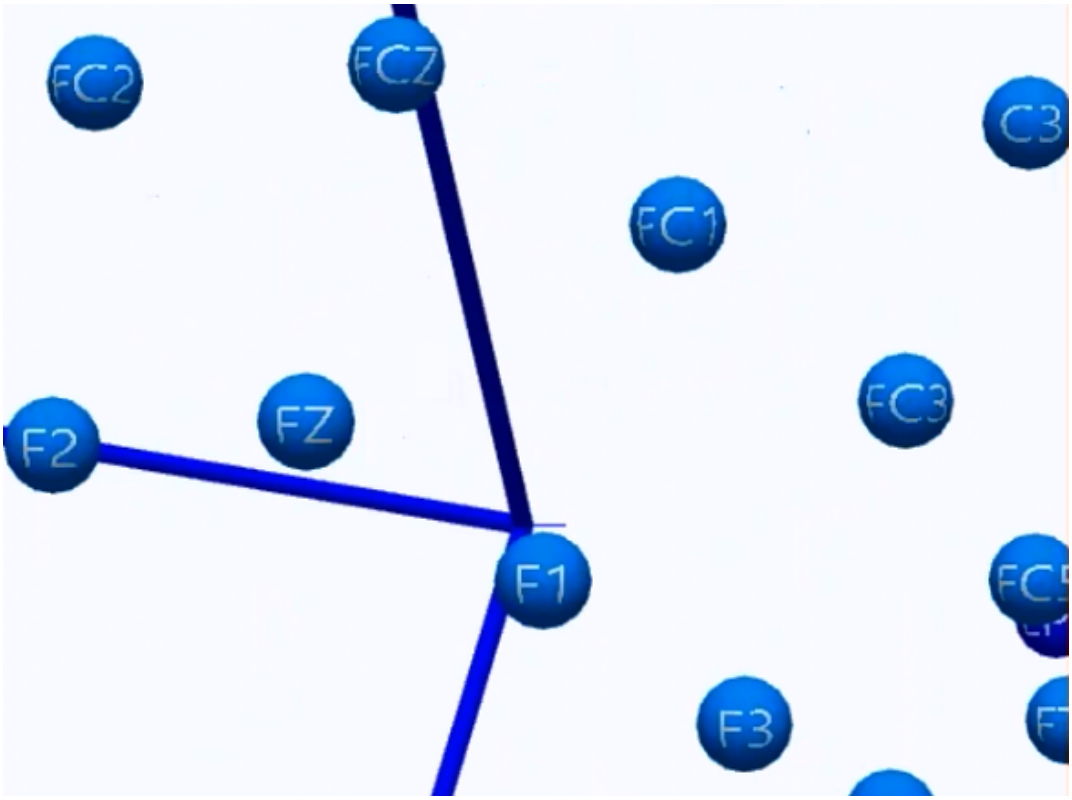


9. In the "guided" Probe mode, you will see the first Landmark flash, indicating that this is the first point to be measured. You will also see several electrodes highlighted. These are user as confirmation points by CURRY to make any refinements. The Probe tool will be used to measure the Landmarks, and then the highlighted electrodes.

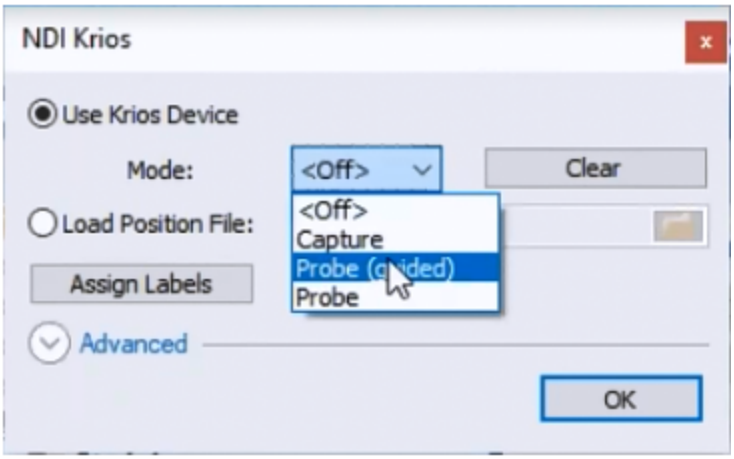
Position the Probe at the designated location, hold the Krios so that the probe and other electrodes are seen, and then press **Button #2** to digitize the position. It will appear in a darker blue shade in the **3D View**.

Continue for the Landmarks and the other highlighted electrodes (including ones that do not have stickers, such as M1 and M2). After that, CURRY will request the remaining highlighted electrodes. These are the five outermost electrodes on the cap (such as T7, T8, FPZ, OZ and CZ). These are used to facilitate the matching algorithm to get the most accurate measurements (optional).

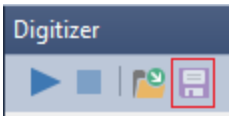
When you are finished you will have all of the positions with their labels, including the "Ref" that was detected automatically.



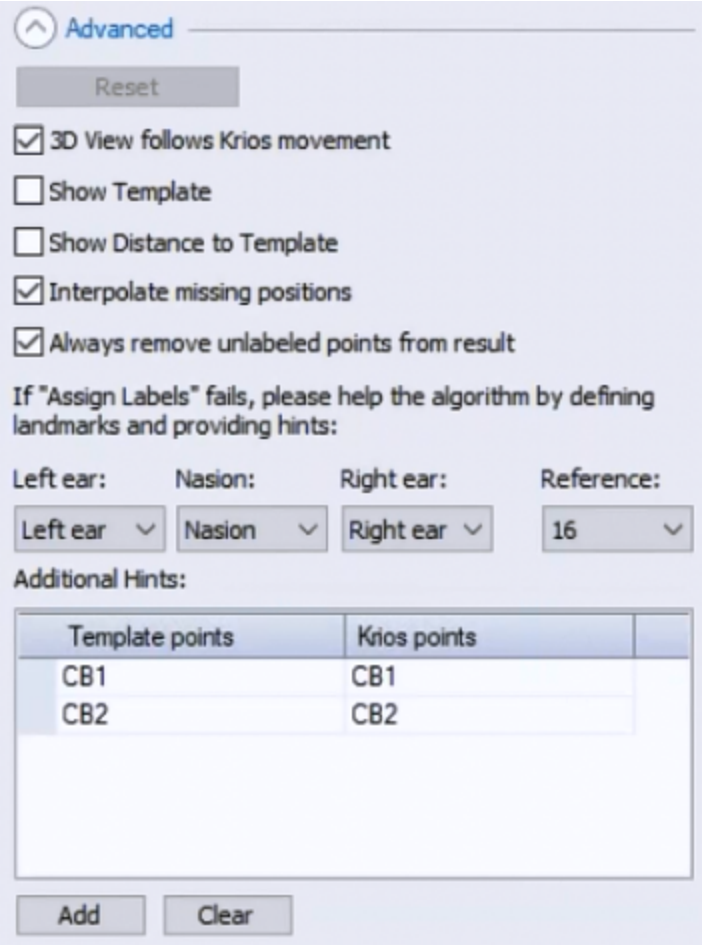
10. If for whatever reason the label matching did not work, the other option is to use the **Probe (guided) Mode** to measure the end points manually (e.g., T7 through CZ), as shown above. After measuring the five designated positions, CURRY will go on to let you measure all of the positions, if desired. This would be for when you want to create a template. Otherwise, press **Button #1** on the Krios to do label matching again. The probed points will appear darker blue.



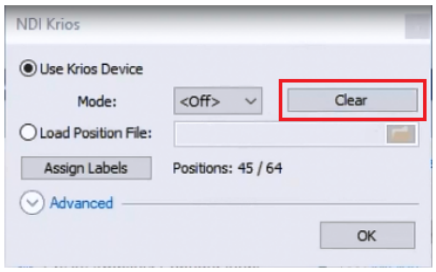
Close the NDI Krios window when finished. Click the **Save** icon at the top of the Digitizer panel to save the positions in a .pom file. Stop the Digitizer.

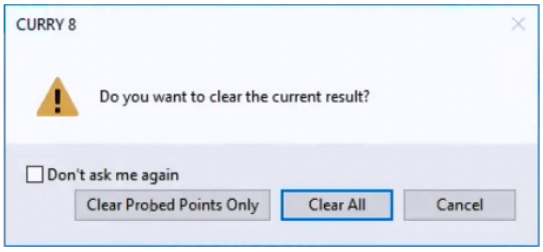


Additional Features
The Krios has some additional features. Some of these are useful if there are problems with the above steps. Most are contained in the **Advanced** section.



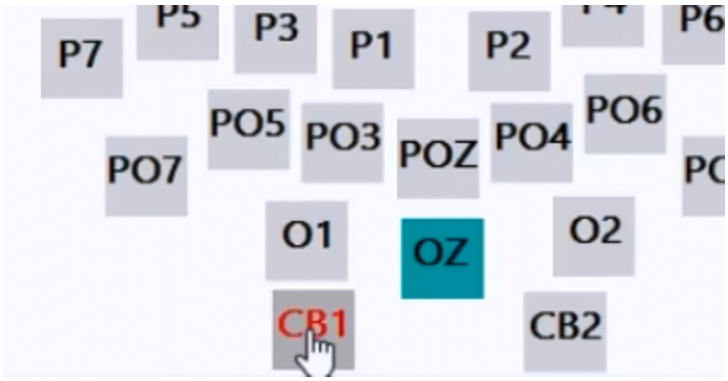
Clear button. You can clear just the Probed points or all of them.



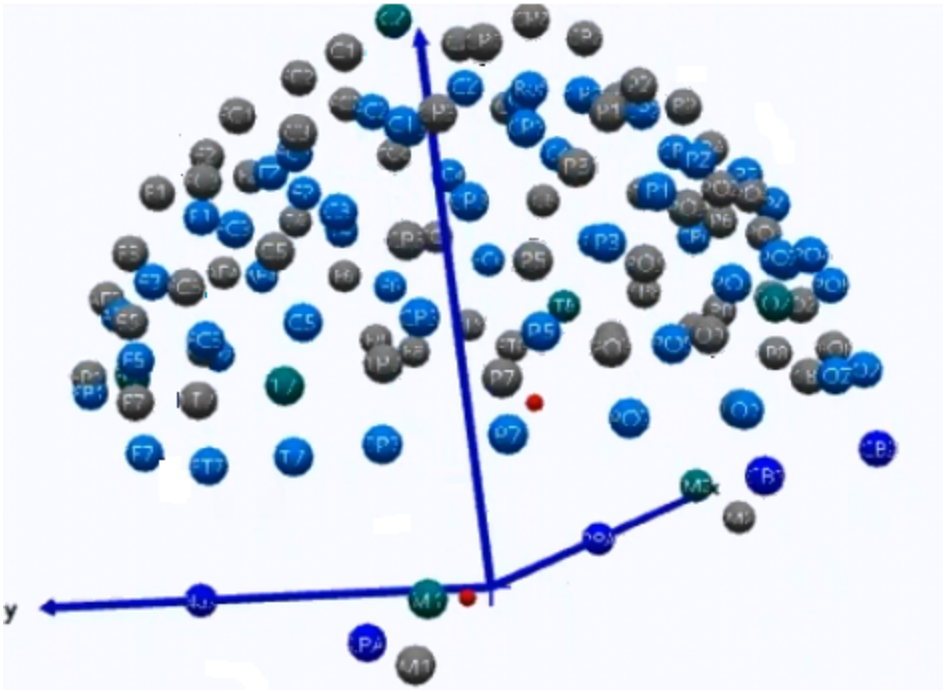


Probe Mode. The non-guided Probe mode lets you measure whatever positions you want, without CURRY guiding you. For example, if you have captured the majority of the positions using the **Capture** mode, but some unmeasured ones remain because they may not have stickers, you cam measure them manually using the Probe mode. For example, if you do not have stickers on CB1 and CB2, you can measure them manually. When you do the usual label matching, you will see the added points.

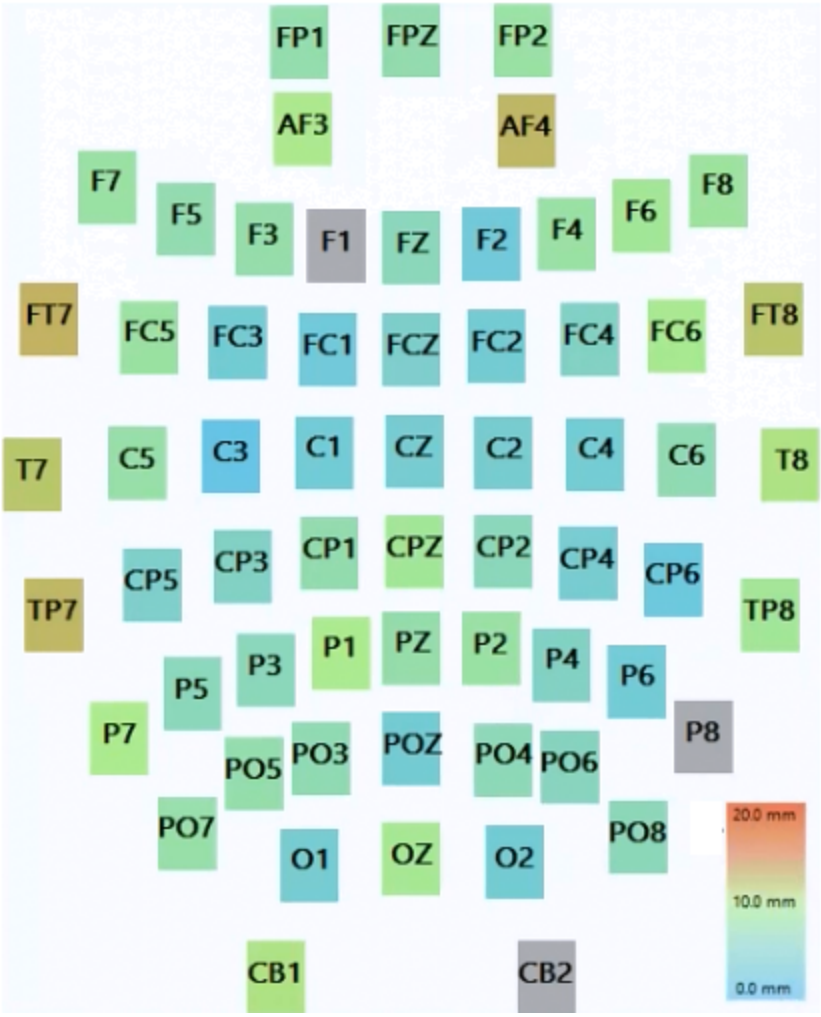
In the **Probe (guided)** mode, you can override the sequence that CURRY is asking for. *Double-click* on a desired electrode and it will flash red until you measure it with the Probe device.



Show Template. One way to determine if the results you get are correct or not is to enable the **Show Template** option. You will see the template points in dark gray, along with your measured points in blue. The template will not match your point cloud exactly, but it should be close.

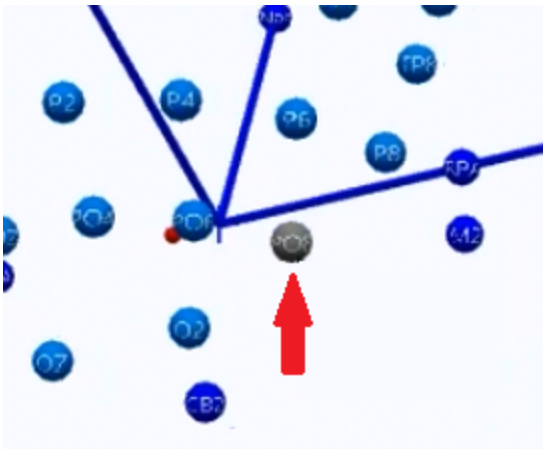


Show Distance to Template. The **Show Distance to Template** option (off by default, since the template you are using is not expected to match exactly the point cloud you are using) will show a colored display with a scale in millimeters, where the colors show the difference between the measured positions and the template. This can be useful if you are making a subsequent recording from the same subject using the same cap, and you want to make sure the cap is fitted as close as possible to the initial recording.



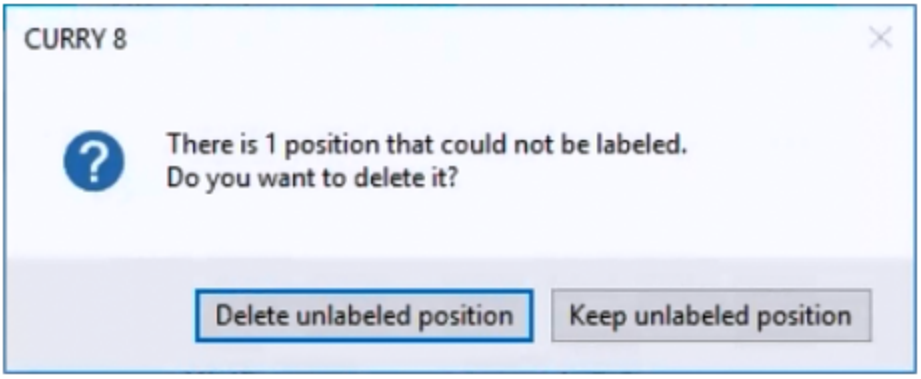
3D View follows Krios movement. When enabled, the 3D model follows the view of the camera, and this is usually the easiest way to view it. If you disable it, the point cloud will be fixed where you set it, and moving the camera will not move the point cloud. This can be useful with the Probe mode, since the Probe point can be seen moving against a fixed point cloud.

Interpolate missing positions. When enabled (default), missing positions will be seen anyway, in gray, in their interpolated positions.In the example below, PO8 has not been measured yet, but still appears in the point cloud. If you disable the option and perform label matching, it will not be seen.

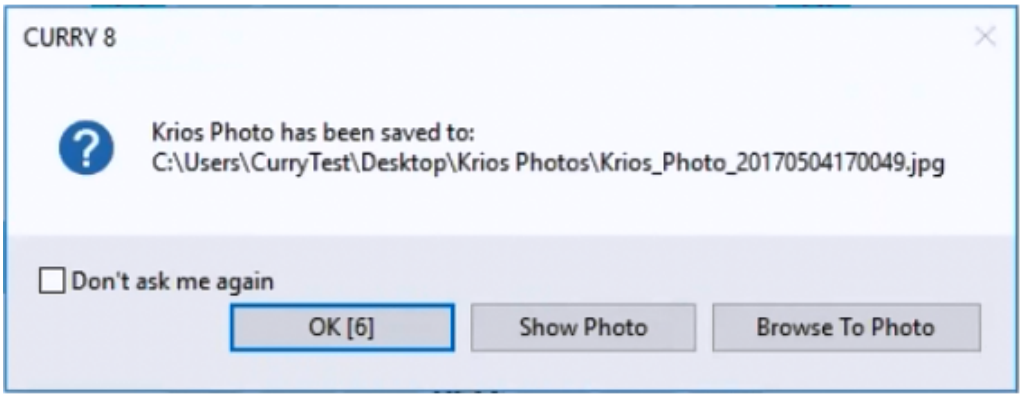


Always remove unlabeled points from result. If you have electrodes with markers yet are not measured, such as the Ground, and without a label, this option will keep from from being included in the result (default). (The Krios works best with the more points that it sees, and that is why the Ground has a marker also).

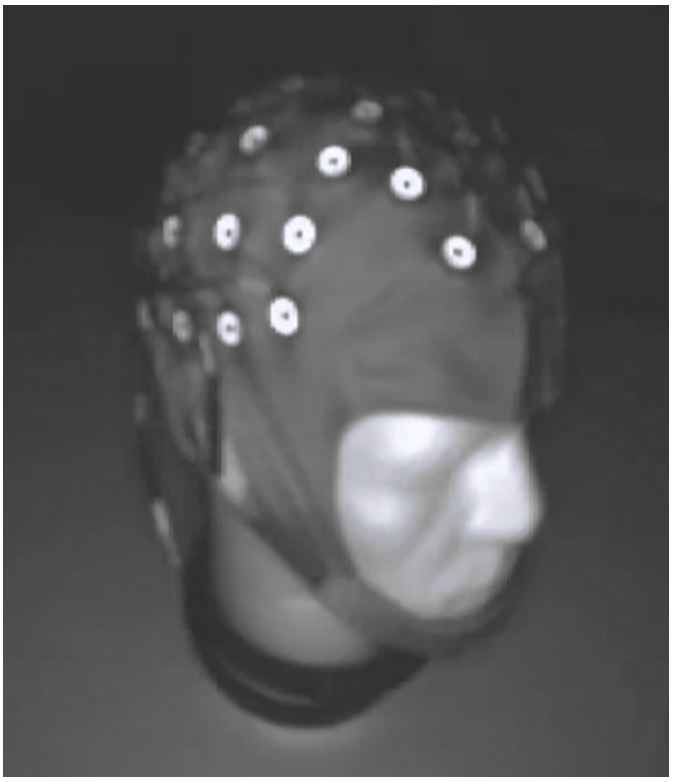
If you have a setup where you have additional markers on the skin (to measure other landmarks) or other places, and you do not want to lose those positions, you can uncheck the option. When you assign the labels Assign Labels, a dialog will appear asking if you want to Delete or Keep the unlabeled positions.



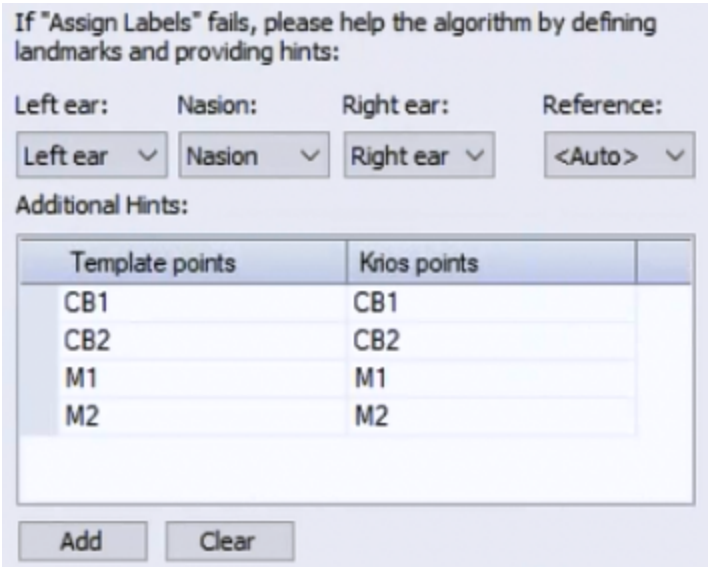
Camera. The Krios can be used as a camera by *double-tapping* **Button #2**. You will hear audio feedback when the image has been captured. This will take a little while.



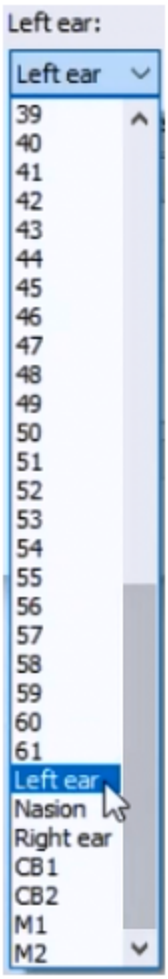
Afterwards, you may Show the Photo. This is be helpful if later on you need to see how a cap was placed.



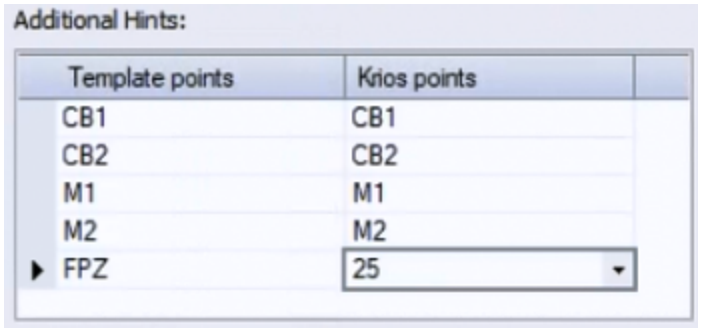
If Assign Labels fails, there is another method you can use. Normally, if you go through the steps above (Capture and Guided Probe modes), you will never need to use these fields. The selections will be made automatically in a way that makes sense, based on the positions you have already measured.



In the list, the items you see are the points that have been detected by the Krios camera (numbers), as well as the points that have been measured with the Probe tool (last 7 items). If, for example, you have a setup where the landmarks also have reflective markers, they will be seen as numbered sites. In that case you can go to the Nasion, for example, and select that number. The default is **<Auto>** so the landmarks will be detected automatically whenever possible. You will have these anyway if you go through the Guided Probe mode.



The **Additional Hints** fields are used in a similar way. Normally the Template points will match up with the Krios points. You can help the algorithm by adding additional "hints". In this case, the FPZ electrode is labeled 25 in the 3D View display. These are now matched together. When you do Label Matching again, this information will be used. The hints will not make any difference if Label Matching already worked successfully. So again, these fields are not needed unless the algorithm needs additional information to work properly.

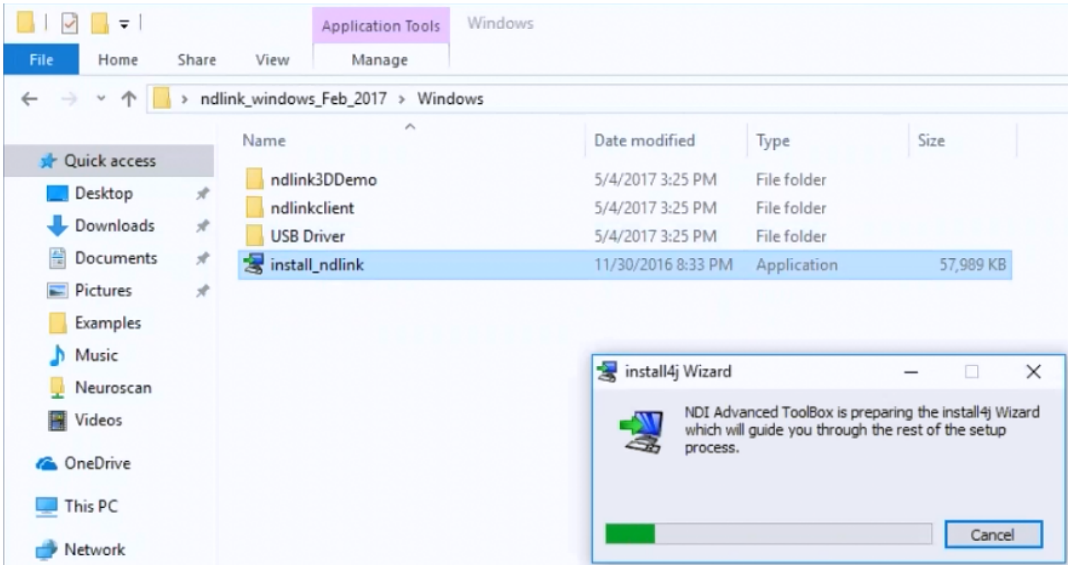


15.4.2.1 Installing the NDLink and NDI Toolbox

It is necessary to install the NDLink and NDI Toolbox software before using the Krios device. If you have not already done so, please see the steps below.

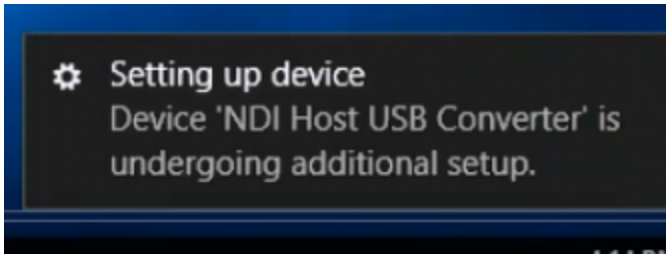
Do not connect the Krios to the computer until step 3.

1. Download and install the NDLink software. You will need to log in to the NDI web site, where you create a user name and password to access the downloads for whatever products you have purchased.

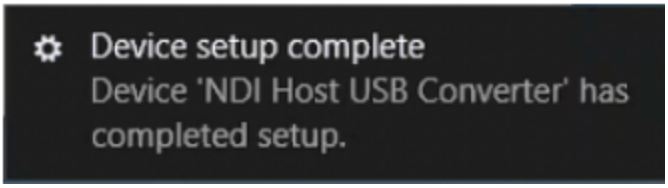


2. The NDI Toolbox is one of the products you will need to download. Go through the setup without changing any of the defaults.

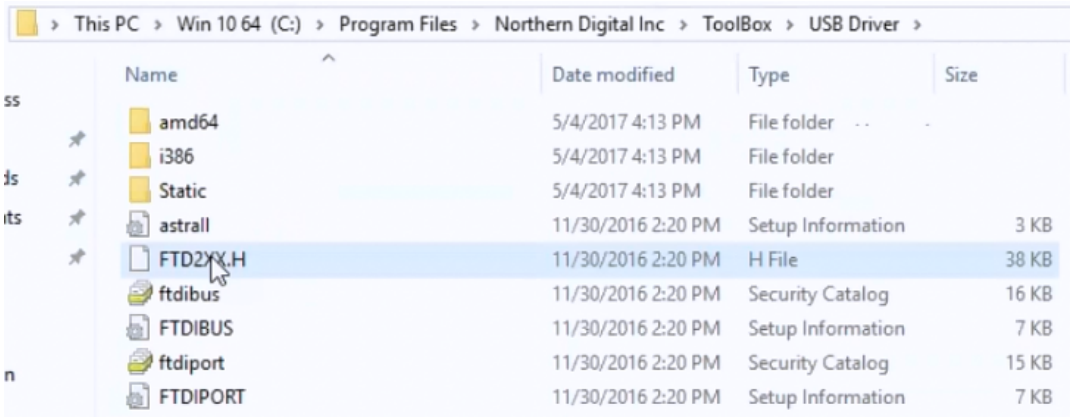
3. Now connect the USB cable from the Krios to the computer. You will see a notice that the device is being set up.



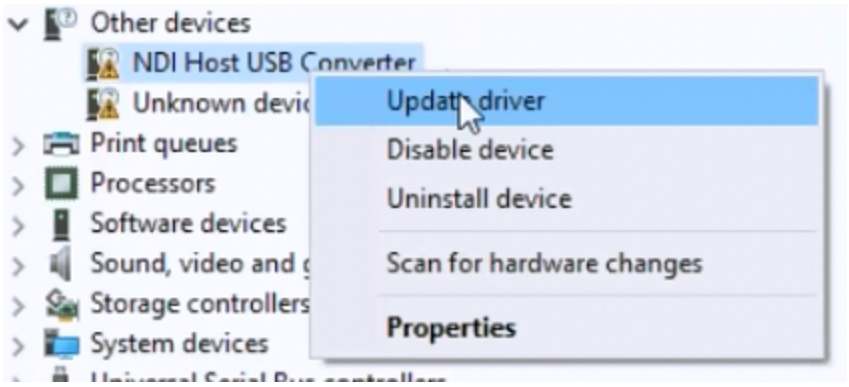
This will take a few moments, so wait until you see the completion message.



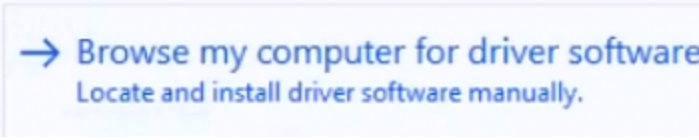
4. It is likely that the NDI drivers will not be installed automatically, so it will be necessary to do this step manually. The folder containing the drivers is as shown. The installer should at least put the drivers in the folder. Copy that path to the Clipboard.



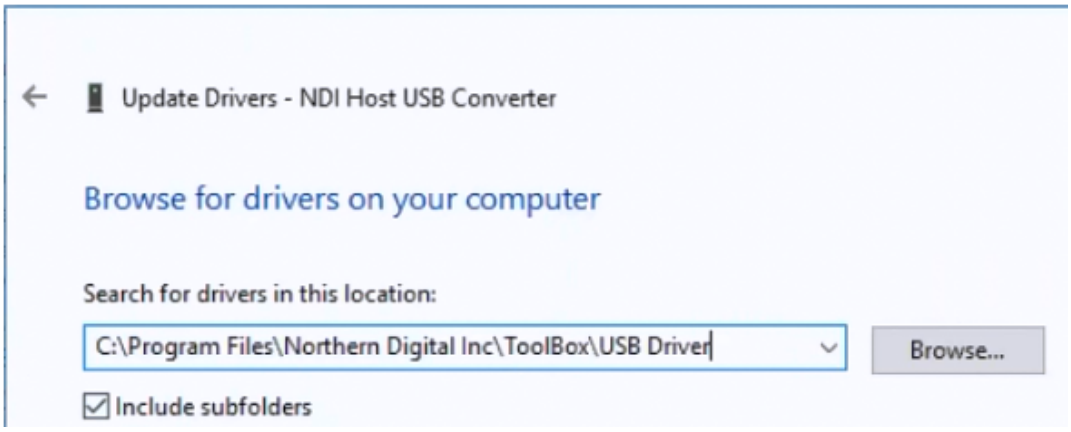
5. In the Device Manager, under Other devices, find the **NDI Host USB Converter**. *Right click* on it and select **Update driver**.



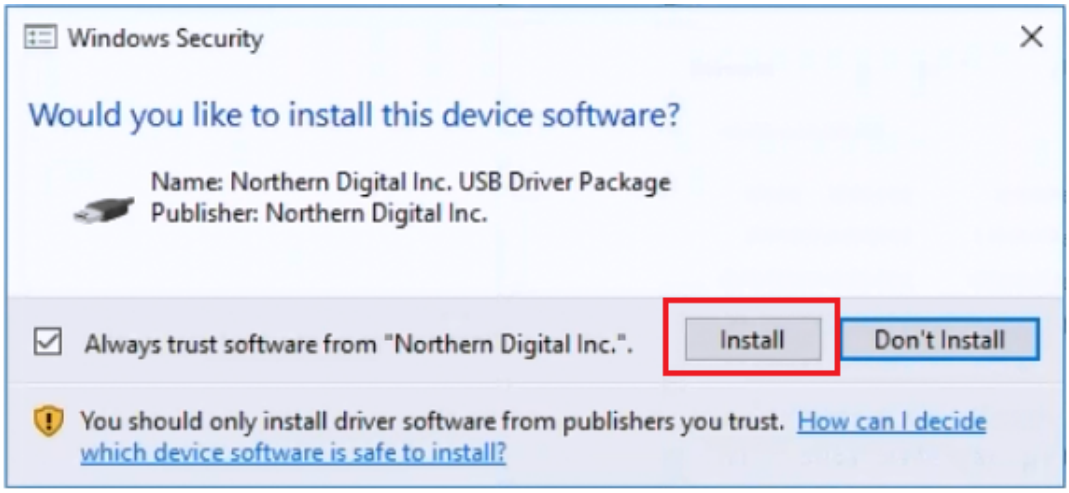
6. Select the option to Browse for the driver software.



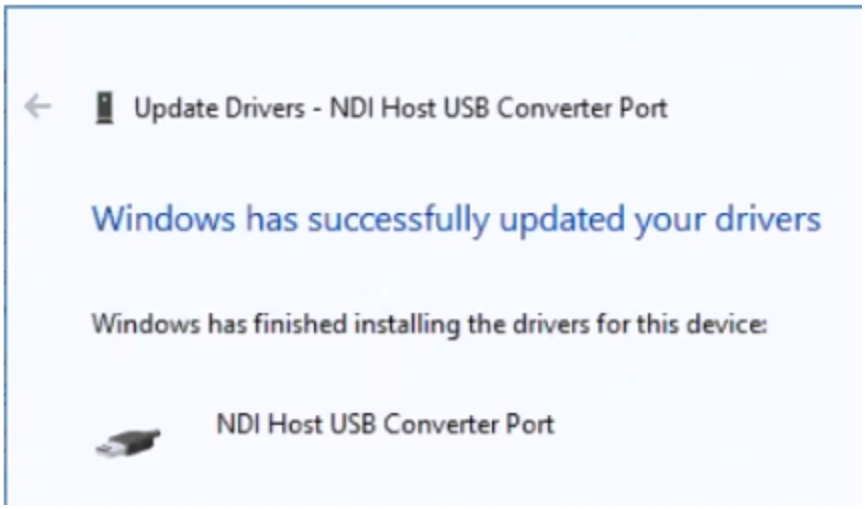
Paste the path from above into the dialog and click **Next**.



Install the software when prompted.

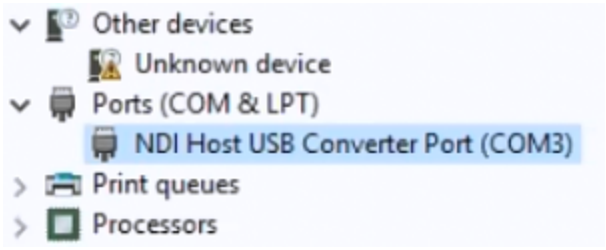


You should see that Windows has successfully installed the software.

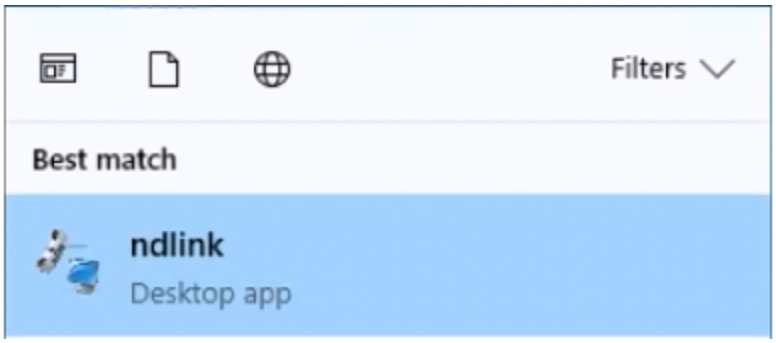


7. Repeat the above steps for the **USB Serial Port** under Other devices in the Device Manager. The **Unknown device** has nothing to do with the Krios and should be ignored.

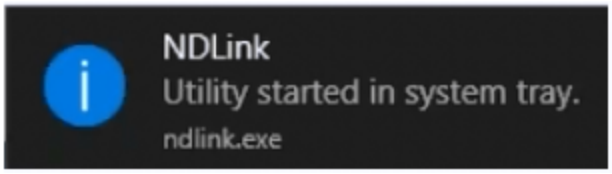
8. You should now see the **NDI Host USB Converter Port** in one of the COM ports. This is what you should see when the Krios drivers have been successfully installed.



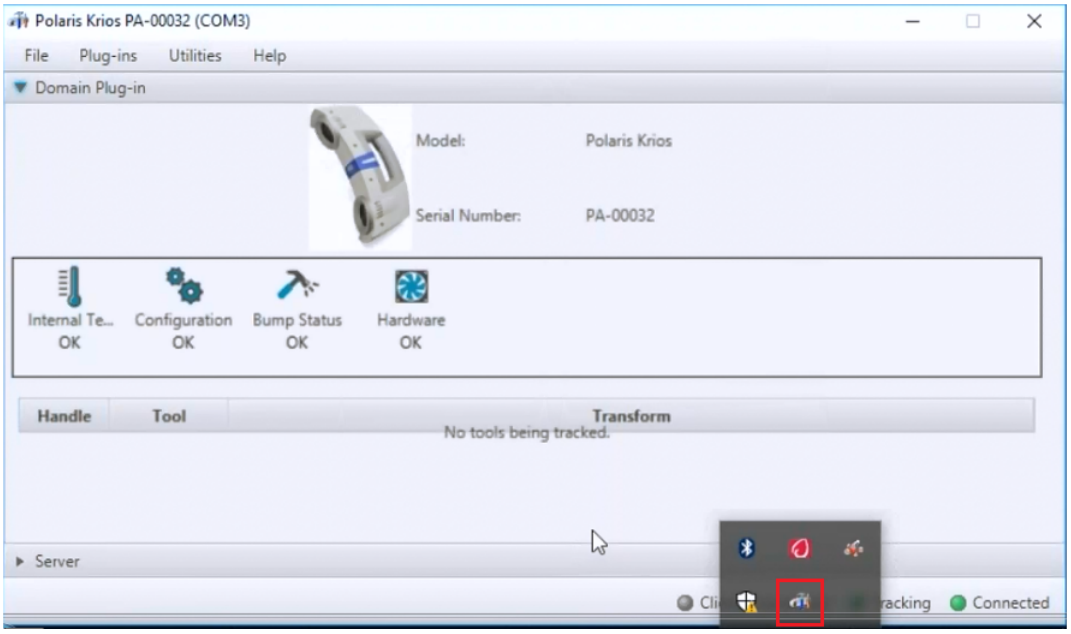
9. The program that you now want to run is the ndlink app on the Desktop.



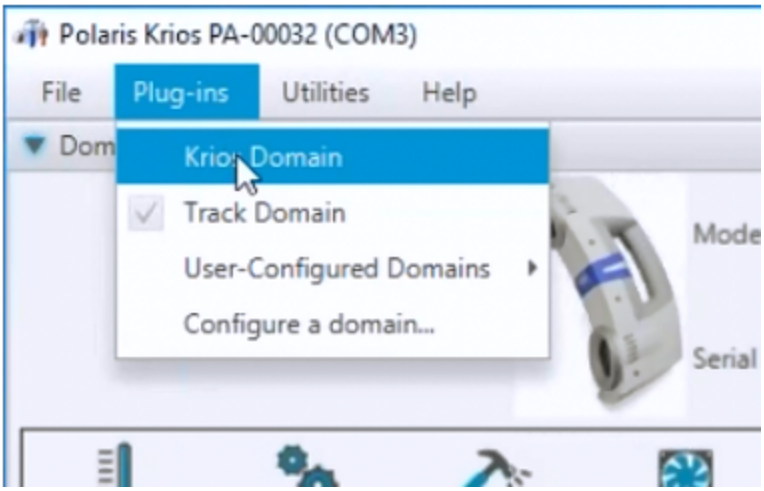
If you get a Firewall message, click **Allow Access**. You will see a message saying that NDLink has started, and you will hear a couple of beeps from the Krios device. The beeps means that NDLink has found the Krios device.



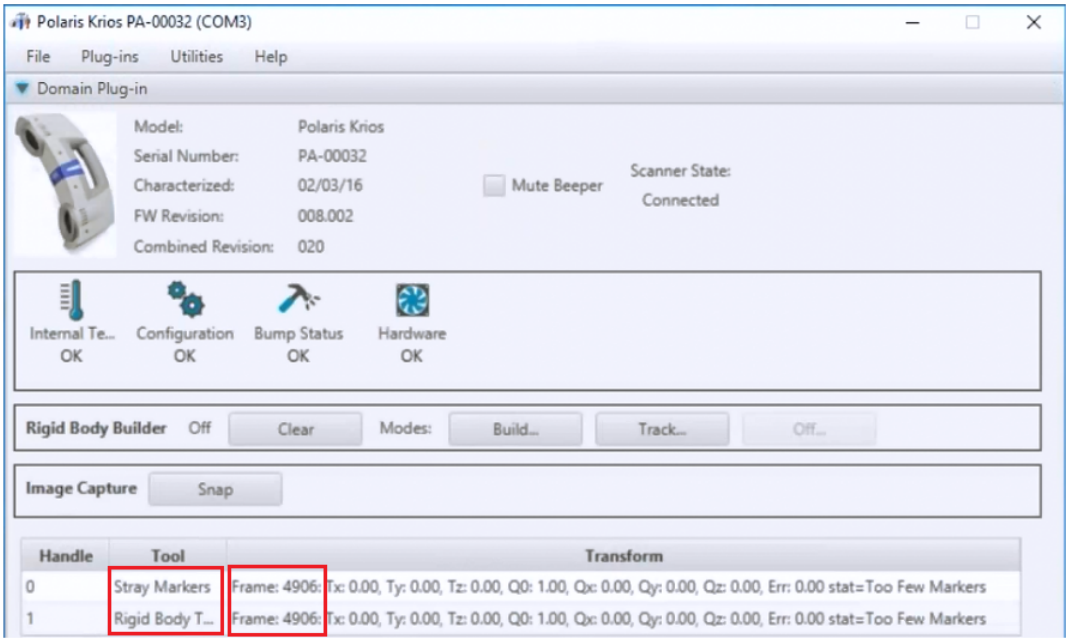
10. The Krios software is now running in the background. You will see its icon on the Taskbar, from which you may open the tool.



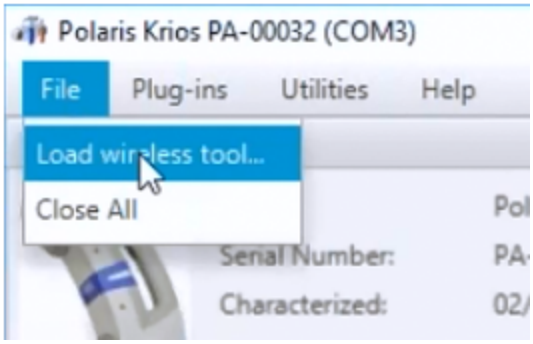
11. To get the Krios to work with CURRY, you must select the **Krios Domain Plug-in**.



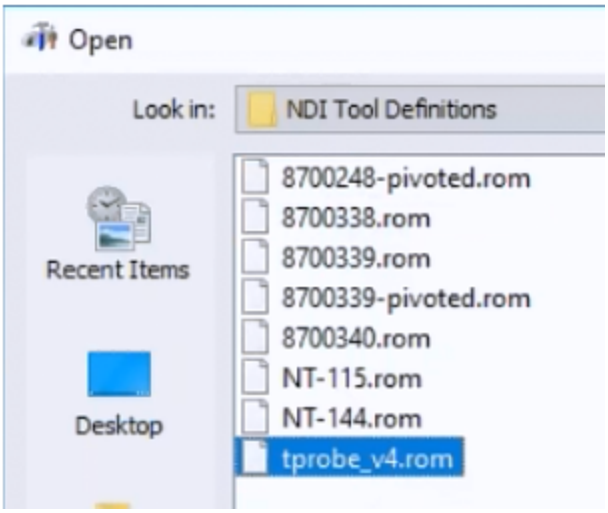
12. You will then see the two Tools, **Stray Markers** and the **Rigid Body Tool**, and you will see the **Frames** incrementing. The Rigid Body is the point cloud that will be created with the positions. Stray Markers appear intermittently before they are added to the Rigid Body.



13. The Probe Tool will be used, so it will be necessary to add it. Under **File**, select **Load wireless tool**.



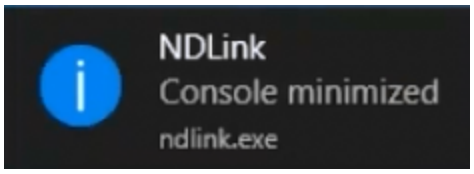
Select the indicated .rom file (*C:\Program Files\Neuroscan\Curry 8\Digitizer\NDI Tool Definitions\tprobe_v4.rom*):



It is likely that in future versions of CURRY this file will have a more user friendly name.

14. Now you see a third Tool appear (Unknown).

This is all that is needed in the NDLink tool. When you close the dialog you will see that it is still running in the background.



All of the settings you made have been saved, and will be present when you restart the computer. You will hear the two beeps again when the tool has restarted and found the Krios. You only have to set up the tool this one time.

Now when you start CURRY, it should find the Krios.

16 Functional Data File Import

The **Functional Data Parameter Wizard** has multiple functions, including setting data file parameters, channel parameters, and selecting files with sensor and landmark position data for co-registration. Its output parameter file (.dpa extension, replaces the previous .dap and .rs3 files) is read when the same data files are loaded subsequently.

Data Parameters

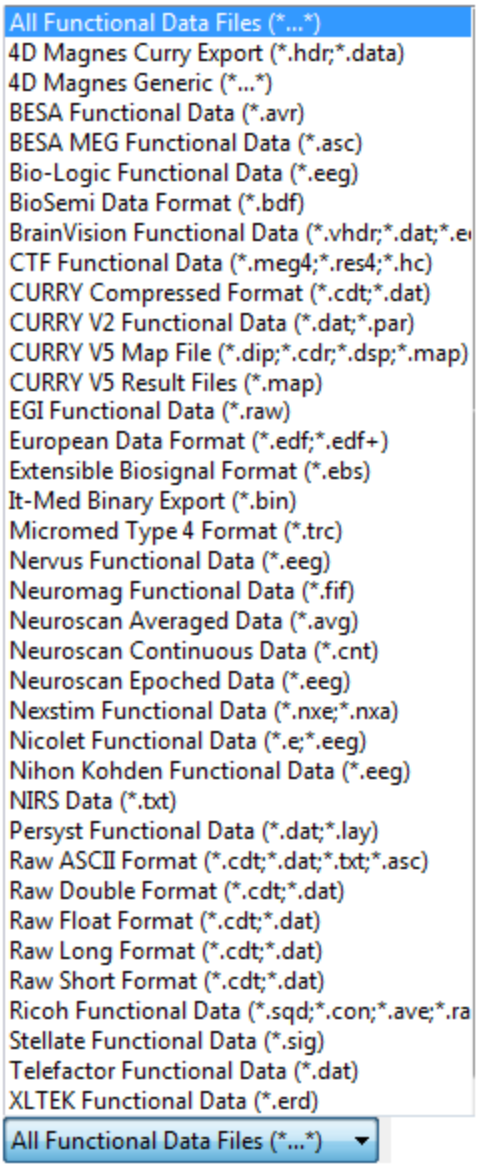
For each data file, CURRY needs to know what kind of data it contains. Each data acquisition system may be seen as a measuring device. Supported devices are:

- EEG. More than one group of EEG channels can be used.
- MEG. More than one group of MEG channels (e.g., magnetometers and gradiometers) can be used.
- Others. Channels that are not used for source reconstruction, e.g., ECG channels, trigger channels, or StereoEEG electrodes. These channels can still be used for display.

As CURRY supports multi-device data files, individual channels in a data file have to be assigned to devices (described in the **Functional Data Parameter Wizard** section below).

Autodetected Data Parameters

CURRY will read the displayed file formats. The functional data file may or may not contain all of the necessary information about the data and sensors, including sensor locations and landmarks. If the information is detected, the file will be displayed after *right clicking* and selecting **Open File**. If not, the **Functional Data Parameter Wizard** will appear and display the available information. You may then add the missing information - typically, sensor and landmark locations. When the wizard is finished, all of the information is written to the .dpa file. When the files are accessed the next time the data file is loaded, the .dpa file is seen as belonging to the data file, the information is detected, and the wizard will not open. To revert, *right click* on the data file and click **Delete CURRY 8 Parameter Files**, or invoke the wizard by clicking **Data Parameters**.

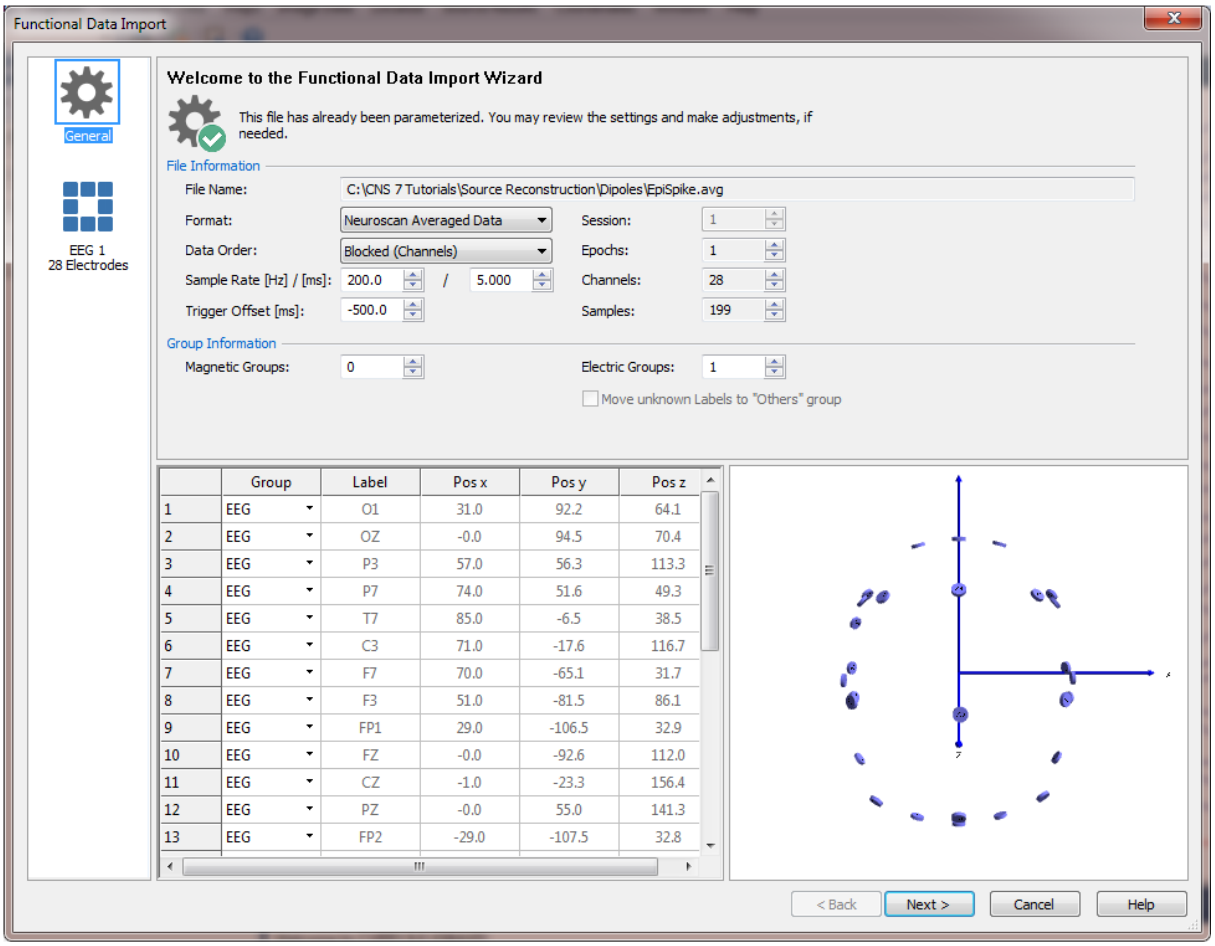


16.1 Functional Data Parameter Wizard

When you first load a data file, CURRY will look for its related parameter file. This contains sensor position information, labels, sampling rate, etc. CURRY creates this file (.dpa) after the Wizard has been completed. If no parameter file is found and if missing information is identified, you will see the Functional Data Import Wizard. This will guide you through the data import, as well as perform a co-registration with the image data, using [generally] the left and right pre-auricular points and the nasion, if available.

Note
Starting with CURRY 8, the single .dpa parameter file replaces the .dap and .rs3 files that were created in prior versions of CURRY.

The following screen shows a data file that has not been loaded before. CURRY will attempt to identify as much information as possible from the file contents. In this case, the file was recognized correctly as a Neuroscan Averaged Data file. If the format could not be autodetected, a drop-down list will be available. For raw data files, select **Raw ASCII Format** or **Raw Float Format** (**Raw Short**, **Raw Double**, etc., are supported as well).



File Information

File Name. The file name and originating folder are shown.

Format. The autodetected format of the file is displayed, where recognized.

Session. This is a feature that is used with some files, where each file can store multiple "sessions" with different channels, samples, and sampling rate.

Data Order. This is the way channels and samples are stored. **Measured (samples)** means that the file starts with measured data for all channels of the first sample, followed by all channels of the second sample, and so on. This is a typical way to store continuous files, because data are written as they come. **Blocked (channels)** means that (per Epoch) measured data for all samples of the first channel are followed by all samples of the second channel and so on. This is

typical for averaged files. The autodetected Data Order is displayed. If the sample order could not be autodetected, the drop-down list will be available.

Epochs. This is the number of epochs in the file. Epochs can be trials (in the case of evoked response data), or they can be a way to organize continuous data in a file of **Blocked** Data Order.

Sample Rate [Hz] / [ms]. This is the Sampling Rate in Hz (the inverse of the sample time), and the Sample Time in ms (the inverse of the sampling rate). While most acquisition systems require that all channels must have the same sampling rate for all channels, some systems, such as Stellate, let you use different sampling rates for some channels. In those cases, the fastest sampling rate is detected, and slower rates are upsampled to match the fastest rate.

Channels. This is the total number of channels in the data file.

Trigger Offset (ms). This is the Trigger Offset in ms. If you have a single or multiple sweep data file, with a prestimulus interval, the Trigger Offset will be the latency of the first data point (e.g., -500 ms).

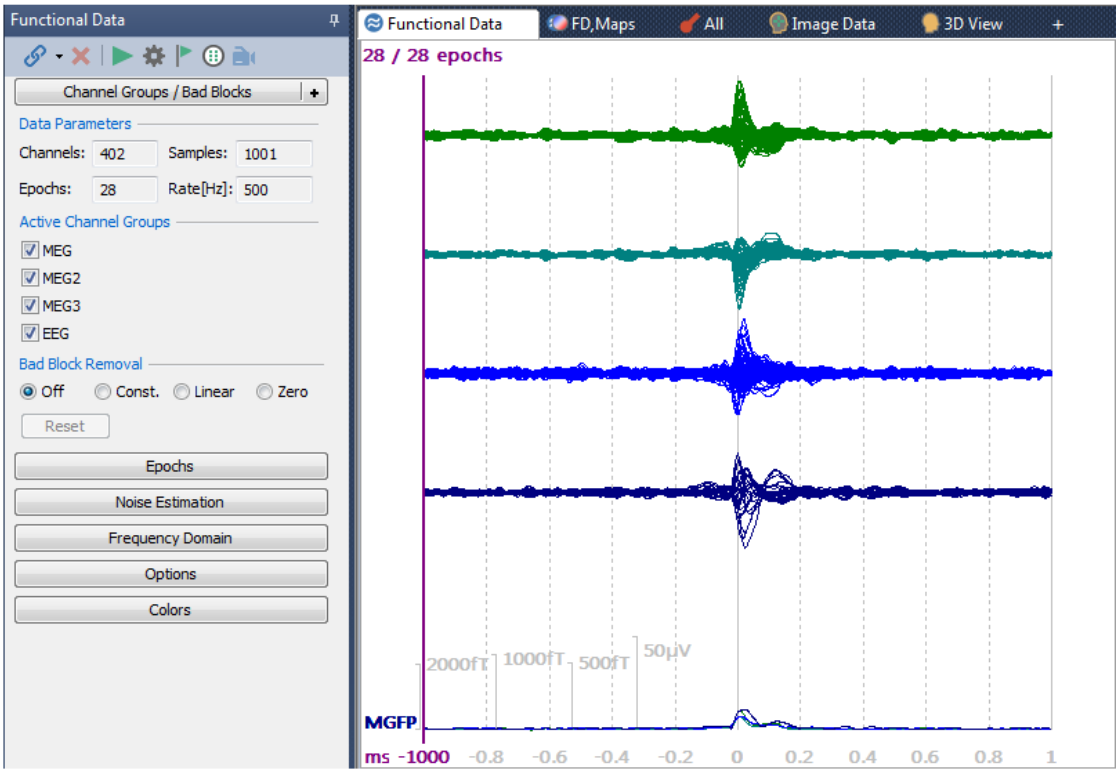
Samples. This is the number of samples per epoch/trial, or the total number in the continuous case.

Group Information
If the file has a combination of device groups, say, one Magnetic and two Electric groups, we would verify that they were detected automatically. You will see additional icons on the left. Each device will have another dialog screen for additional information.

Magnetic Groups. This is the number of MEG Groups (cryostats or groups of coils) in the file. For EEG data, this is **0**.

If you are importing Elekta MEG data, Curry divides the MEG data into three "channel groups", the first of which is magnetometers, followed by two sets of planar gradiometers. The last channel group is EEG. For source analysis, all active

channel groups are used, which includes the ability to combine EEG and MEG. Channel groups can be (de)selected in the user interface.



Electric Groups. If the data file contains electrical data, the number of Electric Groups used will be indicated. For EEG data, this is typically **1**.

The total number of channels in all devices must match the number of channels in the data file.

The sensors and landmarks can be selected per device. The device to be treated is displayed and can be changed by setting the desired device to 1 (or beyond if there is more than one), and the undesired device to 0.

Note
Only the common offsets and the common scaling factors for all of the channels in a device are directly accessible from the window. The calibration factors for each individual channel as well as the channel-to-channel crosstalk compensation matrix and the sensor coupling matrix needed for some MEG systems can only be modified by editing the .dpa file by hand (an extremely rare occurrence). File converters take care of crosstalk and scaling automatically.

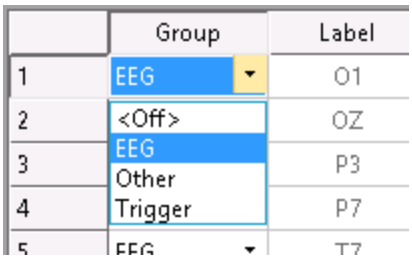
Care
When editing data parameters, make sure that *all* devices are specified. If the number of channels of the device that is selected for editing does not match the number of channels in the data file, look at the other devices as well.

Note

If the ordering of the channels in the data file is *not* Magnetic Sensors 1, 2, 3, Electrode Set 1, 2, Others, the .dpa file can be modified manually (using a text editor) to reflect the channel correspondences (an extremely rare occurrence). File converters take care of the channel ordering automatically.

Move unknown Labels to "Others" group. When enabled (default), channels that would not be detected via Label Matching are set as "Other" channels. "Other" channels are excluded from many of the operations in CURRY, where their inclusion would distort the results. If you look at the drop-down list in the Group column, you will see an "Other" option there as well. This allows you to set *any* channels as "Other" channels, regardless of whether they would be recognized via Label Matching.

Channel Information. Here, the channels as contained in the file can be reviewed, and the devices can be assigned, if necessary. With EEG data, for example, note that each channel can be designated as an **EEG** channel or an **Other** channel. Other channels are typically those that are recorded, but are not included in subsequent analyses. The artifact channels and the pulseometer channels are often designated as Other channels. Any bad channels that you wish to exclude completely may be set as Other channels. If you set them as **<Off>**, they will not be displayed (or even loaded) with the Functional Data at all. This can be a useful feature when you are trying to merge files with different channel counts.



Trigger is a special purpose selection when you have a dedicated channel that carries voltage triggers. If you are using STIM2, or other stimulus presentation software that uses TTL pulses for the triggers, you will not have a Trigger channel. When using the Trigger option, you can configure triggering parameters using the *triggers.cfg* file, found in the *...\Neuroscan\CURRY 8* folder. For more information and help with configuration, please contact *curry8help@neuroscan.com*.

```
#
# This file defines how to create events based on data in channels of type "Trigger"
# Trigger channels can be defined on the first page of Functional Data Parameters
#
# A file of this name is searched in the following folders, in the following order:
# functional data file folder, user folder, install folder
#
TRIGGERINFO START
   Bitmask          = 65535  # use this (16-bit) number to mask out trigger bits
   KeepGeneric      = 0      # if '1', keep "generic" events already contained in the functional data file
   PositiveFlanks   = 1      # if '1', react on positive flanks (0 -> 1)
   NegativeFlanks   = 0      # if '1', react on negative flanks (1 -> 0)
   BinaryMode       = 0      # if '1', generate event for each changing bit (e.g. a "3" will generate a "1" and a "2")
   GlobalOffset     = 0      # event type offset to add for all generated events (to prevent clashes with existing events)
   ChannelIncrement = 0      # event type increment after each processed channel (to prevent clashes between "Trigger" channels)
TRIGGERINFO END
```

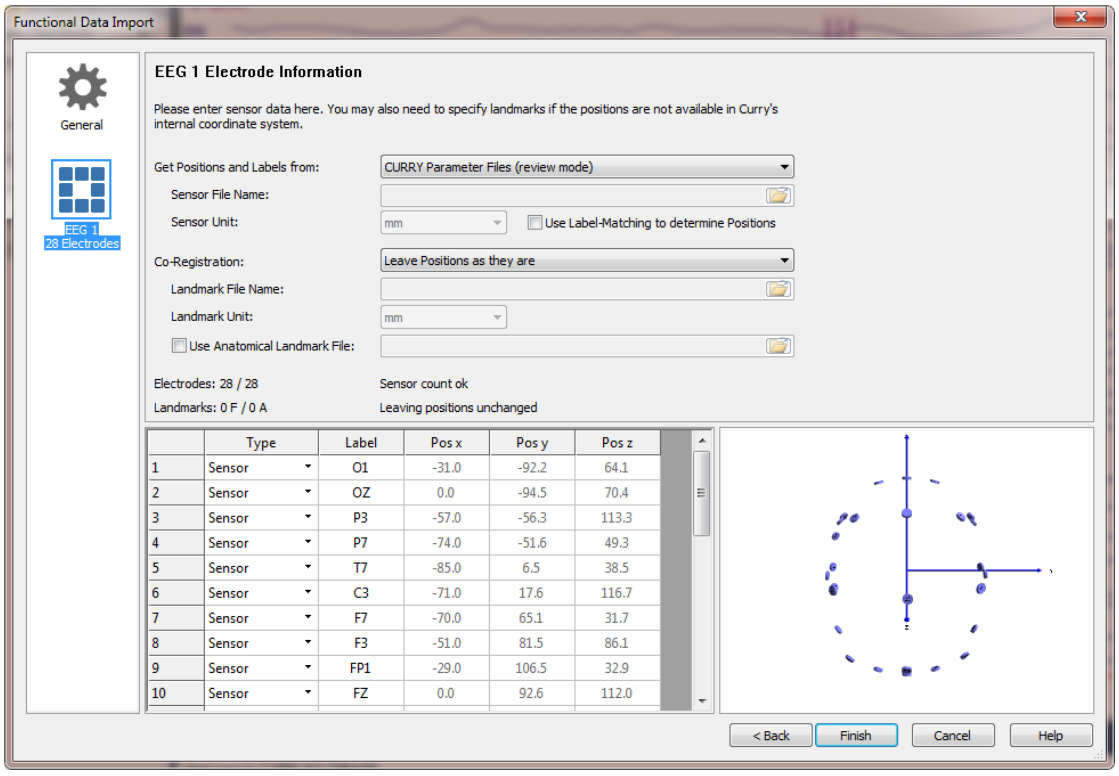
The labels and locations are for reference only; this information is edited in the next parameter page(s). Groups of controls can be selected (*Shift+mouse*) and changed

simultaneously by typing the first letter of one of the options (such as, typing E will change all selected channels to EEG).

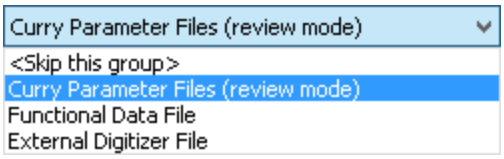
The XYZ fields will be empty if the data file contains no position information (as when the file is loaded for the first time, unless the information is contained in the data file itself).

	Group	Label	Pos x	Pos y	Pos z
1	EEG	O1	31.0	92.2	64.1
2	EEG	OZ	-0.0	94.5	70.4
3	EEG	P3	57.0	56.3	113.3
4	EEG	P7	74.0	51.6	49.3
5	EEG	T7	85.0	-6.5	38.5

Click the Next button to see the first, or only, Group (depending on the type of data file you are using). If you have multiple devices, you can select the device from the column of icons on the left (only one shown below). In the figure below, the data file has been loaded before, and thus the "review mode" text.



You will be asked first to supply the Position and Sensor Label information.



<Skip this group>. Select this option if you cannot locate a proper digitizer file. All positions become invalid and are set to 0.

Curry Parameter Files (review mode). If the file has been loaded before and the parameter files have been written, you may select this option to review the settings.

Functional Data File. In some cases the position and label information is contained in the data file itself (especially with MEG file formats).

External Digitizer File. In some cases the position and label information is contained in a separate file created when you digitized the positions (such as, the .3dd file from the Scan software). For example, if you have a 128 channel recording from Scan, with numbers for the labels, you will have received a Quik-Cap CD that has the corresponding .3dd file, or you may have digitized your own positions. After selecting the External Digitizer File option, the **Sensor File Name** field will become active. Click the **Browse** button to select the digitizer file. At that point there is a lot of information that should appear. If the digitizer file is in an unknown format, the **Digitizer File Wizard** will appear.

1. You should verify that the **Sensor Units** are correct (**mm**, in this case).

2. In the **Co-Registration** field, the **Use Landmarks from Sensor File** was selected, since the functional landmarks were identified in the sensor file.

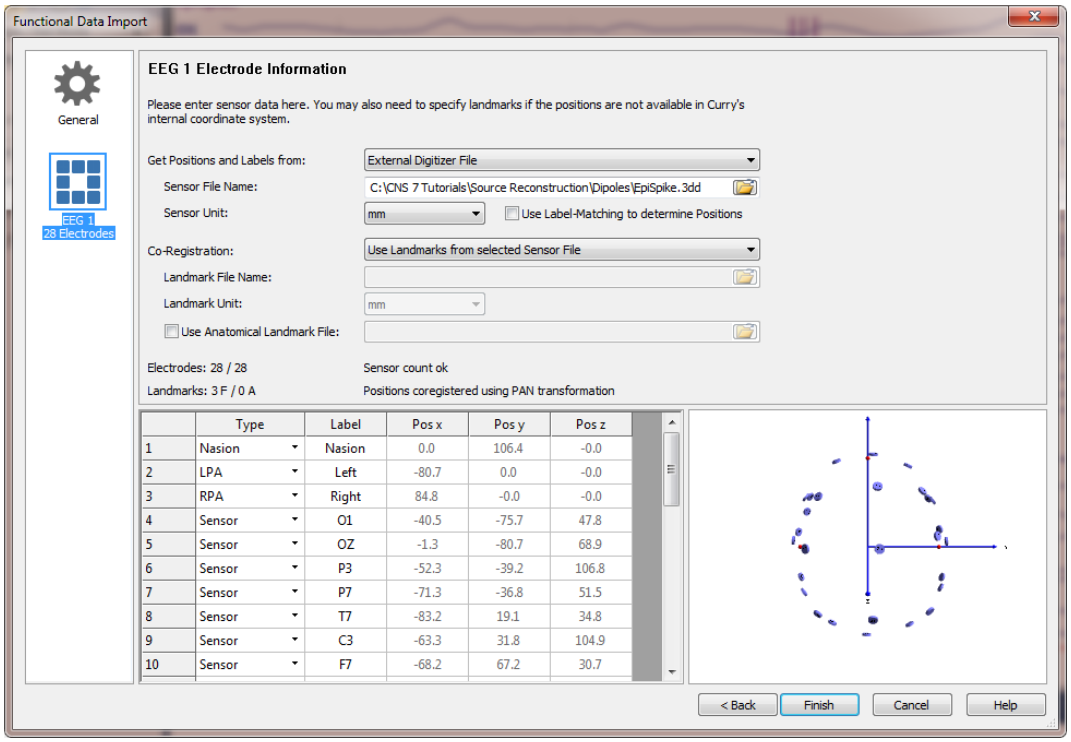
3. **28** of **28** electrodes were recognized, and there is a comment that the **Sensor count** is **ok**. This is the number of sensors identified in the Sensor and Landmark List, vs. the number of sensor in the device. If these numbers do not match, the missing trailing positions are filled with zeros.

4. The number of Functional and Anatomical landmarks identified in the Sensor and Landmark List and the anatomical localization file is shown. If landmarks are to be used, at least three of them are needed. Co-Registration between the functional (measured with the digitizer) landmarks and the "known" anatomical (MRI) landmarks was successful using the PAN (Pre-Auricular and Nasion) transformation. A PAN transformation is almost always used. The advantage is that you have to specify the landmarks only for the functional data, since the anatomical side is clear (the program "knows" where the Nasion, LPA, and RPA are). In contrast is the SVD transformation, where 3 (or more) arbitrary functional landmarks plus the same number of anatomical landmarks are needed for co-registering the data sets. PAN transformation uses just the three PAN functional landmarks - be sure to use the same "**PAN**" definition as CURRY uses.

The MRI data had already been imported in this example, and the anatomical landmarks were identified as part of the image data import (discussed in the Image Data Wizard below). See the **Additional Messages** section below for other examples.

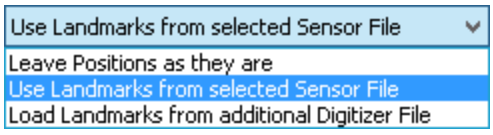
5. The XYZ coordinates for the landmarks and the electrodes were added to the table.

6. The display in the lower right displays the electrodes and the landmarks (red). Note that you can use the *mouse wheel* to enlarge/reduce the display, you can use *Shift+left mouse* to reposition the display, drag the display to change the viewing position, and *right click* in the display to select viewing options.



Use Label-Matching to Determine Electrode Positions indicates that sensor locations will be determined based on the sensor labels. Not enabled indicates that the sensor file contains sensor locations in CURRY coordinates. This is the case if the data file was written by CURRY (see **Leave Position as they are**). This option is also used if sensor locations are not available at all and the data shall only be viewed as traces.

Co-Registration. These fields determine how the sensor information is used to yield sensor locations in CURRY coordinates.



Leave Positions as they are. This option (no transformation / shift) is used when (re)loading files that come from Localize, i.e., when the positions are already in the internal CURRY coordinate system.

Note
If the sensor file *is* a digitizer file, do not use this option but the next one.

Use Landmarks from selected Sensor File indicates that the sensor file (defined above) contains not only sensor locations, but also landmark locations. These landmarks appear in the Sensor and Landmark List, and if these are the **Nasion**, **PAL**, and **PAR**, this can be specified.

Use Landmarks from additional Digitizer File indicates that the landmarks stem from a different file than the sensor file. This digitizer file can be selected using the File Open button  . Select the proper Landmark Unit (mm, cm, inches, etc.). (This is only used for some legacy CURRY V2 file formats).

Sensor Positions from Sensor Labels

For EEG data files that contain sensor labels but no sensor locations, labels are compared with an extensive list of predefined sensor locations that fit to the warped MRI dataset. These locations are used in the initial montage. They can, of course, be overridden using a digitizer file.

The following electrode labels are recognized (based on: Oostenveld R and Praamstra P. The five percent electrode system for high-resolution EEG and ERP measurements. Clinical Neurophysiology 112 (2001) 713-719):

AFp10h	FCC2h	AF10h	FFC6	PPO6	FC6h	AF5	PO8	I1
AFF10h	FCC4h	FT10h	FFT8	PPO8	FT8h	AF3	F9h	F9
FFT10h	FCC6h	TP10h	FTT9	POO9	OI1h	AF1	F7h	F7
FTT10h	FTT8h	PO10h	FTT7	POO7	OI2h	AFz	F5h	F5
TTP10h	TTP9h	AFp10	FCC5	POO5	Fp1h	AF2	F3h	F3
TPP10h	TTP7h	AFF10	FCC3	POO3	Fp2h	AF4	F1h	F1
PPO10h	CCP5h	FFT10	FCC1	POO1	AF9h	AF6	F2h	Fz
POO10h	CCP3h	FTT10	FCCz	POOz	AF7h	AF8	F4h	F2
AFp9h	CCP1h	TTP10	FCC2	POO2	AF5h	F10	F6h	F4
AFp7h	CCP2h	TPP10	FCC4	POO4	AF3h	FT9	F8h	F6
AFp5h	CCP4h	PPO10	FCC6	POO6	AF1h	FT7	T9h	F8
AFp3h	CCP6h	POO10	FTT8	POO8	AF2h	FC5	T7h	T9
AFp1h	TTP8h	AFp9	TTP9	P10h	AF4h	FC3	C5h	T7 (T3)
AFp2h	TPP9h	AFp7	TTP7	PO9h	AF6h	FC1	C3h	C5
AFp4h	TPP7h	AFp5	CCP5	PO7h	AF8h	FCz	C1h	C3
AFp6h	CPP5h	AFp3	CCP3	PO5h	PO10	FC2	C2h	C1
AFp8h	CPP3h	AFp1	CCP1	PO3h	TP10	FC4	C4h	Cz
AFF9h	CPP1h	AFpz	CCPz	PO1h	FT10	FC6	C6h	C2
AFF7h	CPP2h	AFp2	CCP2	PO2h	AF10	FT8	T8h	C4
AFF5h	CPP4h	AFp4	CCP4	PO4h	TP11	T10	P9h	C6
AFF3h	CPP6h	AFp6	CCP6	PO6h	TP12	TP9	P7h	T8 (T4)
AFF1h	TPP8h	AFp8	TTP8	PO8h	FT11	TP7	P5h	P9
AFF2h	PPO9h	AFF9	TPP9	T10h	FT12	CP5	P3h	P7 (T5)
AFF4h	PPO7h	AFF7	TPP7	TP9h	HEOG	CP3	P1h	P5
AFF6h	PPO5h	AFF5	CPP5	TP7h	VEOG	CP1	P2h	P3
AFF8h	PPO3h	AFF3	CPP3	CP5h	SP1	CPz	P4h	P1
FFT9h	PPO1h	AFF1	CPP1	CP3h	SP2	CP2	P6h	Pz
FFT7h	PPO2h	AFFz	CPPz	CP1h	F11	CP4	P8h	P2
FFC5h	PPO4h	AFF2	CPP2	CP2h	F12	CP6	O1h	P4
FFC3h	PPO6h	AFF4	CPP4	CP4h	T11 (MN1)	TP8	O2h	P6
FFC1h	PPO8h	AFF6	CPP6	CP6h	T12 (MN2)	P10	I1h	P8 (T6)
FFC2h	POO9h	AFF8	TPP8	TP8h	P11	PO9	I2h	O1
FFC4h	POO7h	FFT9	PPO9	F10h	P12	PO7	OI1	Oz
FFC6h	POO5h	FFT7	PPO7	FT9h	CB1	PO5	OIz	O2
FFT8h	POO3h	FFC5	PPO5	FT7h	CB2	PO3	OI2	M1
FTT9h	POO1h	FFC3	PPO3	FC5h	Fp1	PO1	LPA (PAL)	M2
FTT7h	POO2h	FFC1	PPO1	FC3h	Fpz	POz	RPA (PAR)	A1
FCC5h	POO4h	FFCz	PPOz	FC1h	Fp2	PO2	Nz (NAS)	A2
FCC3h	POO6h	FFC2	PPO2	FC2h	AF9	PO4	Iz (INI)	T1
FCC1h	POO8h	FFC4	PPO4	FC4h	AF7	PO6	I2	T2

The **Use Anatomical Landmark File** field is used, when needed, to retrieve a file containing the anatomical landmarks (e.g., .pom file) for the MR data. If landmarks (from the sensor file or an additional digitizer file) are present, and these landmarks *cannot* be identified as **Nasion**, **PAL**, and **PAR** in the Sensor and Landmark List below, you will need to add an Anatomical Localization file containing the locations of the landmarks in CURRY coordinates.

Note

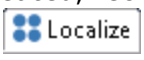
If this file does *not yet* exist, do not select this checkbox and finish the Wizard anyway. Then, after defining the image data set to be used, open the Localize window and use **Create and Edit Anatomical Localization** and **Save and Use Anatomical Localization** to generate and use anatomical landmarks.

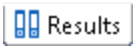
To summarize:

- If you have digitized the PAL, PAR and Nasion landmarks, and are using the averaged, or warped, MR data set, you do **not** need to specify an

Anatomical Landmark file. The anatomical landmarks are already contained within CURRY.

- If you have digitized the PAL, PAR and Nasion landmarks, and are using a subject's MR data, the Anatomical Landmarks are measured during the data loading process. These are retained in the parameter file, and you do **not** need to specify a .pom file in the Data parameters.

- If you have digitized other landmarks than PAL, PAR and Nasion, or if you have created, recreated, or modified an individual's Anatomical Landmarks via the 

display, you **do** need to use that .pom file for co-registration. If the landmarks are incompletely defined in the middle table (such as, it has only "Landmarks" and no labels), you **do** need to use a .pom file for co-registration. You can insert the pom file into the Image Data folder in the Database, you can retrieve it in the Functional Data Parameters Wizard, or you can select **Save and Use As Image Data Landmarks**  from the **Localize** panel under 

(after determining the positions).

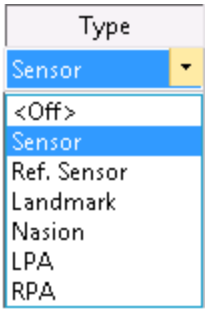
 **Note**
Whenever you select an option for the Sensor, Co-Registration, or Anatomical Landmarks options you should examine the effects on the preview display, and the message regarding co-registration. Note also the 

button. If it is grayed out, that means that there is a problem. If necessary, go **Back**, and make any corrections.

Sensor and Landmark List. All sensors need to be identified here, i.e., their **Type** must be set to **Sensor** or the correct **Landmark**. The number of sensors identified must match the number of sensors in the device, which stems from the channel list in the first page and can be seen in the Sensors field below. **Landmarks** can be used or switched **Off** (if they are to be disregarded). At least three landmarks are necessary for successful co-registration. If exactly three landmarks are used, and these are **Nasion**, **PAL**, and **PAR**, no further co-registration information is necessary. If this is not the case, an anatomical localization file is needed (see above).

	Type	Label	Pos x	Pos y	Pos z
1	Nasion	Nasion	0.0	106.4	-0.0
2	LPA	Left	-80.7	0.0	-0.0
3	RPA	Right	84.8	-0.0	-0.0
4	Sensor	O1	-40.5	-75.7	47.8
5	Sensor	OZ	-1.3	-80.7	68.9
6	Sensor	P3	-52.3	-39.2	106.8
7	Sensor	P7	-71.3	-36.8	51.5
8	Sensor	T7	-83.2	19.1	34.8
9	Sensor	C3	-63.3	31.8	104.9
10	Sensor	F7	-68.2	67.2	30.7

Make sure that the Labels, Type and Landmark lines are correct. Check the channels throughout the list and verify that the Type is correct. Turn Off channels that are not contained in your data file. Make sure the Sensors and Landmarks are correctly indicated. The Reference Sensor will append one extra "null" channel (increases the SNR). For example, if you have a data file that has 64 channels in it, and you load 65 electrode positions into the wizard. Select the Reference sensor, and you will see 65 ("64 + 1") channels on the screen. The reference channel contains just zeros, but this in fact adds information to your data, since "0 µV" is information.



Note
Bad channels must not be deselected (turned off) here; otherwise, the number of sensors will not match the numbers of channels, and you will not be able to continue.

Additional Messages
The message section mentioned above provides information regarding the outcome of the PAN or SVD transformation. If you are not using Anatomical Landmarks (that is, a separate .pom file), a PAN transformation is used for co-registration. If you are using Anatomical Landmarks (from a retrieved .pom file), an SVD transformation is used.

In the case of the PAN transformation, the statement does not mean that the anatomical landmarks, measured when the MR data were loaded, are being ignored, rather, it means you do not need a separate .pom file.

If instead you see other messages, this means that sensor position data were not detected for some or all sensors. You should provide the information if available. There are several ways to do this.

1. If you have a Neuroscan SCAN system with a digitizer, you will have created a .3dd file in 3DSpaceDx. This contains the functional landmarks and electrode positions. You can merge that information with the data file in EDIT. Retrieve the data file, *right click* to see the **Load 3D Electrode positions** option, and save the file with the information in it. CURRY will autodetect the information when you enter the Data Parameters.

2. You can load the .3dd file directly into the Study in the Database, or in the Data Parameters. Use the Browse button for the **Sensors** field to retrieve the .3dd file from the same subject as the data file. Generally, this step will result in a successful PAN transformation (provided there are valid PAN landmarks in the .3dd file), and you can continue.

3. With EEG and MEG data from other sources, there may be additional files that contain the electrode labels, the sensor positions, and the landmarks. These were reviewed above. Use the Browse buttons  to load the files in their respective fields.

4. All sensors with unknown positions may be assigned to the "Other" group (in the previous Parameter File Information screen). MEG channels (file formats with multiple MEG groups), however, cannot be "re-grouped". This is generally not an issue, since those files always provide valid coil positions.

The example above used electric data; the display for magnetic data is very similar.

When you have all the correct information entered, click the 

button to complete the import. The parameters are written to the generic parameter file (.dpa). This file will later be read along with the functional data file, overriding information from the file itself.

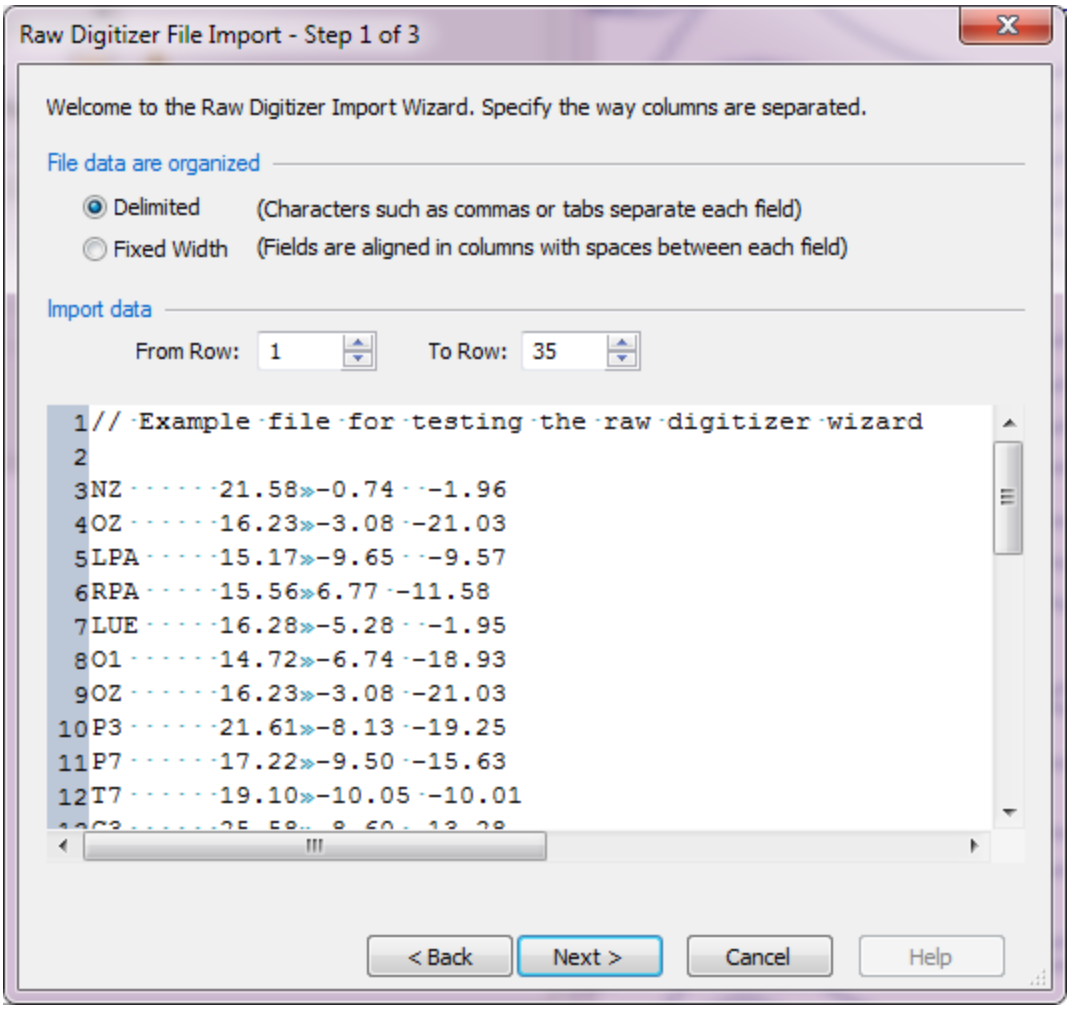
Parameter files. The Parameter file is a text files created by CURRY (.dpa) containing all of the parameters for the particular file. The .dpa file is created in the last step. When a file is opened subsequently, the .dpa file is read, overriding information from the file itself.

16.2 Digitizer File Wizard

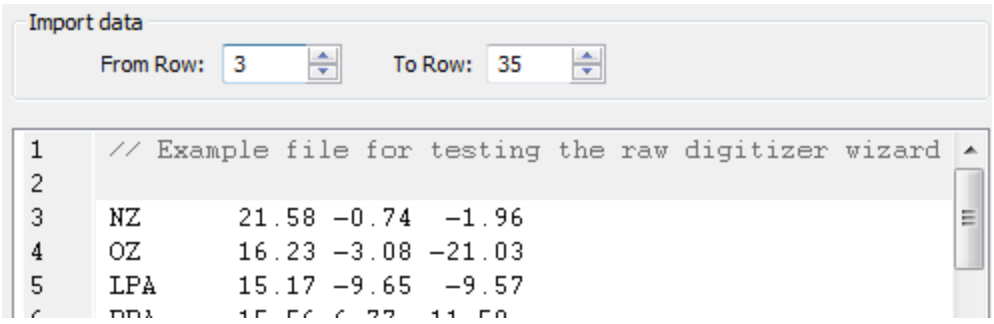
If CURRY is unable to recognize a digitizer file you have retrieved, you will see the **Digitizer File Import** screen appear.

Step 1. Select the option describing how the data in the file are organized: **Delimited** or **Fixed width**. Then select the range of rows that you wish to import. Verify the information in the lines of text, then click **Next**.

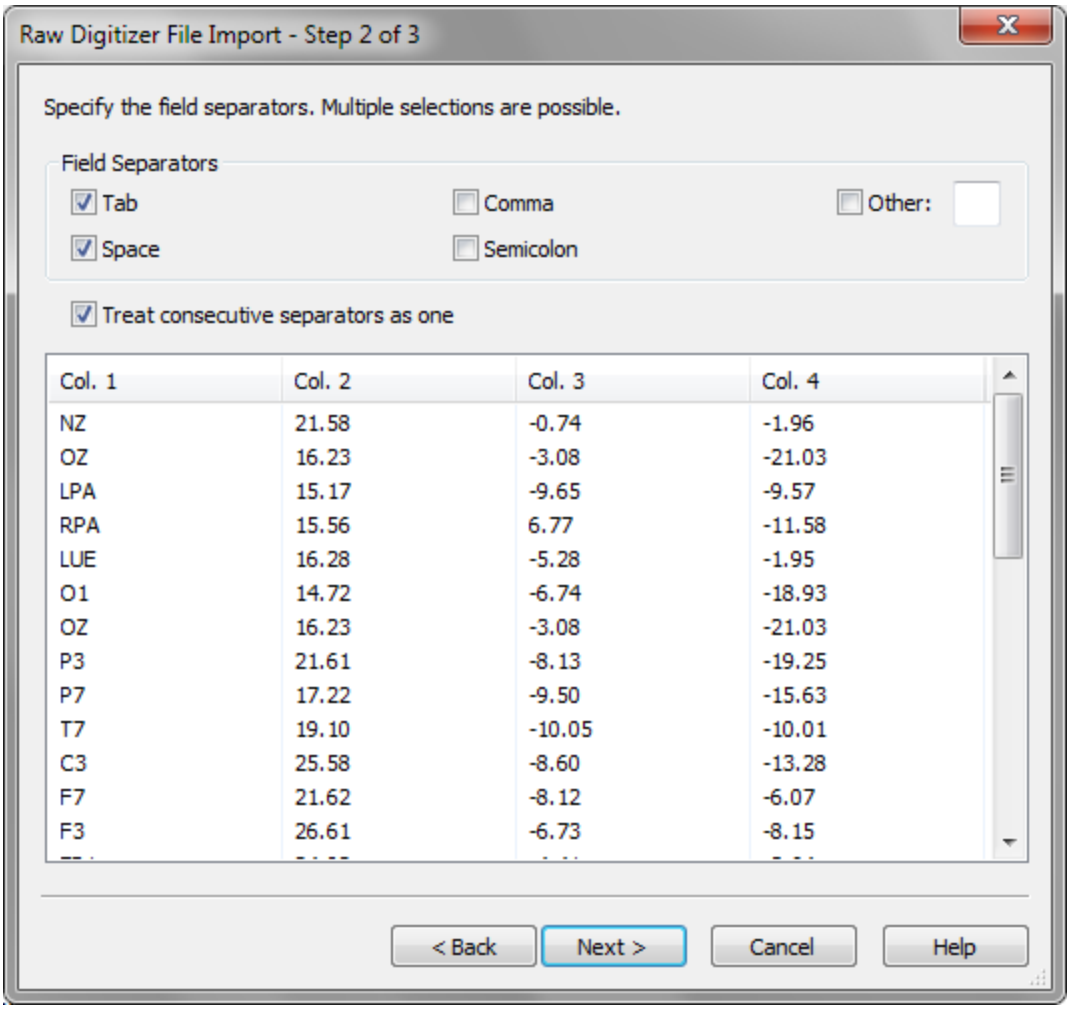
Delimited should be selected if columns are separated by characters such as commas or whitespace. This is the default. An example of a **Fixed Width** type file is shown, where all rows are selected.



In **Fixed width** mode, it is assumed that each column has the same width, and the gaps between columns are filled with whitespace. This option may be useful if labels consist of more than one word. Some files have information in the header that uses the first few lines. You can delete those lines by setting **From Row** to the first data line.



Step 2. If you selected the **Delimited** option, you will see the following dialog screen. Select the delimiters that separate the columns on this page.

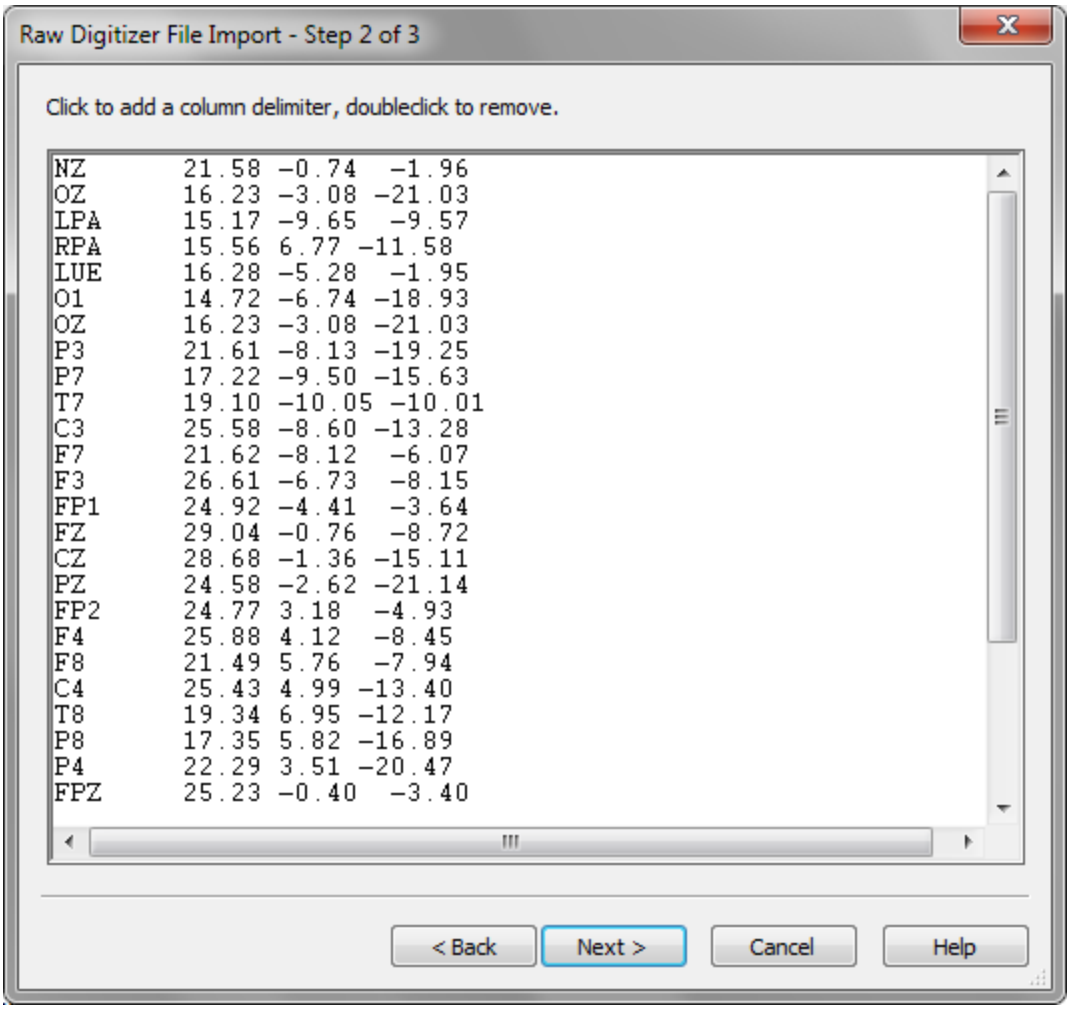


Field Separators. These are the types of non-exclusive definitions of tokens (i.e., separators) that separate each column. Available are **Tab**, **Space**, **Comma**, **Semicolon**, and **Other**, for user-defined token(s).

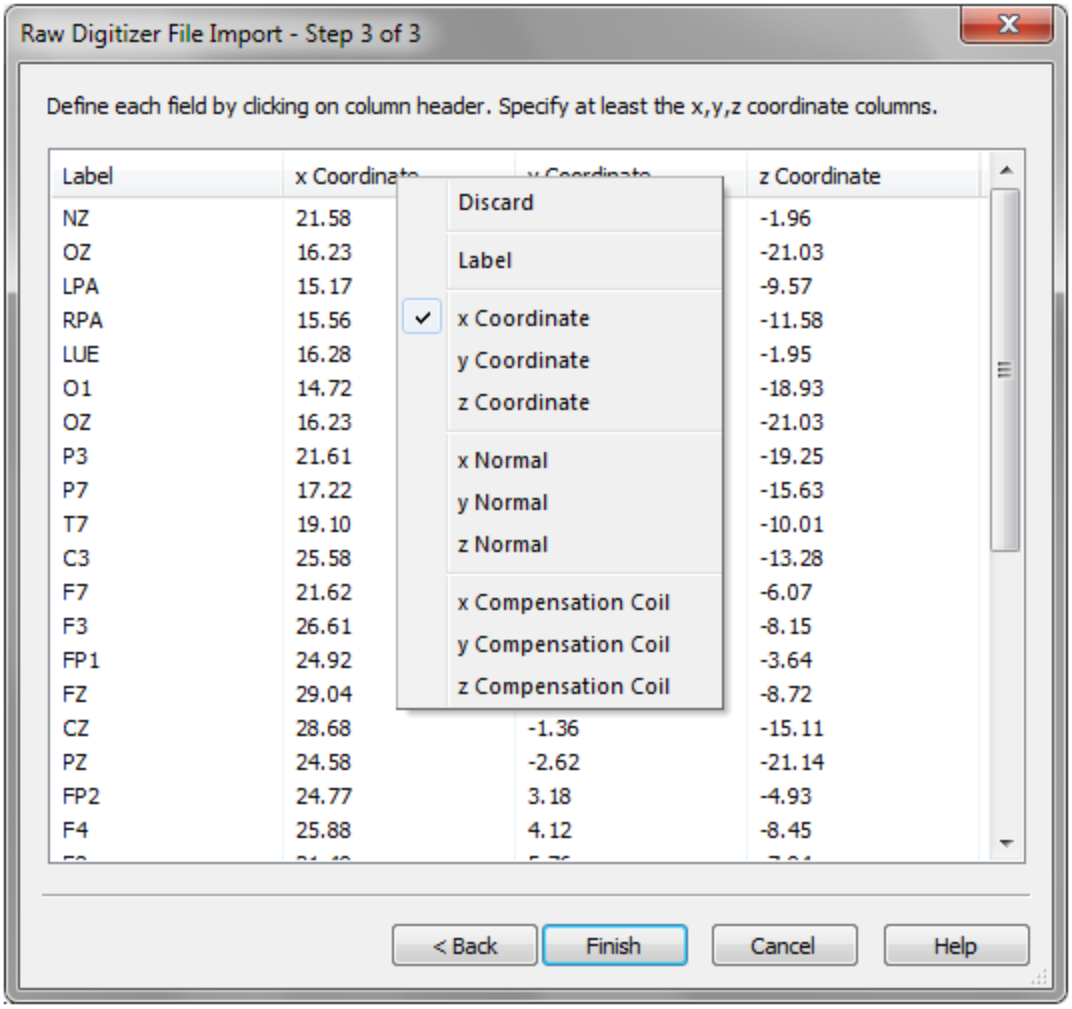
Treat consecutive separators as one. With this option enabled, the import wizard combines successive tokens to a single one. For example "Nasion,,,10.0" would result in two columns, not in four.

Click **Next** to continue.

If you selected **Fixed Width**, you need to define the column margins in the display. Click in the screen once to add a column break between the columns, or twice to remove one. Click **Next** to continue.



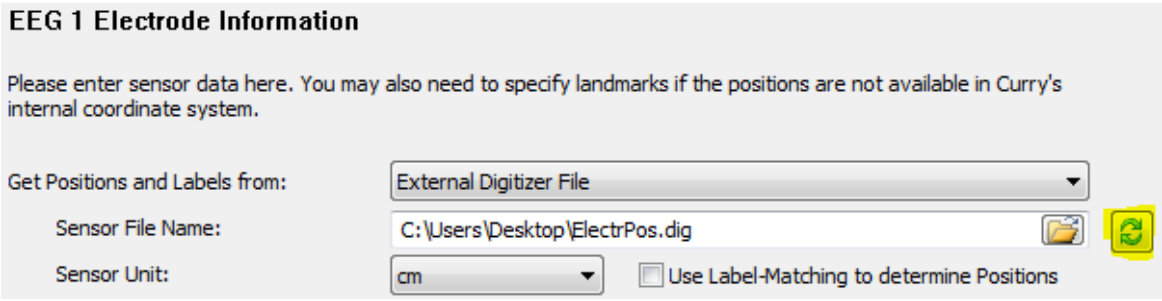
Step 3. Click the column header for each field to define what each column contains.



Clicking on the column header specifies the type of the selected column (the column content is auto-detected). **Discard** rejects the column's content, **Label** defines the sensor label, **x,y,z-Coordinate** define the sensor position, and **x,y,z Normal** define the sensor normal (necessary for MEG/MCG only). With MEG files, you will see the Compensation Coil coordinates (if you are importing gradiometers).

Clicking the **Finish** button closes the wizard and writes the information obtained to a .dpf file (**D**igitizer **P**arameter **F**ile), where the .dpf extension is added to the file name (*example.dig* → *example.dig.dpf*).

To re-invoke the wizard, delete the .dpf file (**Remove Column Info** from the **Database** context menu) and re-access the digitizer file. "Raw" digitizer files will also display a small cog wheel if a .dpf file is present. You can also "re-parameterize" the digitizer file if you make a mistake by using the button indicated below.



16.3 Co-Registration Details

This section describes details regarding CURRY's more specific requirements and operations pertaining to co-registration.

Sensor Locations

This section describes the definition of EEG or MEG sensor positions in functional and anatomical coordinates.

Source localization and reconstruction methods require more than just the functional data: knowledge of the precise 3D coordinates of the sensor positions is also necessary. To use image data along with functional data, the coordinate systems have to be co-registered. Depending on the available information, CURRY supports a variety of methods for importing 3D sensor coordinates and co-registration.

EEG

The positions of the electrodes on the subject's skin must be determined.

MEG

The position(s) of the cryostat(s) with respect to the subject's head or body is sufficient, since the geometric arrangement of the sensors within the cryostat is known.

Sensor locations must either be known in image (anatomical) coordinates. Then, co-registration is unnecessary. Or, the locations of some landmarks must be available in anatomical *and* in sensor (functional) coordinates. These landmarks are then used for coordinate system matching. They may be:

- landmarks such as the nasion and the auricular points.
- a subset of the sensors themselves.
- MEG localization coilsets fixed on the skin.
- any other points, normally located on the skin.

Combinations

The following methods for determining and co-registering sensor coordinates are supported:

- Label-matching where sensors are identified by their labels and locations are taken from a built-in list,
- PAN transformation using a digitizer file containing sensor locations and the PAL, PAR, Nasion landmark locations,
- SVD transformation using a digitizer file containing sensor locations and arbitrary landmark locations plus a file (created in CURRY) containing the same landmark locations in image data coordinates,
- International 10/20 or 10% electrode system locations calculated in CURRY based on the individual subject's skin segmented from MRI or CT,
- Identification of EEG or ECoG electrode locations in the individual subject's image data, and
- Identification of ECoG grid cornerpoints in the individual subject's image data. CURRY can use these to calculate the grid layout.

In the following sections, the strategies and files for specifying sensors and landmarks are described.

Planning to use Landmarks

When landmarks are used for co-registration, several points have to be kept in mind.

- At least three landmarks must be used, else the registration problem has no unique solution.
- The highest registration accuracy is obtained around the center-of-mass of the used landmarks.
- Registration accuracy is less sensitive to errors in the individual locations the more landmarks are used.

This implies that at least three landmarks must be used. Landmarks at the nasion and the preauricular points are good choices as their center-of-mass is near the center of the head. The inion is a good choice for an additional point.

If there is the possibility to use image markers (vitamin E capsules), landmarks can be placed at arbitrary positions, e.g., at the four just named.

If image markers cannot be used, landmarks must be recognizable in the image data itself. For the nasion and the preauricular points, this should be no problem. If the inion can be found in the image data, it should also be used.

 **Note**

Instead of the preauricular points, any uniquely identifiable locations in the vicinity of the ears can be used, e.g., the frontal parts of the ear-hole borders.

 **Care**

When landmarks are digitized using a stylus, the manually applied pressure must be controlled. Different pressures can result in differences on the order of millimeters.

 **MEG**

If localization coilsets are to be used as landmarks and image markers (vitamin E capsules) are available, the spatial resolution of the MEG system has to be

considered. Coilsets have to be placed in a region where the spatial resolution is high.

Sensor and Landmark Files

Sensors and landmarks can be read from various third-party file formats, the most flexible of these being the .3dd and .dig digitizer file formats.

Digitizer files can have several different extensions: .3dd, .dig, .pom, etc. They are typically entered either into the **Functional Data Import Wizard**. (In the SCAN program, you may merge the .3dd file with the data file, so all of the information is contained in the data file).

Digitizer files contain the locations of sensors and/or landmarks in an arbitrary coordinate system. They must adhere to the following conventions:

- One row per sensor or landmark.
- The three location coordinates and an optional label must always be found in the same columns.
- The units used must be 100μm, mm, cm, dm, m, or inches.
- The ordering (not the exact rows) of the sensors must be the same as in the data file.
- The ordering (not the exact rows) of the landmarks must be the same as in the anatomical localization file. When the latter is created, this has to be accommodated.

Neuroscan Electrode and Functional Landmark Position Files

Neuroscan electrode and functional landmarks are created in the Digitize part of CURRY 8 using the FasTrak or Vicra digitizers. 3dd files created with 3DSpaceDx and SCAN will also be read by CURRY 8. You may:

- Merge the .3dd file with the Neuroscan data file in EDIT (*right click* between electrode displays and select Load 3D Electrode positions, then save the file with the changes. In that case CURRY will read the position data and you will not have to load it explicitly.
- Load the .3dd in the **Functional Data** folder in the Database (this is just a convenience - the .3dd file will be preselected in the Wizard).
- Load the .3dd file in the Functional Data Parameters Wizard.

BESA Electrode Position Files

BESA electrode position files .eps or .elp, optionally along with their accompanying electrode label files .ela may be used for specifying electrode positions.

For all BESA files, the organization of the data into columns must not change between lines in the file, i.e., the x, y, and z, with respect to theta, phi, factor coordinates (and possibly the labels) must appear in the same columns in all lines. Also, the units used to specify the coordinates must be the same for all of the electrode positions in the file.

BESA electrode position files and electrode label files must have the same basename. Either, *but not both*, can be entered into the Database in the Functional Data folder.

EGI Electrode Position Files

CURRY supports EGI's .nsi files.

Free-Format Digitizer Files

Line-oriented ASCII files can be used as sensor/landmark files and parameterized using the Digitizer File Wizard (described above).

Sensor Files from Existing CURRY Studies

It is possible to use (or reuse) sensor and landmark locations from other Studies (.rs3 files) as digitizer files.

Anatomical Landmark Files

Anatomical landmark files are generated within CURRY with the .pom extension. They store the landmark coordinates in anatomical (image) coordinates, and thus define the coordinate system into which the sensor locations are transformed. Anatomical landmark files are needed for SVD transformation only. Anatomical landmark files are entered into the **Image Data** folder, or in the Anatomical Landmarks field in the Data Parameters. They are created using the **Localize** options, described below.

 **Care**

The ordering of landmarks is important. Landmarks in the anatomical localization file must have the same order as in the digitizer file or the montage.

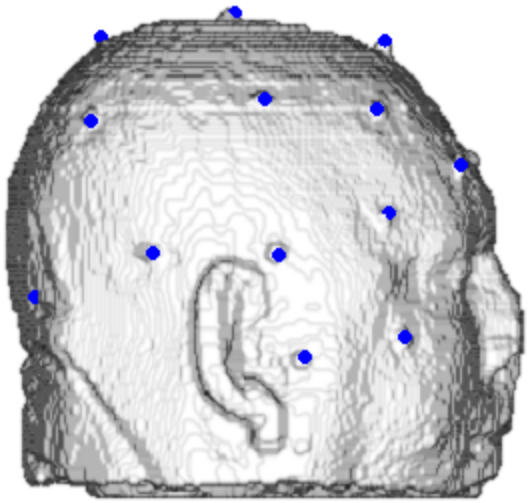
Digitizer Files Created Within CURRY

It is possible to create an individual EEG montage for a specific anatomy, based upon the individual image data. In such a montage, the sensor locations are already in CURRY coordinates. Individual montages are generated in the **Localize** window and they contain sensor locations obtained from image markers at the electrodes.

There are several ways this can be accomplished. One way is to identify the individual electrode positions by clicking on them, as shown in the next sequence. Other ways are to use the 10/20 system setup and the ECoG grid computation. These are described in the **Localize, Context Menu** section below.

The basic procedure is as follows:

1. Load the MR data and go to the **Localize** window. In this subject, the electrode locations are clearly marked.

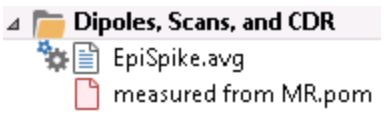


2. While in Append Mode, click on the electrodes one at a time, in the same order as in the data file, and see the positions in the **Localize** table. Relabel the electrodes accordingly (if desired).

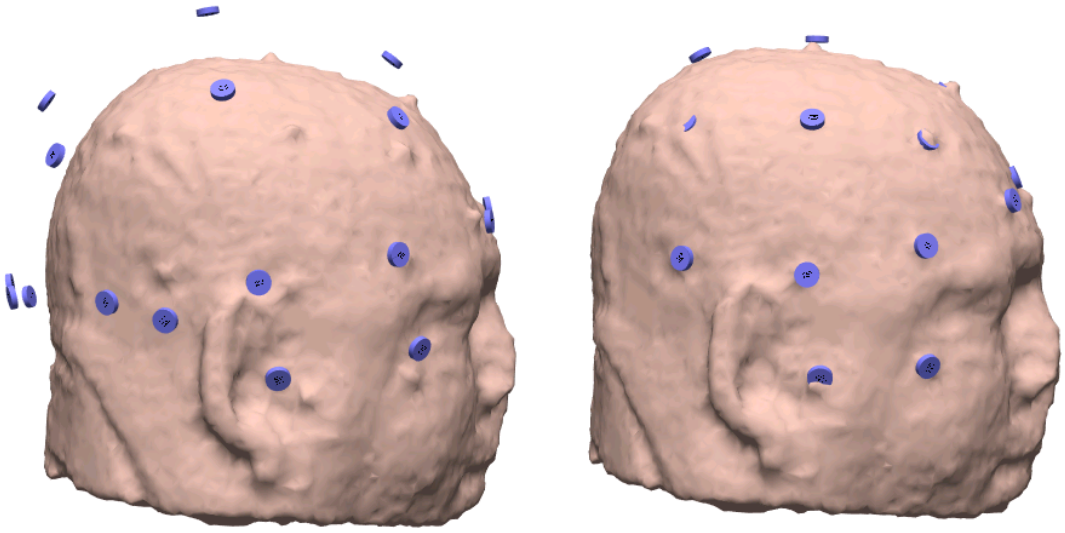
	Label	x [mm]	y [mm]	z [mm]
1	O1	-16.1	-68.5	83.3
2	OZ	3.5	-69.7	84.1
3	P3	-52.9	-18.6	112.6
4	P7	-71.2	-31.1	62.2
5	T7	-81.8	17.7	38.6
6	C3	-55.0	27.7	103.6
7	F7	-67.0	70.6	33.7
8	F3	-52.5	60.4	83.2
9	FP1	-27.2	102.9	37.5
10	FZ	2.4	90.1	90.9

3. When you are finished, click the **Save and Use As Digitizer File** button (select a folder and enter a file name for the .pom file).

4. The .pom file is added automatically to the Database's Functional Data folder. The second screen of the Wizard will open.



5. In this example, we initially used Label-Matching to determine the electrode positions (left). We then selected the digitizer file, which applied the measured positions in the .pom file. The accuracy of the measured electrode positions is seen clearly on the segmented skin surface.



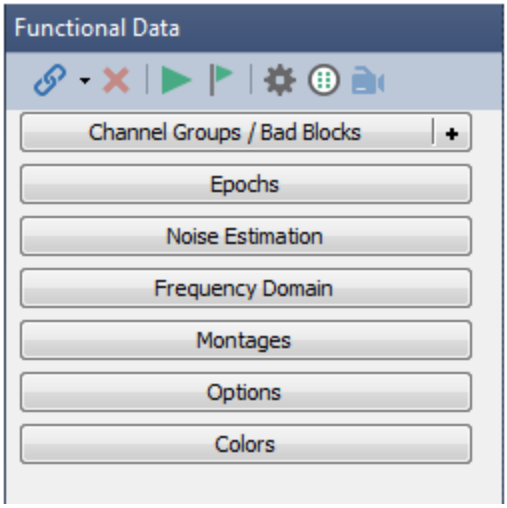
Label-matching

Measured positions

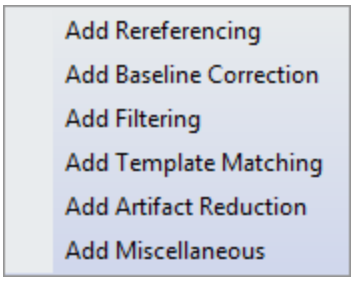
The measured electrode positions may result in more precise localization.

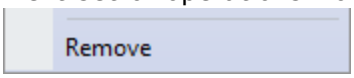
17 Signal Processing

The basic signal processing options are contained in the Functional Data parameter panels. When you first open a Study, you will see only a few of parameter panels. This simplifies the display, letting you select only those operations that are relevant to your analyses.

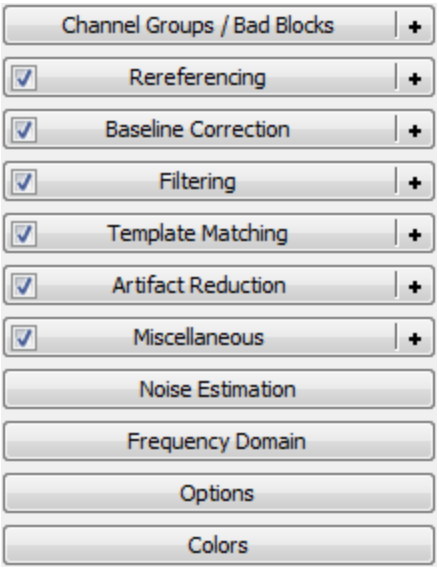


Click the + sign to see additional parameter panels.



Add them in the order you expect to apply them. Note that each one has its own + sign, letting you select the next set of operations from that list. Each has it own option to remove the selection 

. The check box ☑ allows you to set the parameters, but then not apply them by unchecking the box.



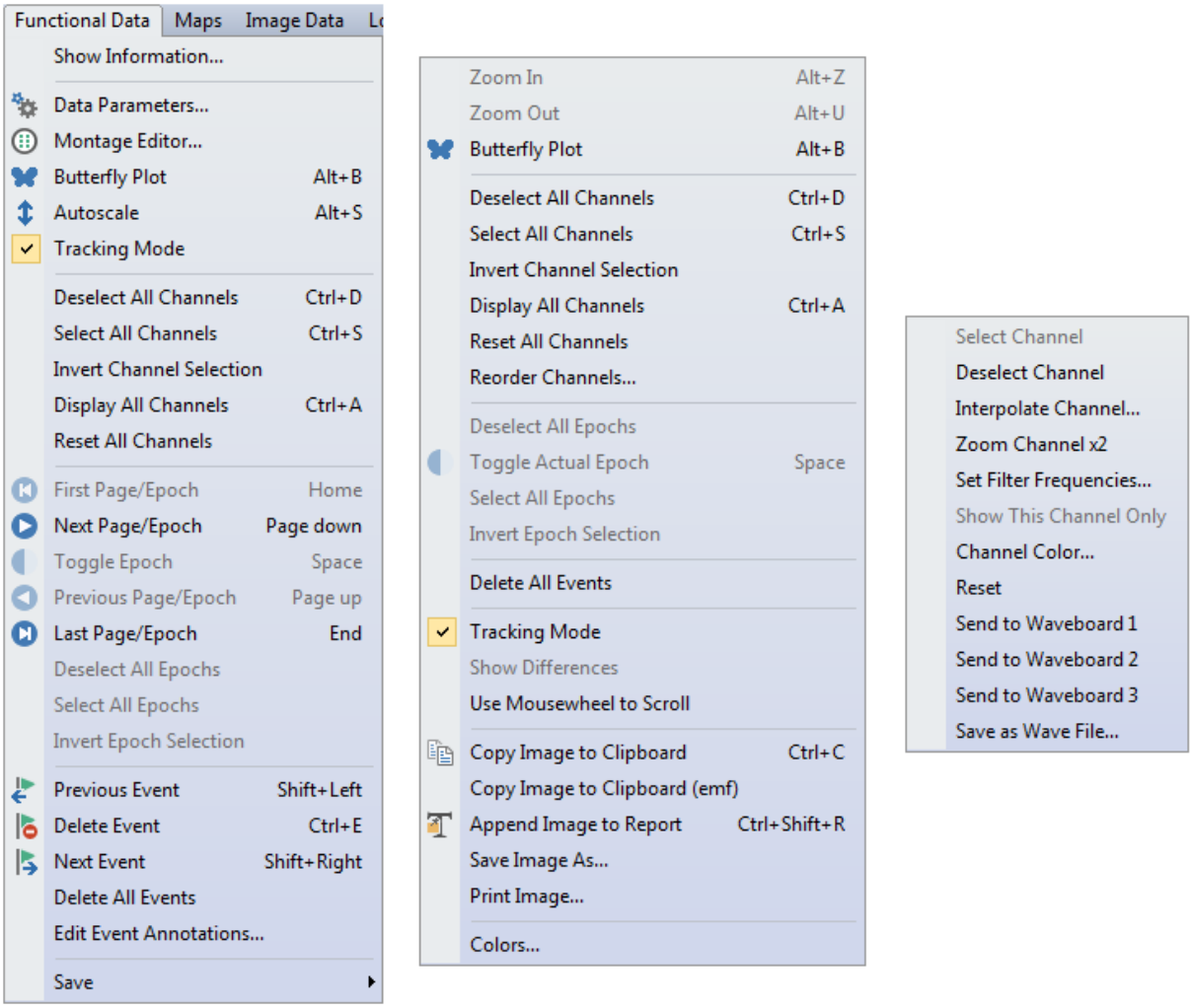
You may have multiple instances of the same parameter panel. For example, you may wish to have two Artifact Reduction processes, reducing two different types of artifact. Or, you may wish to scan the file for more than one class of feature, such as, epileptic spikes from different regions. Or, you can do some initial filtering and later do some further filtering, if desired.

You may drag and drop the panels to change their order.

The Functional Data Toolbars have shortcuts to many of the options you will use. The first is found at the top of the Functional Data parameter panel. The second is seen when you position the mouse in the upper left corner of the data display.

Additional options are found in the Functional Data drop-down list on the Main Menu Bar (left), the context menu accessed by *right-clicking* in the Data Display (middle), and the

context menu accessed by *right clicking* on an electrode label (right). These are described in the following sections.



17.1 Functional Data

Viewing Data

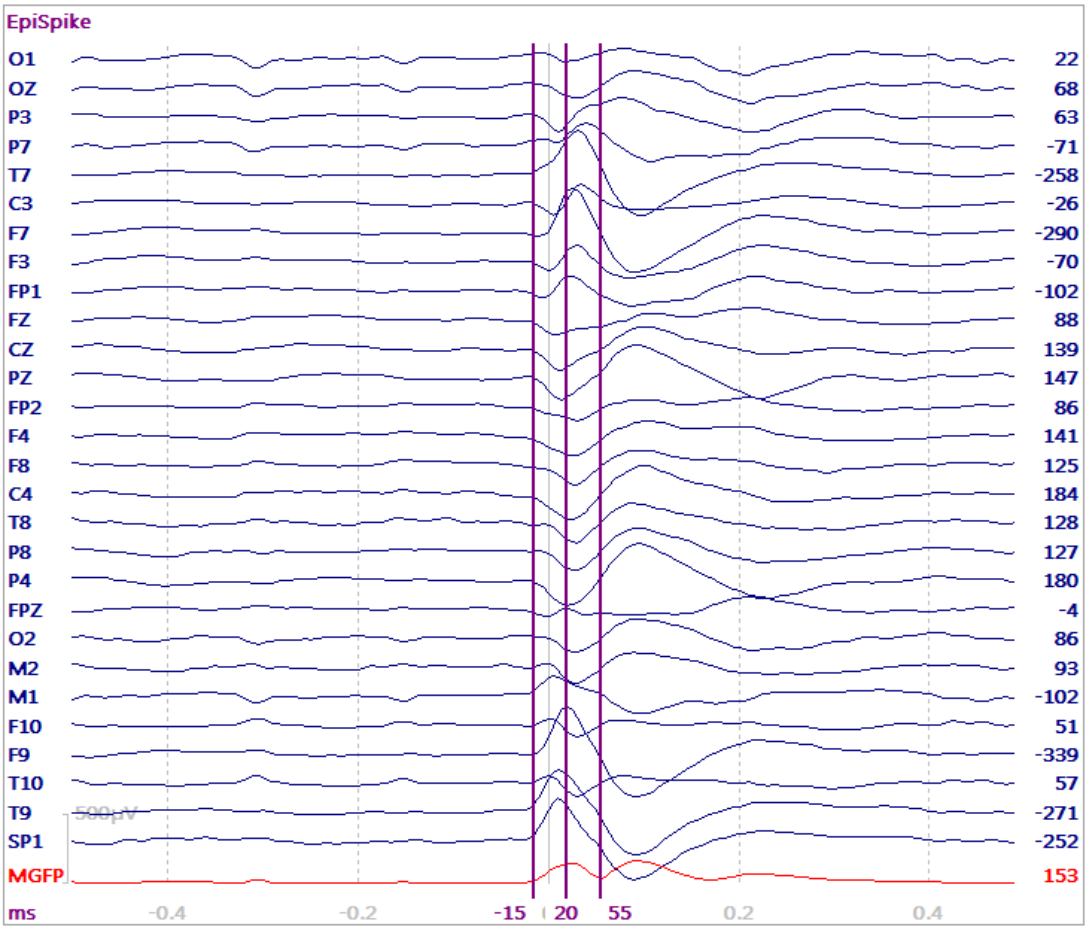
Assuming that your data file(s) has now been loaded into the Database and the parameters have been detected or modified as needed, the data are displayed by *right clicking* on the Study name and selecting Open option (or *double-click* the *Study* name, or by clicking the icon). The Functional Data window (or any display containing the Functional Data) will display the waveform data.

The display of the single sweep data file, or of the first epoch of a multiple sweep file, or the first page of a continuous measurement file is seen. It shows all or some of the channels from the selected device, together with the mean global field power (MGFP), if selected. The data for each channel are filtered according to the settings chosen in

the Filtering panel, and displayed according to the settings chosen in the Colors and Options panels. These are described below.

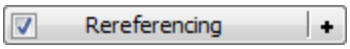
Viewing Single Sweep Data

Neuroscan averaged (.avg files), or other similar single sweep files, may be retrieved and displayed as shown. Voltages for each channel for the latency of the cursor are displayed on the right side. The display options are accessed primarily from the **Options** panel in the **Functional Data** options, and are described in that section below.



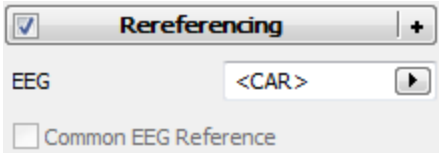
Briefly, you can rescale the data, select/deselect individual channels, show the data in a Butterfly Plot, change the polarity, create a power spectrum, and select a different reference channel in the Rereferencing panel. You can change colors in the Colors panel.

If you have loaded multiple average files in the Study, the individual files may be seen by dragging the sliding bar below the display, or using the Toolbar icons  .

The data (all file types) are displayed using whatever Reference you have selected (in the 

panel under 

). CAR is the Common Average Reference. If you deselect the Active Channel Group, you will see the file with its original reference (as it appears in, for example, the EDIT program in SCAN; you must select a CAR if you are performing source analysis).



Viewing Epoch or Trial Data

Neuroscan epoched (.eeg), or other similarly formatted files, may be retrieved and displayed sweep-by-sweep. Voltages for each channel for the latency of the cursor are displayed on the right side. Step through the sweeps using the Toolbar icons  , the arrow buttons, or drag the cursor bar through the file. *PgDn* and *PgUp* will step through the file sweep by sweep ( and ). *Home* returns to the beginning of the file (); *End* goes to the end of the file ().

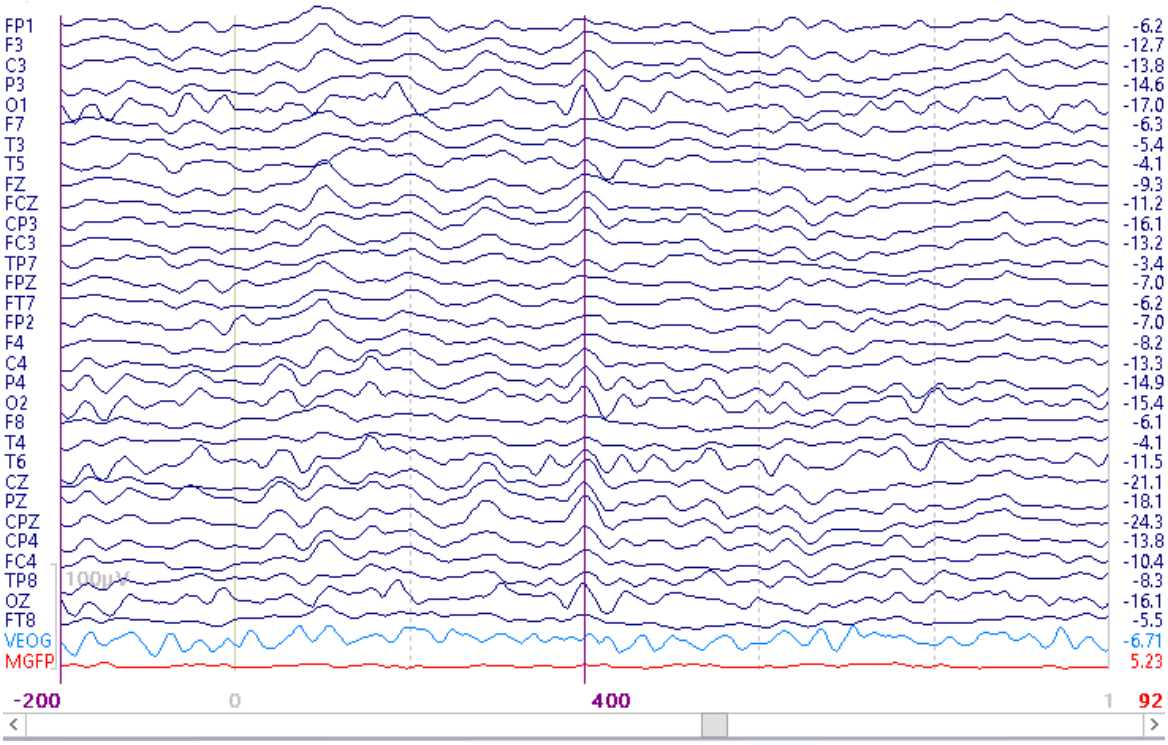
Right click in the data display and enable **Use Mousewheel to Scroll** to go through the epochs using the mouse wheel. In this case, you can use the up and down arrow icons on the Toolbar to scale the data, or use the + and - keys by the number pad on the keyboard.

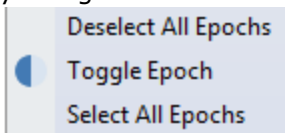
The sliding bar can be dragged to a new location with the mouse, or may be moved using the arrows keys on the *keyboard*. Use the autoscale button  to rescale the data display, or the *up* and *down arrows* on the keyboard. The epoch duration is determined by the number of samples 

(seen in the **Functional Data Wizard** ). In the example below, the AD rate was 250 Hz and the dwell time, or time between data samples, is shown as 4ms 

. In this file, the zero point was offset by 200 ms, as seen with the 

field in the Wizard. The 0 ms latency is indicated by a light gray vertical line in the Functional Data display.



The sweep number is displayed in the lower right hand corner (92). You may accept/reject each displayed sweep by pressing the *space bar* (rejected sweeps are in gray), or by using the button on the **Functional Data** Toolbar. You have the options to 

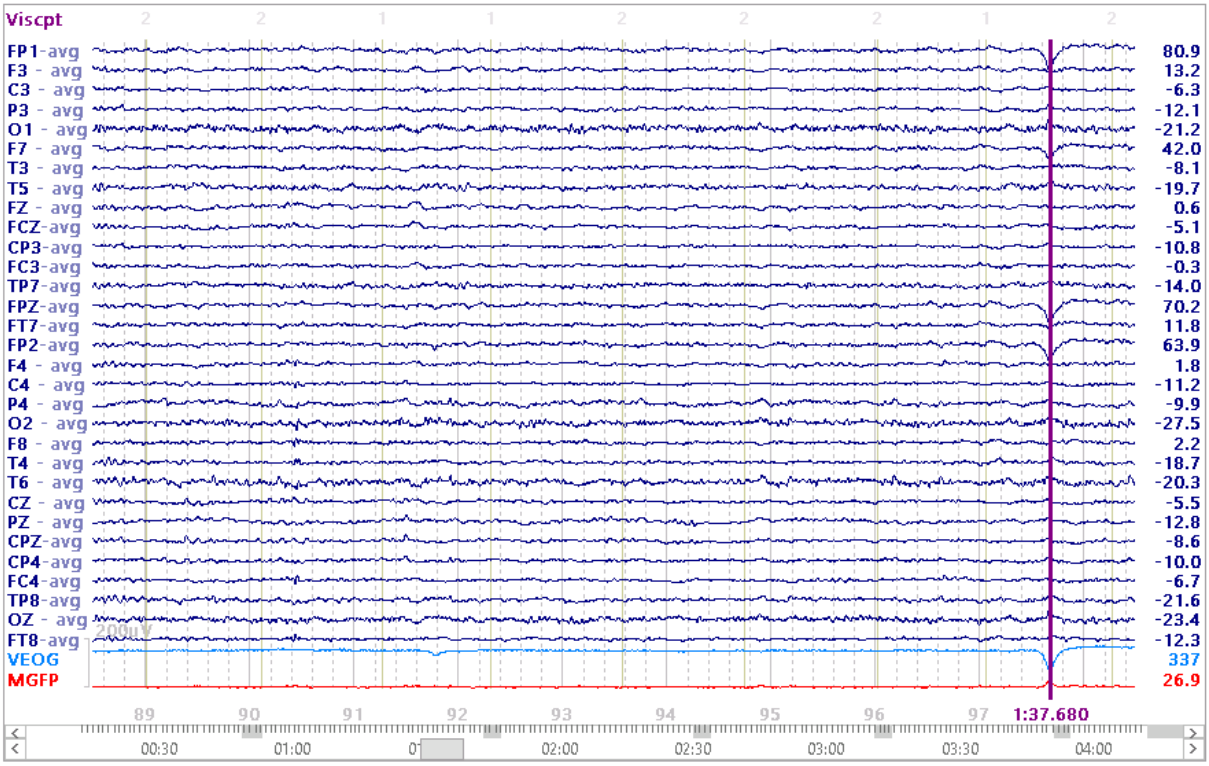
, accessed by *right clicking* in the data display. You can average the sweeps by selecting the 

option in the 

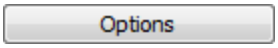
panel.

Viewing Continuous Data

If you load a continuous type of data file, you will see the file displayed as shown below. The voltages per channel at the cursor position are shown on the right side. The events are seen at the top. Channels that have been designated as "Other" channels (typically the artifact channels), are always autoscaled (seen in blue below).



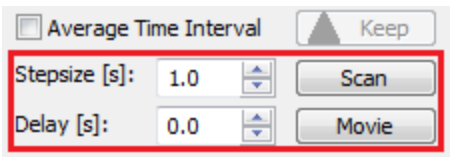
There are several ways to navigate through the file. You can use the icons on the Toolbar  . The left and right arrows move page by page. The arrows with the vertical lines move to the beginning and end of the file. If there are Events (from **Event Detection**) in the file, use the  and  buttons to move to the previous and next events. (Use the  button to delete the event). Drag the sliding cursor bar to any point in the file. Click to the left or right of the sliding cursor bar to advance or go back by the number of displayed seconds (the number of displayed seconds is set by the 

option in the 

under 

). The *PgUp* and *PgDn* keys have the same function. *Home* returns to the beginning of the file; *End* goes to the end of the file.

You may also use the Scan Data options, found in the **Options** panel. This is described in the **Options** section below.

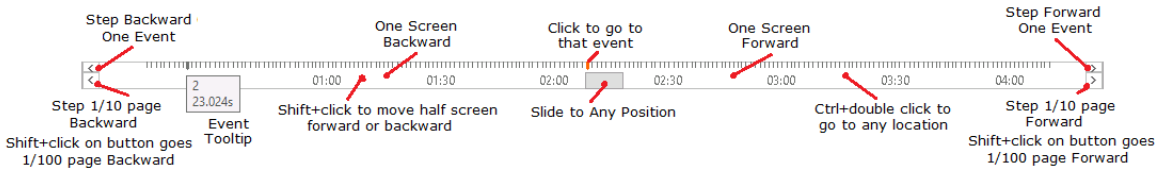


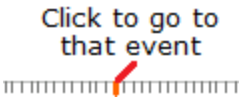
Note
While you can select the number of seconds to display, CURRY actually reads data before and after the seconds that are displayed. Additional samples are read to give a total number of samples that is a power of 2. This is needed when you perform an FFT

(**Spectra** option under Frequency Domain). When using tapering, the extent of the taper may or may not be visible in the continuous data display, depending on how may samples are being read and the extent of the taper (set by the **Width [%]** field in the Advanced Settings under Filtering). When performing artifact reduction, you may see, for example, three blinks in the data display, yet a fourth blink may be seen in the hash marks below the data file. The extra blink is from the section of data being "read" but not displayed.

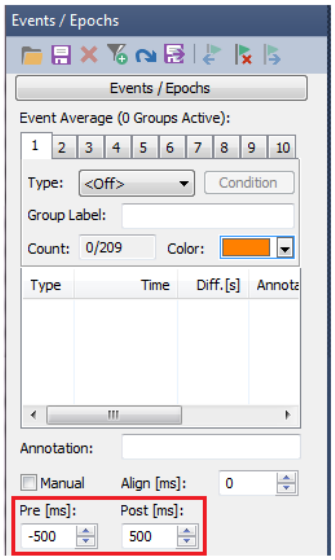
Note also that there is an event bar. Each tick represents the position of an event in the file. Position the mouse over an event and a Tooltip will display the type of event and the seconds into the file. Use the smaller arrows at each end of the event bar to step forward or backward one event.

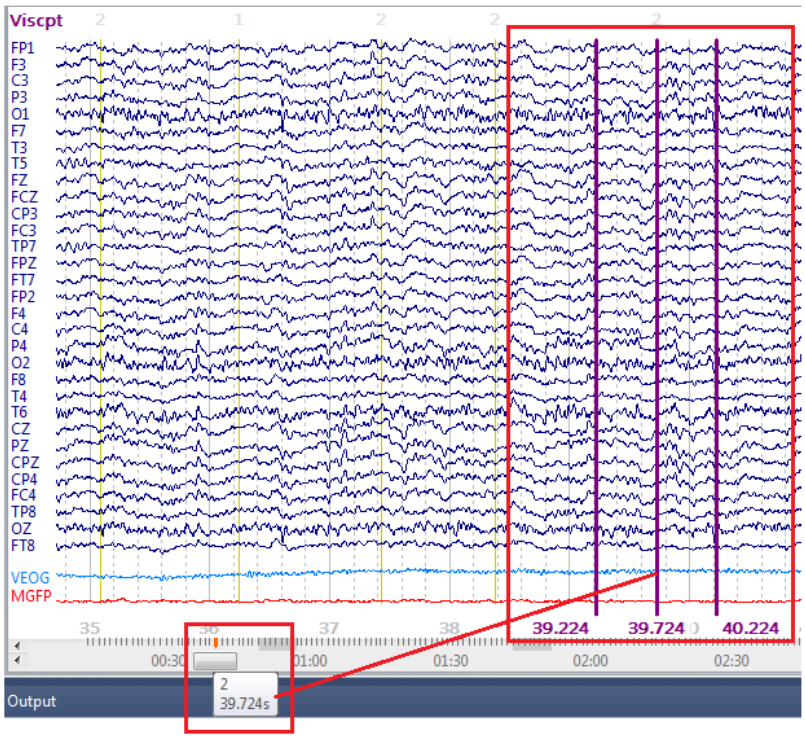
All of the scrollbar modifiers are summarized in the figure below. Note the various uses of the *Shift* and *Ctrl* button.



If you click on one of the event ticks 

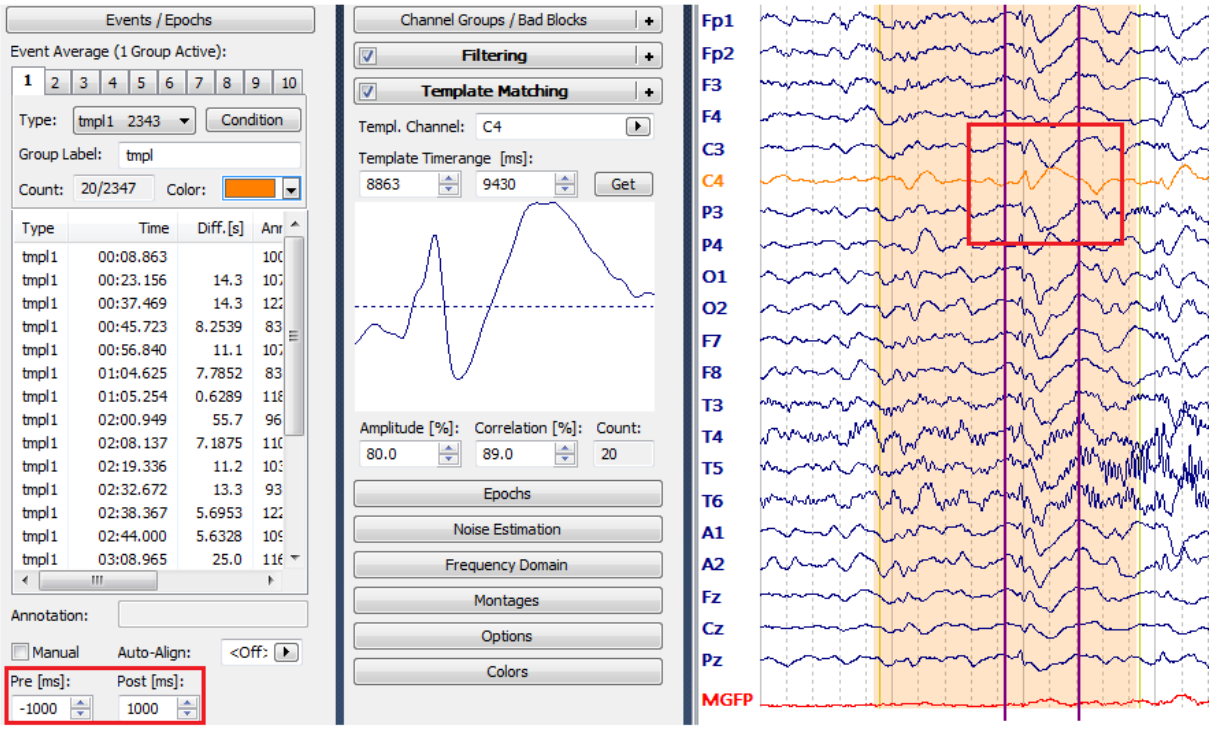
, the cursor will be placed on the event, even if it is not selected in the Event List. *Double-clicking* on an event sets the left and right cursor according to the **Pre [ms]** and **Post [ms]** times in the **Event List**. The middle cursor is set to the event latency.



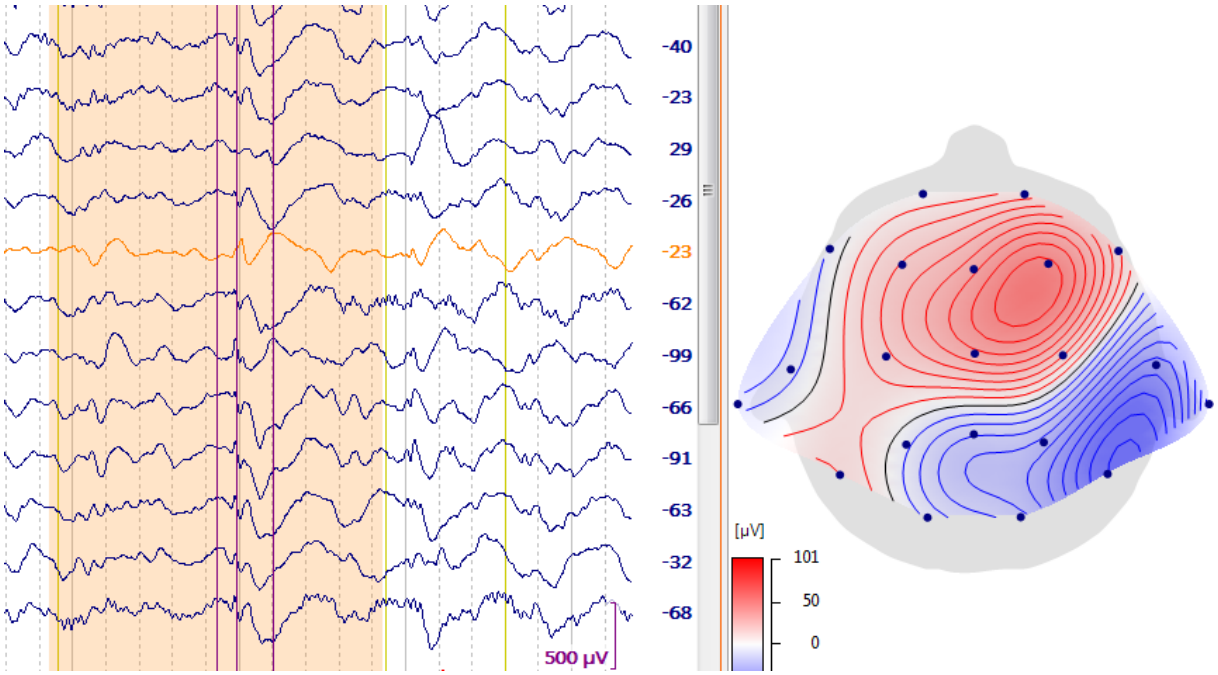


If you the left, middle, and right cursors manually around an event (for example, to select a different time point than the event itself for source reconstruction), the relative position toward the event will be kept if the middle cursor is within +- 1 sec of the previously selected event. For example, imagine there are spikes events where you want to jump from one spike to another, but the time point of interest (for maps or source reconstruction) is not the time point of the event, but slightly before or after it. You can let CURRY mark the event time point, as usual. You then manually shift it slightly. If you now jump to the next event, this slight shift is kept
- relative to the position of the original event. If you shift the middle time cursor more than 1 sec away from the currently selected event, CURRY assumes you no longer want to concentrate on this event and re-centers the middle cursor the next time you jump to a new event.

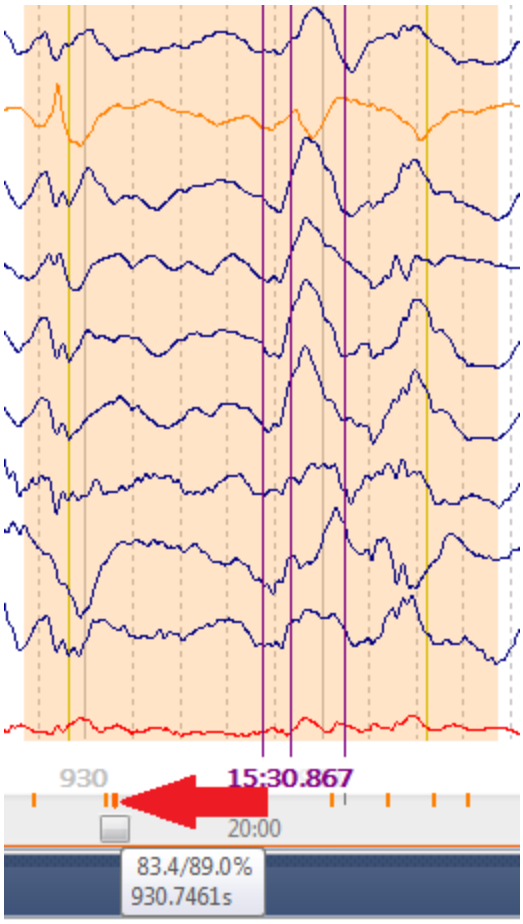
In the example below, Template Matching was used to detect the spike and slow wave patterns in the file. The two vertical cursors define the Timerange that was used for template matching. The orange is defined by the **Pre [ms]** and **Post [ms]** fields in the Event list. If we want to look at the Maps for the peak, we would need to set the middle cursor. If we set it for All maps, that would be a map for every data point, which could be a lot of maps. If we want to do source reconstruction, the entire Timerange would be used, yielding many results that would not be of interest.



We can reset the outer cursors to define a smaller Timerange, and place the middle cursor at a point of interest. The single map corresponds to the middle cursor position. Source Reconstruction would use the smaller Timerange.

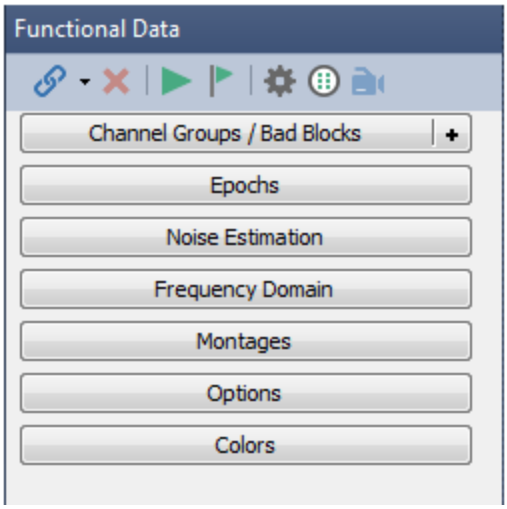


When we click on a different event mark (tick mark), CURRY will go to that event, maintaining the Timerange and relative position to the original event. This greatly facilitates mapping and source reconstruction for each spike, since you do not need to change the cursor positions.



Right click in the data display and enable **Use Mousewheel to Scroll** to go through the file using the mouse wheel. Use *Shift + mouse wheel* to scroll through half a screen at a time. In this case, you can use the up and down arrow icons on the Toolbar to scale the data, or use the + and - keys by the number pad on the keyboard.

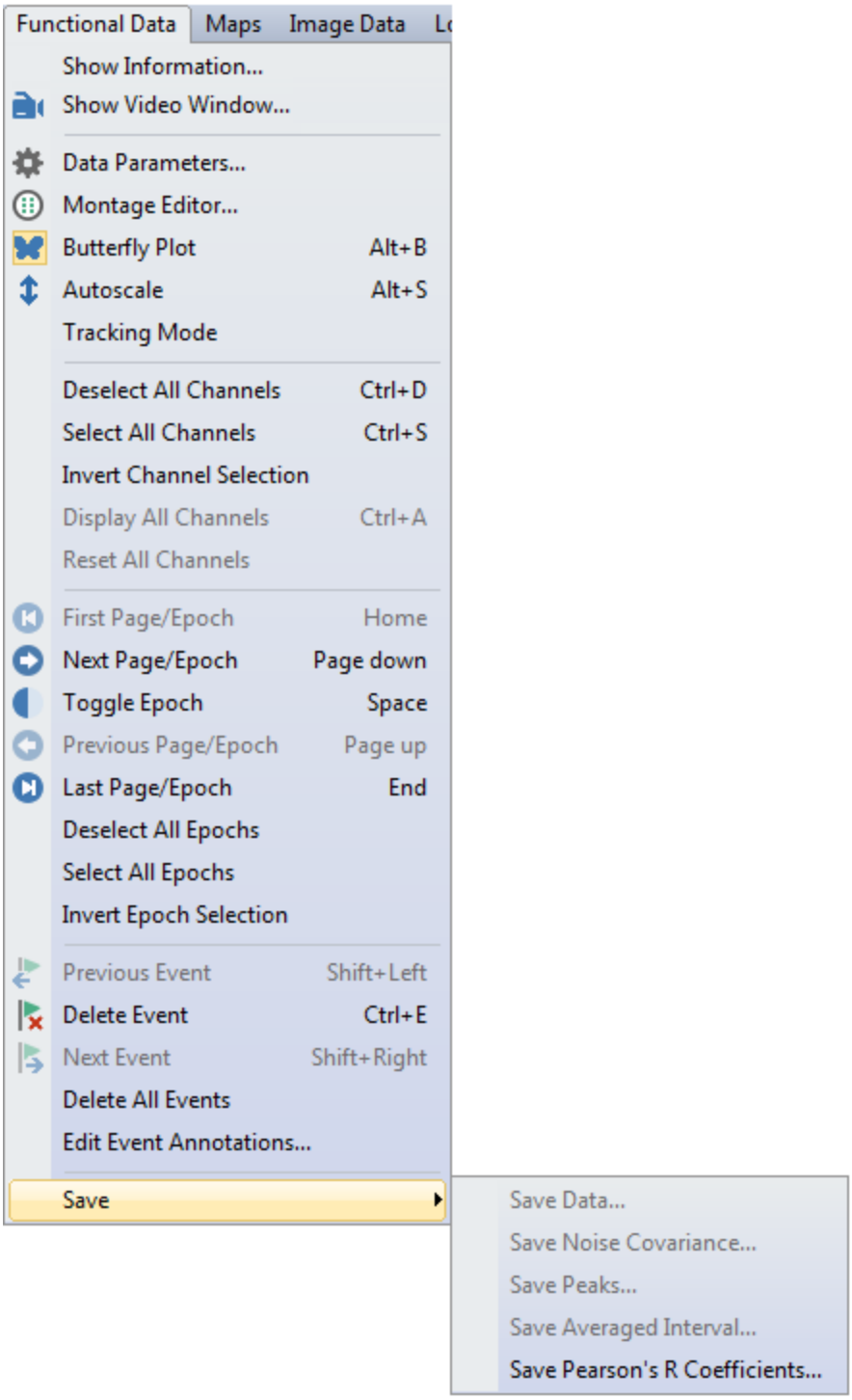
The Functional Data panels are used primarily for data preprocessing, including artifact removal, baseline correction, filtering, noise estimation, and event detection. You can set the colors for the Functional Data display components, as well as additional options. Press *F9* at any time to display the panels.

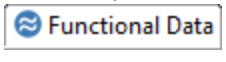


The Functional Data options are associated with the Functional Data display.

Some of the options pertaining to Functional Data are found on the Main Menu Bar.

The items pertain to the display of waveform data, navigation through the file, and exporting data.

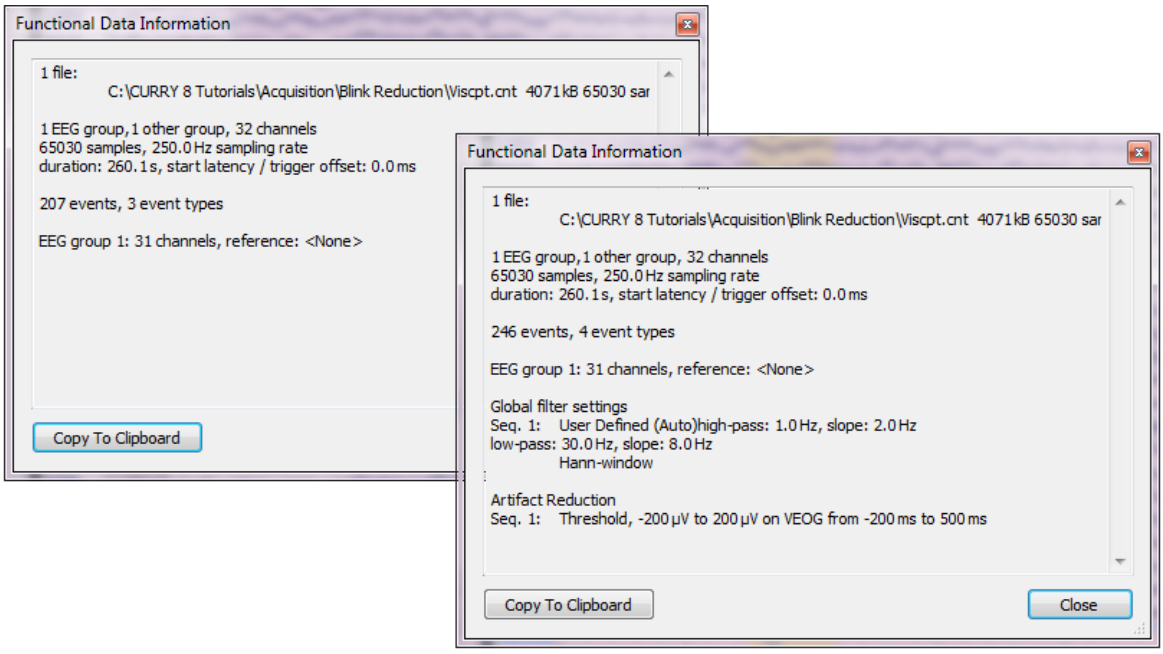


Many of the options may be accessed from the Toolbar icons at the top of the **Functional Data** parameters panel  , and also are seen when you position the mouse in the upper left corner of the 

display  .

Some of the options will not be accessible unless you have retrieved a continuous or epoched file, and have identified events.

Show Information. This displays information about the file(s) in the currently open Study. Changes you make as you go along will be seen in the file.



Show Video Window. Displays Video window.

Data Parameters  . Invokes the Functional Data Parameters Wizard.

Montage Editor  . Provides access to the Montage Editor (described below in the **Options** section).

Butterfly Plot  . Toggles the Butterfly Plot display on and off (or *Alt+B*).

Autoscale  . Autoscales the display of the functional data (or *Alt+S*).

Tracking Mode. When enabled, a single vertical dashed cursor may be positioned by clicking the mouse on a position, or by grab-and dragging the cursor to a position. The voltages for each channel at the cursor position are displayed on the far right of the Data Display. *Shift+left mouse* also disables Tracking Mode; double-clicking the left mouse button enables it.

If you disable Tracking Mode, there will be three vertical cursors for positioning. The two outer cursors are used to define the Timerange. the middle cursor defines the specific time point within the range. The Timerange is used for Noise Estimation, Source Reconstruction, Zooming, etc.

Deselect All Channels. All selected channels will be deselected.

Select All Channels. All deselected channels will be selected.

Invert Channel Selection. Selected channels will become deselected channels, and deselected channels will become selected channels.

Display All Channels. Restores the display of all channels.

Reset All Channels. Restores the default settings for the channel attributes, including color, interpolation, etc.

First Page/Epoch (or *Home*), **Last Page/Epoch** (or *End*). Moves to the First or Last Page (continuous data files) or Epoch (epoched data files).

Next Page/Epoch (or *Page down*), **Previous Page/Epoch** (or *Page up*). Moves to the Next or Previous Page (continuous data files) or Epoch (epoched data files).

Toggle Epoch. Toggles the Accept or Reject state of the current epoch (or *Space bar*).

Deselect All Epochs. All epochs will be deselected.

Select All Epochs. All epochs will be selected.

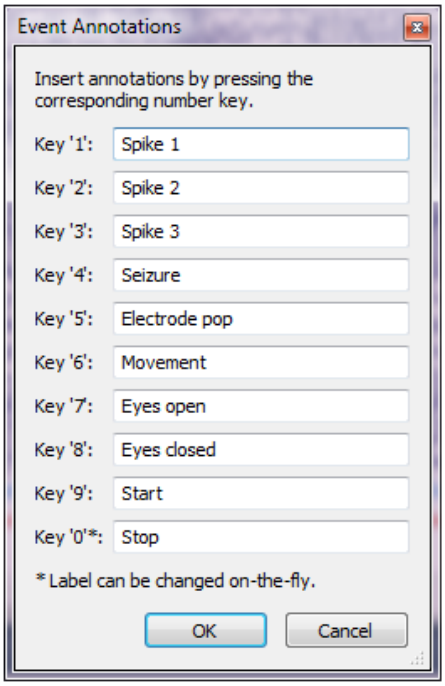
Invert Epoch Selection. Selected epochs will become deselected epochs, and deselected epochs will become selected epochs.

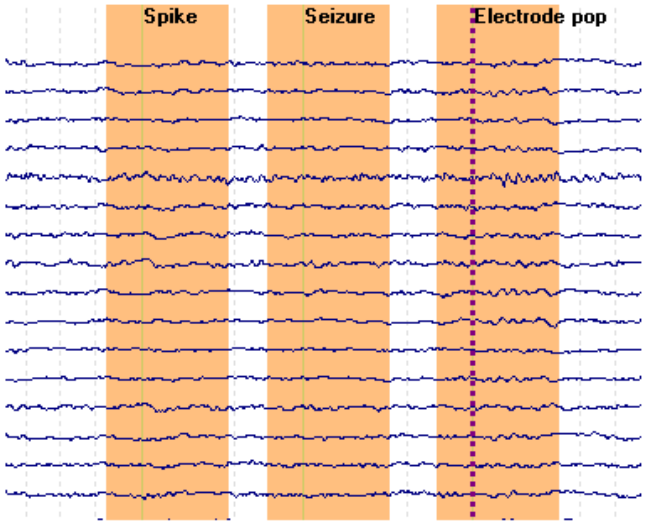
Previous Event (or *Shift + Left arrow*), **Next Event** (or *Shift + Right arrow*). Move to the Previous or Next Event (in continuous data files where events have been detected).

Delete Event. Removes the highlighted event from the continuous data file.

Delete All Events. All Events in the data file will be removed. Click the button at the top of the Events / Epochs panel to reload the original events.

Edit Event Annotations. When you are inserting events manually (using the Manual option under the Event List), the default labels will be m0, m1, m2, etc. You may define the events using **Edit Event Annotations**. The new text will be seen in the data display when you insert the events. See the **Manual** option in the **Event List** for details.

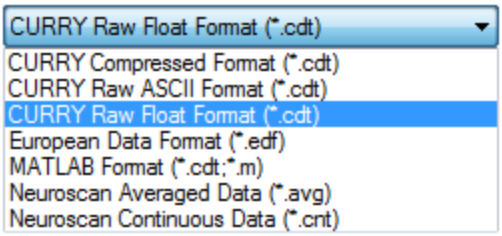




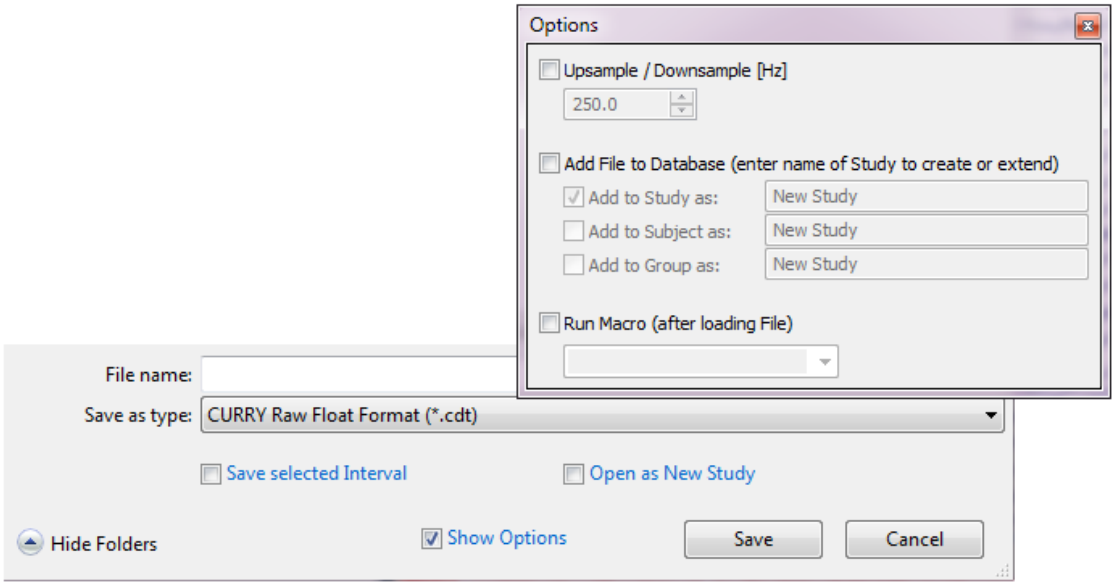
Save

Save Data. As a general "rule", CURRY saves/exports the data you see on the screen - what you see is what is saved. There are exceptions, most notably with montages. CURRY will save the original data, not the montaged data. In most instances, the changes you make will become permanent when you explicitly save/export the file.

The functional data may be exported as a .dat file, using either Raw Float Format or Raw ASCII Format, or as a Neuroscan Continuous Data or Neuroscan Averaged Data file. In general, the default file type may have speed advantages over the Neuroscan file types; use the Neuroscan file types if you are planning to open the files in the Scan software.



There are several additional options in the lower part of the window.



Save selected Interval. By default, the entire displayed interval will be saved. If you want to save less than that, set the two outer cursors to define a Timerange that you want to save, and then enable the option.

Open as New Study. Enabling this option will open the file (or Study containing the file) automatically.

Show Options. Clicking this option displays the **Options** dialog.

Upsample or Downsample. This is where decimation occurs. For example, you can save a file sampled at 5000 Hz to 500 Hz (every 10th point would be saved). Low pass filtering should be used first with downsampling to avoid aliasing. Upsampling uses a spline fit for the added points.

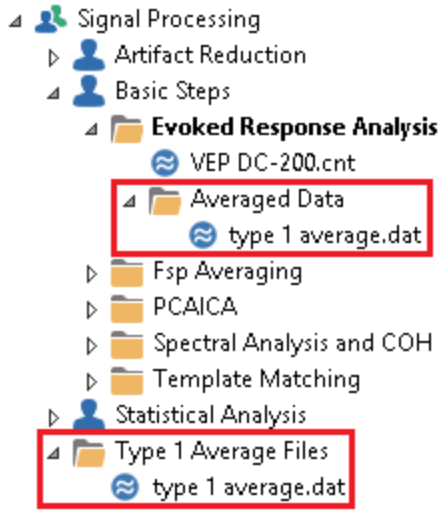
Add File to Database. These are very useful options when you are using a Database to organize your files.

Add to Study as. Imagine you start with a continuous data file, and from it you have created an averaged file. You want to save this file in a subfolder (derived folder) under the Study with the continuous data file. You would then enable the option and add a new file name (Averaged Data). If you had used an existing Study name (under the continuous data Study), the averaged file would be added to that folder.

Add to Subject as. In this case, you could also create a new folder under the Subject, or add this averaged file to an existing folder under the Subject.

Add to Group as. This option, as well as the previous one, are used, for example, when you want to create grand averages of the average files we are creating. Recall that you can only average files when they are found in the same Study folder. In this case, we are saving the

averaged data file under the continuous data file from which it was created, as well as in a new Study called "Type 1 Average Files" that will be created at the Group level. Other averages could then be saved to the same Group level folder so that all averages would then be in the same Study, and could then be averaged to get the grand average. (Note: the files are not saved in the Database - only the paths to the file that are stored on the hard drive).



The averaged file is added as a new subfolder under **Evoked Response Analysis**, as well as under the Group.

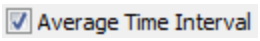
Run Macro. If you enable this option, you can enter or select a macro file to run automatically when the file opens (this is used to, for example, link two macros together without user intervention).

Save Noise Covariance. Noise covariance can be saved to an .noi file, which can then be recalled for **Noise Estimation** using the **From File** option.

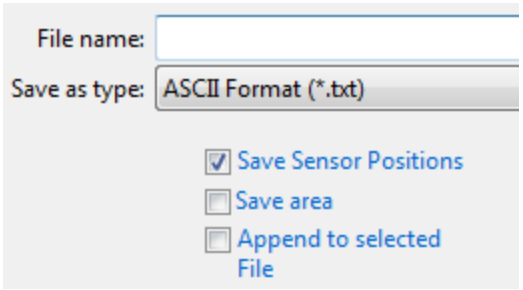
Save Peaks. A text file is created that contains the maximum and minimum voltages for each channel, using the Timerange that has been defined. A section of the text file is shown below.

The header displays whether the file contains time or frequency domain data, how many channels were in the file, and how many samples were in the Timerange. The Timerange limits are shown. Following that are the channel labels, the XYZ coordinates of the electrode, the minimum and maximum values, with their respective latencies.

```
# time domain
# channels, tested samples
   28    35
# -10.0 - 165.0 ms
# channel labels, positions[mm] [x y z], min max[µV], latencies[ms]
O1    42.41    89.90   -22.07  -41.660   74.237  165.000   80.000
OZ     2.31   105.41   -13.35  -77.856  123.474   30.000   90.000
P3    50.05   103.18    40.49 -106.807  133.718   10.000   80.000
P7    71.86    67.31     6.47 -114.699  160.610  110.000   40.000
T7    82.98    20.07    31.22 -291.703  317.704   95.000   30.000
C3    59.11    55.26    84.52  -81.522  135.944    5.000   35.000
F7    66.92   -14.84    58.08 -289.796  318.092   90.000   25.000
F3    46.40     7.96    99.55 -122.205  114.874   85.000   30.000
FP1    30.69   -37.77    88.94 -110.196  105.032   90.000   25.000
FZ   -15.30     7.64   117.27 -107.602   44.049    5.000  110.000
```

Save Averaged Data. After setting a Timerange, use the 

option under **Options** to see the averaged values in the column on the far right. Save these values using Save Averaged Data. At the bottom of the Save As dialog, you will see options to Save Sensor Positions and Append the results to an existing file (as opposed to overwriting it).



For time domain data, you will see a file similar to the following. The average for each channel across the -10 to 65ms Timerange is found in the column on the right.

```
# time domain
# channels, averaged samples
   28    15
# -10.0 ... 65.0 ms
# channel labels, [µV]
O1 - avg          15.893
OZ - avg         -22.083
P3 - avg          10.732
P7 - avg          84.218
T7 - avg         149.003
C3 - avg          23.067
F7 - avg         109.829
F3 - avg           6.727
```

For frequency domain data, there are columns for each frequency band (delta, theta, etc.), showing the averages for each band, and the overall average in the far column on the right. In the example below, the cursors defined a frequency

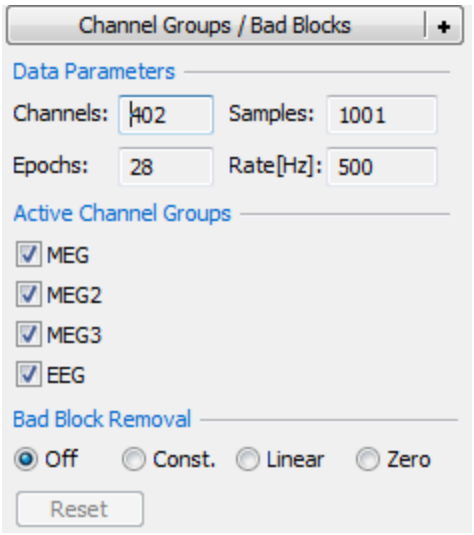
range of 0 to 70.4Hz. The numbers in brackets are the number of frequency bins in each band, as well as the overall number of bins.

```
# frequency domain
# channels: 28
# averaged frequency ranges [bins]:
# 0.000...3.000 Hz [50]
# 3.000...8.000 Hz [83]
# 8.000...12.000 Hz [67]
# 12.000...30.000 Hz [296]
# 30.000...70.000 Hz [656]
# 59.000...61.000 Hz [33]
# averaged frequencies (cursors):
# 0.000...70.374 Hz [1154]

# channel labels, [µV]
FP1-avg    0.020       0.229       0.695       0.172       0.018       0.010       0.111
PZ - avg   0.018       0.286       1.474       0.255       0.013       0.005       0.179
FP2-avg    0.020       0.255       0.739       0.168       0.017       0.008       0.113
OZ - avg   0.013       0.251       0.710       0.172       0.015       0.007       0.112
F3 - avg   0.016       0.255       0.681       0.161       0.013       0.006       0.106
FC5-avg    0.012       0.170       0.571       0.137       0.012       0.003       0.087
F4 - avg   0.019       0.299       0.729       0.170       0.014       0.005       0.115
FC6-avg    0.013       0.197       0.615       0.139       0.011       0.004       0.091
C3 - avg   0.010       0.164       0.482       0.140       0.011       0.004       0.082
CP5-avg    0.012       0.174       0.520       0.142       0.011       0.005       0.085
C4 - avg   0.010       0.190       0.538       0.136       0.011       0.003       0.086
CP6-avg    0.010       0.173       0.474       0.150       0.011       0.004       0.084
P3 - avg   0.015       0.257       0.840       0.204       0.012       0.005       0.126
CP1-avg    0.012       0.197       0.631       0.188       0.012       0.004       0.106
P4 - avg   0.013       0.256       1.212       0.223       0.014       0.004       0.153
CP2-avg    0.012       0.203       0.914       0.198       0.011       0.003       0.125
O1 - avg   0.015       0.301       0.916       0.224       0.022       0.009       0.144
PO1-avg    0.018       0.347       1.388       0.280       0.015       0.005       0.185
O2 - avg   0.014       0.247       0.744       0.180       0.012       0.005       0.114
PO2-avg    0.016       0.300       1.442       0.230       0.014       0.005       0.171
```

17.1.1 Channel Groups / Bad Blocks

The **Channel Groups / Bad Blocks** panel contains the following groups or parameters.

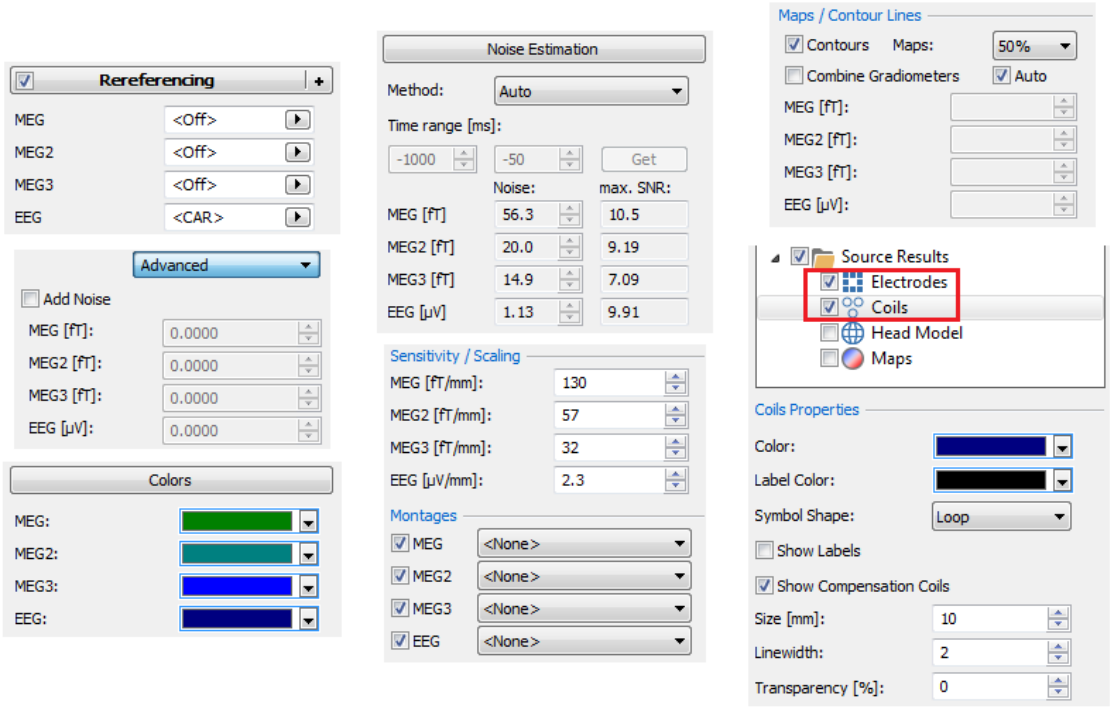


Data Parameters. The first four fields are informational only, displaying the number of **Channels** in the data file, the number of **Samples** (data points) per channel/sweep (or overall for continuous data), how many **Epochs** were detected, and the sampling **Rate [Hz]**.

Active Channel Groups. If you have specified multiple channel groups (devices), you will be able to select the active devices independently. Only data from the **Active Channel Group** will be used for further processing.

Note
This is the only location to switch between EEG and MEG if both are in the same Study.

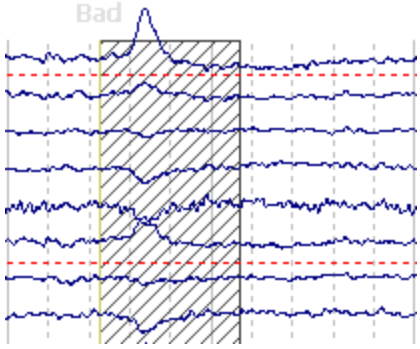
When using multiple devices, you will see information or options for both in various places in CURRY. In addition to the **Active Channel Groups**, these include **Noise Estimation**, individual **Scaling**, **Filtering**, **Montages**, **Colors** (Functional Data), **Contour** line settings for **Maps**, and display options in **3D View**.



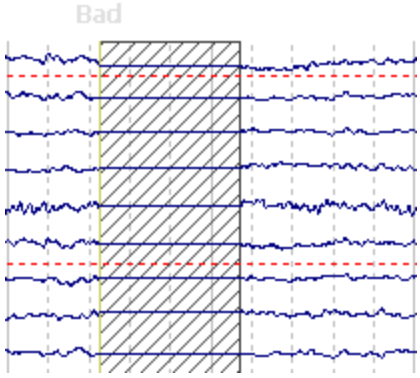
Bad Block Removal. You must first define a bad block within the data file. This is done using the Mark Block icon  on the **Functional Data Toolbar**. Click at the beginning and end of the section to be designated as a bad block, or *click-drag* with the mouse to define the bad block. When the context menu appears, select **Mark Bad Block**. Alternatively, you may use *Ctrl+Alt+mouse drag* to create bad blocks.

Once you define the bad block, you may select how you wish the data in it are to be treated.

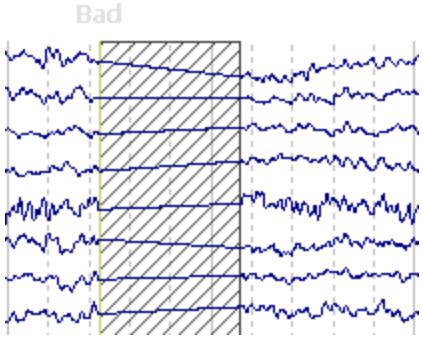
Off. No action is performed. The bad block will be excluded from epoching and other operations where to not exclude it would affect the results.



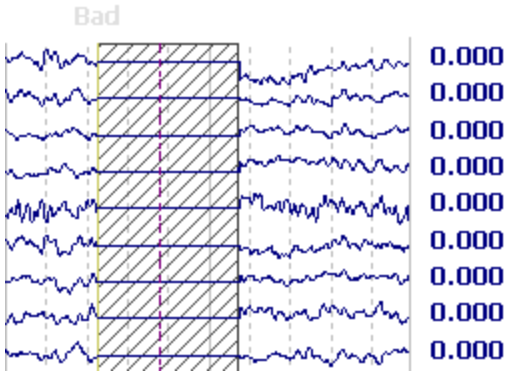
Constant. Flat lines (zero slope) connect the last data point before the bad block to the first data point after the block.



Linear. Sloping lines will connect the last data point before the bad block to the first data point after the block.



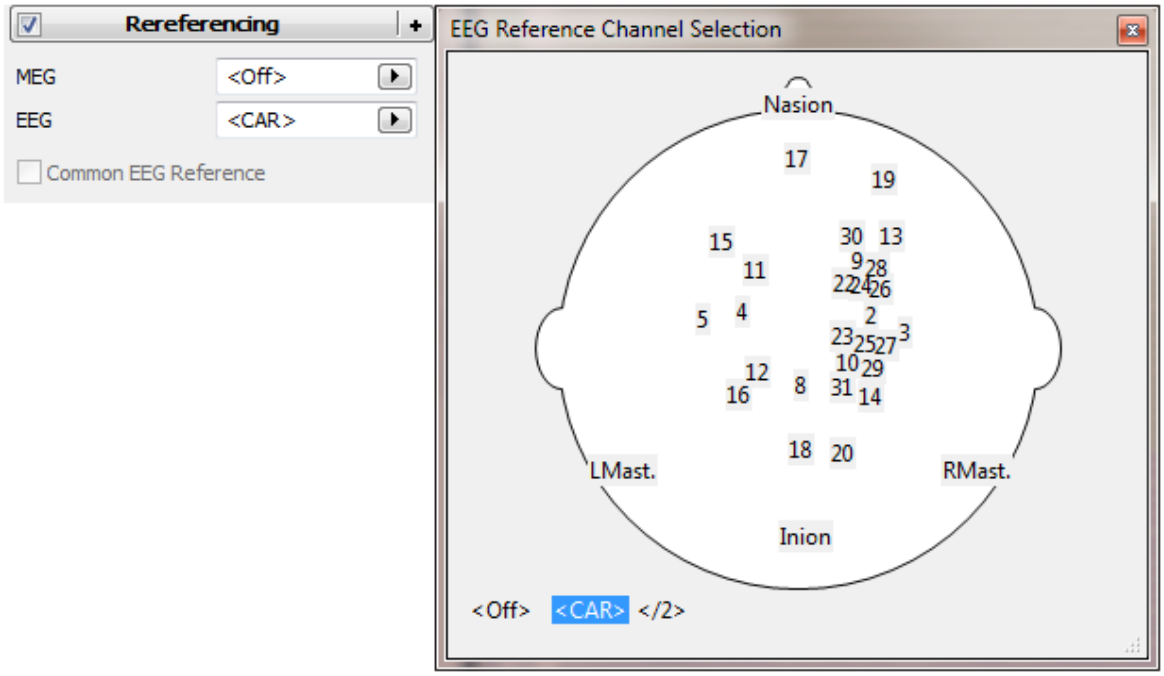
Zero. Zero will set the Bad Blocks to 0μVs (similar to **Constant** above, except that the flat lines with **Constant** are not necessarily at 0μV).



Reset. Clicking the Reset button will reset all manually designated Bad Blocks to be accepted blocks.

17.1.2 Rereferencing

The Rereferencing panel allows you to change the reference to the Common Average Reference (CAR), or to a single reference channel, or to other options, as described. The Reference can be selected independently for the channel groups; you will see multiple Groups depending on how they were designated.



The **Reference** is selected from the montage dialog. **<Off>** displays the data as recorded. **<CAR>** is the Common Average Reference, which is used for source reconstruction (with EEG data). To create a derived reference for any other channel, just click that channel. Use *Ctrl+left click* to select two channels to obtain an averaged reference of those two channels.

Note

CURRY will use a CAR for source reconstruction, despite whatever reference you have selected. For that reason, you should select the CAR when doing source reconstruction so you can see the data that are being analyzed. Again, CURRY computes the source analyses with a CAR regardless of the reference you select.

The **</2>** option is used when you want an averaged ear (or mastoid) reference. For example, say you recorded all EEG channels with an A1 reference, including A2-A1. Now you want an averaged ear reference. Use *Ctrl+left mouse* to select **A2** and **</2>**. This divides the A2 channel by 2, which is all that is needed to create the averaged reference with A1.

 **Care**

Referencing is performed after the filtering to ensure that the data are correctly referenced as they go to the reconstruction. This is necessary because the forward calculation takes the referencing into account as well. For that reason, no reconstructions are possible if no referencing is selected (for EEG data).

 **EEG**

Usually the common average reference (**CAR**) is used for electric measurements. Additionally, it is possible to select a reference channel. The displayed MGFP is always computed with a CAR.

 **MEG**

Since MEG data use absolute magnetic field measurements (not voltage differentials) there is no need for a CAR. The default setting is therefore set to Off. CAR should generally be avoided since one virtual channel will be taken away, and data will be lost in the process).

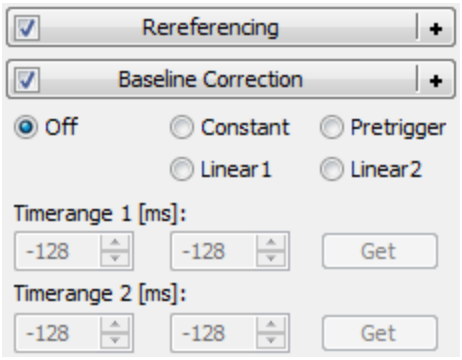
In CURRY 8, as in CURRY 5-7, magnetic CMR (common mode rejection) always equals plain CAR (and is accessed using the **CAR** option for the Reference Channel). Vector-based CMR was an option in CURRY 4.x that is no longer supported.

 **Care**

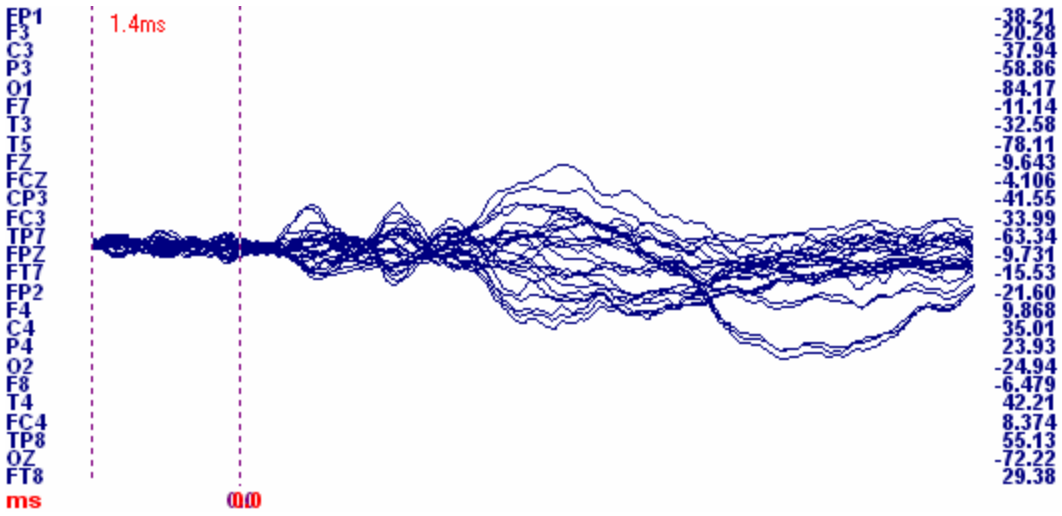
The stability of source reconstructions is highly sensitive to magnetic CMR. When data are processed for which a CMR has been performed previously, the **CAR** setting must reflect this. Otherwise, source reconstruction will fail.

17.1.3 Baseline Correction

These parameters are used to select the method for performing **Baseline Correction**.



The baseline correction option is used to remove a constant or linear DC offset from the data. This can be the entire interval that is displayed, only the pre-stimulus interval (if present), or one or two Timeranges that you select. The Baseline Correction is applied "on the fly" when you select a type of correction or set the Timerange(s).



The Baseline Correction section lets you select the type of correction to apply, as well as the Timerange(s) of the interval to be used.

Constant. For a constant baseline correction, the entire displayed interval is used to determine for each channel the offset that is subtracted from the data. The Timerange to use is specified literally or taken from the momentary time cursor. This option is typically used with continuous or epoched data where there is no prestimulus-interval. When you select Constant with epoched or averaged data, check the Timerange 1 interval to be sure it is set for the range you want to use.

Pretrigger. The Pretrigger interval (pre-stimulus) is used for baseline correction. This is typically used with evoked potential data (and is grayed out with continuous data).

Linear 1, Linear 2. For linear baseline correction, an additional linear drift in the data can be compensated. In this case, it is also possible to specify two Timeranges from which the baseline is determined. Weights are given to the

samples in order to achieve the same overall weight in the linear fit for each of the two Timeranges.

Timerange 1 [ms]. With the channel-wise Linear 1 waveforms correction, a linear drift is fitted to the data within the selected time range for each channel. The data in the whole time range are corrected by the extrapolated linear drift. Set the outer cursors to define the Timerange and then click the Get button. Or, enter the values manually in the fields.

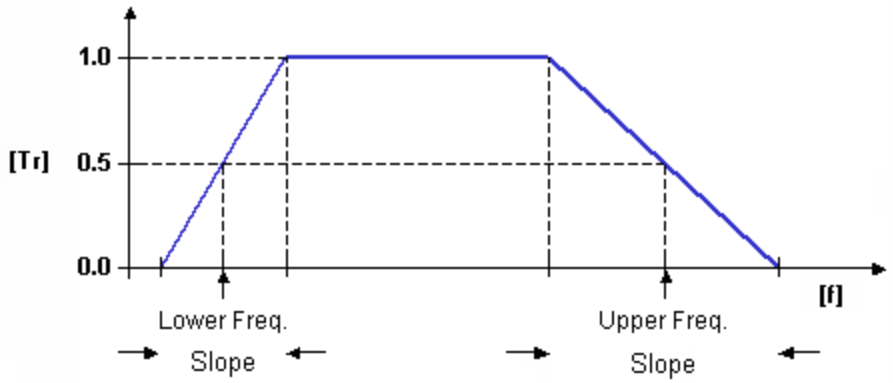
Timerange 2 [ms]. Set the outer cursors to define the Timerange and then click the Get button. Or, enter the values manually in the fields. The drift is calculated via the mean values of the data in the first and second time range.

17.1.4 Filtering

The Filter parameters allow you to apply a bandpass, notch, or bandstop filter, add noise to the data, and change the filter shape.

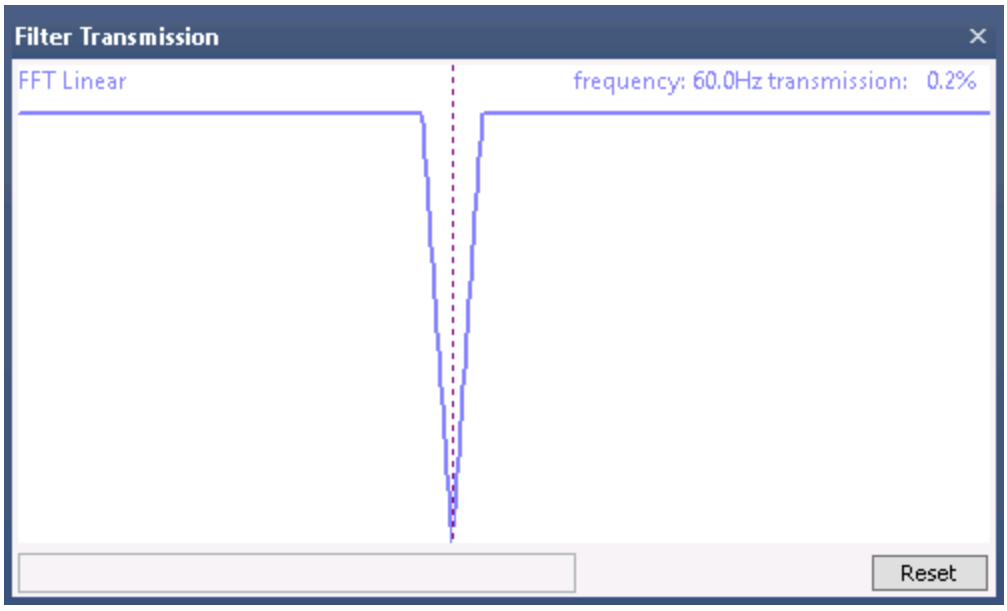
Offline filtering is applied to EEG and MEG channels, but not to "Other" channels. To filter an Other channel, *right click* on the channel label and select **Set Filter Frequencies**.

The parameters control how the transfer function *Tr* increases from 0 to 1 in the frequency range below the lower and decreases from 1 to 0 above the upper limit. For all settings the transfer function is 1 between the upper and lower limits (**Linear** filter shown).

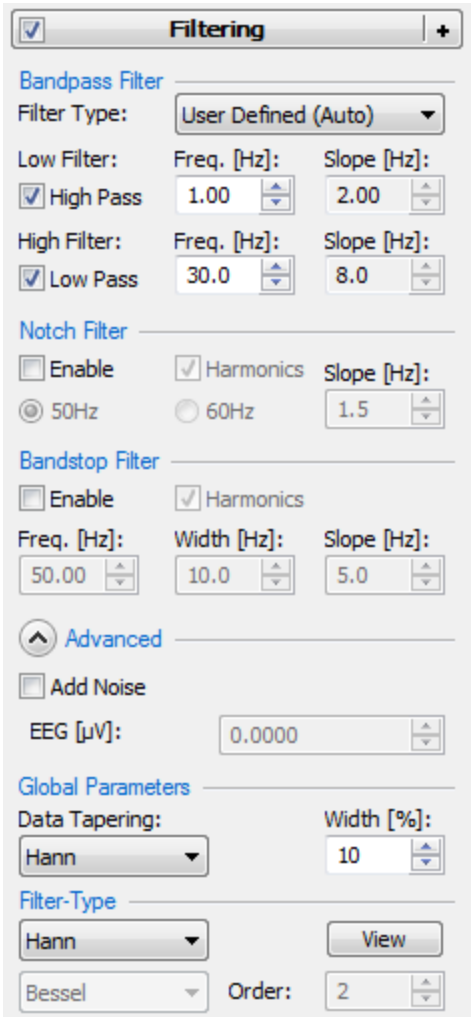


To see the effects of any of the filter parameters you set, click the View button in the Filter-Shape section. The Filter Transmission widow will appear, showing the filtering function. Click the Reset button in that window to clear the display, reset the filter parameters as desired, and click the View button again to see the effects. If you do not click the View button, you may superimpose additional filter functions. A 60 Hz, linear shaped, notch filter function is shown below.

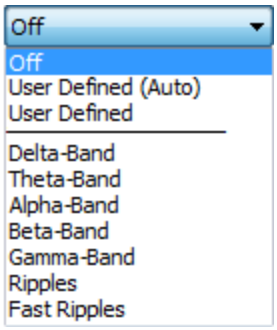
Vary the contents of the display, as follows. Use the *mouse wheel* to change the display scale. Use *Shift+left mouse* to drag the contents of the display. Use *Shift+mouse wheel* to expand the x-axis.



The Filter Parameters panel allows you considerable control over the filter characteristics. The filtering will be applied "on the fly" whenever you have a filtering option enabled. Filtering affects the entire sweep (not just the selected Timerange).



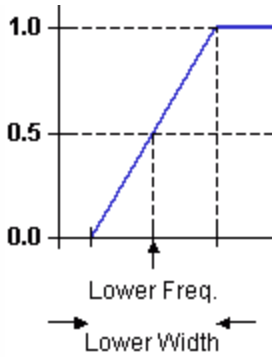
Bandpass Filter. **User Defined (Auto)** sets the slopes automatically; whereas, the **User Defined** option lets you select the desired slopes. Preset bandpass filters for Delta, Theta, Alpha, etc. may be selected. The parameters are seen in the lower fields, and may be edited as desired. **Ripples** and **Fast Ripples** select faster frequency bands to focus on High Frequency Oscillations that have been associated with epilepsy. Ripples sets a bandwidth of 80-200 Hz and Fast Ripples sets a bandwidth of 200-450 Hz (AD rates slower than 1000 Hz will have different upper limits, as the highest low pass filter cannot exceed half the AD Rate). (See for example, Bragin A, Wilson CL, Staba RJ, Reddick M, Fried I, and Engel J. Interictal High-Frequency Oscillations (80–500 Hz) in the Human Epileptic Brain: Entorhinal Cortex; Ann Neurol 2002;52:407–415).



Low Filter (High Pass). Click this option to enable the High Pass Filter (frequencies higher than the entered value will be passed). It is typically used to attenuate low frequency drifts or DC offset.

High Pass. The High Pass filter may be enabled or disabled.

Freq. [Hz]. This is the frequency limit of the High Pass Filter. The figure below is a section of the first figure in this section, seen above. The value that you set for Frequency is the point at which there is 50% attenuation of the amplitude of that frequency. It is the center point of the filter attenuation.



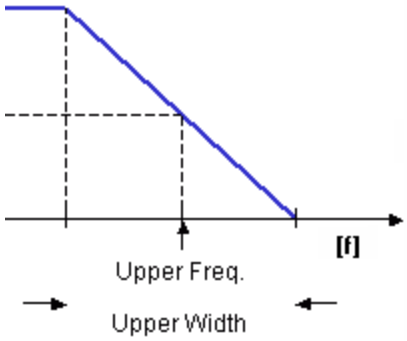
Slope [Hz]. Slope, which can also be thought of as width, is the frequency range from complete attenuation to complete transfer - see the figure above. The greater the Slope, the broader the width, and the shallower the "roll-off".

The Slope should not extend below 0 Hz. If the High Pass Frequency is set for 1Hz, the Slope should not exceed 2Hz. **The User Defined (Auto)** option will set the slope automatically.

High Filter (Low Pass). Click this option to enable the Low Pass Filter (frequencies below the entered value will be passed). It is typically used to attenuate high frequency noise, EMG, etc.

Low Pass. The Low Pass filter may be enabled or disabled.

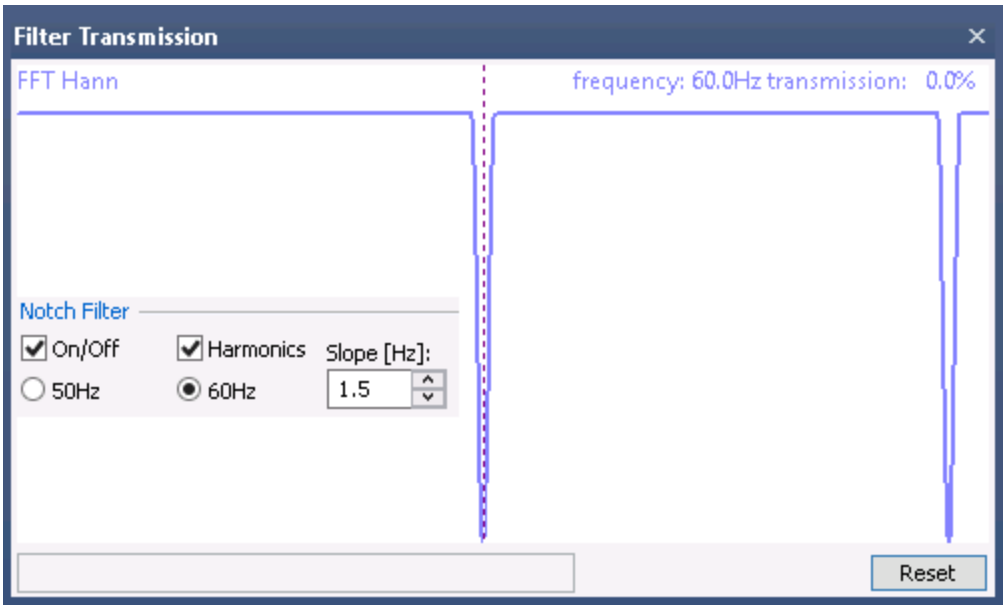
Freq. [Hz]. This is the frequency limit of the Low Pass Filter. The figure below is a section of the first figure in this section, seen above. The value that you set for Frequency is the point at which there is 50% attenuation of the amplitude of that frequency. It is the center point of the filter attenuation.



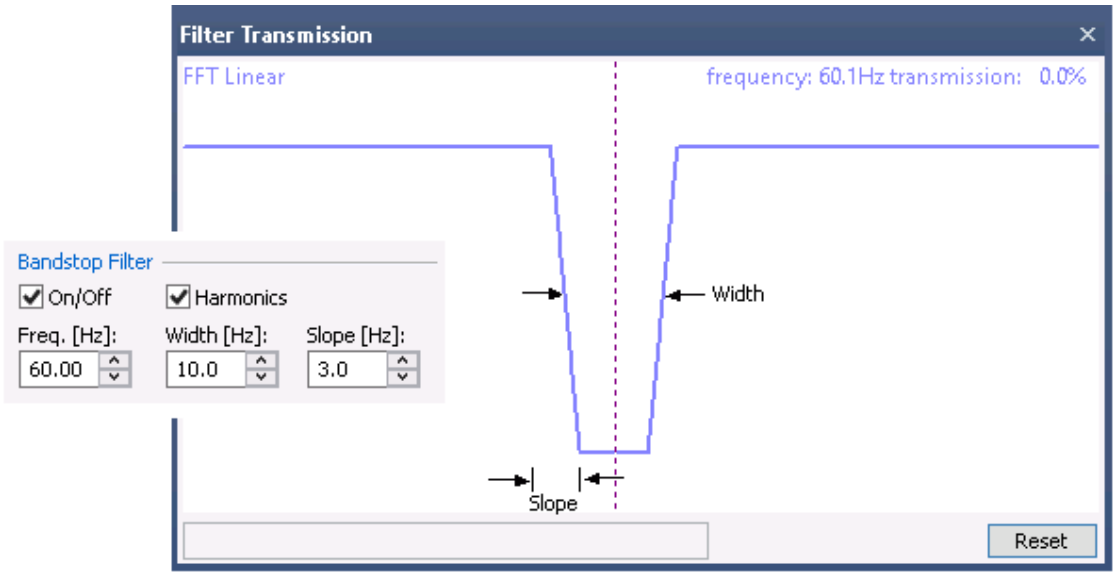
Slope [Hz]. Slope, which can also be thought of as width, is the frequency range from complete transfer to complete attenuation - see the figure above. The greater the Slope, the broader the width, and the shallower the "roll-off".

Notch Filter. A notch filter, centered at either 50 Hz or 60 Hz may be applied to attenuate line noise. The 

setting controls whether harmonics (multiples) of the selected notch filter frequencies are suppressed. If enabled along with the 50 Hz Notch Filter, for example, harmonics of 50 Hz (e.g., 100 Hz) will also be attenuated. Set the desired width of the notch in the **Slope (Hz)** field. Below is a 60 Hz notch filter with Harmonics enabled to show filtering at 60 and 120 Hz.



Bandstop Filter. A Bandstop filter is the opposite of a Bandpass filter. Rather than passing frequencies between the high and low pass limits, the bandstop filter attenuates frequencies about a selected frequency (similar to a notch filter, but broader).



Harmonics. The  setting controls whether harmonics (multiples) of the selected filter frequencies are suppressed.

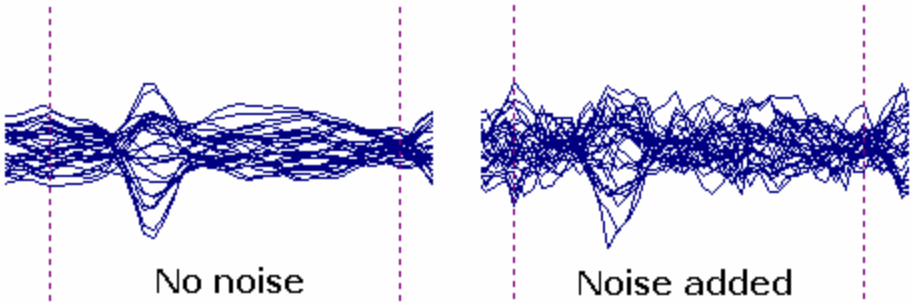
Freq. [Hz]. Center frequency for the bandstop filter. In the figure above, the Frequency was set to 60 Hz.

Width [Hz]. The Width parameter is used in addition to the Slope parameter with Bandstop filtering. Width is the interval from the 50% attenuation points about the center frequency. In the example above, the center frequency is 60 Hz, and the Width is 10 Hz. The frequency values at the two arrows are 55Hz and 65Hz.

Slope [Hz]. The interval defines the frequency span from complete transfer to complete attenuation (shown in the figure above). The Slope is the same on both sides of the center frequency.

Advanced
Click the button to see additional filter settings.

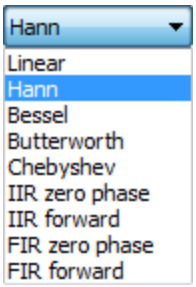
Add Noise, EEG [μV]. Gaussian distributed Noise can be added to the waveforms (e.g., to obtain more realistic simulations). This can be useful in cases where you have simulated data that contains no noise. In that case, the Noise Estimation may lead to erroneous source reconstruction. Enter a level in the **EEG [μV]** field.



Global Parameters

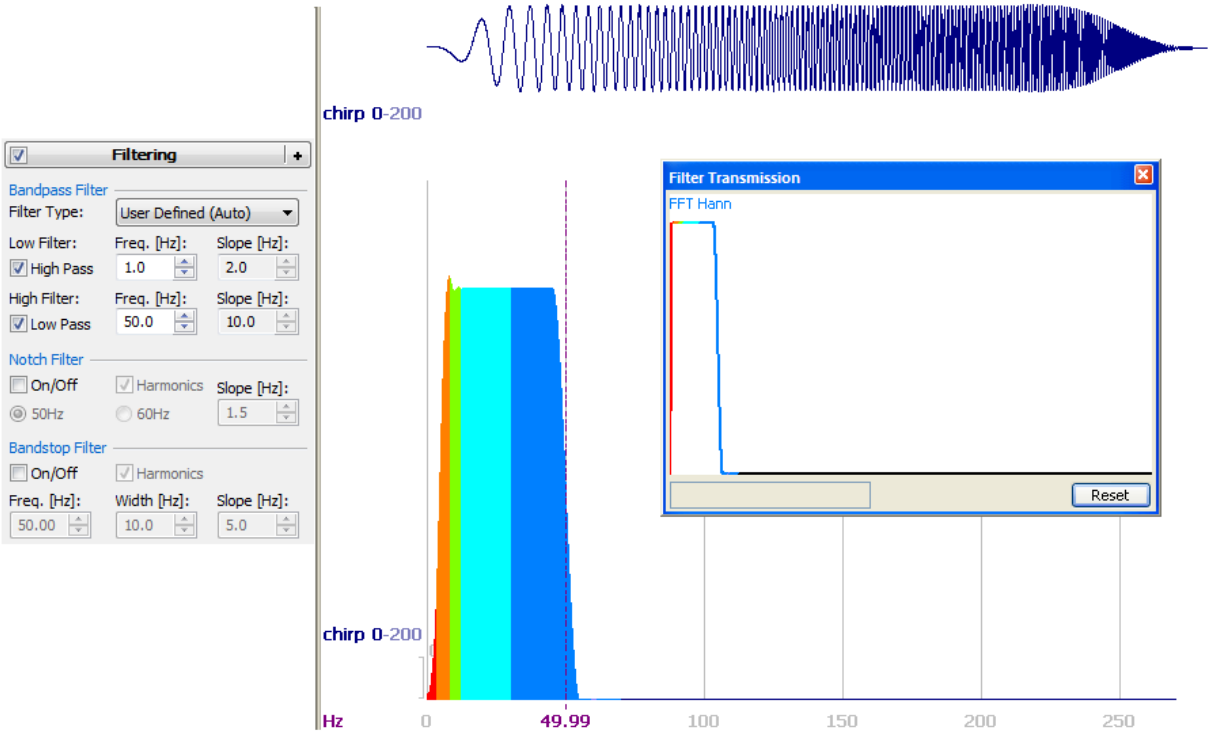
Data Tapering, Width [%]. Windowing, or data tapering, is typically applied when computing spectral distributions to avoid spurious increases that can occur due to abrupt transitions from zero voltage at the beginning and end of an epoch. The different methods - Hamming, Hann, Blackman - have different shapes to the tapers. The Width is the extent of the taper. Data tapering at the beginning of a continuous recording is shown below using 0% and 50% widths (a similar tapering is seen at the end of the file). With epochs, you will see the paper at the start and end of the epoch. Data Tapering is not applied if the Filters are turned off.

Filter-Type. You have the option of applying several different filters. The first 5 are FFT-type filters; the last four are IIR and FIR filters. In general we recommend using the default Hann filters, and selecting **User Defined (Auto)**, as this will set the **Slopes** automatically. See also the *Filtering* tutorial in the *CURRY 8 Installation and Tutorials* manual.

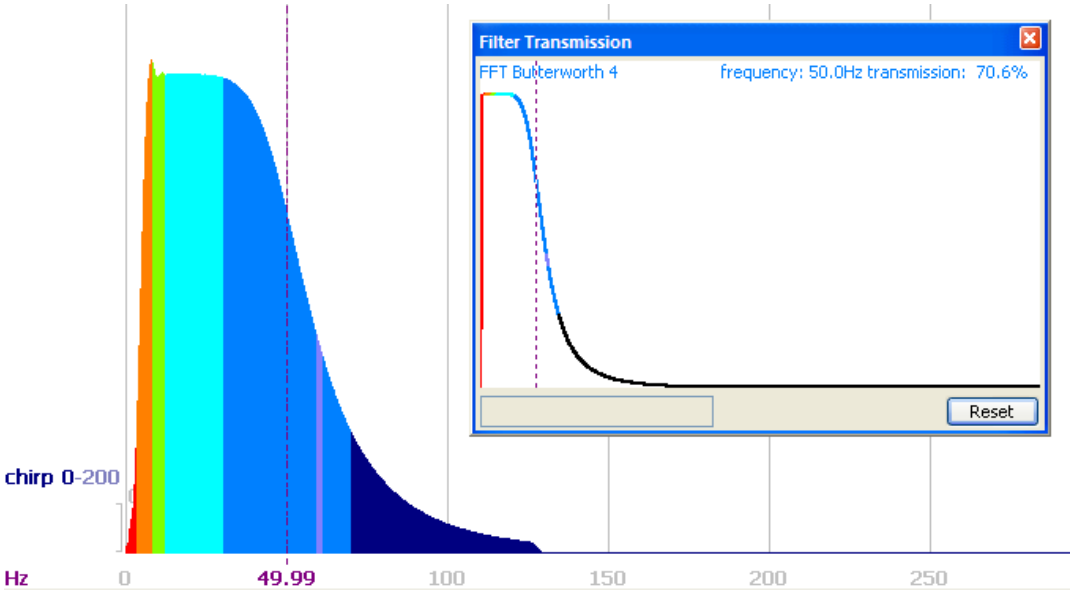


Linear. The filter functions with Linear roll-off slopes. Applying the Linear filter, as displayed in the diagram above, results in a linear attenuation of frequencies below the low limit and above the high limit. There is no phase-shifting.

Hann. A Hann filter (default) has a curved shaped to the roll-off. There is no phase-shifting. In the figure below, a "chirp" file (0-200 Hz) is being filtered at 50 Hz with a Slope of 10 Hz. A 10% Hamming taper has been applied. The Spectra results and the Filter Transmission function (from **View**) are shown. By viewing the various filters in this way, you can compare the differences quite easily.

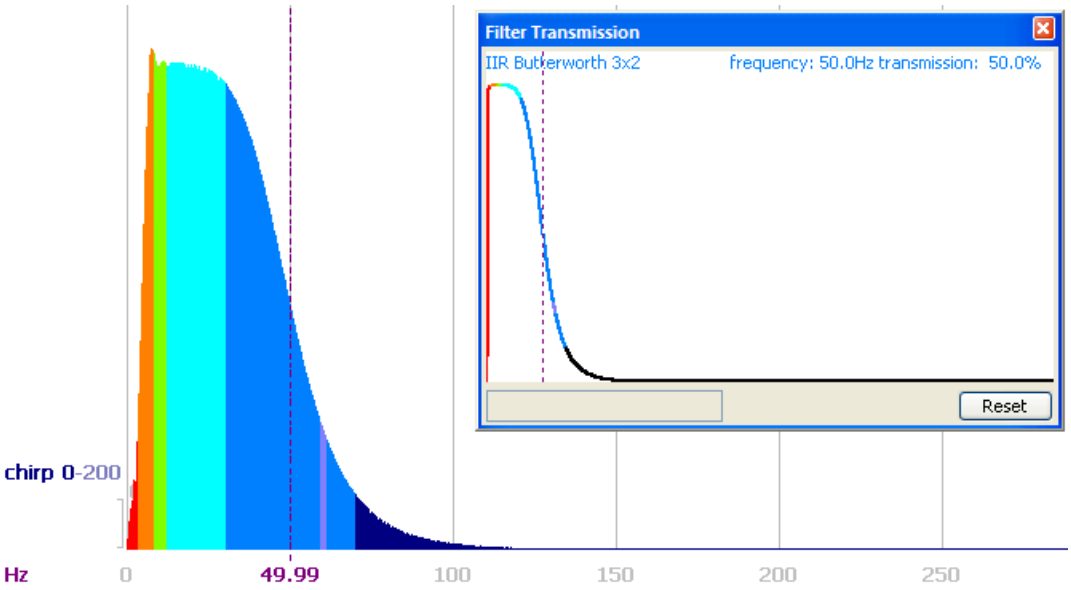


The next three filters - **Bessel**, **Butterworth**, and **Chebychev** - are also FFT-type filters. With these you also can select the steepness of the roll-off using the **Order** field. Below is an example of the **Butterworth** filter using an **Order** of **4**. There are no phase shifts with these filters. (Bandpass parameters were the same as in the figure above - 1-50 Hz).



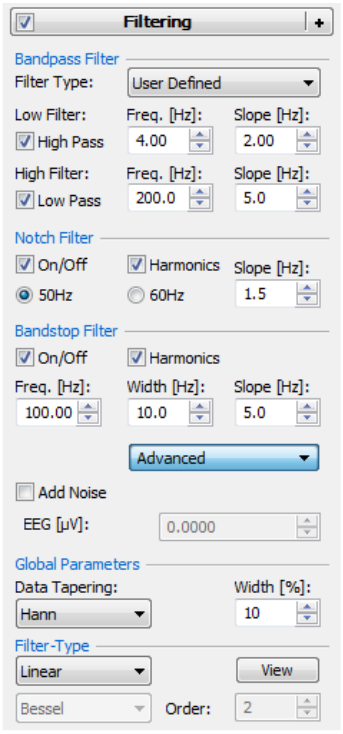
IIR Filters (Infinite Impulse Response). IIR filters can have either zero phase shifts (**IIR zero phase**) or can introduce phase shifting (**IIR forward**). With each, you can select **Bessel**, **Butterworth**, or **Chebechev** filtering, and you

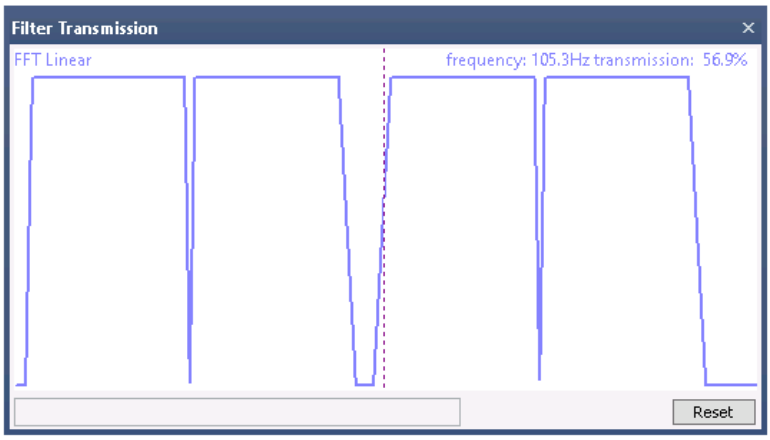
may select an **Order** from **1-4**. With IIR zero phase, the Order is divided by 2 (data are passed on both directions). Below is an example of IIR zero phase, Butterworth, with an Order of 3. The "3x2" in the Filter Transmission window means that this was a 3rd order filter, passed twice. (Bandpass parameters were the same as in the figure above - 1-50 Hz).



View. Click the View button to see the effects of the filter parameters, including those you have set for the High Pass and Low Pass filters (and other parameters).

In the example below, a Linear filter was selected - note that "Linear" appears in the Filter Transmission display. A 50 Hz notch filter was selected, and this is seen as the first sharp dip. A Bandstop Filter was also selected, with a center at 100 Hz, a width of 10 Hz, and a slope of 5Hz. This is the second dip in the display. The overall Bandpass filter was set from 4Hz (slope of 2Hz) to 200 Hz (slope of 5Hz). The vertical cursor is position at 105.3Hz, and the transmission of the signal is at 56.9% of the original.

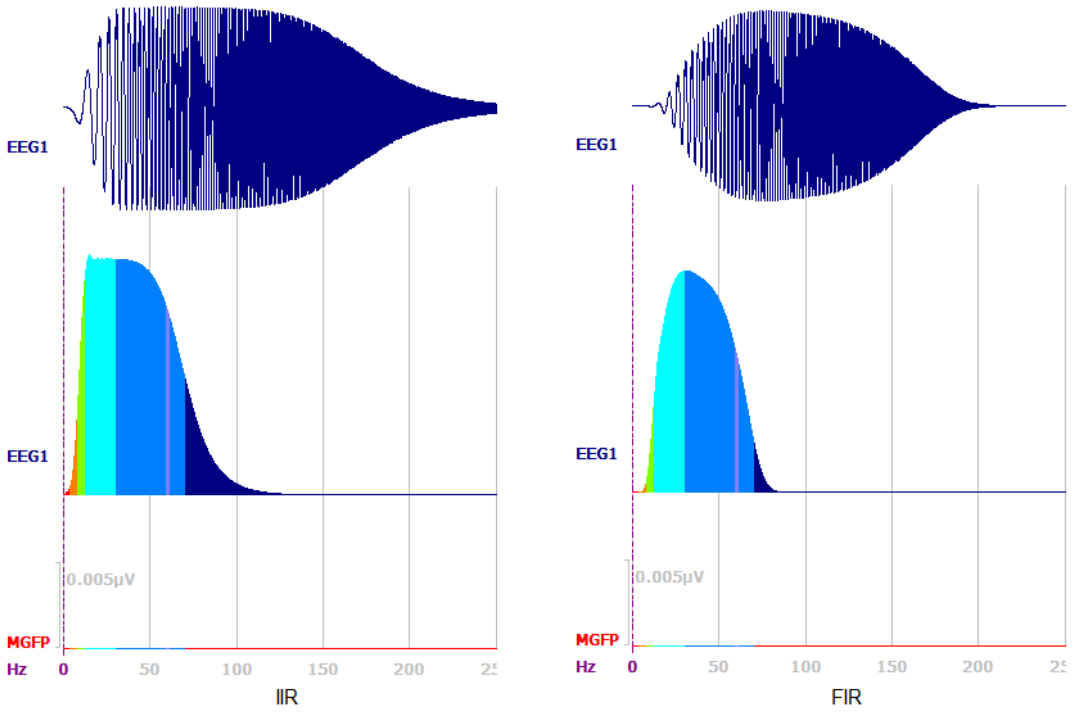




By varying the filter type, cut-off frequency, width, and slope, you can construct a custom filter, and see the effects in the display. If you want to make changes and compare the effects, enter the parameters you want and click View again to see the second graph along with the first. Click the **Reset** button to remove the prior graphs.

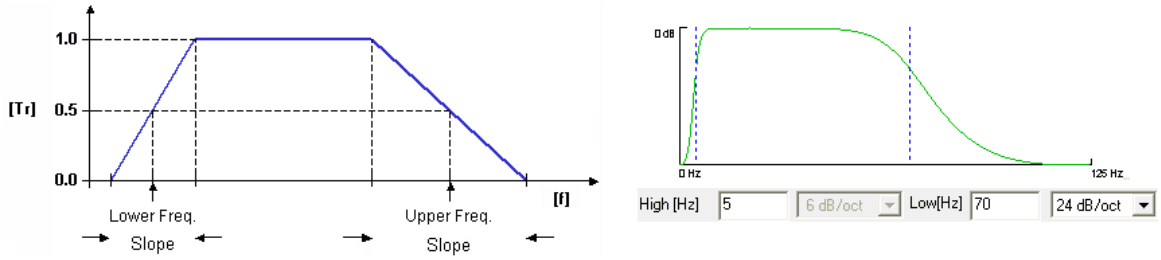
FIR Filters (Finite Impulse Response). FIR filters can have either zero phase shifts (**FIR zero phase**) or can introduce phase shifting (**FIR forward**). An FIR filter is one whose impulse response (or response to any finite length input) is of finite duration, because it settles to zero in finite time. This is in contrast to infinite impulse response (IIR) filters, which may have internal feedback and may continue to respond indefinitely (usually decaying). The default FIR filters in CURRY have an order of 62, and use a Hamming window.

For comparison's sake, an IIR zero phase filter (1-70 Hz, Butterworth, Order 4) is compared with an FIR zero phase filter (1-70 Hz).

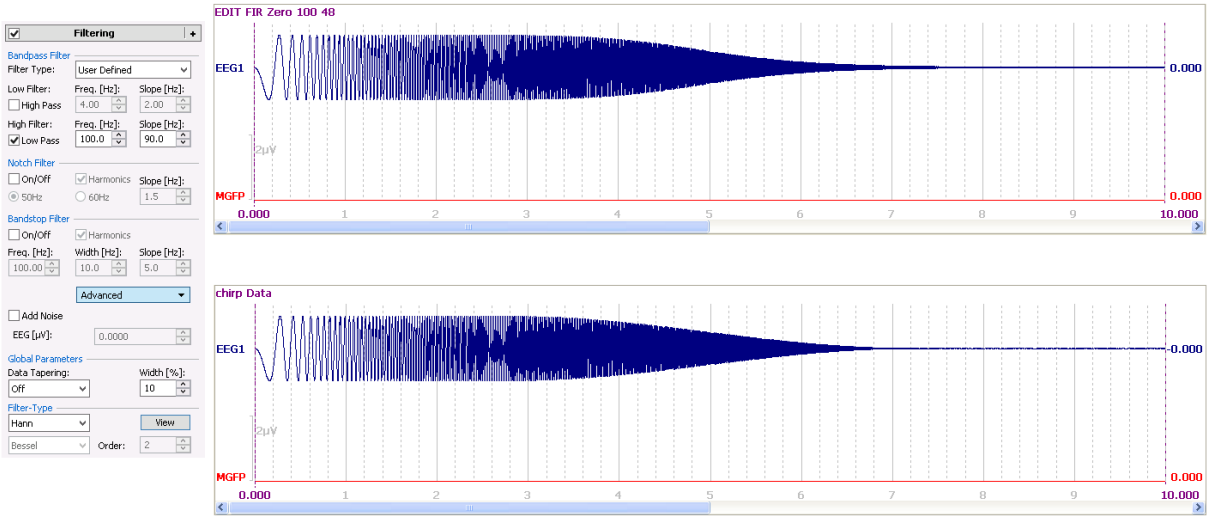


Matching CURRY filters with those used in EDIT or other software

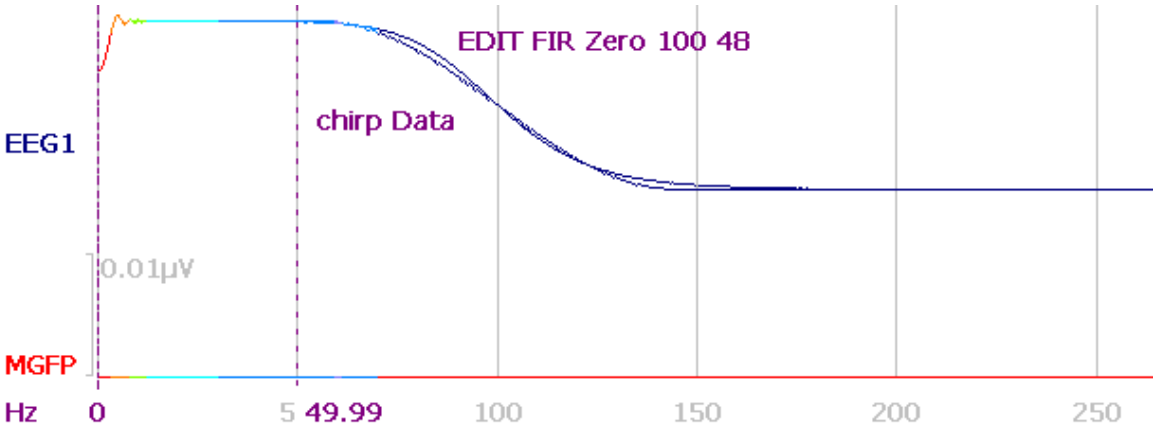
If you already have data from the Neuroscan EDIT program (or other analysis program), and you wish to match the filters as closely as possible to data recorded with CURRY, there is no simple way to perform the conversion. The nature of the filters differs between CURRY and EDIT. In CURRY (left), with Linear filters shown, the 50% (amplitude transmission) frequency and the width of the transition is given; whereas, EDIT (right) uses a more indirect measure (dB/octave) with a non-linear (non-converging) slope.



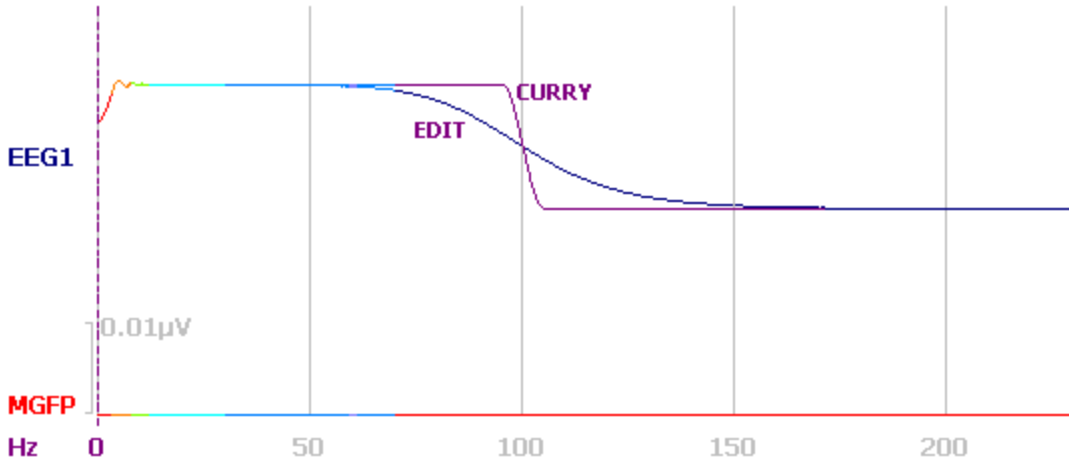
One approach to matching the two is to use a "chirp" file. This is a sine wave with increasing frequency - in this case, 0-200 Hz. When you apply the filters, you will see the effects on the data. In the example below, we filtered the chirp file in EDIT using an FIR Zero Phase filter, set at 100 Hz, with a 48dB/oct roll-off. The idea then is to open that file in CURRY, along with the original chirp file, and try to match the effect. In this case, a basic Hann filter and a 90 Hz Slope is getting pretty close.



Compute the **Spectra** for both and superimpose the results. There are very slight differences as you approach and exceed the cutoff frequency. The slower frequencies are identical.



The filters in CURRY allow you to obtain a much steeper roll-off, preserving more of the data as you approach the cutoff frequency, and excluding more of the activity after the cutoff frequency. Below is a Hann filter at 100 Hz with a 10 Hz Slope, compared to the FIR zero phase filter at 100 Hz with 48dB/oct in EDIT.

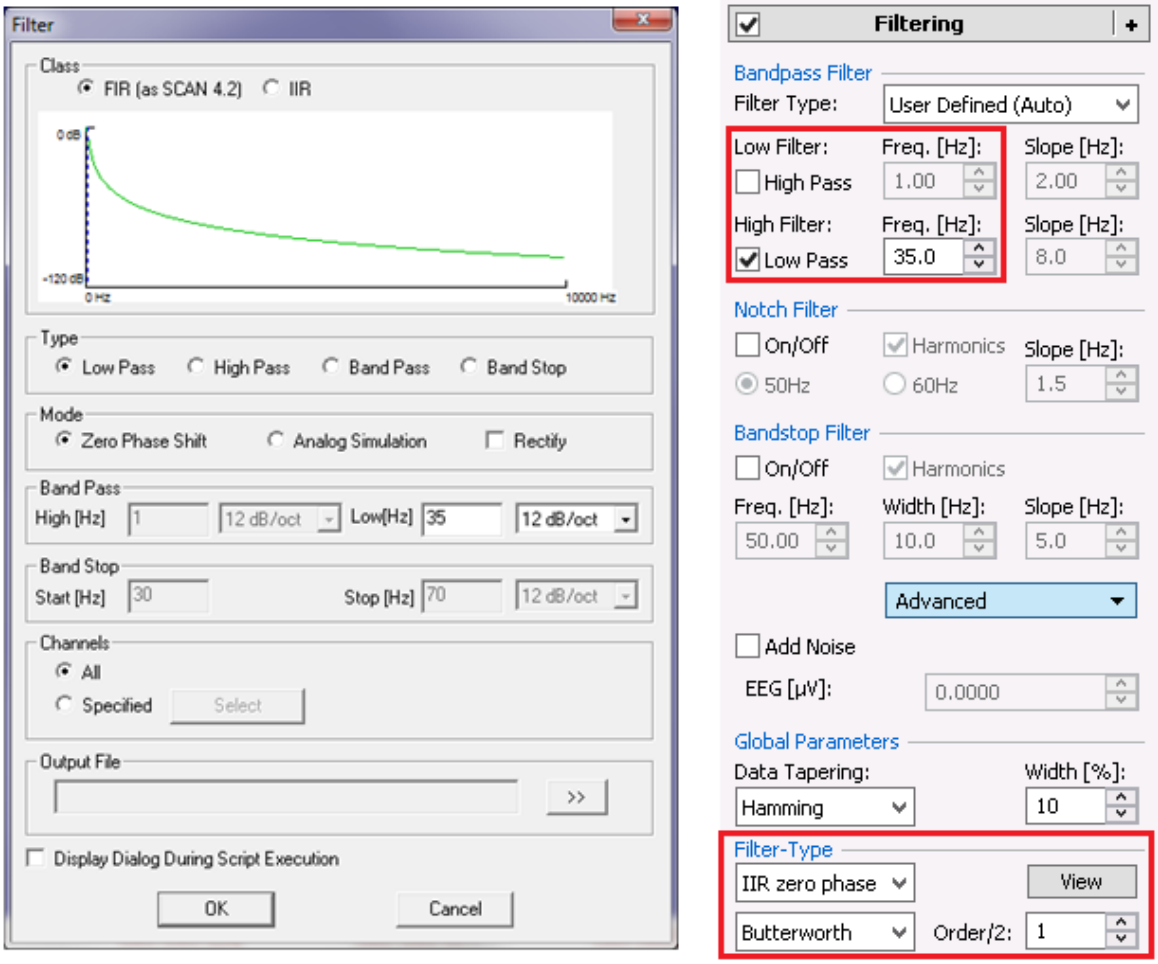


Additional testing with certain filter parameters has resulted in the following equivalences between Scan and CURRY filters.

The FIR zero phase shift filters in Scan are equivalent to IIR zero phase, Butterworth filters in CURRY, where

12dB/Oct in Scan is equivalent to order/2: 1 in CURRY
24dB/Oct in Scan is equivalent to order/2: 2 in CURRY
48dB/Oct in Scan is equivalent to order/2: 3 in CURRY
96dB/Oct in Scan is equivalent to order/2: 4 in CURRY

For example,the filter settings in Scan on the left are equivalent to the filter settings in CURRY on the right.



IIR filters (analog simulation) in Scan are equivalent IIR forward, Butterworth filters in CURRY, where

12dB/Oct in Scan is equivalent to order: 2 in CURRY
48dB/Oct in Scan is equivalent to order: 4 in CURRY

FIR filters (analog simulation) in Scan do not have an equivalent counterpart in CURRY. (The FIR filters in CURRY are sharing the same characteristics as the default FIR filters in the Compumedics clinical EEG software, ProFusion).

Contact curry8help@neuroscan.com if you need help in matching filtering parameters between SCAN and CURRY.

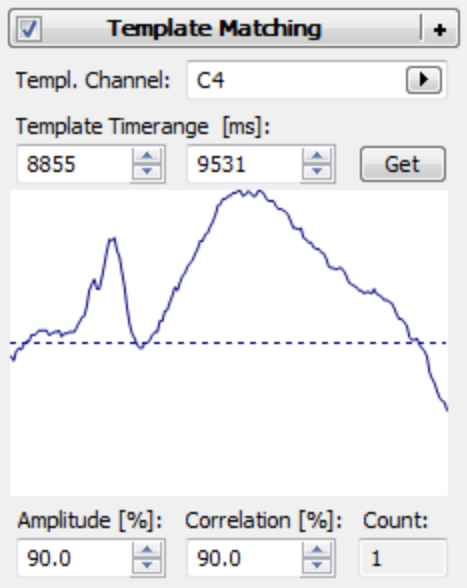
17.1.5 Template Matching

The Template Matching feature is used to detect defined events in the data such as epileptic spikes (for source reconstruction) or artifacts (for removal). You define one or more templates of the spikes(s) or artifacts(s), using one or more Template Matching panels, and CURRY will search through the file for sections that meet amplitude and correlation criteria you set. The event categories can be saved and retrieved automatically as series of sweeps, or epochs. The epochs may then be

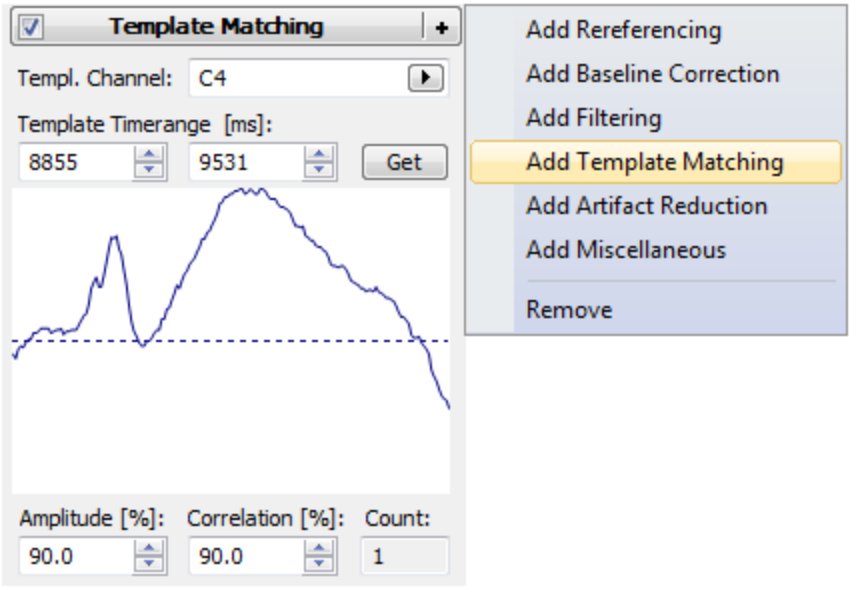
averaged to increase the SNR, thereby facilitating source reconstruction. Or, you may average the sweeps immediately, bypassing individual epochs. Template Matching is frequently used in conjunction with the **Events/Epochs** list.

Care

If the template waveform has all or nearly all positive (or negative) voltages, this will likely result in poor matches. Use baseline correction, filtering, multiple channels, or a wider Timerange to obtain template waveforms that have both positive and negative voltage values.



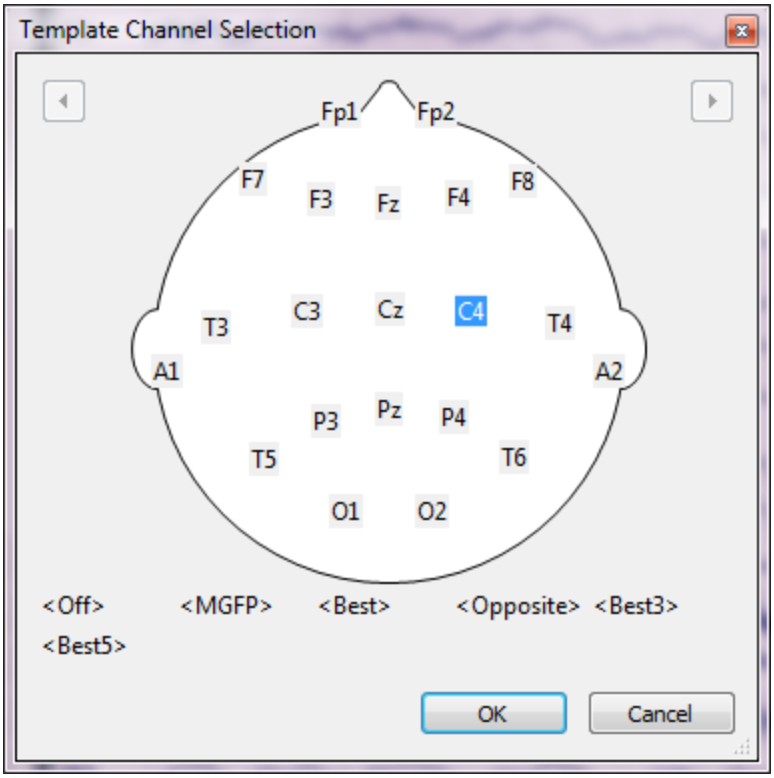
In CURRY 7, you could define up to 5 templates that are scanned in sequence. You can do the same thing by selecting additional **Template Matching** panels from the **+** list.



The use of multiple templates is intended primarily for detection of epileptic spikes, where there can be different classes of spikes in the same file, based on morphology or spatial distribution. Select the first panel and Template Channel that shows the spike clearly. Set the two outer cursors to define the spike, and press the Get button. Then move to the next Template Matching panel and repeat.

The multiple template panels may also be used for detection of different artifacts. When using the **Templates** option in **Artifact Reduction** (offline), the first sequence in Artifact Reduction will use the first template; the second Artifact Reduction sequence will use the second template, and so on.

Template Channel. Select the channel that is to be used for the template. Instead of individual channels, you may select the **MGFP** channel, the channel with the **Maximum SNR**, the **Best 3** channels (the 3 best SNRs), the **Best 5** channels, or **All** channels. **Opposite** selects the same channel as **Best**, and then finds the channel with the largest difference to this signal.



Template Timerange. The Timerange is selected using the two outer vertical cursors to define the template, just as you select the interval for Source Reconstruction. Press the Get button to transfer the cursor latencies to the Event Detection panel (or enter the values from the keyboard).

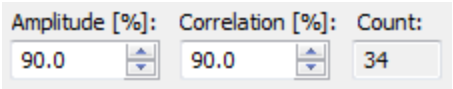
Amplitude [%]. CURRY will search through the file for voltages that are a percentage of the value in the template. **75**% in this field means that CURRY will search (in the designated channel) for voltages (or fT values for MEG) that are at least 75% of the voltage in the template. Larger amplitudes are also included, as follows. If you set the

Amplitude to 50%, that will include amplitudes from 50% of the template to 1/0.5%, or 200% larger. (All potential matches from 30% Amplitude and 50% Correlation are detected, regardless of the values that are entered. The matches that are displayed in the Event List are the ones that fit within the parameters that you set).

Correlation [%]. When the voltage criterion is met, CURRY will perform a correlation between the new region with the same region in the template. If the correlation meets or exceeds the level you set, the new region will be detected as an event (in conjunction with the Amplitude criterion).

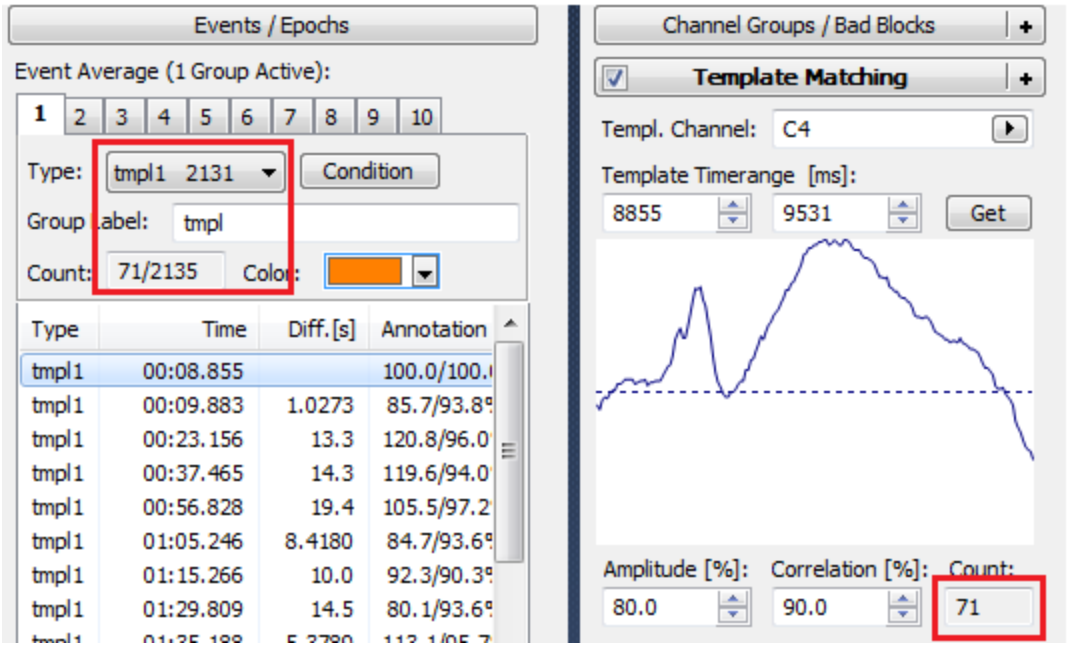
Both criteria must be met for there to be a match.

Count. After scanning the file, the **Count** field will display how many matches there are, using the **Amplitude** and **Correlation** levels that were set. Reduce either criterion to see the number of matches increase. It is generally better to have fewer well matched instances than a large number that are not that well matched.



Scan Templates. Scans through the data and computes matching events that are then shown in the **Count** field as well as in the **Event List**. You will initially see the flashing  button, letting you know that the file has not been scanned yet. After scanning, you will see the  button, letting you know that it has been scanned. If you change the Template Timerange after scanning, you will see the flashing arrow again, letting you know you need to scan the data again. Changing the Amplitude or Correlation criteria will not affect the scan button status. If you subsequently change previous parameter settings, including the Reference, Baseline Correction, and Filtering, these will affect the template matches, and therefore the  button will flash again  , letting you know that the file must be rescanned.

After scanning, you will see the number of matching events in the **Count** field for **Template Matching**, as well as in the **Event List** (first select *tmpl1*). In the example below, there are 2131 potential events in the file, while only 71 of them fall within the Amplitude and Correlation criteria selected. The 2135 number is how many total events there are in the file (not just the tmplx ones).

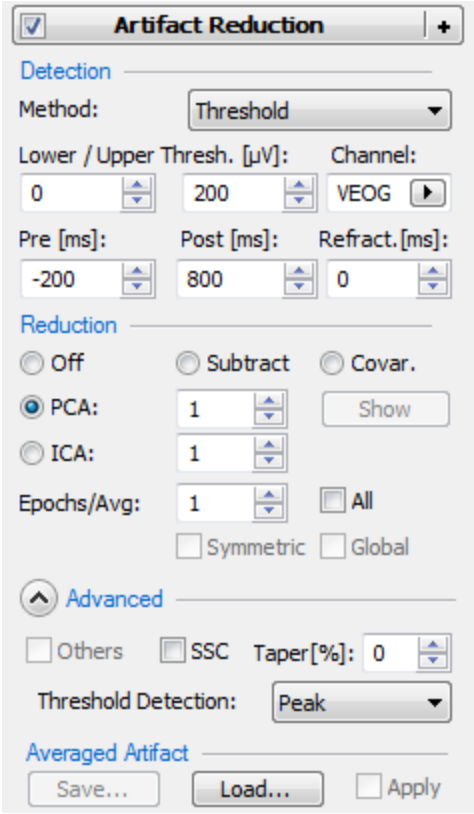


See the *Template Matching* tutorial for an example using epileptic spikes.

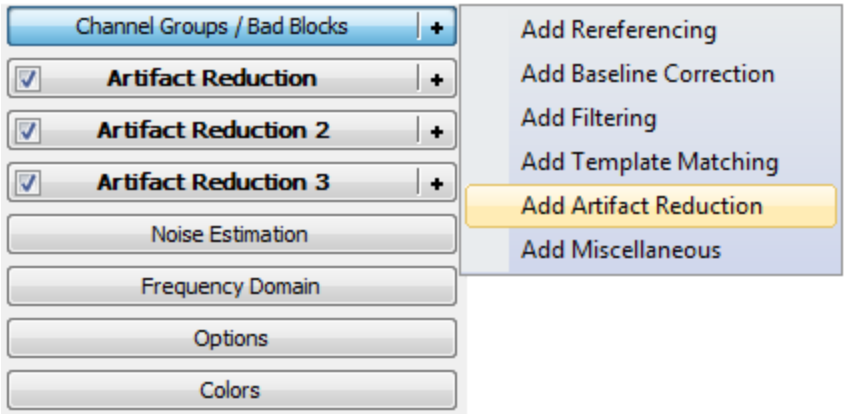
17.1.6 Artifact Reduction

These sections are used to reduce artifact in the data file. Multiple types of artifacts can be corrected by creating a sequence of correction methods.

The methods occur in two parts: Detection and Reduction. The upper fields are concerned with detecting the artifacts, and the lower fields let you select the type of reduction method you wish to use. The **Scan Data** button , found at the top of the Functional Data parameter panels, is used to scan the file for artifacts. Generally, you will need to scan the data before you can select a reduction method. The reduction options will be grayed out in these cases, indicating that you need to scan the data first.



Multiple Reduction Sequences. If you have a file with more than one type of artifact, you can configure more than one Artifact Reduction panel. Click on the **+** and select **Add Artifact Reduction**. You will see the numbered panels.

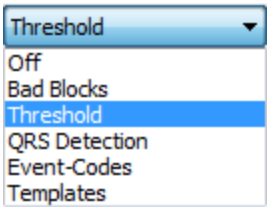


For example, you may wish to remove the eye blinks first and then remove EKG artifact. Set the parameters in the first panel, then set the second one. You will see the Scan Artifacts icon flashing  , letting you know that the file needs to be scanned. It will be scanned one time for each panel you configure. Uncheck the box  if you want to retain the settings without applying them. If you change any of the parameters above or including the Artifact Reduction panel, the Scan button will again flash, letting you know that the file needs to be scanned again.

It is not possible to have overlapping artifact intervals (defined by the Pre Post latencies), and therefore some blinks, for example, may be missed if they occur too closely together. You can reduce the Pre Post interval to avoid the overlap, or you can use a second Reduction Sequence to correct the blinks that were missed in the previous pass. In this case, if you are using a reduction method that does not correct the **Channel** you selected, you will then need to use a different **Channel**. The Threshold(s) should be adjusted accordingly.

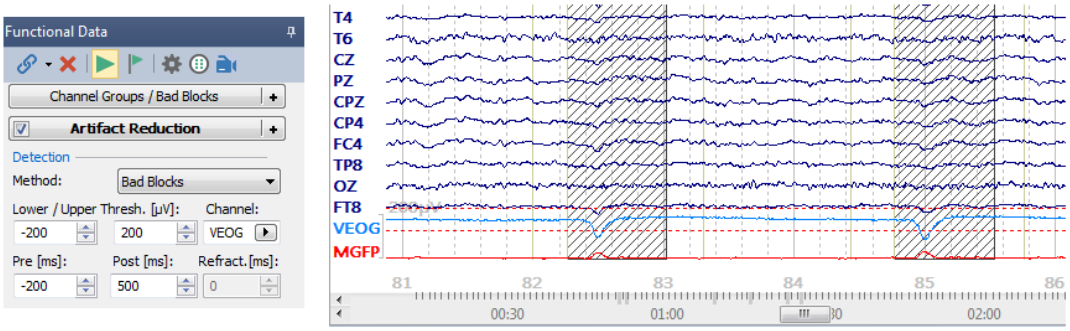
Artifact Detection. There are five different methods for performing Artifact Detection and reduction: **Bad Blocks**, **Threshold**, **QRS Detection**, **Event-Codes**, and **Templates**.

Method. Select the artifact reduction method(s) that you wish to use.



Off. No detection method is selected.

Bad Blocks. This method allows you to reject bad sections in the data file on the basis of a voltage threshold. **Lower** and **Upper Thresholds** are monitored, from the channel(s) you select. The **Pre** and **Post** fields define the region to be rejected. Voltages meeting the criteria during the **Refractory** period (measured from the point where the threshold is detected) will be ignored.

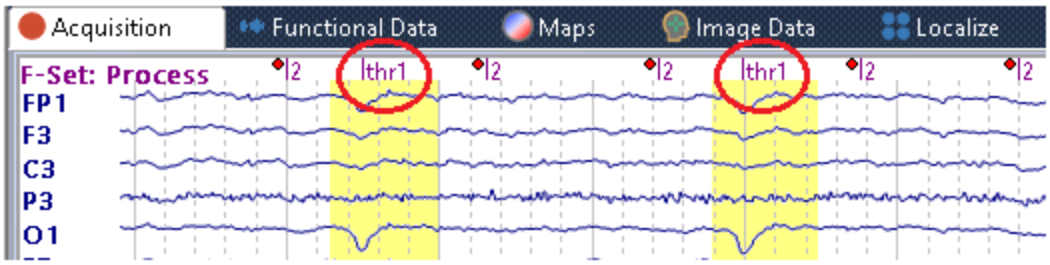


Note

If you designate bad blocks manually, you will be asked if you want to save the changes when you close the Study. If you detect the bad blocks automatically using **Bad Blocks**, you will not be asked if you want to save them, and they will not be saved. They will be saved if you save the Study Parameters, however.

Threshold. Any single channel, including the MGFP channel, collection of channels, or all channels will be scanned for voltages (or fT values for MEG) in excess of the **Threshold** values entered. The **Pre** and **Post** times define the

interval from the point at which the Threshold was detected. The intervals will be shaded in yellow in the data file. The detected artifacts will be seen as "thr1" (or whatever the Reduction Sequence number is) in the Event List.



QRS Detection. This method is designed primarily for reduction of heart beat artifact. The QRS complex is detected automatically and QRS1 events (or what the Sequence number is) are seen in the data file and in the event list.

The QRS Detection method uses an automated QRS Detection routine, based on a public domain algorithm for QRS detection (Open Source ECG Analysis Software Documentation; Copyright © 2002 Patrick S. Hamilton).

The algorithm is used for peak detection and trigger placement. With it, there is no need for the Refractory Period or Threshold parameters. You can still define the duration of the artifact, as well as the channel(s) that are to be monitored for detection.

Briefly, beats are detected in two phases: Filters and Detection Rules.

Filters. The signals are filtered to generate a windowed (time limited) estimate of the energy in the QRS frequency band. This is accomplished by:

1. Low pass filtering,
2. High pass filtering,
3. Taking the derivative,
4. Taking the absolute value of the signal, and
5. Averaging the absolute value over an 80 ms window.

   The final filter output produces what might be called a "lump" every time a QRS complex occurs. T-waves generally produce smaller lumps than QRS complexes.

Detection Rules. After the signal has been filtered, peaks are detected in the signal. Each time a peak is detected, it is classified as either a QRS complex or noise, or it is saved for later classification. The algorithm uses the peak height, peak location (relative to the last QRS peak), and maximum derivative to classify peaks. The following is an outline of the basic detection rules for the algorithm.

1. Ignore all peaks that precede or follow larger peaks by less than 200 ms.

2. If a peak occurs, check to see whether the raw signal contained both positive and negative slopes. If not, the peak represents a baseline shift.

3. If the peak is larger than the detection threshold it is called a QRS complex, otherwise it is called noise.

4. If no QRS has been detected within 1.5 R-to-R intervals, there was a peak that was larger than half the detection threshold, and the peak followed the preceding detection by at least 360 ms, that peak is classified as a QRS complex.

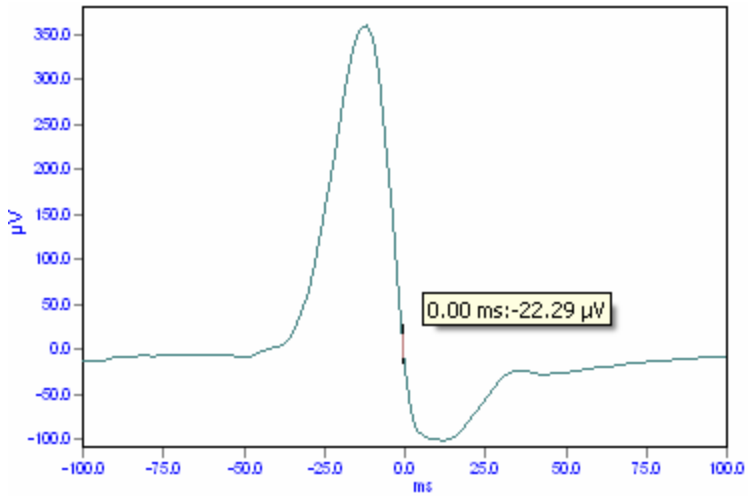
Threshold Estimation. The detection threshold used in 3 and 4 above is calculated using estimates of the QRS peak and noise peak heights. Every time a peak is classified as a QRS complex, it is added to a buffer containing the eight most recent QRS peaks. Every time a peak occurs that is not classified as a QRS complex, it is added to a buffer containing the eight most recent non-QRS peaks (noise peaks). The detection threshold is set between the mean or median of the noise peak and QRS peak buffers according to the formula:

Detection_Threshold = Average_Noise_Peak + TH*(Average_QRS_Peak Average_Noise_Peak)

where TH is the threshold coefficient. Similarly, the R-to-R interval estimate used in 5 is calculated as the median or mean of the last eight R-to-R intervals.

The beat detector must begin with some initial threshold estimate. In order to make an initial estimate, the maximum peaks are detected in eight consecutive 1-second intervals. These eight peaks are used as the initial eight values in the QRS peak buffer, the initial eight noise peaks are set to 0, and the initial threshold is set accordingly. The eight most recent R-to-R intervals are initially set to 1 second.

In practice, you will find that this method places the events not at the R wave peak, but rather between the R and S waves.

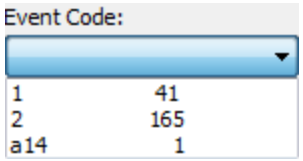


There is a "warm up" period at the beginning of the CNT file where no events are placed (usually 8 beats), then you should see events inserted for each detected QRS complex.

Our experience thus far with the public domain QRS Detection method is that it is very effective in detecting and removing the QRS complex in routine EKG recordings; however, it tends to become less accurate with BCG (which it was not designed to detect).

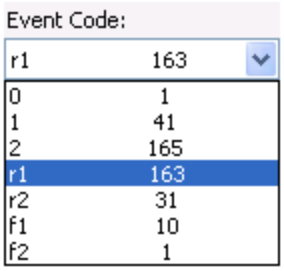
Event-Codes. Rather than using a voltage threshold to detect artifacts, this option uses event codes in the file. For example, in an SEP recording you might have stimulus artifact occurring at and just after the stimulus type codes. Define the duration of the artifact and use Subtract to replace the artifact with flat lines (**Epochs/Avg** = 1) or by subtracting whatever residual EEG is in the average (**Epochs/Avg** = larger value). Try PCA or ICA Projection to project the artifact from the data.

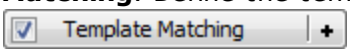
When you select **Event-Codes**, you will see the **Event-Code** field in place of the **Threshold** fields. The drop-down list will display the events in the files.



This is the method used to remove MRI gradient artifact (see the *MRI Gradient and Ballistocardiogram Reduction* tutorial). Briefly, in most MagLink systems, you will select the **Response Type 5** events, and then use **Subtract** to remove the gradient artifact.

If you first merge the behavioral data file from STIM2 (or other source), you will also see the responses in this list. In this case, the 1 and 2s are stimuli, the r1's and r2's are correct responses, and the f1s and f2s are incorrect (false) responses. [To merge the behavioral data, use the **Merge Behavioral Data File** button  at the bottom of the **Event List** dialog, or else use from the **Workflow**].



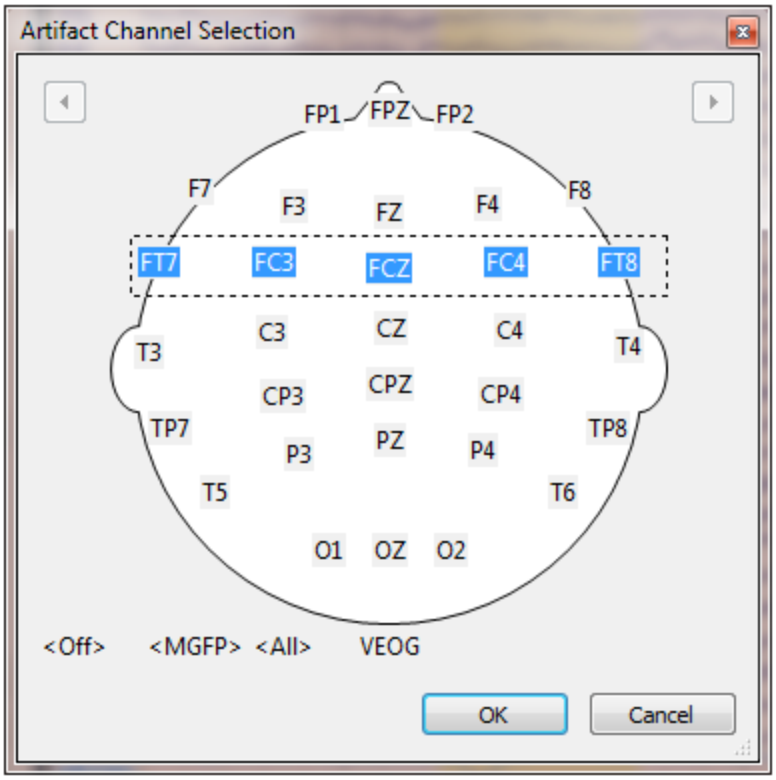
Templates. The **Templates** option is used in conjunction with **Template Matching**. Define the template and scan for matches, as described under  . Select **Templates** for the artifact detection

Method. Click the **Scan Templates** button. Select the type of Reduction method you wish to use. Then proceed with average, etc.

When using multiple template sequences in **Template Matching**, the first sequence in Artifact Reduction will use the first template; the second Artifact Reduction sequence will use the second template, and so on.

Lower/Upper Threshold [μV]. These fields set the voltage (or fT values for MEG) thresholds (positive or negative values). Values exceeding the thresholds (on the channels you select) will result in detection of the artifact.

Channel. You may select a single channel to be monitored (for the Threshold), a combination of channels, the MGFP channel, or All channels (any one can meet the Threshold criterion). Use *Ctrl+click* to select individual channels, or, you may drag a rectangle around a group of electrodes to select them.



Pre [ms] / Post [ms]. Pre and Post define the start and end latencies for the artifact interval. If you are correcting gradient artifact, *and if the triggers are "r5"*, these fields will autodetect the TR interval.

Refract [ms]. Defines the minimum time that must elapse from one threshold detection to the next possible one (voltages that would meet the Threshold criterion during the Refractory period will be ignored). The Refractory period must always be at least the sum of the durations of the **Pre [ms]** and **Post [ms]** spans (no additional events can be detected in the artifact interval). A zero in this field (default) also uses the sum of the Pre and Post [ms] spans. Setting **Refract** to **0** lets you reduce the Pre or Post [ms] intervals without also having to reduce the

refractory period also. "Zero" is a special case that always uses the |sum| of the two intervals.

Artifact Reduction. There are four general methods for reducing the artifact (described below), with additional options that can be used.

Reduction. Select the method of artifact reduction you wish to use.

Off. No method is selected.

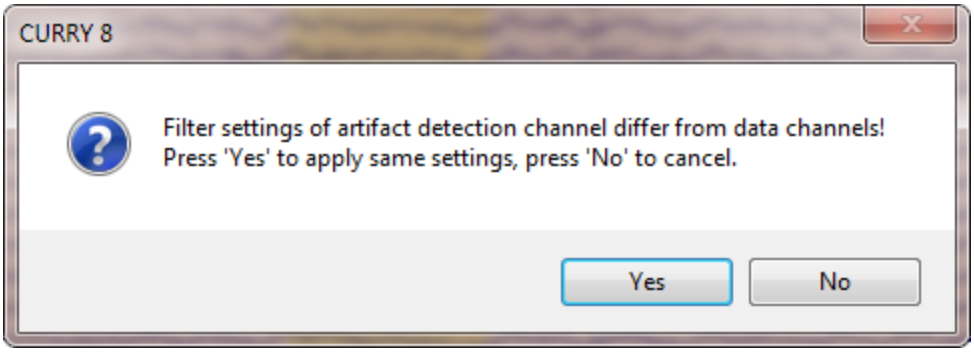
Subtract. When selected, the "rolling" average artifact - based on the number you selected for **Epochs/Avg** (or all artifacts if OAR is selected) will be subtracted from the current artifact.

Covariance. When selected, a covariance analysis is performed between the artifact channel and each EEG channel. Linear transmission coefficients (similar to beta weights) are computed. Based on the weights, a proportion of the voltage is subtracted from each data point in the artifact interval, or, if **Global** is selected, each data point in the file. (The procedure is based on Semlitsch, Anderer, Schuster, and Presslich, 1986).

Listed below are the steps used by the algorithm to reduce ocular artifact:

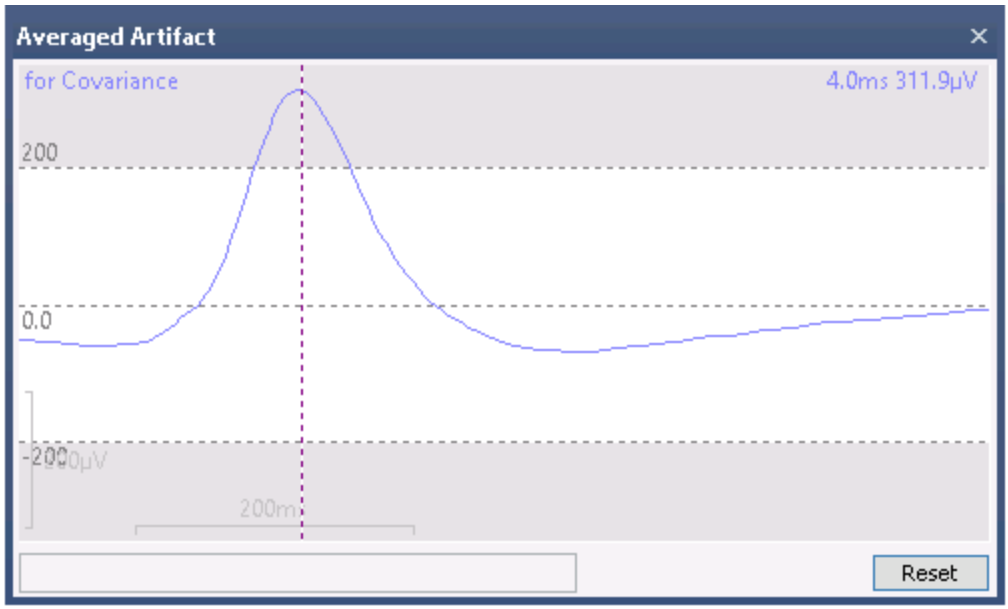
1. A scan is made for eyeblinks that fit the detection criteria you select.

Note
When using the VEOG (or HEOG) channel in artifact reduction, it should have the same filter characteristics as the EEG channels, or the correction will not be optimal. If you have applied filtering to the EEG channels, and if the **Channel** you select for the blink channel is an "Other" channel (which is likely), then, when you select **Covariance**, you will be asked if you wish to apply the same filtering to that channel. Generally, you should click **Yes**. If you select Covariance before Scanning, you can now scan the data file. If you select Covariance *after* Scanning, you will see the message below. If you click Yes, you will see the flashing yellow Scan Data button , and it will be necessary to scan the data again.



2. An average artifact is constructed. The averaged artifact for the selected channel(s) may be viewed, after Scanning, by clicking the

Show button. You will need to also enable the All (33) option, and select Covar.. The Average Artifact window will then be displayed.



From this average, transmission coefficients are computed by estimating the covariance of the averaged potentials of the ocular channel with the EEG channels. The transmission coefficients are computed according to the following equation:

$$b = cov(EOG,EEG)/var(EOG)$$

where b is the transmission coefficient, cov and var are the covariance and variance statistics, respectively. The coefficients are computed separately for all EEG channels.

3. The EOG is subtracted from the EEG channels on a sweep-by-sweep, point-by-point basis in the following manner:

$$corrected\ EEG = original\ EEG - b \bullet EOG$$

The correction is applied only to the data samples in the artifact interval if **Global** is deselected, or to the data samples throughout the file if **Global** is selected.

Scan versus CURRY 8. The most commonly used method for blink artifact reduction in Scan was the **Ocular Artifact Reduction** (OAR) transform. There are some slight differences in how CURRY 8 applies the same correction.

In Scan, the selected channel is first scanned for the maximum voltage. If you reviewed the maxima, you could verify that the maximum voltage was due to a blink, and not some other artifact. Blinks were then defined as the time point at which X%, typically 10%, of the maximum was encountered. If

the maximum blink was 400μV, then any point that met or exceeded 40μV was considered to be the start of a blink (assuming you used the default 10%).

In CURRY 8, simple voltage thresholds (positive, negative, or both) are used to define the start of a blink. If the **Threshold** is set at approximately the same level as the **Threshold %** in Scan, then the same blinks will be detected. You can use **Scan Interactive** to review and accept the desired blinks, just as you could review and accept the individual blinks in Scan. Since you cannot easily determine what the actual threshold would be in Scan, you can only make a reasoned estimate for CURRY. Any differences that exist should be negligible.

In Scan, you set the **Duration** field, which was the interval from the time point where the threshold was met, until the value you selected, typically 400 ms. That interval was used for the covariance analyses. The correction was applied to every data point throughout the continuous data file.

In CURRY 8, you set the **Pre** and **Post** time points. That interval is used for the covariance analyses, and you have the option to correct only those intervals in the continuous data, or to use the **Global** option to apply the correction to all points in the continuous data file.

If you want to set CURRY 8 to be as close as possible to the way it was done in Scan, you should do the following.

1. Obtain a representative estimation of the maximum blink voltage in your data files. Take 10% - or whatever **Threshold %** you used in Scan - of that value, noting whether the blinks were positive or negative. Set the **Upper** or **Lower Threshold** in CURRY accordingly, and turn off the other threshold (set it to 0).

2. In the **Advanced** section under **Artifact Reduction**, set **Threshold Detection** to **First Slope**, rather than the default **Peak**. This will more closely approximate the starting point of a blink.

3. Set **Pre** to **0 ms** and **Post** to the **Duration** value you used in Scan.

4. Use the **Covariance** method. If you see the message saying the filter parameters for the EEG channels differ from those for the artifact channel, say **Yes** to apply the filter parameters to the artifact channel.

5. In the reduction section in CURRY, select **All** and **Global**. This will eliminate the stair-stepping that would otherwise likely occur (Scan does the same thing).

Remember, an averaged blink artifact is created, and it is that average that is used for the covariance analyses. The blink reduction procedures are extremely robust, and are generally not affected by minor differences in the blinks that were selected. If you use comparable parameter settings in CURRY, you should obtain nearly identical results to the OAR method in Scan. In CURRY, you have more flexibility in artifact detection and reduction options, and you may find that other reduction methods (such as PCA

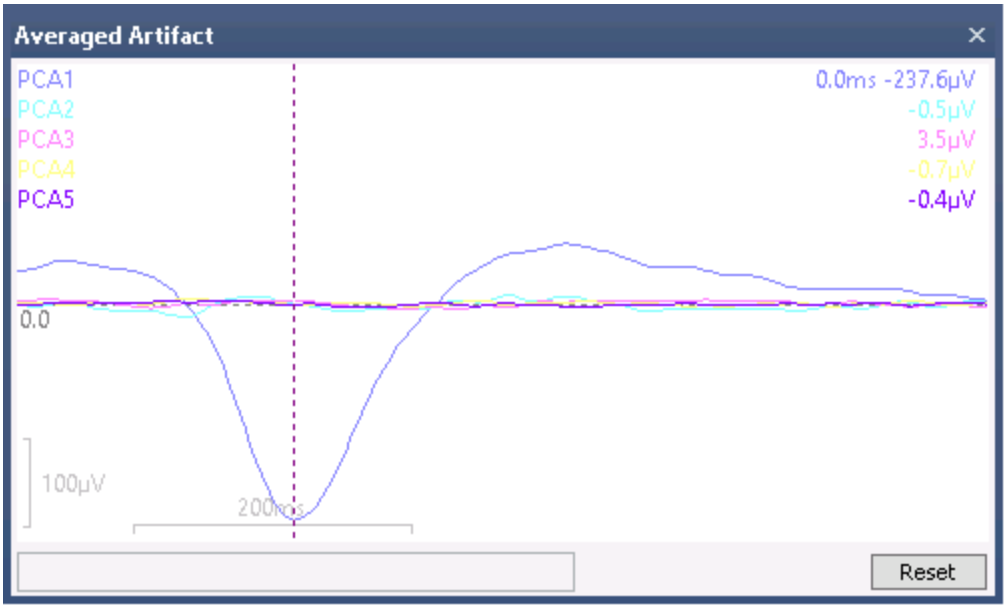
without using Global) give better results. Even if you deviate from the most comparable settings used in Scan, you should still get a very comparable reduction in CURRY. After averaging the evoked responses, any differences should be negligible.

PCA Components. A PCA analysis is performed on the averaged artifact. You may then select how many PCA components you wish to remove. Inspect the corrected data as you increase the number of components. Use only the number that results in artifact removal, while minimizing the effects on the remaining data.

To view the PCA components, you must enable the 

option, and then click the 

button. The PCA components (up to 5) are displayed.



Note

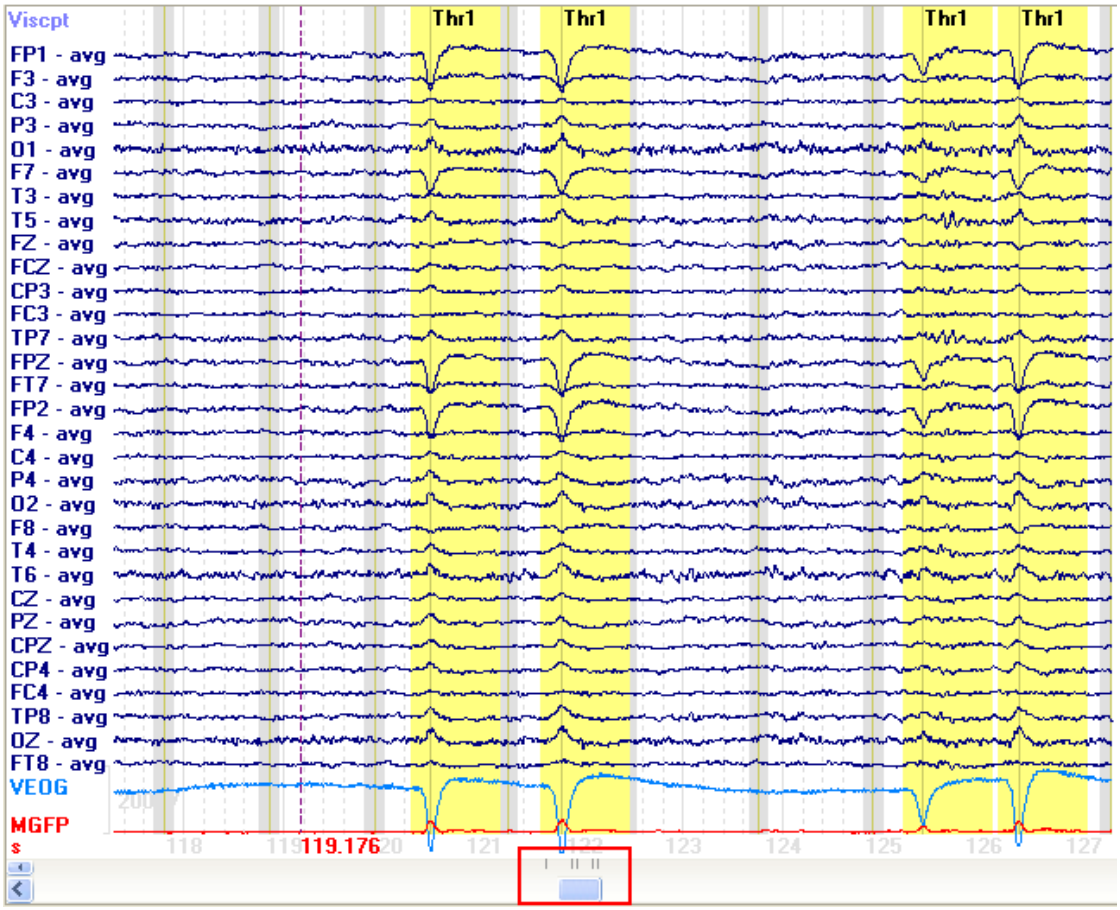
With PCA, the number of epochs that goes into the averaged artifact, and hence used by PCA, varies. If you use the **Global** option, all artifacts in the file are used in the averaged artifact. Otherwise, PCA uses an average of the number of artifacts that are displayed on the screen (or just off the screen), up to the number of **Epochs/Avg** you select. If you select 10 for the number of sweeps going into the average artifact (**Epochs/Avg**), and 5 artifacts are seen in the display, then PCA is performed on the first artifact using the first artifact alone. The second displayed artifact is corrected based on the average of the first two artifacts. The third uses the average of the first three artifacts, and so on up to the five artifacts displayed. If you increase the number of seconds displayed in order to see 10 artifacts, then the tenth one will be corrected using the average of all 10 artifacts. If you display more than 10 (the number of **Epochs/Avg** in this example), the averaged artifact will always use the 10 most recent sweeps (including the current one), and that is the average used by PCA.

ICA Components. ICA artifact reduction is somewhat of an experimental method that takes just the artifact intervals without averaging, then performs an ICA and rejects the leading components. It is a local method since the individual artifacts are treated independently. Since with ICA reduction the data are locally synthesized leaving out the leading components, this approach cannot be done Globally. A **Global** method would require averaging and a projection algorithm (as in PCA or Covariance), and so is not possible. The **Show** option is available only with the **All** option, which is not available with ICA. The **Symmetric** option is also not used with ICA.

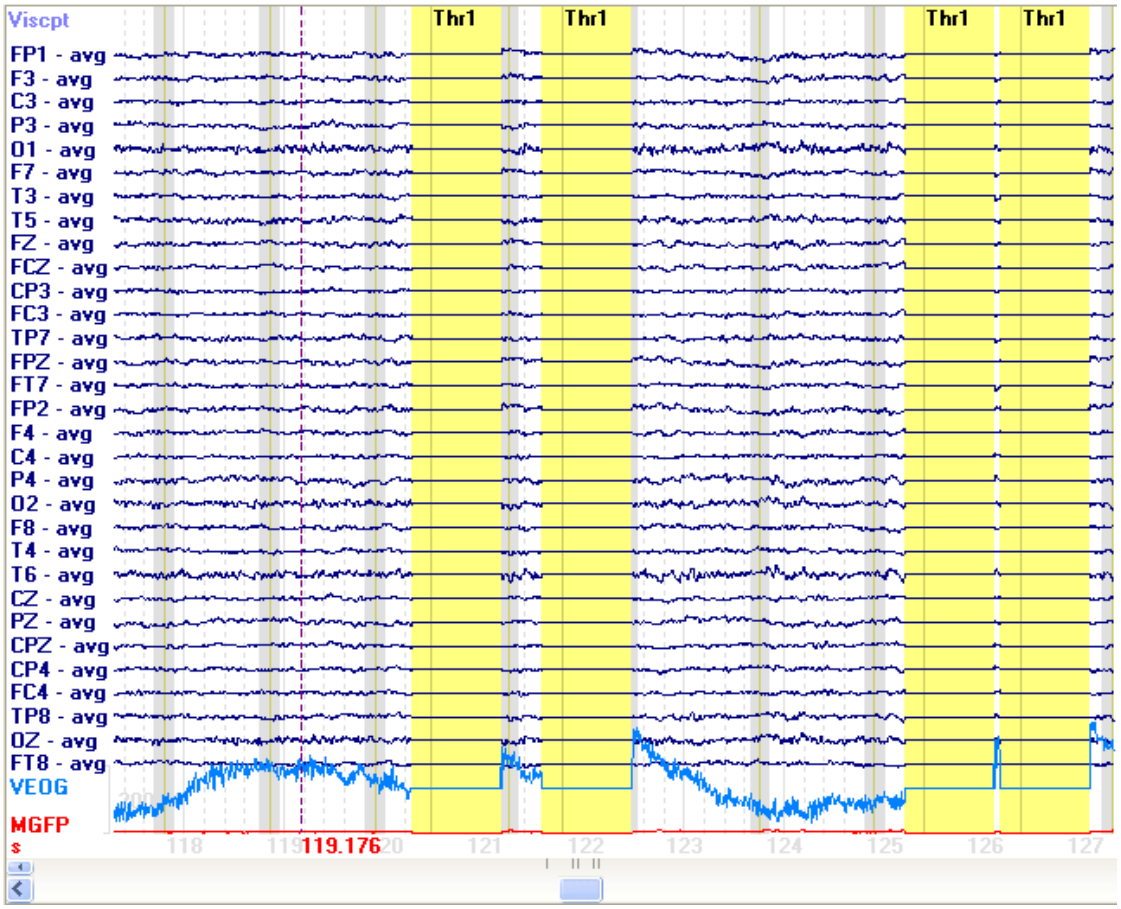
ICA normally works best if the number of samples is at least two or three times the number of sensors, so it is generally not very well suited for short duration artifacts.

Show. The **Show** button is used to display the averaged eye blink or the PCA components, as shown above.

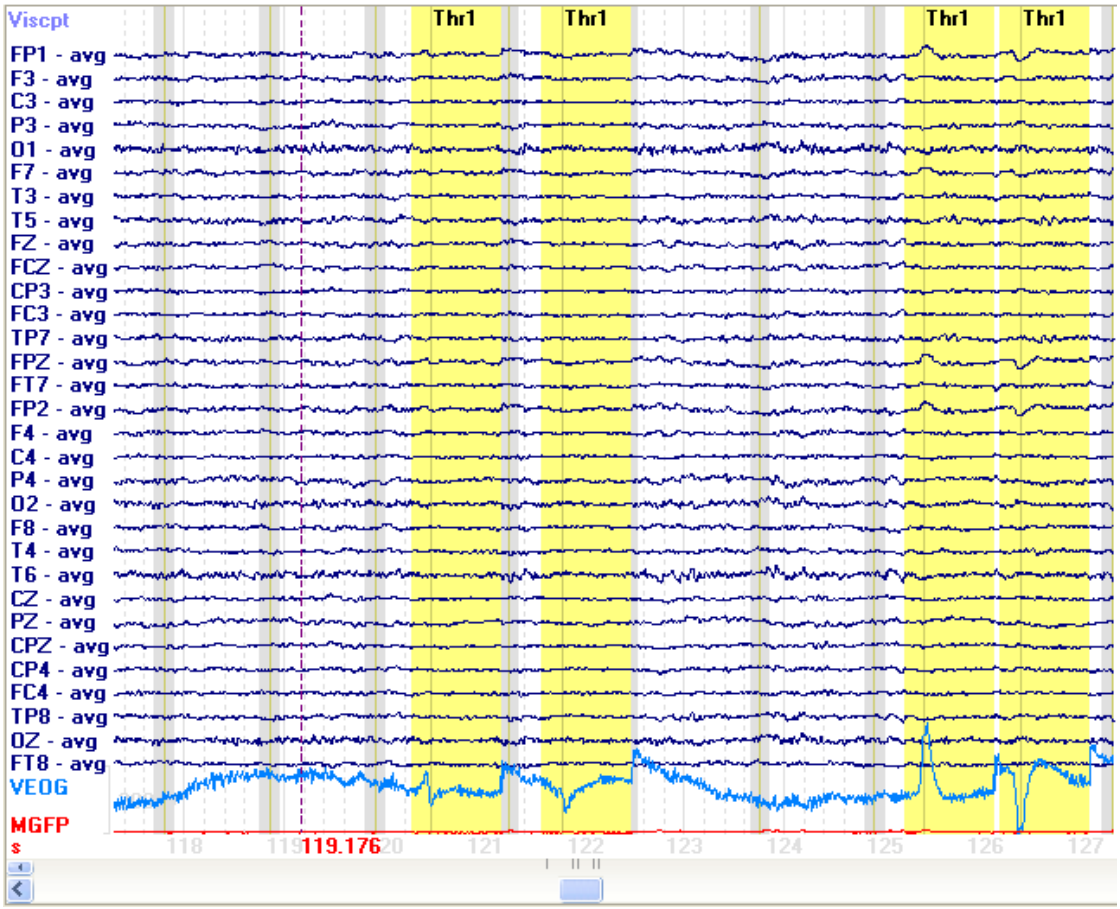
Epochs/Avg. Epochs/Avg has a slightly different function before you click the  button as opposed to after clicking it. Before clicking  , the option gives a preview of the effectiveness of the correction. The important thing to understand is that it is applied to the data that are displayed only, plus sections before (and after) the displayed data. For example, consider the following data display, taken from the middle of a file. Four blinks are seen; however, if you look at the tick marks below the data, there are actually 5 blinks detected, but the first one is off the display, to the left.



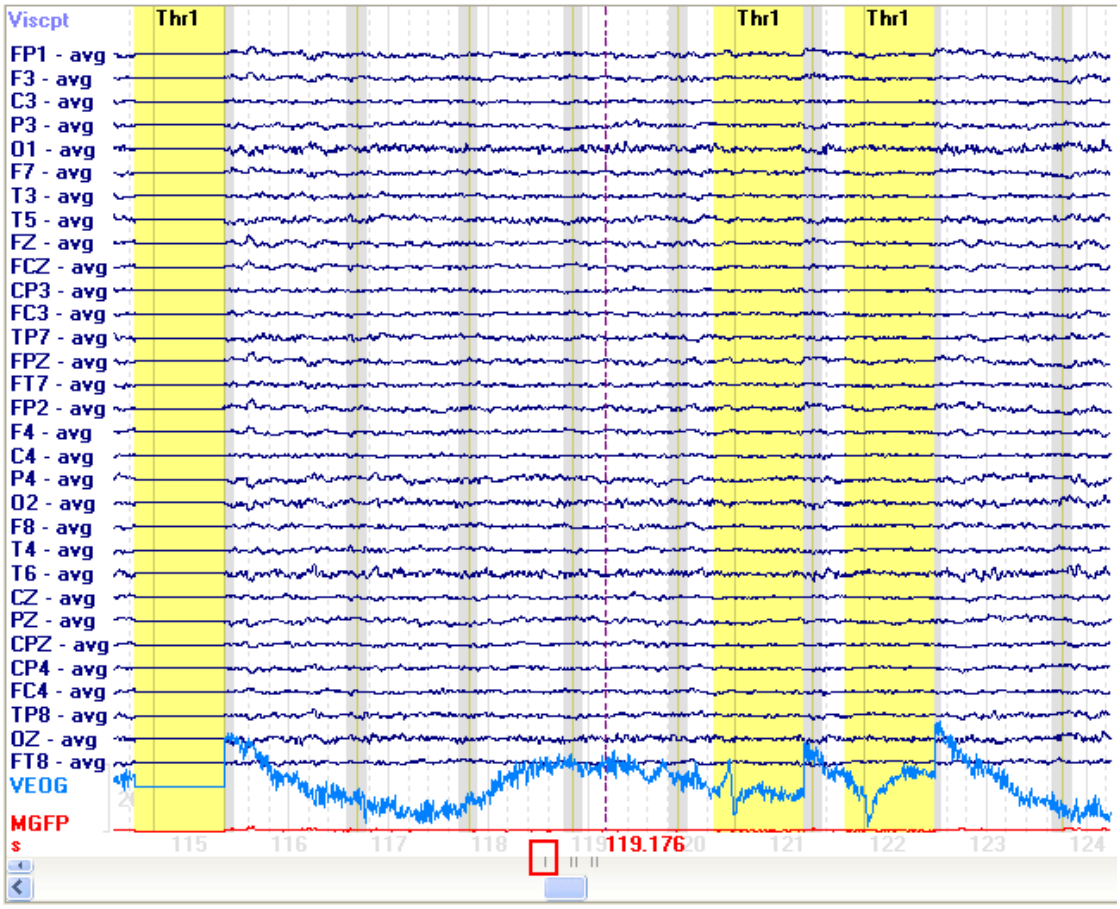
Epochs/Avg has been set to **1**. If you enable Subtract, all of the blinks are replaced with flat lines. With **Epochs/Avg** of 1, each blink is subtracted from itself.



Set **Epochs/Avg** to **2** (with Subtract still enabled). Now the blinks have been reduced.

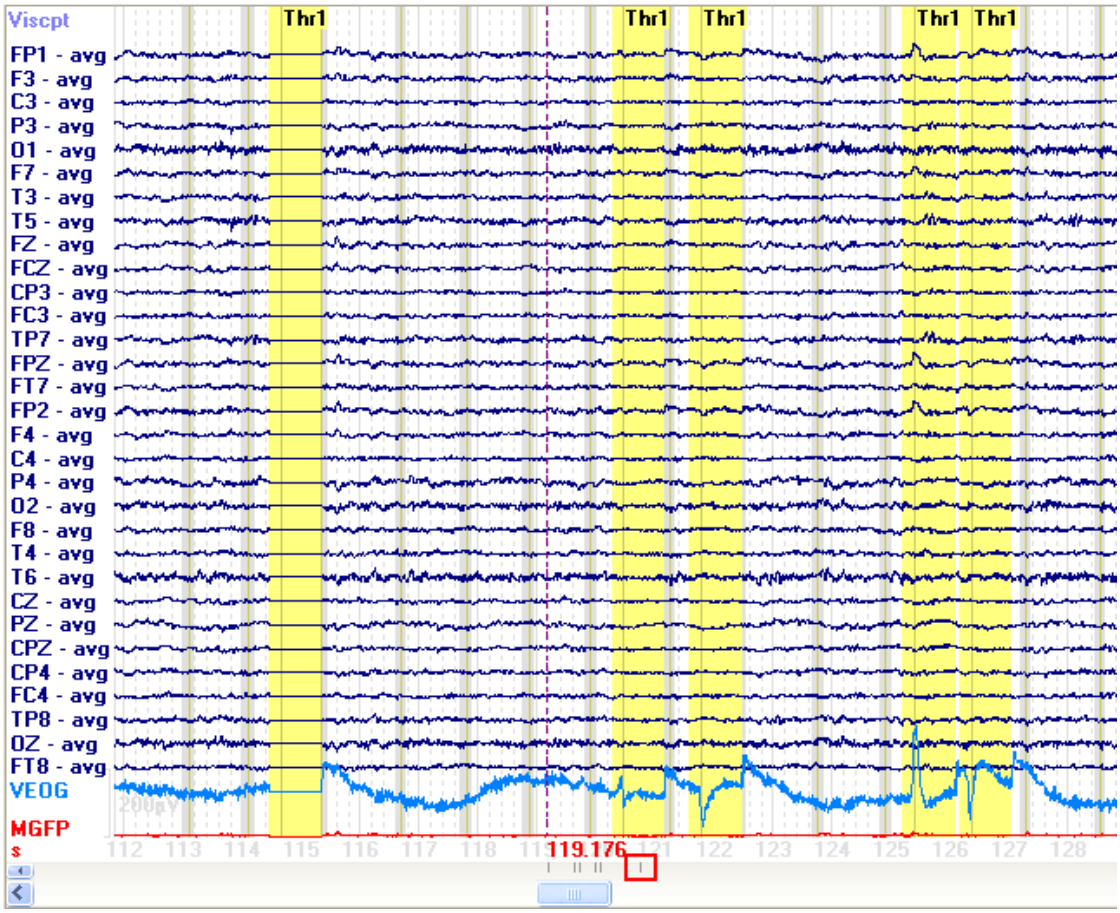


If you move slightly to the left in the file, you will see the first blink that had been off-screen before. It has a flat line.



With **Epochs/Avg** set to **2**, the first blink will have a flat line, since it is subtracted from itself. The second blink will be corrected - the average of the first two blinks is subtracted from it. The next two blinks are subtracted from the third blink, and so on, with the average being based on the two most recent blinks in the display.

With **Epochs/Avg** set to **5**, and with increasing the number of seconds displayed, you can see better what happens. The first blink has flat lines, the second is corrected using the average of the first two blink, the third is corrected using the average of the first three blinks, until the fifth one, which is corrected using the average of the five blinks.



If you look at the tick marks below the data, there is a sixth blink that was detected, but not displayed. If we moved over to see it, it would be corrected using the average of the last five blinks (rolling average), assuming all blinks were still in range of the display.

At this point, before clicking  , the correction is being applied to the data that are displayed, plus the data immediately before and after the display (additional samples are added until the total samples is a power of 2).

After clicking  , all artifacts can be used to create the average by clicking the 

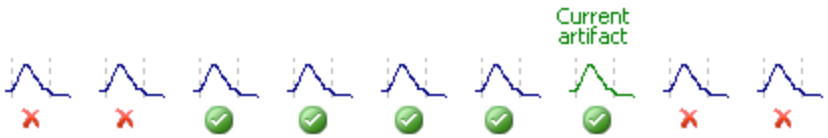
option. The total average of artifacts is then subtracted from each individual artifact (or used in the Covariance, PCA, or ICA analyses).

If you set **Epochs/Avg** to a number greater than the number of artifacts that are in the file, and then Scan the data file, the **Epochs/Avg** field will be reset to the largest number of artifacts automatically.

All. When enabled, all of the detected artifacts will be used to create the averaged artifact. Enabling the option before scanning the file has no effect; after scanning, all artifacts will be used for creating the average artifact.

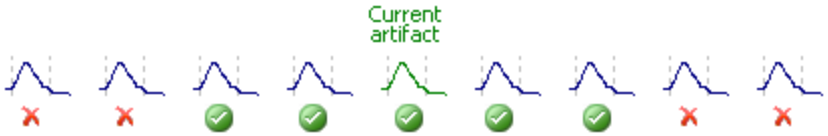
Symmetric. When Symmetric is disabled, the average artifact is based on the current one and the preceding artifacts to total the number you entered for **Epochs/Avg**. When Symmetric is enabled, and **Epochs/Avg** is an odd number, the current artifact is included, and well as half of **Epochs/Avg** - 1 before and after the current one. If **Epochs/Avg** is Even, the average artifact is based on half of the epochs before the current one and half after the current one, omitting the current one.

Symmetric Disabled, **Epochs/Avg** = 5, before , and online. The current artifact and the four preceding ones are averaged to get the average artifact.

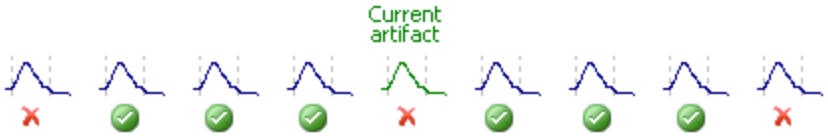


After scanning the data file , the current artifact and the four nearest artifacts (before or after) are averaged. (If you select **All**, all artifacts are averaged).

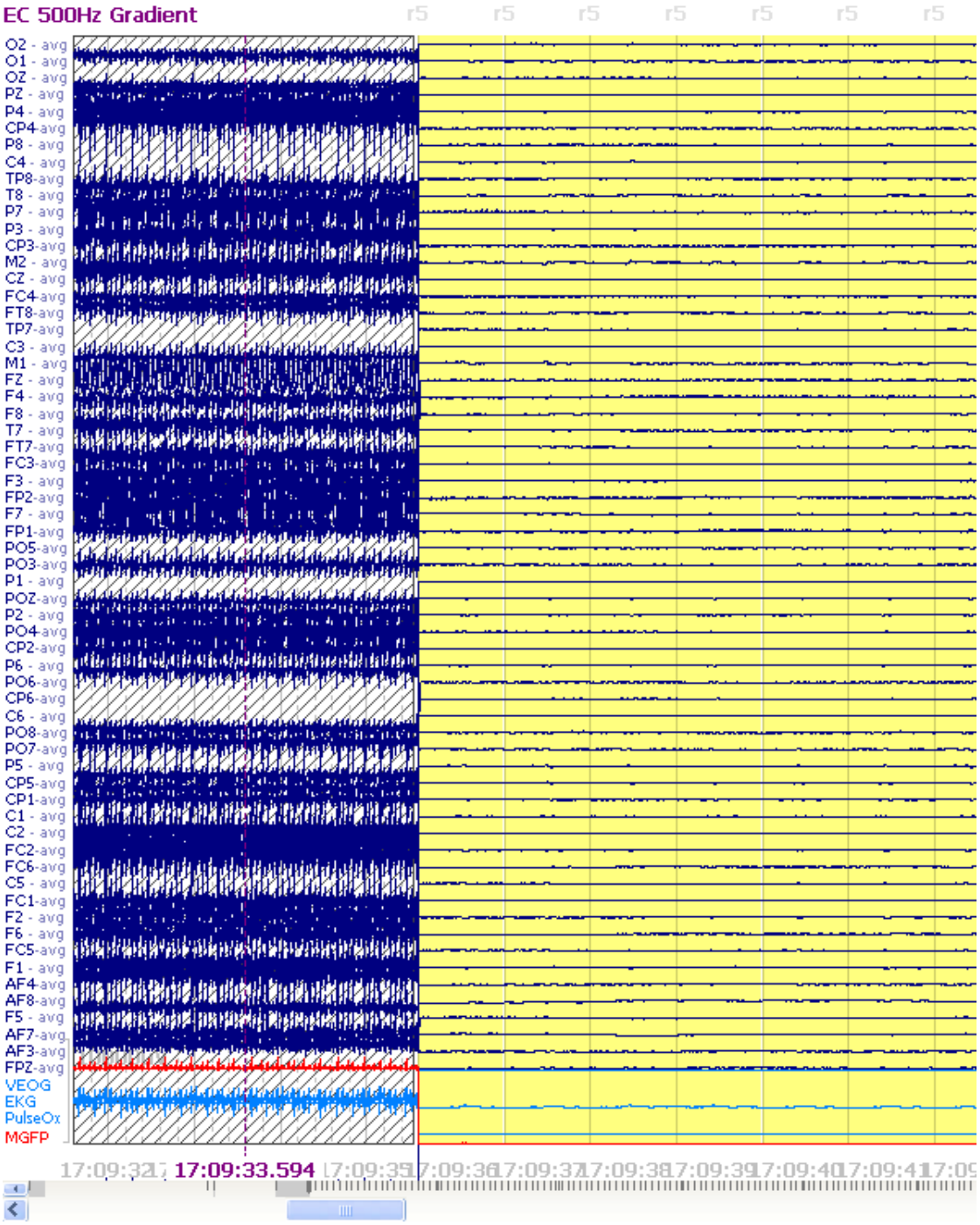
Symmetric Enabled, **Epochs/Avg** = 5. The current artifact, the two before it, and the two after it are averaged to get the average artifact.



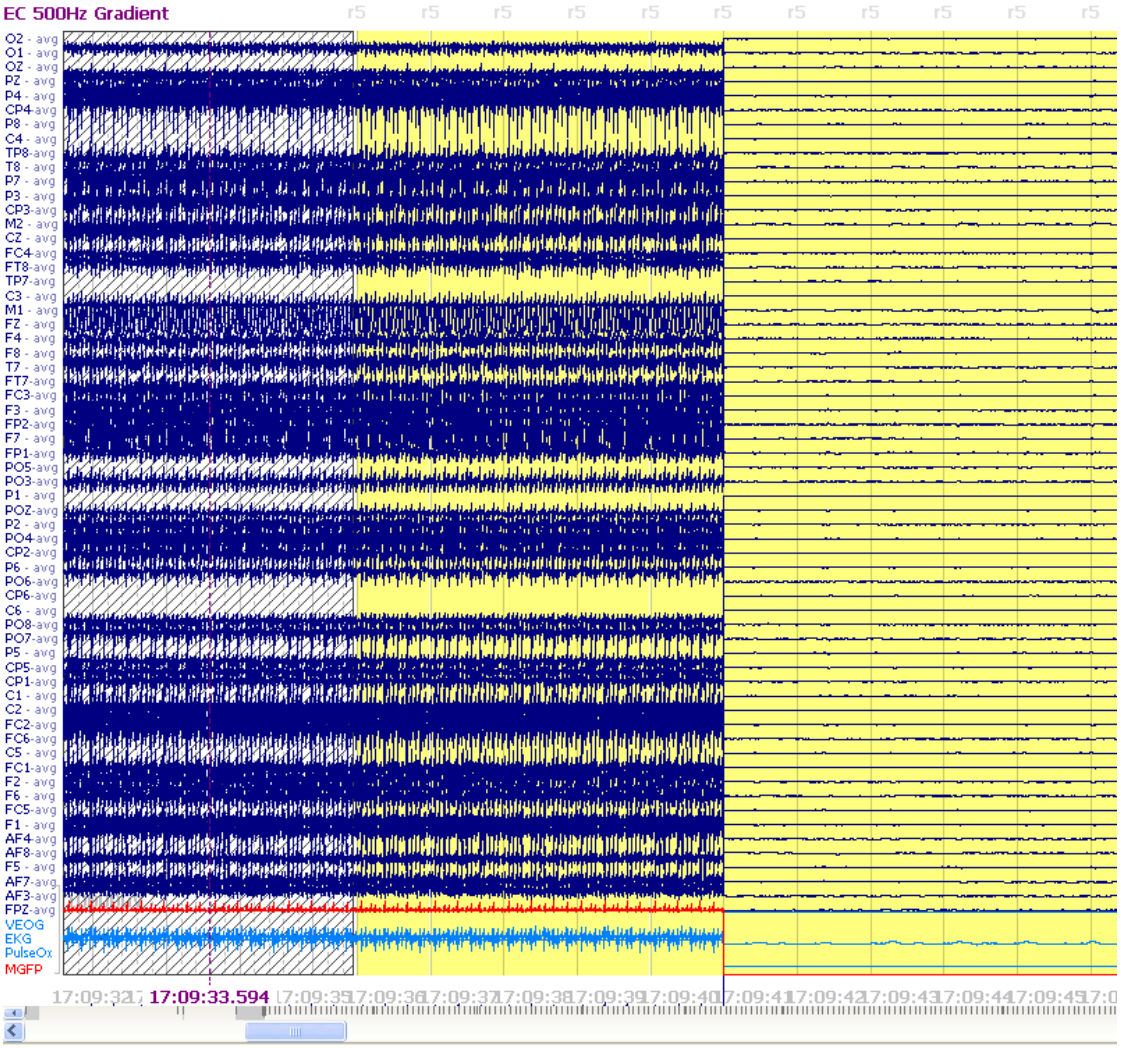
Symmetric Enabled, **Epochs/Avg** = 6. The three artifacts before, and the three artifacts after the current one are averaged to get the average artifact.



The effect of the Symmetric option is most easily seen at the beginning of the data file. In the example below, **Epochs/Avg** was set to **10**, and **Symmetric** was off. The r5's are corrected from the beginning of the file. If Symmetric is off, the program will take the nearest N events to create the average artifact - in this case, events 2-11 are averaged for the first r5, events 1 and 3-11 are averaged for the second r5, and so on until there are 5 events before and after the current on (the 6th event in this case).



With Symmetric enabled, the correction looks like the following. The first 5 r5's are not corrected, because the Symmetric option imposes the condition that the events that are to be included in the averaged artifact must come equally from before and after the current event. That condition is not met until the 6th r5 event.



The intended use of Symmetric is primarily for gradient artifact reduction where there may be jitter in the events from the scanner and additional flexibility is needed to select the artifacts to include in the average artifact. In practice, try the correction with and without the Symmetric option to see if it helps, hurts, or makes no difference.

Global. When deselected, the correction will be applied to the defined Timeranges only (the span of the artifact). When enabled, the correction will be applied to every data point in the file. Prior to scanning the data file, the option will have no effect. After scanning, the file will be corrected globally.

Scan Data. The Scan Data button will appear with a flashing yellow background  or not  . The flashing lets you know that the file should be scanned. You will see it when you first access the **Artifact Reduction** parameters panel, and again when you change a parameter - in **Artifact Reduction** *or elsewhere* (such as **Reference**, **Baseline Correction** or **Filter Parameters**) - that would necessitate a new Scan. Clicking the  button scans the entire data file. Prior to clicking the button, you will see the effects on the section of data that is displayed (and

slightly beyond). After scanning, you will also see the events listed in the **Event List**. The Type of event will vary depending on the Type of detection method you are using. **Threshold** creates **Thr**x events, **QRS Detection** creates **QRS**x events, **Event-Codes** uses the selected events in the file, and **Templates** creates "tmplx" events. The "x" is determined by the Sequence selection.

If you are using multiple **Reduction Sequences**, you need only click  one time, and the file will be scanned for each sequence. After scanning, if you change a parameter - in Artifact Reduction or elsewhere - that will affect the results of the scan, you will see  change back to  , indicating that you must scan the file again. If you have, for example, 3 sequences, and you change a parameter in Sequence 2, you will see that scan button revert to  . The button in Sequence 1 remains  . So you would only need to rescan Sequences 2 and 3 (since the results of the second scan could affect the third scan). If, after scanning, you enable **All** or **Global** for one sequence, you will need to rescan any subsequent sequences. Briefly, when you see the  button, click it. See the *Common Artifact Reduction* tutorial (final example) for a demonstration of using multiple Processing Sequences.

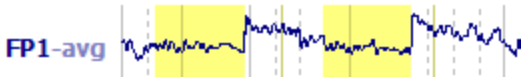
If you have saved the **Study Parameters** and then reopened the file, you will need to again click  .

Advanced. These are options that are generally left with their default settings.

SSC (SubSample Correction). SubSample Correction is used for gradient artifact reduction when the routine [subtraction] correction does not produce reliable results due to subsample jitter about the event marks. A cubic spline is used with a correlation correction to adjust the jitter. If there is no jitter in the file, the **SSC** option will have no effect (and is time consuming), so it should be used only when needed. It can be used with or without clock synchronization, and with any AD rate.

Others. Enabling this option (after scanning) will include channels designated as Other channels in the correction when using Subtract or Covariance (not PCA or ICA).

Taper [%]. On occasion, you may see sharp transitions from the artifact corrected areas to the uncorrected areas.



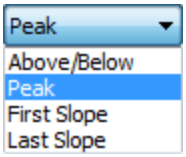
There are several ways to reduce these sharp transitions. One is to apply a taper. Here a 45% taper has been applied.

Other ways are to use a high pass filter (left), and to extend the interval that is being corrected to include more of the artifact (right).

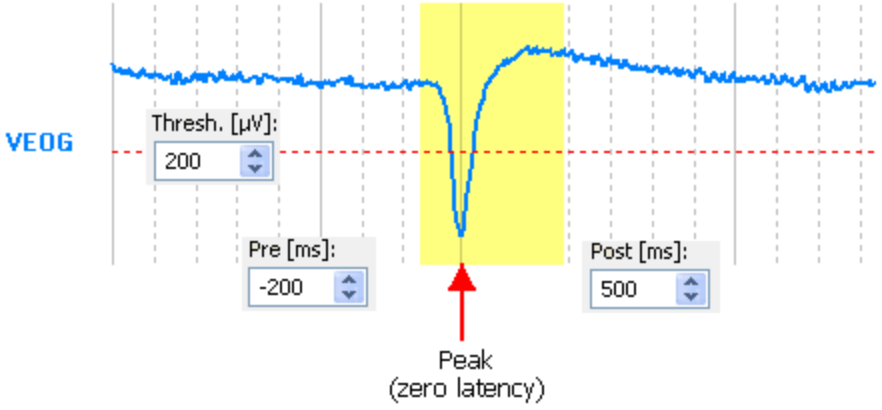
Offline, you can use the **All** and **Global** options, which may provide the best solution.

Threshold Detection: The Threshold Detection options are used to align the peaks of the artifacts (minimize smearing of the average artifact due to latency jitter). They are active only with the **Threshold** method of artifact detection.

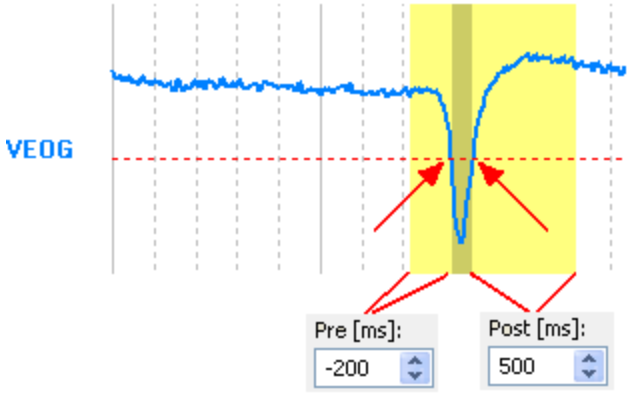
The default setting is **Peak**, and that is generally sufficient in most cases.



In that case, the "peak" is defined as the greatest voltage (positive or negative) between the two Threshold crossings (red dashed line). The **Pre [ms]** and **Post [ms]** intervals are measured from the zero latency point at the peak.



Above/Below. This option uses the intersection with the first Threshold as the end of the **Pre [ms]** interval, and the intersection with the second Threshold crossing as the start of the **Post [ms]** interval. This option is used primarily with MagLink data files, where there may be occasional jitter from the scanner pulses. Note that this is the only option where the width of the complete artifact interval can vary from one instance to the next. This is a problem only if you want to average the artifact events from the Event List - you cannot average epochs having differing widths. (This is not an issue when the artifacts are averaged in the process of Artifact Reduction).



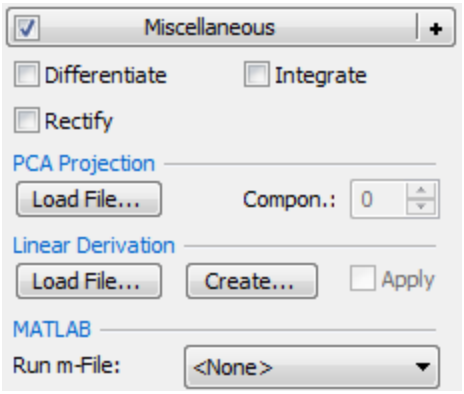
First Slope. The zero latency point is where the first crossing of the Threshold occurs.

Last Slope. The zero latency point will be where the second crossing of the Threshold occurs.

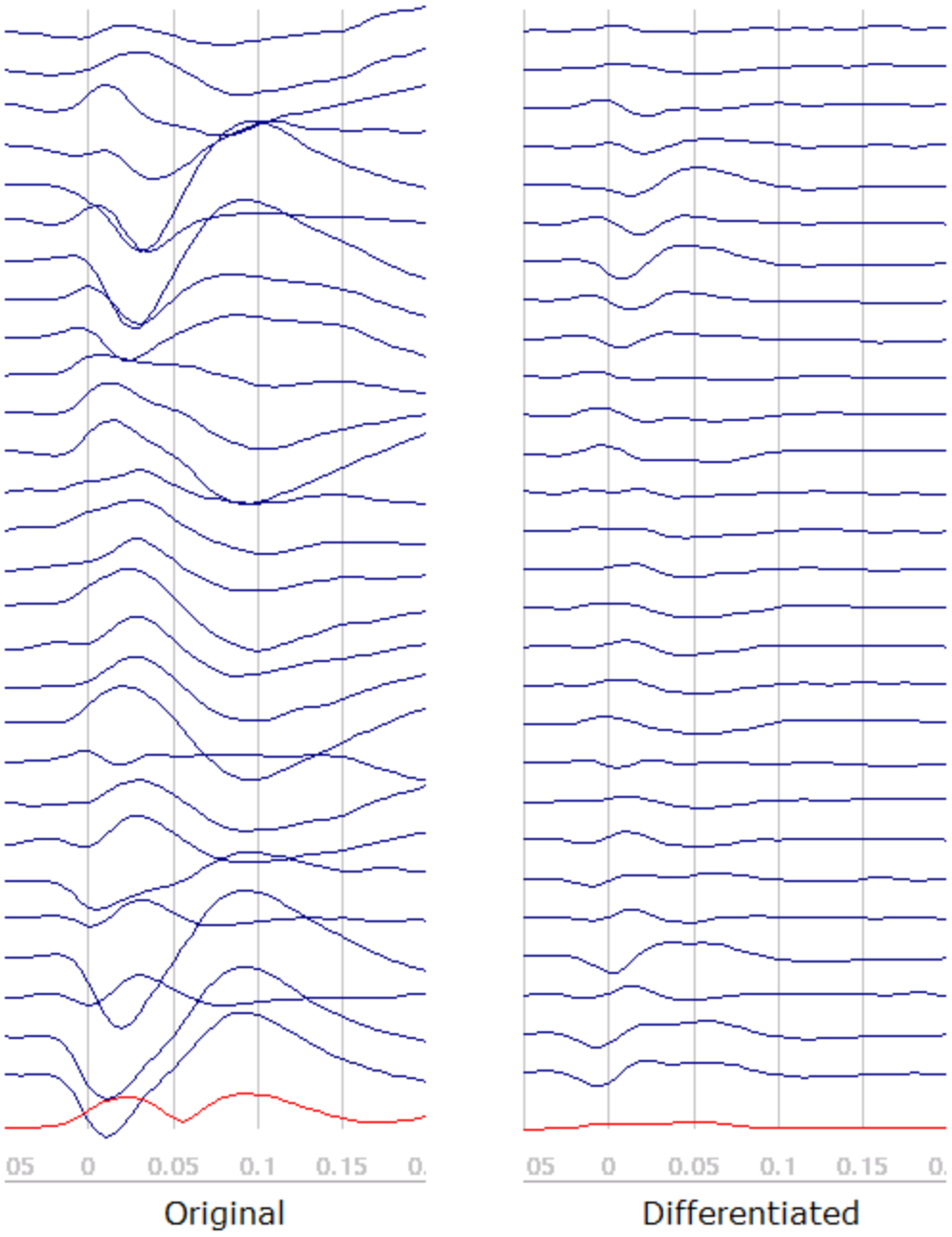
Averaged Artifact. This option will save the averaged artifact (with a .art extension), after the regular artifact reduction procedure has been completed. Click Save... to select a folder and file name for the file. The average can then be used with subsequent recordings with the same subject, as long as there is no reason to think the morphology or distribution of the artifact has changed. Click Load... to select the file, then Apply.

17.1.7 Miscellaneous

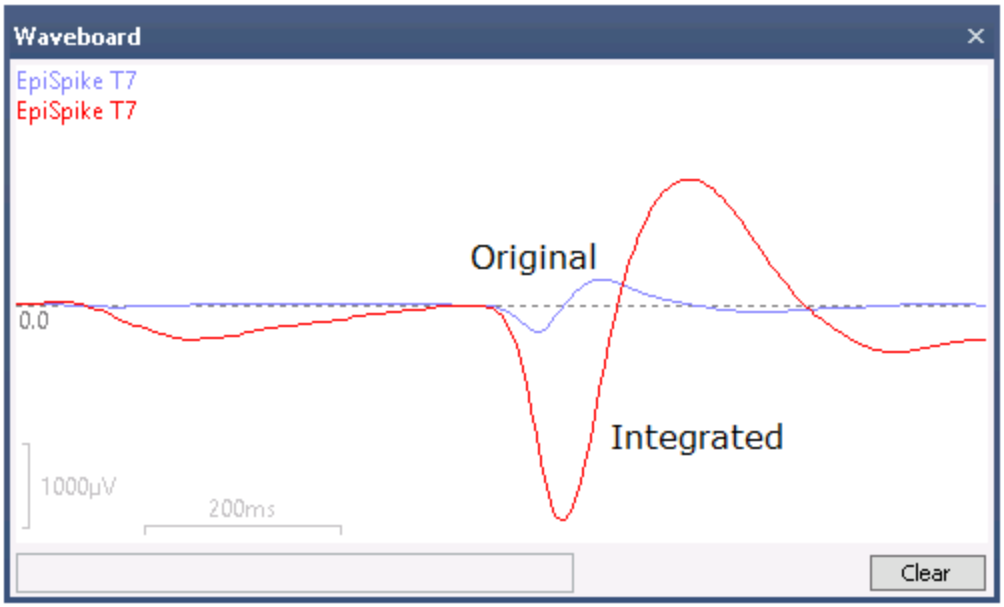
As the name implies, The Miscellaneous panel contains options that do not fit well in other panels.



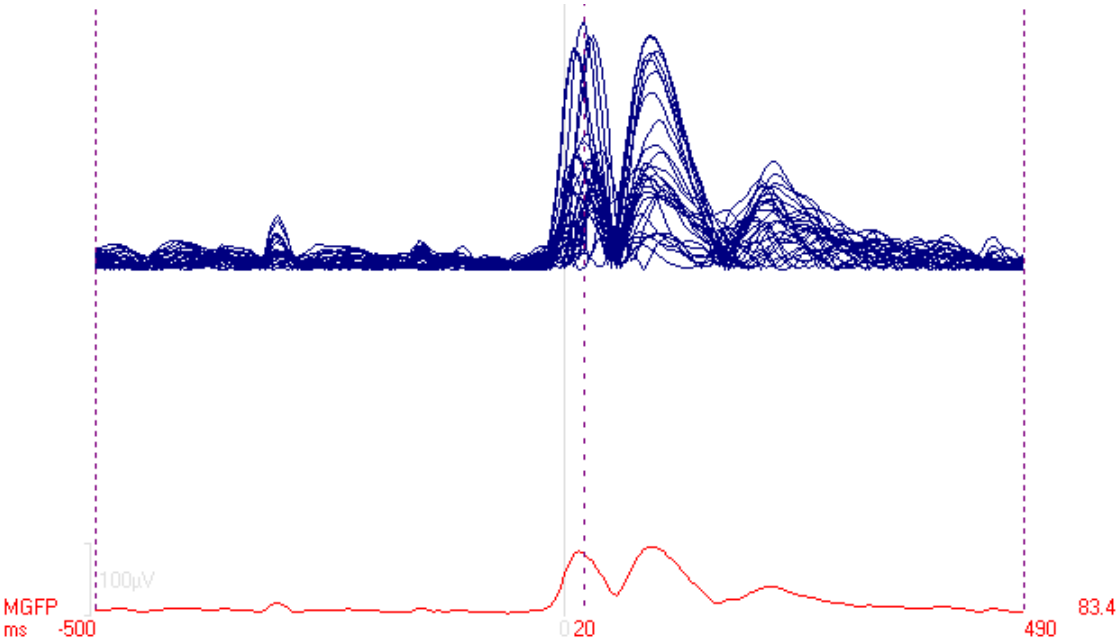
Differentiate. This is the first derivative of the waveforms.

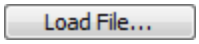


Integrate. A cumulative voltage function is created for each channel. The first point stays the same, the second point is the sum of the original first and second points, and so forth (the n-th new sample is sum of all preceding original samples plus the n-th original sample).



Rectify. Rectify converts all voltages to positive values.



PCA Projection. Artifact suppression can be accomplished using results from the PCA analyses. Perform PCA on the user-determined artifact interval. N number of components will be detected and selected for export. Go to **Maps** → **Save** → **Save PCA Results** to save the results. Select that file after clicking the 

button, and decide how many of the components to include 

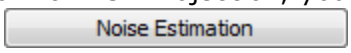
. Those should be the components representing the artifact. The selected number of components will then be projected from the data.

How does **PCA Projection** differ from the **PCA** option under **Reduction**? PCA Projection is the same as the PCA option, if the same blinks have been chosen to create the average artifact and if **Global** is selected with the PCA option. PCA Projection gives you more control over the principle component analysis. Once you obtain the averaged artifact, you can easily vary the Timerange and see the immediate results in the PCA. In the PCA display, you can see the distribution of the components, the SNRs for each, and you can save more than three components (the limit with the PCA option under Reduction).

Additionally, you have more control over which artifacts are included in the average. For example, if you select **Threshold** for the detection method, all blinks that meet the criteria (and are not in Bad Blocks) will be included in the average. You can review them further in the continuous data file. The only difference in this case is that, with PCA Projection, you are averaging the artifacts manually, and the SNR rejection method can be used. If, however, you are using the Threshold or Eyeblink detection methods, the **Average** field comes into play. The average artifact is rolling, being recreated with the N most recent artifacts. PCA (and ICA) will use the rolling average, rather than all blinks in the file, unless you use the **Global** option. Therefore, you have more control over the sweeps that are used to create the average artifact.

 **Note**
Note, however, that *CURRY 8 always uses an internal CAR (Common Average Reference) data when computing PCA and ICA in Maps, even if you have turned off the CAR option in Functional Data*. If you are using the PCA results from Maps to project artifact from your data in the **PCA Projection** option under **Artifact Reduction**, you must enable CAR to see the expected effect.

When using PCA Projection, you can start with a single instance of an artifact or, more commonly, the average of multiple artifacts (to reduce the background noise). If you are using a single instance, just define a Timerange to capture the artifact, and then do the PCA analysis. If you want to use the average of multiple instances, you will first need to use one of the Detection methods (described below).

Also with PCA Projection, you must select the **User Defined Noise Level** option for 

(see **Noise Estimation** below). You will see a message to that effect if you save the PCA results without having selected the User Defined Noise Level. You do not need to enter a noise level - use the value displayed.

The basic steps for using PCA Projection are as follows (please see the *Artifact Reduction* tutorials for more thorough demonstrations):

1. Use one of the Detection methods to identify the artifacts, such as, the Threshold method.
2. In this case, we do not want to reduce the artifacts, but rather average them together.
3. Average the artifacts via the Event List.
4. Set Noise Estimation to User Defined Noise Level.
5. Select a Timerange for analysis.

6. Set Maps for PCA, and determine the number of components that you want to export.
7. Export the components as a .pca file.
8. Revert to the continuous data file and select that file for PCA Projection.
9. Vary the number of components that are projected from the data.
10. Save the Study Parameters, if desired.

When using PCA Projection, you may need to try removing several components, while verifying that the remaining activity has not been affected.

If you export components containing more than one artifact, you can remove them individually by selecting the PCA components for inclusion in the removal. While blinks were demonstrated above, you can remove other types of artifact - anything that can be decomposed accurately in the PCA analyses. (See also the *Common Artifact Reduction* example in the *CURRY Tutorials*).

File. Select the .pca file you have created.

Components. Adjust the number of components you wish to project from the data.

Linear Derivation

Linear derivation files (LDR) were created in Scan for a number of purposes. CURRY 8 can create simple LDR files, and it will read and apply certain ones from Scan. For example, if you have created LDR files to reduce artifact using the Ocular Artifact Reduction transform, or from the Spatial Filter transform, those LDR files will work in CURRY 8 as long as the number of channels and the channel order are the same (otherwise you will get a message saying the matrix must be square). The labels are ignored in the LDR file, therefore, if you try to reorder the channels with an LDR file, the channels will change, but the labels will not. If you change the labels in the LDR file for any reason, such as renaming an interpolated channel, the labels will not be changed in CURRY (although the channel will be interpolated). [These restrictions may change in subsequent versions of CURRY].

Click the 

button to select an existing LDR file and the **Apply** field to apply it.

Click the 

button to create an identity matrix LDR file. An identity matrix is one that has 1's down the diagonal, from top left to lower right. All other cells have 0's. If you apply the identity matrix LDR file, there will be no changes - the output file is the same as the input file. In some cases, you may wish to create a special purpose LDR file, in which case you can edit the identity matrix as needed, save it, and then Load and Apply it. Please see the **Creating LDR Files** section below.

MATLAB

Run m-File. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

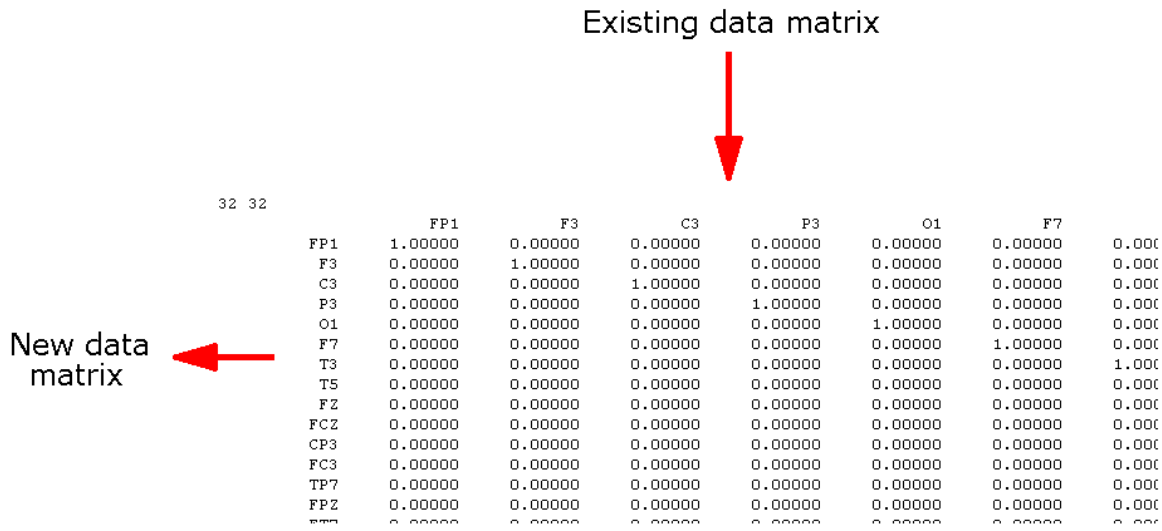
17.1.7.1 Creating LDR Files

In certain situations, you may need to create your own special purpose LDR file, where you do not have access to the Scan EDIT program. In that case, you can create a basic LDR file in CURRY and then modify it using a text editor. LDR files have an .ldr extension (e.g., *blink reduction.ldr*). If you have Scan, please see the Montage Editor appendix at the end of the EDIT manual (or, for older versions of Scan, see the separate Montage Editor manual) for directions for creating LDR files.

Background. LDR (linear derivation) files allow you to create new channels that are linear combinations of existing channels.

You have an existing data matrix, where typically the columns are the channels and the rows are the data points over time. You want to create a new data matrix that has the same form, but the cells are changed in a certain way. With LDR files, each data point for each channel is multiplied by a number, and then the results are added linearly per row to create modified data points.

The example below is a simple example of an LDR file. The existing FP1 data point is multiplied by 1.0, and all of the other channel data points (F3, C3, etc.) are multiplied by 0.0. Summing across that row gives the same value for FP1 - no changes. The same thing happens in the second row for F3, and so on. This is called an Identity Matrix (in Scan terms). An identity matrix has 1.0's down the diagonal and 0's for all other cells. The output file will be the same as the input file.



32 32

	FP1	F3	C3	P3	O1	F7	
FP1	1.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
F3	0.00000	1.00000	0.00000	0.00000	0.00000	0.00000	0.00(
C3	0.00000	0.00000	1.00000	0.00000	0.00000	0.00000	0.00(
P3	0.00000	0.00000	0.00000	1.00000	0.00000	0.00000	0.00(
O1	0.00000	0.00000	0.00000	0.00000	1.00000	0.00000	0.00(
F7	0.00000	0.00000	0.00000	0.00000	0.00000	1.00000	0.00(
T3	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	1.00(
T5	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
FZ	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
FCZ	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
CP3	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
FC3	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
TP7	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(
FPZ	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00(

Note the "32 32" in the top left corner. This means there are 32 input channels and 32 output channels. *In CURRY, you must always use a square matrix, with the same number of input and output channels*. When creating an LDR file, you still need to include those two numbers in that position.

The next line has the existing channel labels. *These must be in the order that they appear in the data matrix*.

A simple example of an LDR file is one that creates bipolar channels. In CURRY, you would of course use the Montage Editor to create a bipolar montage. The point here is to illustrate how LDR files work. If you want FP1-F3, just enter a -1.0 for F3 on the

first line. For F3-C3, enter -1.0 in the second line under C3. For C3-O1, enter -1.0 on the third line under O1, and so on. The first channel in the new file will be the mathematical difference between FP1 and C3, the second line will be the difference between F3 and C3, etc. *CURRY does not recognize any changes you make to the output labels*, and instead will use the same labels as the input channels. If you wish to change the labels, you can do so in the first page of the Functional Data Import Wizard.

	FP1	F3	C3	P3	O1	
FP1	1.00000	-1.00000	0.00000	0.00000	0.00000	0.00
F3	0.00000	1.00000	-1.00000	0.00000	0.00000	0.00
C3	0.00000	0.00000	1.00000	0.00000	-1.00000	0.00

You can use LDR files to create composite channels. For example, let's say you wanted to combine all of the frontal channels into a single channel. You have two options. You can enter 1.0's for each of the frontal channels to get the *sum* of those channels. Or, you can enter 1/N for the multiplier to get the *average* of all of the channels. In this case, there were 8 frontal channels, and so the multiplier was 0.125. For the remaining channels, you can leave them as they are, which will create identical channels in the new file, or you can change the 1.0's to 0.0's, which will create flat lines. In either case, you can deselect the unwanted channels and resave the file with the single frontal channel. Again, use the first page of the Functional Data Import Wizard to change the label.

	FP1	PZ	FP2	OZ	F3	FC5	F4	FC6	
FP1	0.12500	0.00000	0.12500	0.00000	0.12500	0.12500	0.12500	0.12500	0.0
PZ	0.00000	1.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.0
FP2	0.00000	0.00000	1.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.0
OZ	0.00000	0.00000	0.00000	1.00000	0.00000	0.00000	0.00000	0.00000	0.0
F3	0.00000	0.00000	0.00000	0.00000	1.00000	0.00000	0.00000	0.00000	0.0
FC5	0.00000	0.00000	0.00000	0.00000	0.00000	1.00000	0.00000	0.00000	0.0
F4	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	1.00000	0.00000	0.0

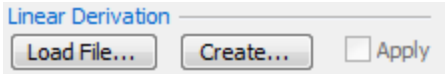
LDR files can get more complex. Here is a section of an LDR file that performs artifact reduction using the Covariance method. Looking at the first line, there is a 1.0 for FP1 and -0.38476 under VEOG. The values in the VEOG column are the transmission coefficients produced in the covariance and regression-like analysis. For each row of data, the VEOG value is multiplied by some value, which should be a negative number. The new FP1 data point is (FP1 * 1.0) + (VEOG * -0.38476). A proportion of the VEOG channel is therefore subtracted from the FP1 channel. This happens for all data points for all channels.

	FP1	F3	C3	P3	OZ	FT8	VEOG
FP1	1.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.38476
F3	0.00000	1.00000	0.00000	0.00000	0.00000	0.00000	-0.20196
C3	0.00000	0.00000	1.00000	0.00000	0.00000	0.00000	-0.11961
P3	0.00000	0.00000	0.00000	1.00000	0.00000	0.00000	-0.05123
O1	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.00989
F7	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.26672
T3	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.09538
T5	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.04139
FZ	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.16006
FCZ	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.11564
CP3	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.09034
FC3	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.13928
TP7	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.05992
FPZ	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.35224
FT7	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-0.17707

Here is a section of a more complex LDR file. This is a spatial filter LDR file created in the Scan software.

	FP1	F3	C3	P3	O1	F7	
FP1	0.65237	0.40627	-0.35570	-0.01601	-0.02478	-0.24763	0.12
F3	-0.15581	1.18209	-0.15942	-0.00718	-0.01111	-0.11099	0.05
C3	-0.08224	0.09611	0.91585	-0.00379	-0.00586	-0.05858	0.02
P3	-0.05209	0.06088	-0.05330	0.99760	-0.00371	-0.03711	0.01
O1	-0.01914	0.02237	-0.01958	-0.00088	0.99864	-0.01363	0.00
F7	-0.22913	0.26778	-0.23444	-0.01055	-0.01634	0.83678	0.07
T3	-0.08294	0.09693	-0.08487	-0.00382	-0.00591	-0.05908	1.02
T5	-0.03714	0.04340	-0.03800	-0.00171	-0.00265	-0.02645	0.01
FZ	-0.12871	0.15042	-0.13170	-0.00593	-0.00918	-0.09169	0.04
FCZ	-0.08712	0.10182	-0.08914	-0.00401	-0.00621	-0.06206	0.03
CP3	-0.06358	0.07430	-0.06505	-0.00293	-0.00453	-0.04529	0.02
FC3	-0.10963	0.12813	-0.11218	-0.00505	-0.00782	-0.07810	0.03
TP7	-0.05201	0.06079	-0.05322	-0.00240	-0.00371	-0.03705	0.01
FPZ	-0.32635	0.38140	-0.33392	-0.01503	-0.02327	-0.23247	0.11
FT7	-0.14454	0.16892	-0.14790	-0.00666	-0.01031	-0.10296	0.05
FP2	-0.30908	0.36122	-0.31625	-0.01423	-0.02204	-0.22017	0.10
F4	-0.12826	0.14990	-0.13124	-0.00591	-0.00914	-0.09136	0.04
C4	-0.06741	0.07878	-0.06898	-0.00310	-0.00481	-0.04802	0.02

If you have an LDR file from Scan, or its equivalent from some other source, or one you have created, you can apply it offline in CURRY using the **Linear Derivation** option near the bottom of the **Miscellaneous** panel. Load the file and then **Apply** it. See the online equivalent in the online **Artifact Reduction** panel.



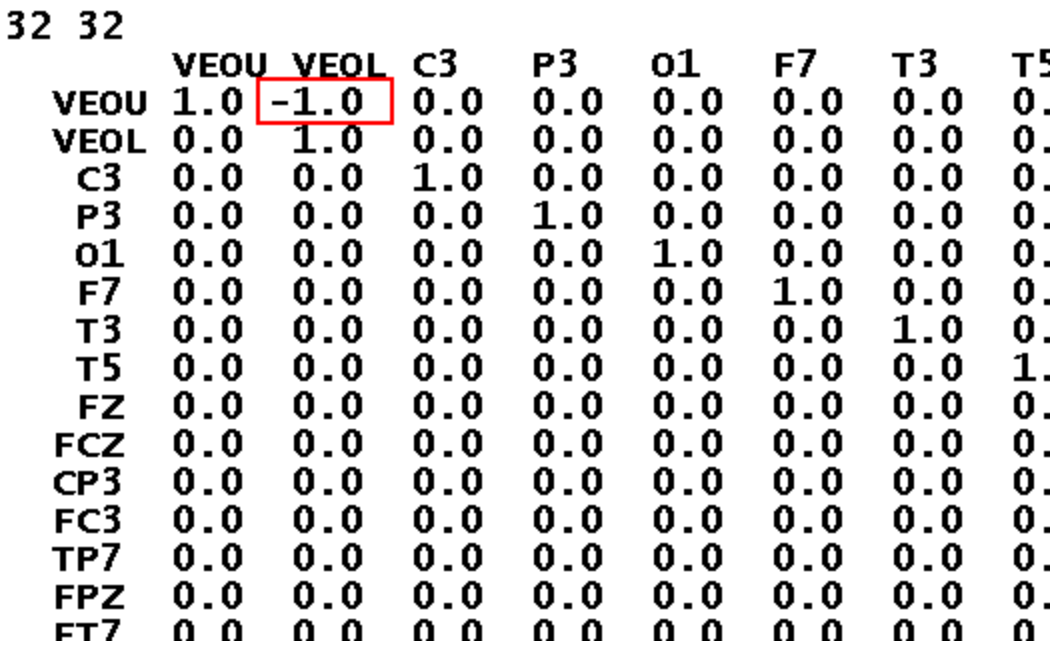
LDR Files with NuAmps

A common use of LDR files occurs with NuAmps users. With NuAmps, where all channels are referential channels, including the blink channels, you may wish to create a bipolar channel for VEOU-VEOL.

Click the 

button to create the identity matrix file, and then open that file in a text editor, such as Notepad or Wordpad. The VEOU and VEOL have been positioned at the top left part of the file below, for convenience. You may see them elsewhere, more toward the lower right, but the modification is the same.

What we want is a bipolar channel, where VEOL is subtracted from VEOU. To do this, change the 0.0 on the VEOU line, in the VEOL column, to a -1.0. Then save the LDR file.



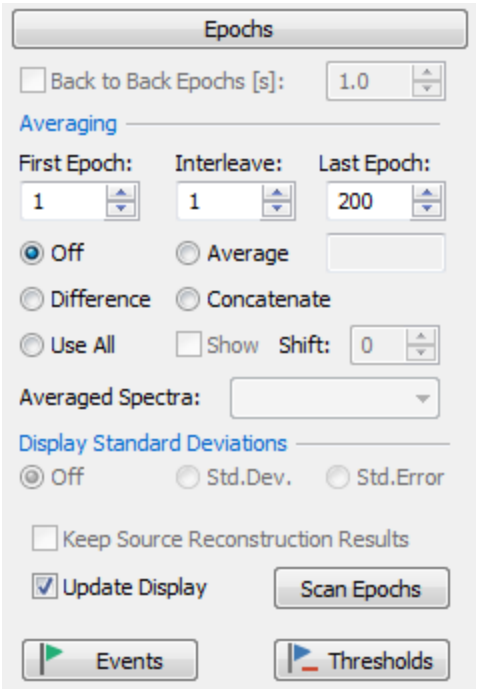
32 32

	VEOU	VEOL	C3	P3	O1	F7	T3	T5
VEOU	1.0	-1.0	0.0	0.0	0.0	0.0	0.0	0.
VEOL	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.
C3	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.
P3	0.0	0.0	0.0	1.0	0.0	0.0	0.0	0.
O1	0.0	0.0	0.0	0.0	1.0	0.0	0.0	0.
F7	0.0	0.0	0.0	0.0	0.0	1.0	0.0	0.
T3	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.
T5	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.
FZ	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.
FCZ	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.
CP3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.
FC3	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.
TP7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.
FPZ	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.
FT7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0

Use Load File... to select that file, and enable Apply to apply it. The VEOU channel will now be VEOU-VEOL, even though the label does not change. It is the new bipolar channel that will then be used for Artifact Reduction, etc. If desired, you can save the continuous data file, with the derived bipolar channel, and then open that file. Go to the first page of the **Functional Data Import Wizard** and change the label for VEOU to VEOU-VEOL (click **Next** and **Finish**). Then you will see the new label in the data display.

17.1.8 Epochs

The Epochs panel contains multiple options pertaining to the creation and averaging of epoched data files.



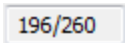
Back to Back Epochs [s]. Enter a value for the epoch interval and enable the option. The resulting file has back-to-back epochs with the duration you select.

Averaging

First Epoch, **Interleave**, **Last Epoch**. If you have a data file open with multiple sweeps, CURRY will compute the average of the sweeps. The total number of sweeps is displayed. You can determine the sweeps to be averaged by selecting the **First Epoch** and **Last Epoch** to be included (such as, the first or last 50 epochs). **Interleave** will automatically exclude epochs. An Interleave of 1 includes all sweeps. An Interleave of 2 includes every other sweep (1, 3, 5, etc.). An Interleave of 3 includes every third sweep (1 accepted and 2 and 3 deselected; 4 accepted and 5 and 6 deselected, etc.).

Off. Deselects **Average**, **Difference**, **Concatenate**, or **Use All** options.

Average. The 

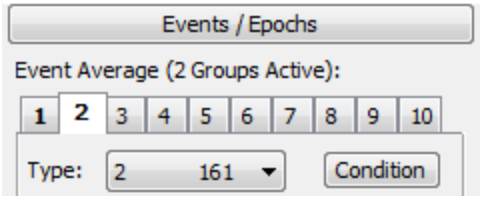
option is used to average *selected* epochs. It is not used with continuous data. The field to the right 

will display how many epochs are included in the average. You can also Accept and Reject individual sweeps manually by stepping through the file and using the  button on the **Functional Data** Toolbar to toggle the state of each sweep (or press the *Spacebar*), or you can use the automatic voltage threshold option (described below).

Averaging multiple AVG files
You can average up to approximately 1000 compatible averaged data files (same number of channels, same channel labels, same AD rate, same Start point). Load the files as usual in the **Functional Data** folder (any **Study** folder).

After clicking **Open Study** (if needed, the **Functional Data Parameters Wizard** will appear for the first file only and use those parameters for all files), you will see the first file displayed as usual, with a sliding bar beneath the Functional Data display. As you slide the bar across, you will see the individual data files. Use the Average option to average the files together. Deselect any files you do not wish to include in the average. You can then perform further analyses on the averaged file.

The Average option may be used in conjunction with the Event Average groups (under Events / Epochs) to average epochs based on type codes.



The following rules apply.

1. If you have different event types in the epoched file (Type 1s and Type 2s, for example), and you do not specify them in any way in the Event Average groups, then all event types will be averaged together.

2. If you specify the event types in the Event Averages, such as, Group 1 has the Type 1's, Group 2 has the Type 3s and Group 3 has the group 5s, then all of the 1s, 3s and 5s will be averaged together. In other words, any event types you specify will be averaged together, regardless of what group they are in.

3. Similarly, if you specify Types 1-5 in Event Average group 1, all of the Types 1-5 will be averaged. Again, any event types you specify will be averaged together, whether they are in individual Event Averages or all in the same Event Average group.

4. If you want to selectively average just one Type, select only that Type for a single Event Average group.

5. If you want to create multiple *individual* averages, set them up using multiple Event Average groups (Group 1 has the 1s, Group 2 has the 2's, and so on), and use **Export Epochs** instead of the Average option.

6. If you plan to use any of the methods for rejecting bad epochs under Threshold Criteria, you may want to include All epochs when Scanning for the epochs to reject. This will let you select the criteria based on all of the epochs. When you average the groups individually, you will still need to use Scan Events under Threshold Criteria for each group you are averaging.

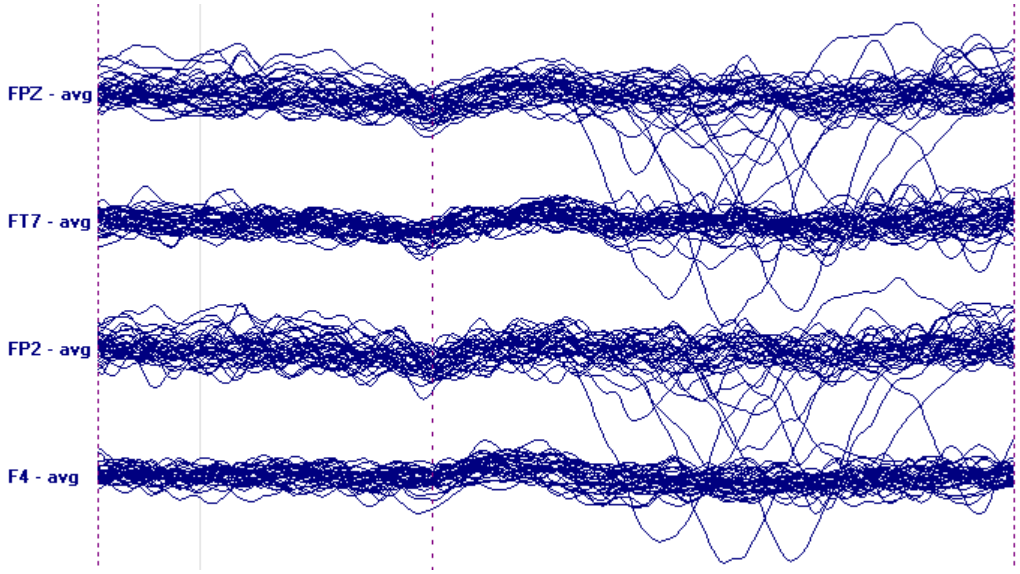
Please see the *Evoked Response Analysis* tutorials for an example of the above.

Difference. Alternates the sign from selected epoch to the next selected epoch. If you have multiple epochs, the result will be the same as averaging the even selected sweeps and subtracting that from the average of the odd selected sweeps. In effect, you are subtracting the signal from the noise, and this can be used in noise estimation. If you just have two epochs selected (or present, as in the case, for example, of two average files) the second epoch is subtracted from the first one.

Concatenate. When **Concatenate** is enabled, the individual epochs/files will be placed back-to-back in a continuous file display. The events that are in the file are then seen in the Event List. This means you can alter the **Pre** and **Post [ms]** latencies, and thereby redefine the epochs. You should not expand the limits beyond the existing ones, as that would include discontinuities in the data. This function also means that you can impose **Conditions** to decide which epochs to include in the average (see the *Conditional Statements* tutorial). You can also use the full extent of **Artifact Reduction**. MEG data may be output as back-to-back epochs, rather than continuous data.

Use All. Enabling this option will overlay all of the epochs in the file. If you have multiple averaged files in the Study, enabling the options will superimpose all of them. If you want to superimpose only selected epochs or averages, deselect the ones you wish to exclude (*right click* and select **Toggle Actual Sweep**, or use the *spacebar*).

In the figure below, 34 uncorrected epochs are overlain, and it is obvious which ones contain the blink artifact.

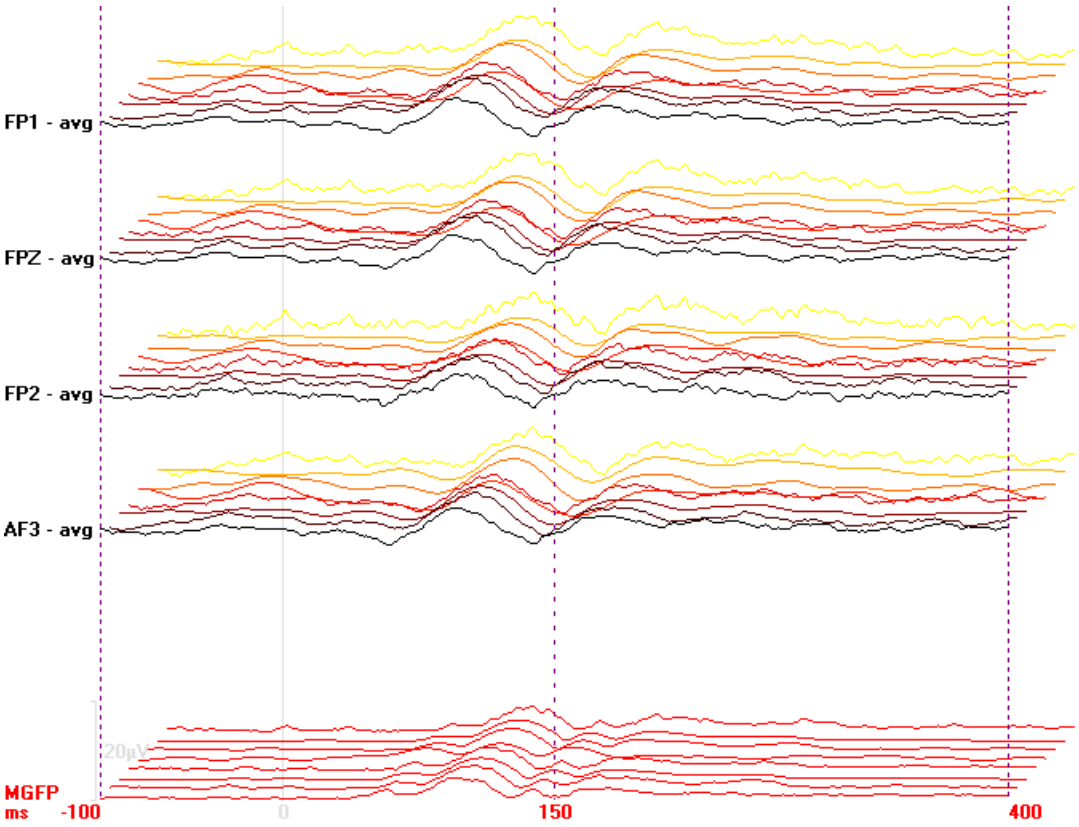


The **Use All** option is generally selected when you are performing statistics with functional data. It has the same function as enabling the **Use All Selected Epochs** option in **Result Statistics**. It can be time consuming to overlay all of the epochs, and the final displayed result may have little value when performing statistics. Deselecting the **Show** button disables the

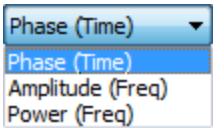
display of the overlain epochs, while for statistical purposes the epochs are overlain.

Show. The Show button is a convenience option that will disable the display of the overlain epochs (when you enable **Use All**). The default state is disabled. This is a time saving option when computing statistics with functional data, since displaying large numbers of overlain epochs can take a while.

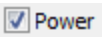
Shift. Displays multiple epochs or files in a cascade or landscape display. In this case, only 4 channels are being displayed for 8 subjects (**Shift** of **6**), and a color scale was selected for **EEG**, under Colors.

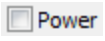
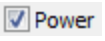


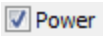
Averaged Spectra. These three options, combined with the Power and Power options in the Frequency Domain panel, provide 6 different ways to compute the power spectrum. These options will be active after you select Spectra from the Frequency Domain panel.



Phase (Time). If this option is selected, the actual waveforms will be averaged first (time domain averaging), and then the FFT will be computed. The results will be displayed in μV or μV^2, depending on whether you

selected  or  . In this case, the phase relationships are taken into account.

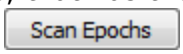
Amplitude (Freq). If this option is selected, the FFT is applied to each epoch first (frequency domain averaging), scaled for *amplitude* (μV), and then the epochs are averaged. The results will be displayed in μV or μV^2, depending on whether you selected  or  . In this case, the phase relationships are not taken into account.

Power (Freq). If this option is selected, the FFT is applied to each epoch first (frequency domain averaging), scaled for *power* (μV^2), and then the epochs are averaged. The results will be displayed in μV or μV^2, depending on whether you selected  or  . In this case, the phase relationships are not taken into account.

Display Standard Deviations

If you select **Std.Dev.**, the +/-1SDs for the single epochs are displayed. If you select **Std.Error**, the SDs of the mean, or standard error of the mean, are displayed (SD divided by the square root of N).

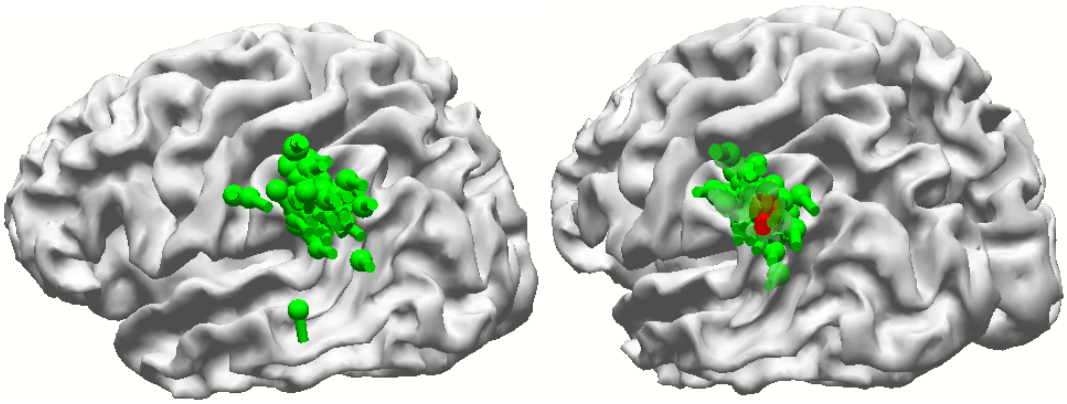
Keep Source Reconstruction Results. There are times, such as when you are looking at the source solutions for multiple individual epileptic spikes, where you want to superimpose all of the individual spikes on one display. In earlier versions of CURRY, you had to compute the solutions one spike at a time and use Keep Results. This is fine if you have only a few spikes, but can quickly become tedious if you have many spikes.

Beginning in CURRY 8, there is an icon, **Dipole Cluster**  , at the top of the Source Reconstruction parameters, that has the same function as **Keep Source Reconstruction Results** and the  button. Both methods will create one set of Kept Results that contains all of the spike solutions.

You need to have epoched data to use this option. With spikes, you can use **Template Matching** to detect the spikes, or manually place event marks on the spikes. Then create an epoched file.

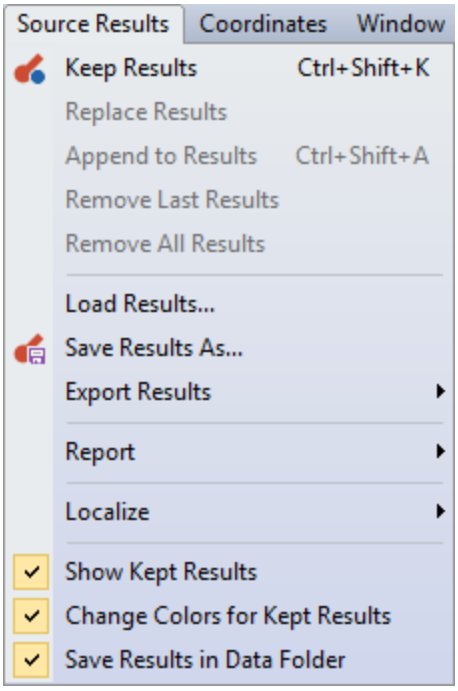
Select a **Head Model** and **Dipole Type**. After the initial dipole results have been computed, enable the **Keep Source Reconstruction Results** option and click **Scan Epochs**, (or just click the **Dipole Cluster**  button).

A dipole solution will be displayed for each epoch. At the end of the scan, you will likely find some inconsistent solutions. *Double-click* on one of them and you will see that epoch. You can then decide if you want to deselect the epoch or not. Click **Scan Epochs** again to rerun the scan with the deselected epochs omitted. A new set of **Kept Results** will be seen. You can also select the **Average** option under **Events / Epochs** to see the solution for the average of the selected epochs (red dipole in right side figure below).

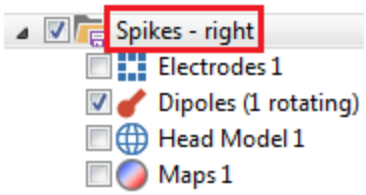


Tips
If you cannot *double-click* on a bad solution because it is inside the cortex, disable the display of the cortex.

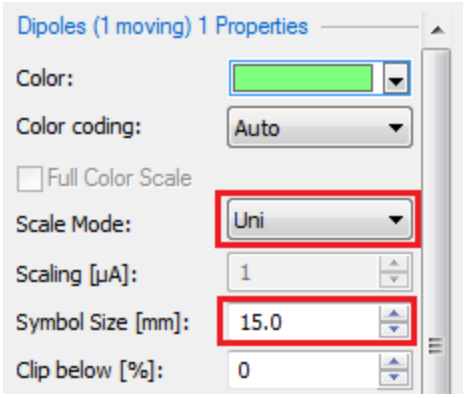
Note the various "Results" options under **Source Results**. For example, use **Remove Last Results** or **Remove All Results** before running the final **Scan Epochs**.



You can Rename the Kept Results by highlighting "Kept Results" and pressing the *F2* key.



You may likely see dipoles of different sizes, where one may be very large and the others may be very small. You can set the dipoles to be the same size with the **Uni** option for **Scaling** in the **Dipoles Properties** (for the Kept Results). Use **Symbol size** as desired to change the overall dipole sizes. Instead you can enable the Uni Size for Kept Results option under **Source Results**.



Update Display. When enabled, you will see the waveforms in each epoch as the epochs are scanned. This gives you a quick review of the epochs, although it can be time consuming. If you are sure the epochs are good and you want the scan to go faster, disable Update Display.

Scan Epochs Scan Epochs. The **Scan Epochs** button has a similar function as the Scan Epochs in the Threshold Criteria panel, although there are times where you may wish to use it independently, such as in conjunction with **Keep Source Reconstruction Results**.

Events Events. This is a convenience short-cut option to display the Events / Epochs panel.

Thresholds Thresholds. This is a convenience short-cut option to display the Threshold Criteria panel.

17.1.9 Noise Estimation

Noise estimation is the central task in preprocessing in the sense that subsequent source reconstruction processes may fail if the noise estimation is incorrect. The following procedures depend on the estimated noise level with respect to the estimated value of the signal to noise ratio (SNR):

- Confidence Ellipsoids,
- Sensor weighting,
- Regularized Dipole Fits,
- Regularized Dipole Scans, and
- Current Density Reconstructions.

Care
Only a correct noise estimate leads to correct or useful regularization parameters for dipole fits and current density reconstructions. As a general rule, the number of data samples used for noise estimation should be the same as the number of samples used for the signal interval.

The weight that is attributed to the functional data of any sensor is inversely proportional to its noise. Sensors are weighted relative to each other
- between data groups and
- within a data group, if channels have different noise levels.

Noise Estimation Methods

Three methods for the noise estimation are available within CURRY, and it is strongly recommended that you estimate noise values using all estimation methods which are appropriate for the data at hand and check the results for consistency. The noise can be estimated from:

- a specified time interval.
- the 50% of samples with the lowest signal.
- the noise level can be entered directly by the user.

For the noise estimation from an interval, the noise is estimated as the variance of the data, i.e., the RMS deviation from their mean, or the RMS deviation from the best fitted linear background. Two options for choosing the interval (i.e., the selection of samples that are defined to consist of noise only) are available:

- The **Percentile 20** and **Percentile 50** methods (described below).
- For measurements with a pre-trigger range this time range can be used by selecting a **User Def. Interval** for noise estimation (described below).

For these methods, in addition to the individual noise level of each channel, the full noise covariance matrix is also estimated if the number of samples used for noise estimation is larger than twice the number of channels. It is displayed in the **Output** window.

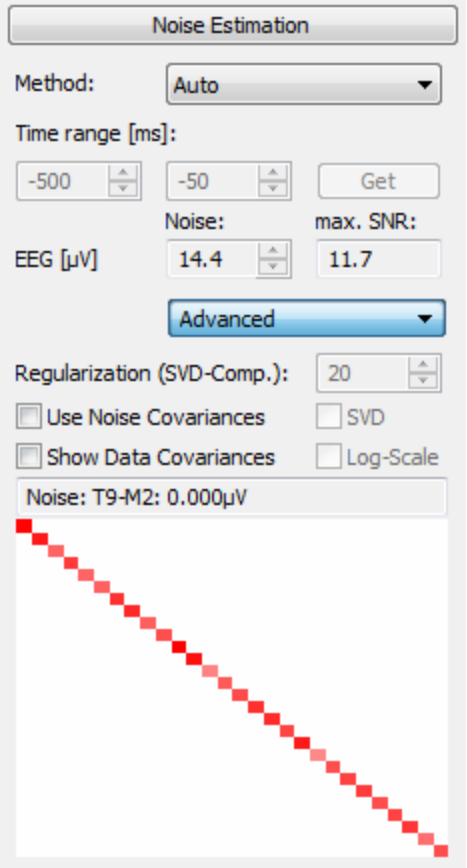
Note
For source reconstruction, only the diagonal elements of the covariance matrix are used, although the off-diagonal elements are also estimated and displayed in order to visualize the noise correlations between the different sensors.

For most methods, the individual noise level of each channel is calculated and used for the reconstruction. In the user interface the average over all channels of each group is always displayed. More detailed information is printed in the **Output** window.

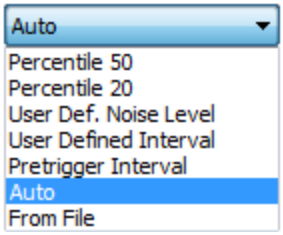
Note
For CURRY version 7.0.6.6 and newer, there has been a slight change in the way noise is estimated. The new method uses the standard deviations of the selected channels over time averaged over the selected channels for the noise estimation, instead of using the standard deviation over the channels and averaging over time.

This change allows you to compute noise and SNR with single channel data, which was not possible before.

CURRY performs a real-time noise estimation as soon as you select **Open Study**. The default method is the **Auto** method, which uses the pre-stimulus interval if there is one, and the entire interval if there is not one. You should verify that the best method for your data is being used. For a given Study, you may save the **User Def. Interval** (or **User Defined Noise Level**) and the start and stop points in the **Study Parameters**.



Method. There are six methods available for noise estimation.



Percentile 50. The standard deviation of the *50 percent* smallest signal values in the entire latency range are used for noise estimation. In most situations, this provides a rough estimate of noise level, and is intended for use in cases where there is no "signal free" interval (such as a prestimulus interval). Depending on the

actual data, the use of the **User Defined Interval** method is strongly recommended for further data processing and reconstruction.

Percentile 20. The standard deviation of the *20 percent* smallest signal values in the entire latency range are used for noise estimation. In most situations, this provides a rough estimate of noise level, and is intended for use in cases where there is no "signal free" interval (such as a prestimulus interval). Depending on the actual data, the use of the **User Defined Interval** method is strongly recommended for further data processing and reconstruction.

User Defined Noise Level. This option lets you set the noise level (same for all channels) manually. When selected, the **Noise** field will become active. Enter the value manually (using the arrows or the *keyboard*). This option is helpful if none of the other methods yields satisfying results, or if you want to overrule the estimated value. Also, if the estimated noise levels vary too much over the channels, e.g., when a small number of samples are used for noise estimation, the noise covariance matrix can thus be chosen to be proportional to the unity matrix by switching the estimation mode to **User Defined Noise Level**.

User Defined Noise Level must be used when saving the results from PCA. PCA is done in the "unitless" space. The Percentile 50 and User Defined Time Range (and the special case of it, Pretrigger) modes use each channel individually. That is, noisy channels are downweighted since they get smaller (SNR) values after the transformation. If each channel is treated individually (regarding noise transformation), the values that would be saved to disk would be incorrect. With the User Defined Noise Level mode, all channels are simply divided by a factor, and the backtransformation to unit space is trivial (just multiply the factor again).

User Defined Interval. Noise is estimated using the standard deviation of the user defined time interval (determined by positioning the two outer cursors and clicking the 

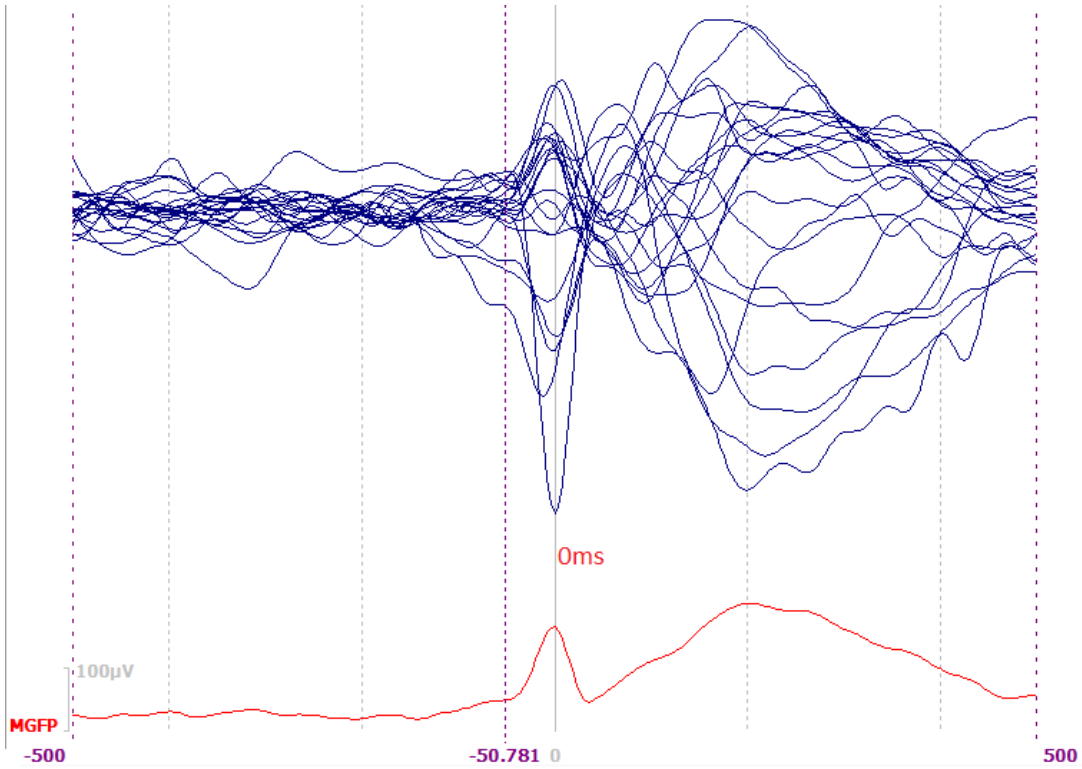
button, or entering the values manually). This is the recommended option unless you have no "signal free" interval in the data.

Pretrigger Interval. This is a convenience option. Rather than select **User Defined Interval** and then designate the pretrigger interval, just select this option.

Auto. The Auto option will automatically detect and apply the most likely method for noise estimation. With continuous data (> 10s), or data without a pretrigger interval, and if you have selected **<None>** for the **Scope**, this is equal to **Percentile 50**. With continuous data (> 10s), or data without a pretrigger interval, and if you have selected **Curry 7** for the **Scope**, this is equal to **Percentile 20**. For averaged data (< 10s) with a pretrigger interval, the Pretrigger Interval is used for noise estimation.

Note
The Auto and Pretrigger options have a special setting when the pretrigger interval is 490 ms or longer. In that case, the noise estimation is made with an ending time of -50 ms (or closest latency, depending on the AD Rate), instead of 0 ms. The reason for that is when you are analyzing epileptic spike data, where the spikes have been detected manually, the 0 ms point occurs at the peak of the spike. You

typically create epochs from -500 to 500 ms. If you use the -500 to 0 ms interval for noise estimation, that will include part of the spike, and result in an abnormally high noise estimate. CURRY therefore uses the -500 to -50 ms range for noise estimation, when you select either Auto or Pretrigger. If you have a pretrigger interval that starts less than -490, e.g., -400 ms, then the noise estimate will be based on that value to zero (-400 to 0 ms). You can, of course, override these values by selecting User Defined Interval and entering in the desired interval.



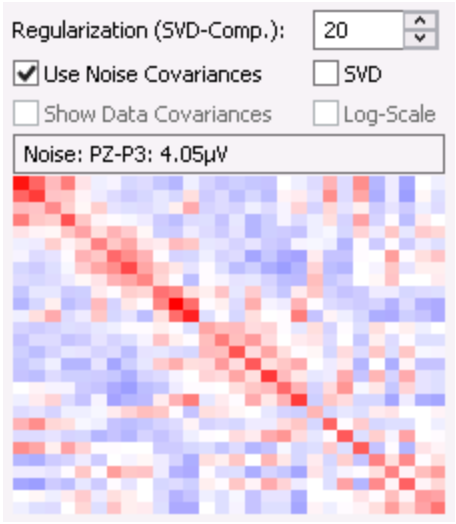
From File. In some cases you may wish to use a data file where no subject was connected during the recording as a measure of noise. Or, in order to get enough samples for accurate noise estimation, you may need to select other sections of the continuous data file for noise estimation. Use From File to select the file, assuming it has the same number of channels, same labels, etc.

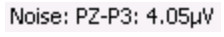
Timerange [ms]. These fields become active when you select **User Defined Interval**. Select the Timerange to use for noise estimation either by setting the outer two cursors and clicking the Get button, or by entering the values manually.

EEG [µV], **Noise**, **SNR**. In all but the User Defined mode, the **Noise** field is read-only and shows the estimated noise level. In User Defined Noise Level mode, you may enter the noise level here. The **SNR** field displays the best (maximum) SNR (signal to noise ratio). The information is also displayed in the **Output** window.

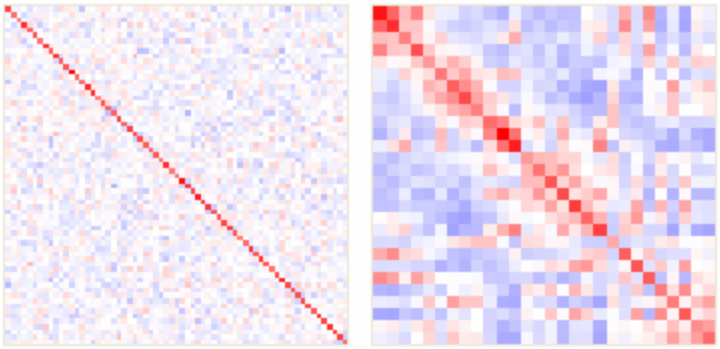
Advanced
Regularization (SVD-Comp.), **Use Noise Covariances**, **SVD**, **Log Scale**, and **Show Data Covariances**. When **Use Noise Covariances** is enabled, the full covariance matrix is used for the SNR-transformation, otherwise just the diagonal is used (which is appropriate in most circumstances). At least twice as many samples as the number of

selected channels should be used to obtain a meaningful measure. The noise covariance method is only meaningful if there is a huge amount of signal free background samples (~10,000), so that a reliable estimation of the whole matrix is possible. Otherwise it can give spurious source reconstruction results. These options are special purpose research tools (used more, for example, with MEG recordings).



The Noise window displays the estimated noise covariances as a matrix. Individual Noise levels may be seen by positioning the mouse in the display and reading the level in the Noise field above it 

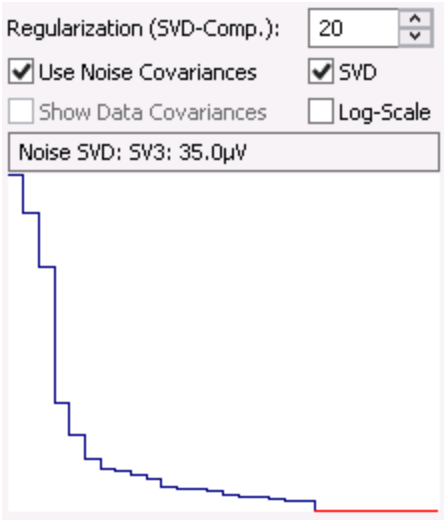
. The color scale used can be changed using the **Colors** panel, under **Functional Data**. It can be seen how channels differ in their noise statistics. In the simulated data file below (left), 1µV noise was added to a file with no noise. Each channel's noise level is nearly independent, which is approaching the same situation as disabling the Use Noise Covariances (where the non-diagonals are all 0.0 and excluded). The second file (right) is a genuine data file with representative noise, showing the correlation among channels. The larger the correlation, the more questionable is the assumption of white Gaussian noise existing in the channels.



For the SNR-transformation, the inverse of the covariance matrix is also required. When using the full covariance matrix, this matrix has to be inverted. The **SVD** option (singular value decomposition of the noise variance) allows a regularized, truncated SVD inversion, which removes instabilities from the low amplitude components.

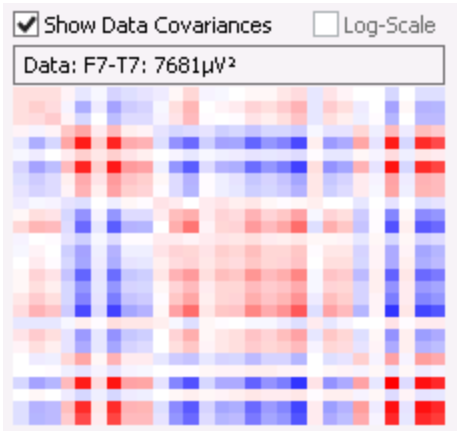
The SVD checkbox also switches the display so the sorted SVD weights can be seen

(on a linear or **Log-Scale**). The red colored range indicates the truncated small components. In the example below, the 20 leading components are used for the inverse, and are colored blue (blue is the device color - with more devices more curves will be displayed).



Alternatively, the data covariance matrix (of the full page Timerange) is displayed for information purposes (when performing a Beamformer scan, this matrix is actually used).

The **Show Data Covariances** option can be displayed, and the covariance between any two channels can be seen in the field above the matrix by positioning the mouse cursor in the display.



Care

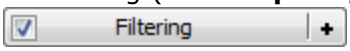
In the noise estimation, only uncorrelated noise in the data due to background noise, amplifier noise, etc., is calculated. Errors due to incorrect calibration factors, wrong sensor positions, and incorrect head models are not measured.

Care

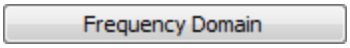
Enabling Use Noise Covariances and changing the number of SVD components can affect the source reconstruction results. These options should not be used in routine operations.

17.1.10 Frequency Domain

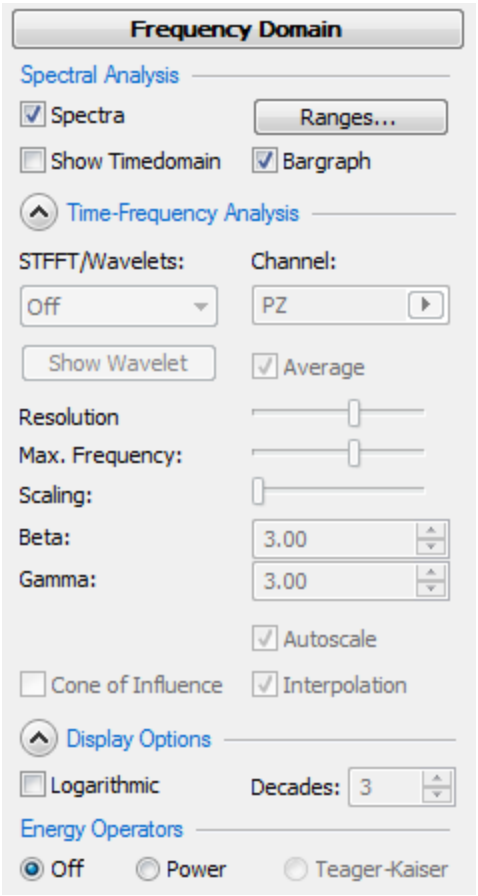
The Frequency Domain options are used to perform FFTs (Fast Fourier Transforms) and wavelet analyses.

Whenever you are performing power spectral analyses, it is necessary to apply windowing to the data to avoid spurious increases at the ends of the interval. Windowing (**Data Tapering**) is found in the **Advanced** settings under 

.

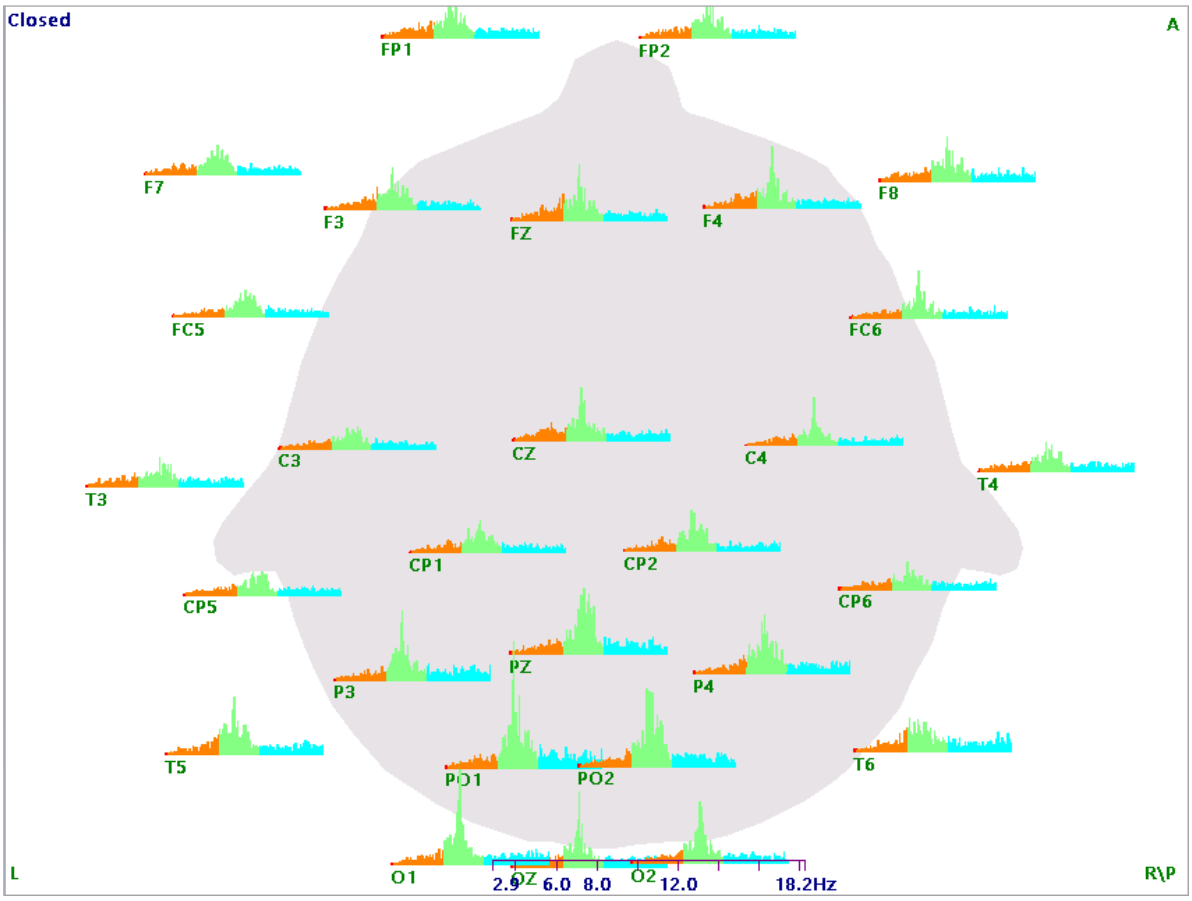
The 

parameters panel contains the other settings.

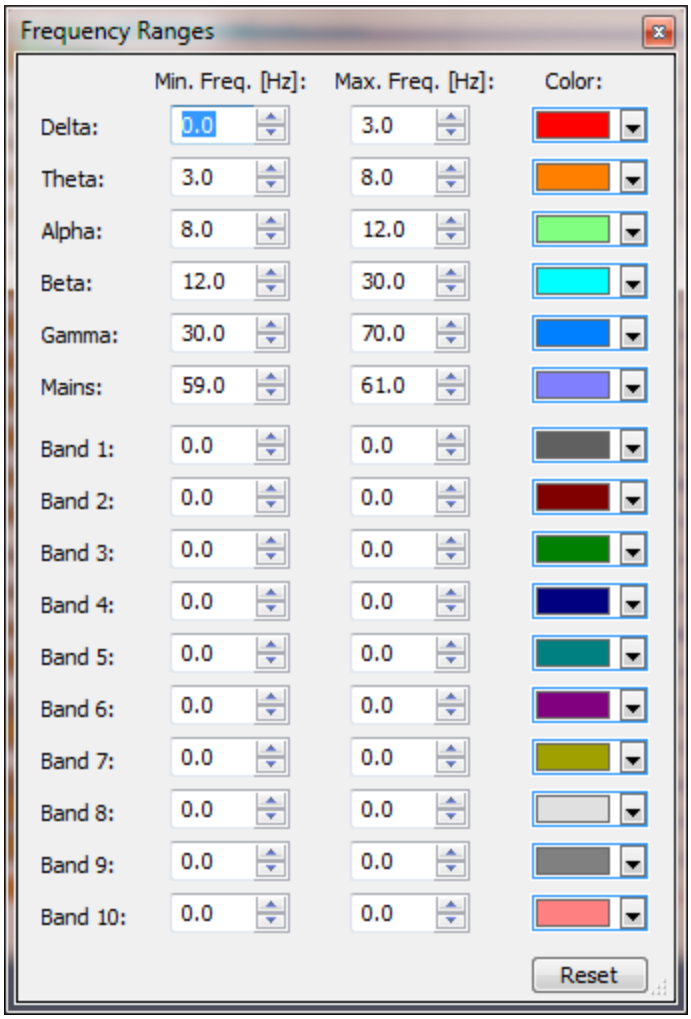


Spectral Analysis
Spectra. An FFT spectral analysis is computed *over the data that are displayed* (the Timerange is ignored), plus enough extra samples at the beginning and end of the file in order to achieve a number of samples that is a power of 2. Change the number of seconds that are displayed to focus in or spread out the section that is displayed. Once the power spectrum is computed, you can zoom in to the frequency range of interest. With epoched data, you do not need the epoch

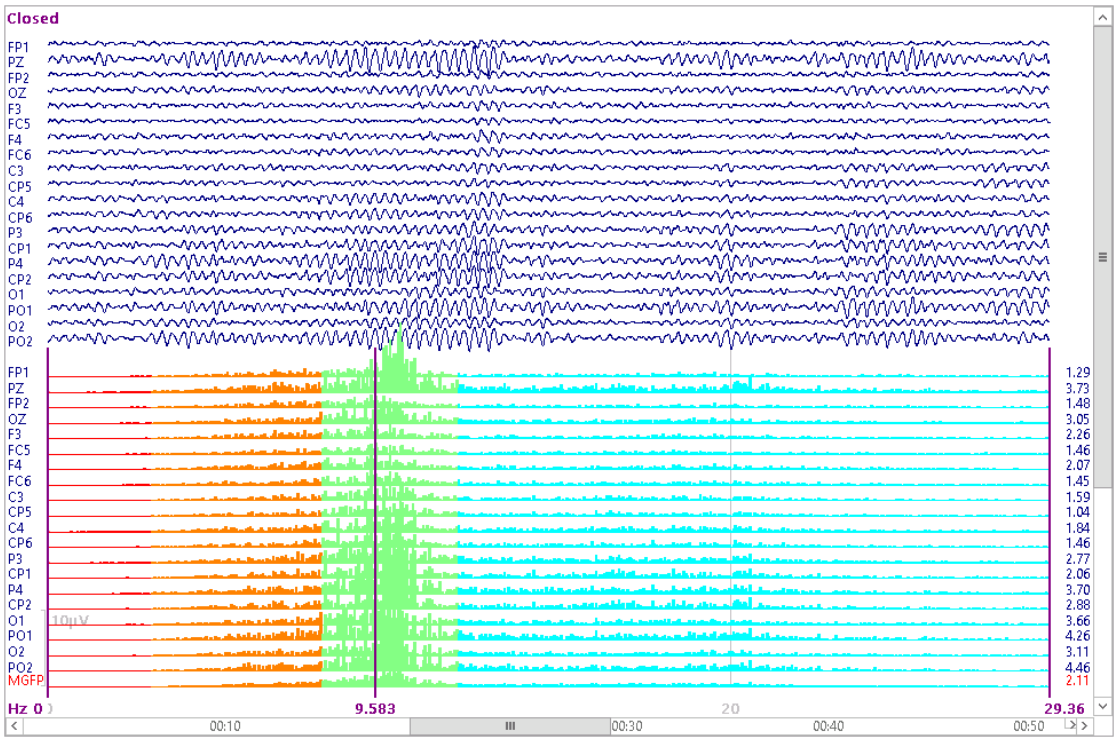
interval to have a power of 2 samples. Epochs can be of any duration - zero padding is used to make up the difference.



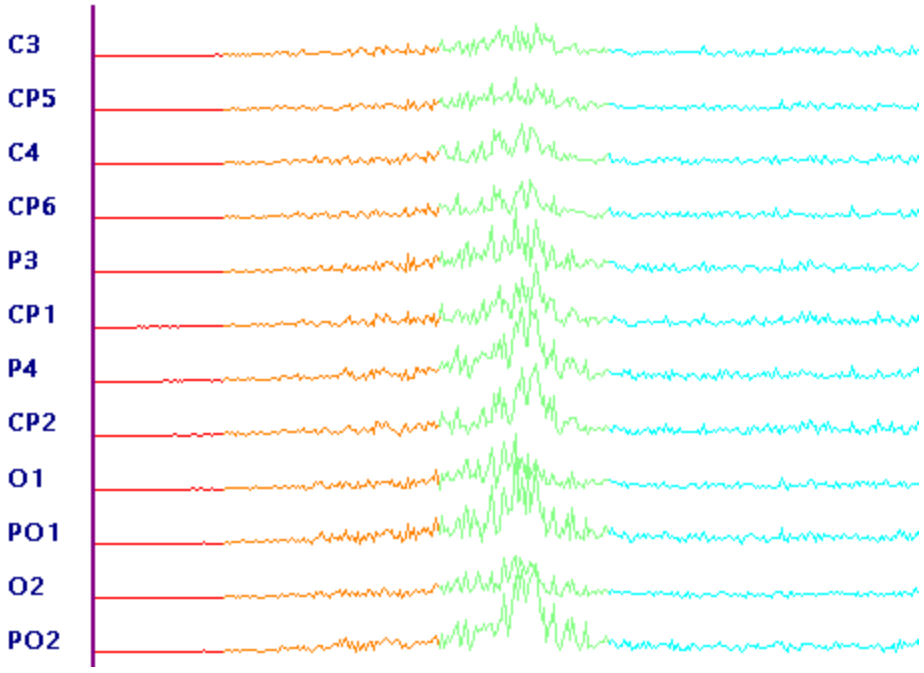
Ranges. This option allows you to redefine the Frequency ranges and colors. You can also include up to 10 additional ranges. These will take precedence over any overlapping conventional ranges. For example, if you set Delta to 0-3.0 Hz in Red, and Band 1 from 0-5.0 Hz in Dark Gray, you will see only the dark gray.



Show Timedomain. This option allows you to display the waveform data at the same time as the spectral data. Moving through the file will show the changes in both. Amplitude scaling works for the spectral data only. To rescale the waveform data, deselect **Spectra**, change the functional data scale, and reselect **Spectra**.



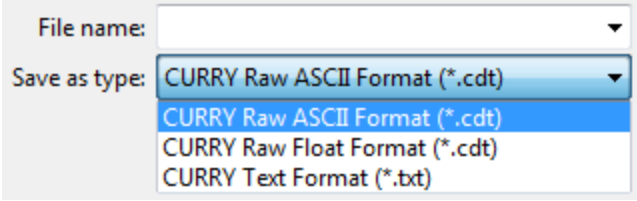
Bargraph. This allows you to view the FFT data in bar graph display (above). When disabled, data are displayed in a line graph (below).



Exporting the FFT Data

There are 3 options for exporting spectral data files. Briefly, the **ASCII** export creates a text file that can be read back into CURRY. The values are not simple amplitudes, as seen in CURRY. See the next section for details. The **Raw Float**

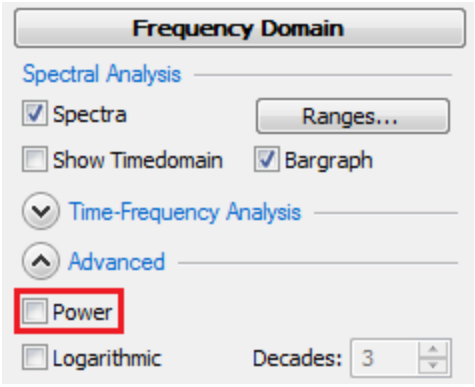
format is the basic format used in CURRY. The **Text** format creates a text file with the actual amplitude/power values that can be read into, for example, Excel, but not back into CURRY. This is the preferred option if you are exporting the spectral data for further analysis outside of CURRY in Excel or in a statistical package. See below for more details.

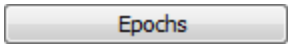


CURRY Raw ASCII Format (*.cdt).
There are a couple of things that should be understood when exporting files to ASCII (as opposed to the CURRY Raw Float Format).

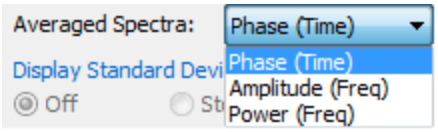
1. The values that are contained in the ASCII .cdt file are half of the *amplitude* values seen in CURRY. If you are performing further analyses of the ASCII data, multiply them by 2 first. If you open the ASCII .cdt file in CURRY, the amplitude will be the same as when the file was saved (the x2 is performed internally).

2. When you export spectral data to an ASCII .cdt file, it is always the Amplitude (microvolt) values that are saved. This is irrespective of the **Power** option selection under **Frequency Domain**, which affects the display only.



The saved results are affected by the **Averaged Spectra** selection only (in 

). This means that if you, for example, compute **Power (Freq)** values and save the ASCII file, it is the square root of those values (only Amplitude values are saved), divided by 2, that are contained in the .cdt file. Multiply the values in the .cdt file by 2, then square them to obtain the values seen in CURRY. When reopening the file in CURRY, the x2 is performed internally; select the **Power** option to see the squared values.



Real and imaginary values are saved.

For example, say you are exporting 69 channels of an averaged file of amplitude spectra data sampled at 1000 Hz.

First, the .dpa parameter file contains the description of the data and the geometry description of the sensors that are contained in the .cdt file.

In this example, spectra were saved ([DPA] FrequencyDomain = 1). The .cdt file then contains the (amplitude) spectra of all channels, the columns address the channels ([DPA]NumChannels = 69 in this case), the rows (lines in ASCII-format) address the frequency bins ([DPA]NumSamples = 4096 in this case -> 2048 frequencies, see below), so the first row contains the 69 real part amplitudes of frequency 0 Hz.

Two consecutive rows contain the frequency bins, first the real (R), and second the imaginary (I) part, so for example row three and four contain real and imaginary parts of the second frequency bin (0.2441Hz, see below). The frequency bin amplitudes are calculated from sqrt (R*R + I*I).

The maximum frequency (Nyquist frequency) is given by: sampling frequency / 2 ([DPA]SampleFreqHz = 1000 Hz / 2 = 500 Hz in this case). The frequency resolution is given by: max. frequency / number of frequency bins = sampling frequency / 2 / ((NumSamples / 2) = 1000 / 2 / (4096 / 2) = 0.2441Hz.
The Nyquist frequency (sampling frequency / 2 = 500 Hz) is not displayed in Curry, so there the maximum displayed frequency is sampling frequency / 2 - frequency resolution = 500 - 0.2441 = 499.8Hz.

Nyquist and 0 frequencies are special cases since they have no imaginary part: 0 Hz amplitude is in the real part of bin 0 (first row / line), Nyquist frequency (500 Hz) is in the imaginary part of bin 0 (second row / line).

If you want to calculate *power* spectra, the amplitude values have to be squared (R*R + I*I).

If you are saving epochs, rather than the average of the epochs, the same conventions apply.

CURRY Raw Float Format (*.cdt). This is the basic CURRY binary float format. Files saved with this option can be opened by CURRY; a parameter file is created automatically. The files may be read into MATLAB as well, although this format is generally used only within CURRY.

CURRY Text Format (*txt). Use this option for exports outside of CURRY. A simple text file is created. In this case the values are the same amplitude/power values you see in CURRY (as opposed to the CURRY Raw ASCII Format). A matrix is created where the channels are the columns and the frequency bins are the rows. If you are exporting multiple epochs, you will see the values for the first epoch first (channels by bins), then the second epoch, and so on.

The entire spectrum is saved, even if you select a smaller frequency range.

The frequency of a bin is calculated as (sampling rate / number of rows) x 0.5 x (current row - 1).

For example, if your file has a sampling rate 1000Hz and your FFT export contains 2048 values (1024 pairs of real and imaginary values), the frequency resolution of each bin is 1000/2048 = 0.49Hz. (The more correct formula would be: maximum frequency / number of bins = 500Hz / 1024, but the other formula creates the same result.) If you multiply this by the current row count (you have to subtract a 1, because the first bin shows the 0Hz bin), you get the starting frequency of each bin.

Below is a section of an epoched data file. The channels are the columns, and the epochs and frequency bins are the rows. Note that the far column on the right gives the starting frequency for each bin. With continuous data, the file is similar but without the epochs.

FP1	F3	C3	P3	O1	F7	T3	T5	FZ	FCZ	Freq[Hz]
Epoch 1										
2.8013	2.8885	0.15085	0.35286	2.254	1.1458	1.9198	0.80396	5.1454	0.56868	0.00
2.7573	2.8904	0.96856	0.78613	1.4786	1.6016	1.323	0.44692	3.8007	1.2846	0.49
5.3456	4.104	1.4461	2.2213	2.6294	3.4742	2.4846	0.86751	4.3659	2.5136	0.98
5.0195	3.1053	1.0739	2.1049	2.1753	3.4009	2.1106	0.76044	2.1585	2.2237	1.46
2.35	1.4619	0.89386	0.38519	0.24454	1.6563	0.52357	0.32833	1.0827	2.0559	1.95
1.2829	2.2105	3.6891	1.577	0.86667	0.82747	1.8477	0.77678	3.7188	4.9343	2.44
0.82507	2.0138	3.6043	2.4116	2.6421	0.3192	1.9123	0.78772	3.6047	4.67	2.93
0.69316	2.1181	3.791	2.6273	2.5354	0.69016	2.254	1.2292	2.5753	4.5909	3.42
2.3416	3.0716	3.7789	1.9907	1.4794	1.7299	2.1886	1.1883	3.0499	4.5605	3.91
2.3545	2.2863	0.73212	0.74017	1.4655	1.621	0.90429	0.53212	1.8038	1.2762	4.39
1.1599	0.78651	0.67237	0.74272	0.48195	0.59884	0.7984	0.65501	1.2305	1.0971	4.88
1.0919	0.70853	0.11314	0.654	0.75737	0.73625	0.42709	0.44681	1.483	1.2181	5.37
1.7831	1.7928	0.47526	0.034851	0.8546	1.7926	1.2327	0.27301	1.0666	1.014	5.86
1.8813	1.857	0.69651	0.53294	0.70242	1.9111	1.1846	0.15592	0.56777	1.2708	6.35
0.7596	1.0567	0.80033	0.61294	0.80741	1.1563	0.41702	0.15136	0.72994	1.1824	6.84

Time-Frequency Analysis
STFFT/Wavelets

EEG/ERP data are generally presented as amplitude changes across time. When you perform a spectral analysis, the data are presented as amplitude changes across a frequency range. Wavelet transforms provide time and frequency information simultaneously, hence giving a time-frequency representation of the signal.

Please see the following articles for more information about Wavelets and STFFT.

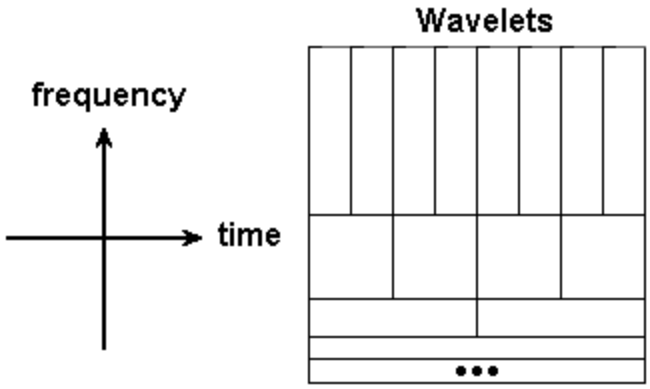
For Wavelets:

A.N. Akansu, W.A. Serdijn, and I.W. Selesnick, Wavelet Transforms in Signal Processing: A Review of Emerging Applications, Physical Communication, Elsevier, vol. 3, issue 1, pp. 1–18, March 2010.

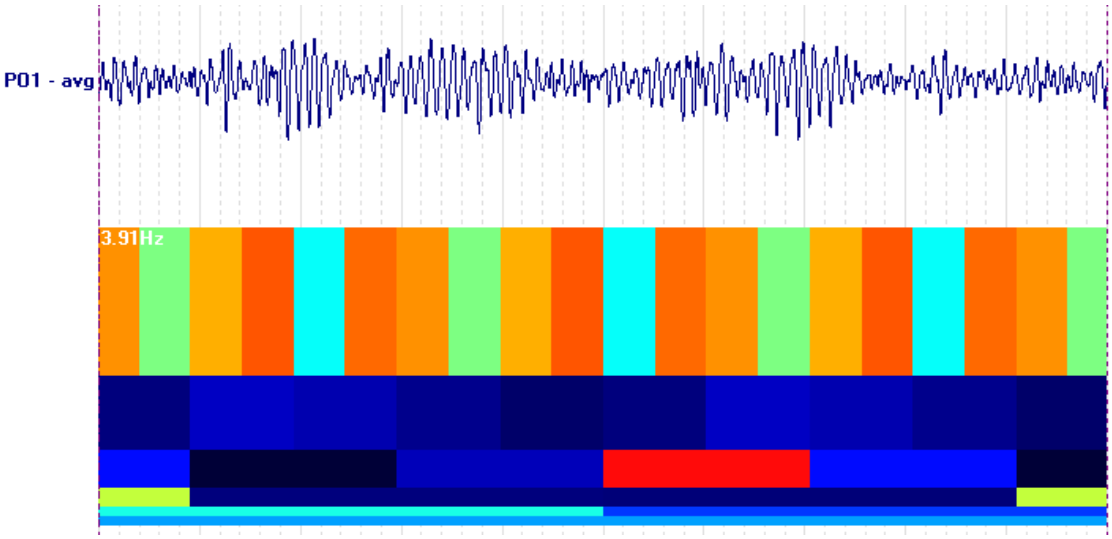
For STFFT and Wavelets:

B. Boashash. Time Frequency Signal Analysis and Processing: A Comprehensive Reference. Oxford, Elsevier, 2003.

With wavelets there is a relationship between frequency and time resolution. Slower frequencies have better frequency resolution with poorer time resolution, and faster frequencies have poorer frequency resolution with better time resolution. This is shown schematically in the following figure,



and graphically in the actual results.

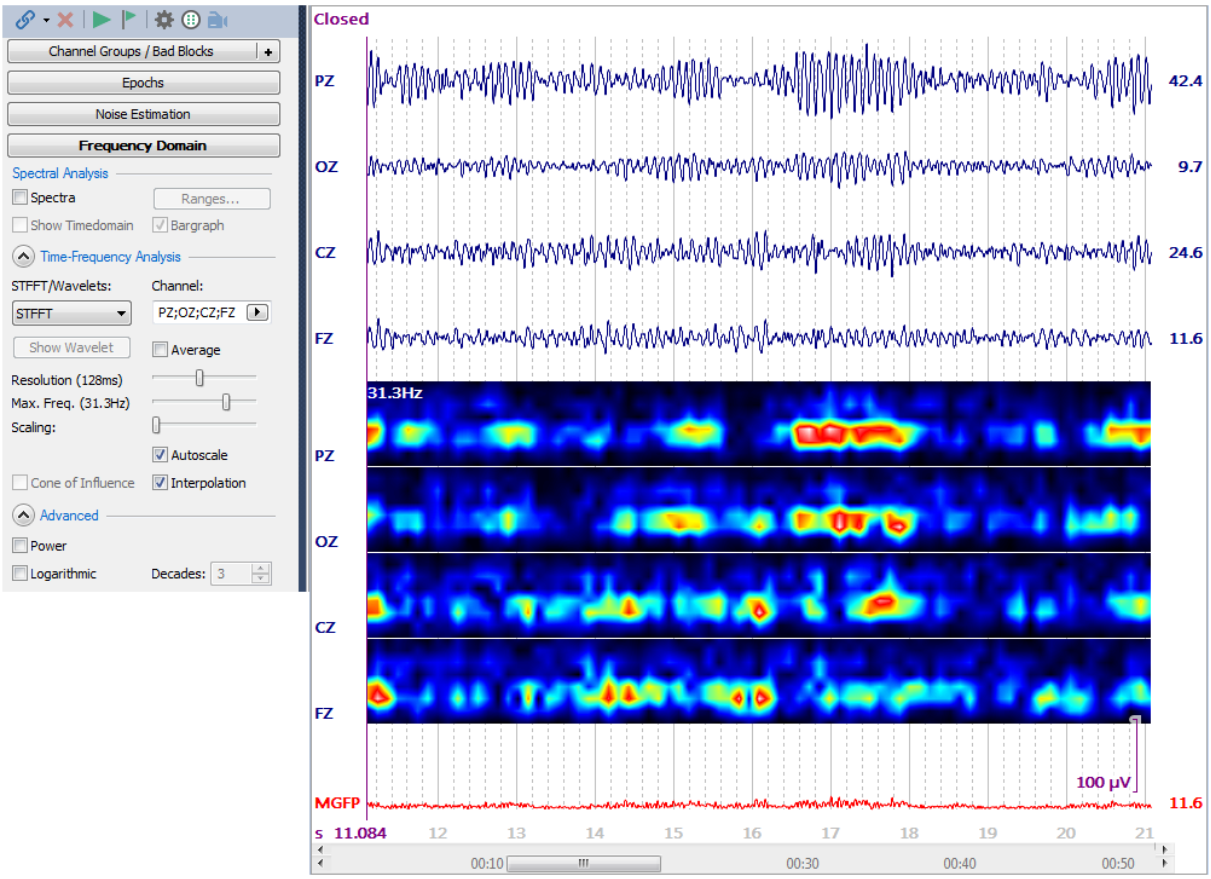


There are many types of wavelets that can be computed. CURRY includes the wavelets shown below. **STFFT**, or Short Time FFT, is an alternative to wavelets. It is well beyond the scope of this manual to describe the computational differences among the options, or the advantages/disadvantages or applications of each. Briefly, STFFT is generally more effective for ongoing EEG, while wavelets are generally better for transient phenomena, such as spikes.

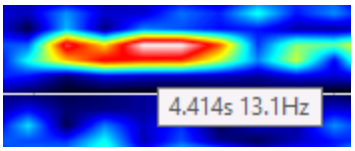
STFFT. The algorithm is called short-time FFT, and it is an alternative to wavelets. The spectra are displayed for all selected channels, or averaged over all selected channels.

The STFFT is meant more as a qualitative, not a quantitative measure since the results strongly depend on the pagesize and resolution (see below), and this is why the absolute values are not shown or saved.

In all of the STFFT and Wavelet displays, the y-axis is frequency, and the x-axis is time, corresponding to the waveform data being displayed. It is generally helpful to reduce the number of channels being displayed in order to see the wavelet display more clearly. In the example below, a montage was created to display only the midline channels. The STFFT results are for the selected channels only (the midline channels). If the **Average** option had been enabled, we would see only the average of the four channels. If you have "Other" channels, such as artifact channels, these will not be included in the wavelet displays.



Position the mouse cursor in the display, and a Tooltip will show the time into the file and the frequency for that position.



When you select STFFT or one of the wavelets, the **Channel**, **Resolution**, **Max. Frequency, Scaling** and **Average** controls become active.

Channel. Select one, some, or all channels.

Show Wavelet. Displays the wavelet's waveforms.

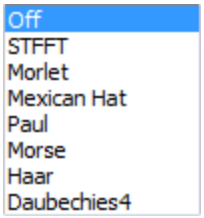
Average. When enabled, the display will be based on the average of the selected channels. Otherwise, you will see the results for each selected channel.

Resolution. Selects the temporal/frequency resolution. There is always a tradeoff between frequency and time. Dragging the cursor to the left gives better frequency resolution, with wider time intervals. Dragging to the right gives better time resolution, with broader frequency intervals. With wavelets, resolution chooses greater or fewer frequencies for inclusion in the analyses, which affects the computational load (more detail is present in the y-axis), without affecting the x-axis. For the STFFT the data are segmented into a power of 2 samples depending on the resolution you choose (for example a pagesize of 10s corresponds to 10001 visible samples (1 kHz sampling rate) and 16384 samples are loaded and processed in the background, for each STFFT segment e.g. 16384 / 32 = 512 samples are used).

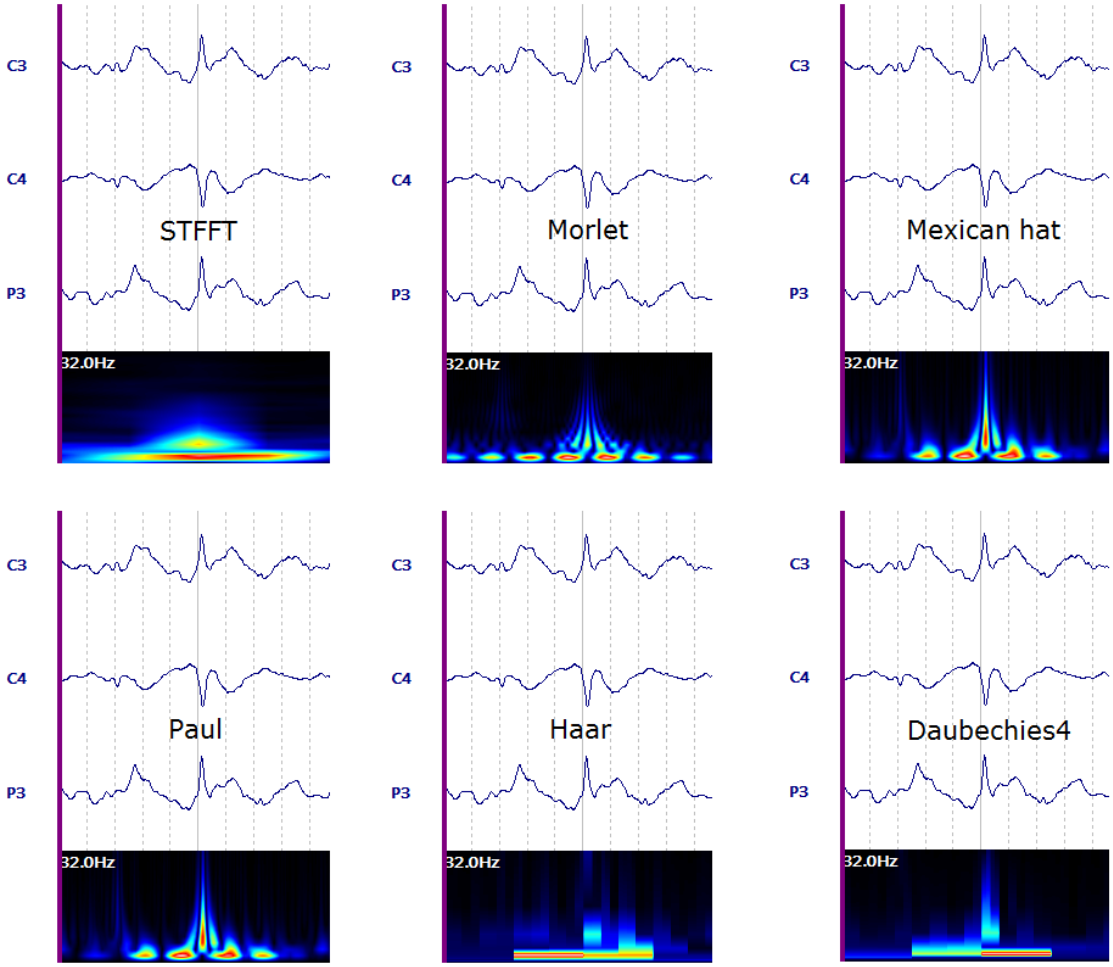
Max. Frequency. Moving the control will increase or decrease the maximum frequency that is displayed (the maximum frequency is displayed in the upper left corner). The absolute maximum is determined by the sampling theorem (sampling frequency/2).

Scaling. This controls the sensitivity of the color scale.

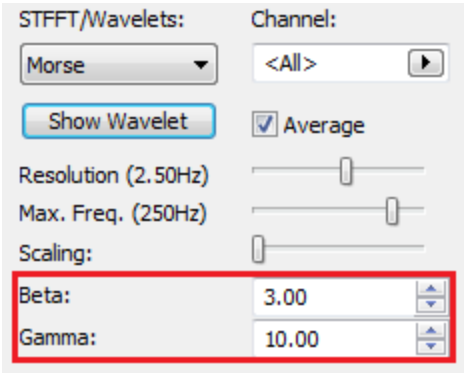
Wavelets. CURRY includes the following wavelets.



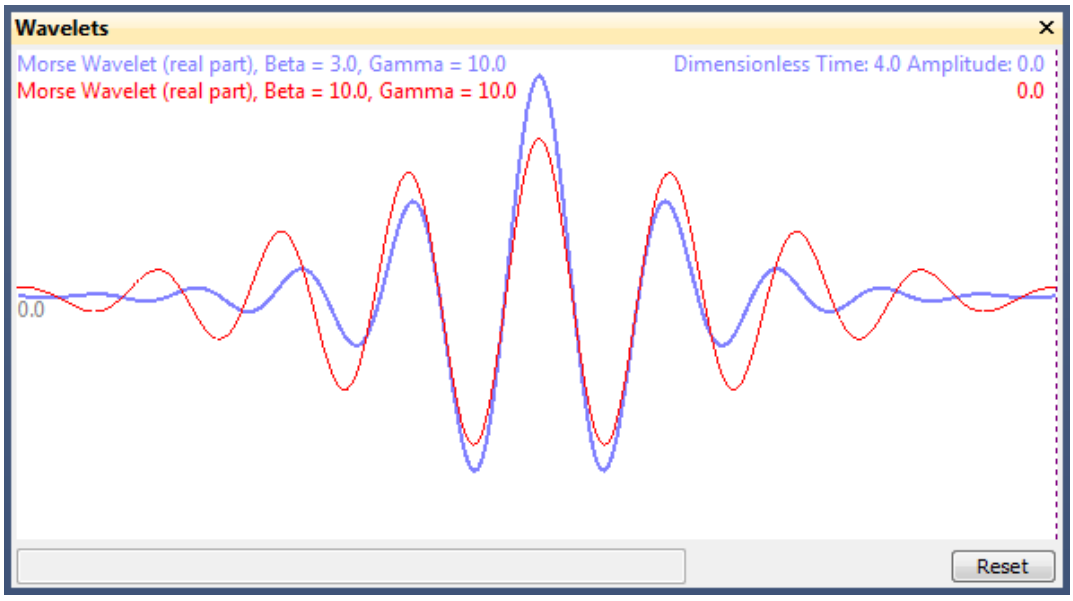
Very briefly, you can see some of the differences among the wavelets in comparison to the STFFT below. The Mexican hat has one oscillation, whereas Morlet has many, which may make it simpler to work with. Paul is very similar to the Mexican hat, although it actually has more oscillations (not really seen below). The Mexican hat may be better for spikes because it has fewer oscillations, which tends to create a temporal smearing that simplifies the pattern. Morlet, Mexican hat, and Paul may all be preferable to the STFFT for transient patterns like spikes.



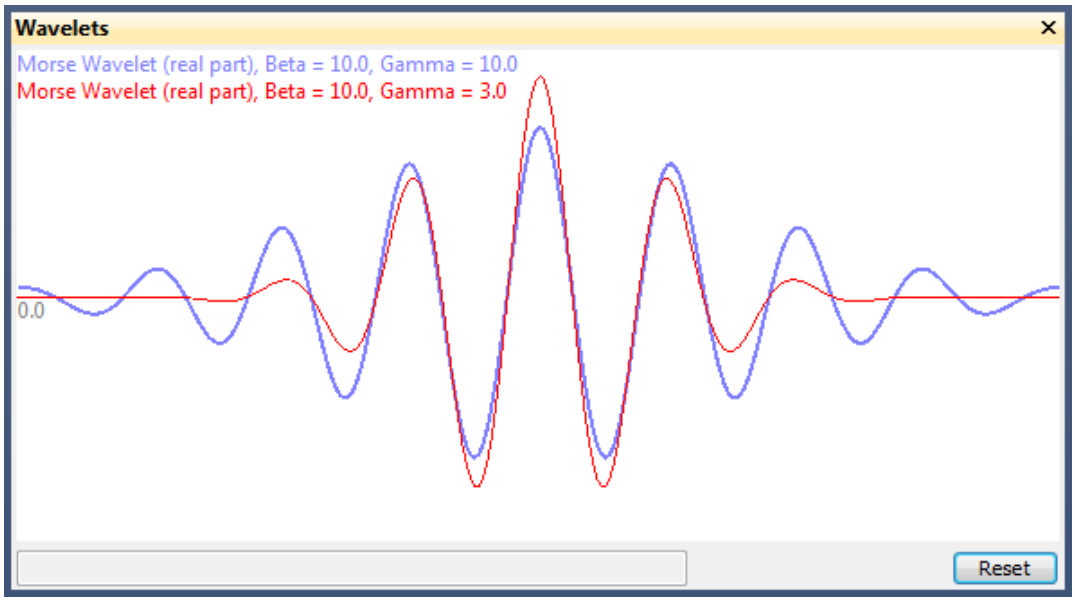
The **Morse** wavelet is particularly useful with high frequency oscillations. It is a little different in that it has two fine-tuning settings: Beta and Gamma. Adjusting these will let you fine tune the wavelets, and also allow you to reproduce many of the other wavelets.



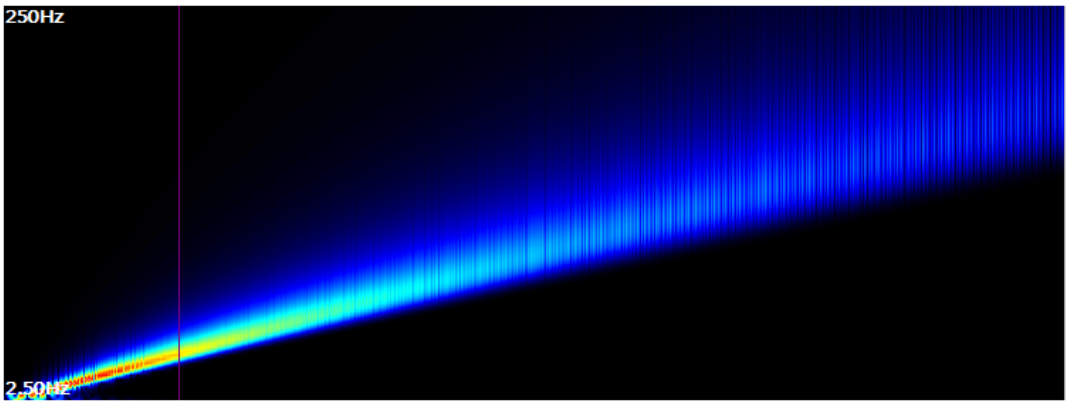
Beta. This is the Morse time decay. Higher values increase the wavelet length, allowing more oscillation. In this example, Beta was increased from 3 to 10.



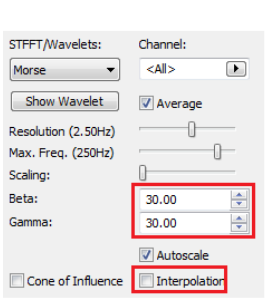
Gamma. This is the Morse frequency decay. Higher values produce more oscillations in time and make the wavelet narrower in the frequency domain. In this example, Gamma was decreased from 10 to 3.

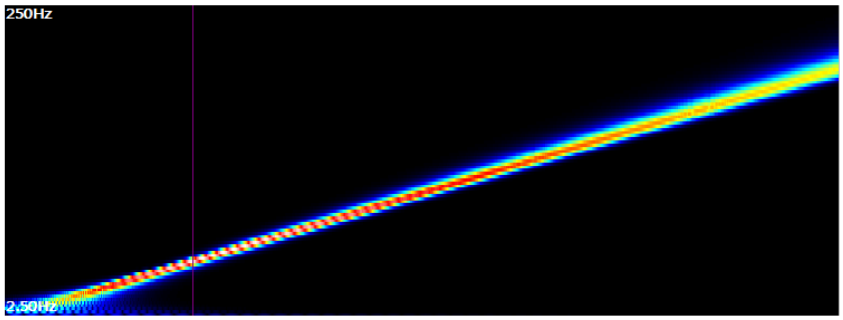


See the effects in the color wavelet display as you change the settings.

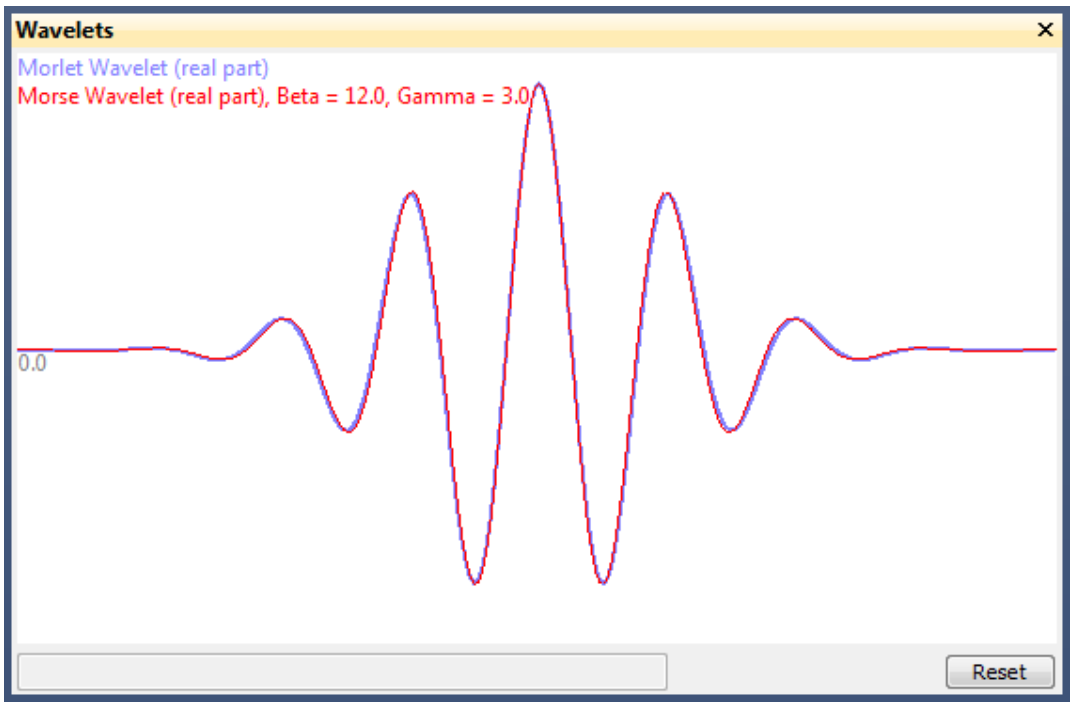


Here we have increased both Beta and Gamma to increase the frequency resolution of the faster frequencies. In this case it was helpful to turn **Interpolation** off.

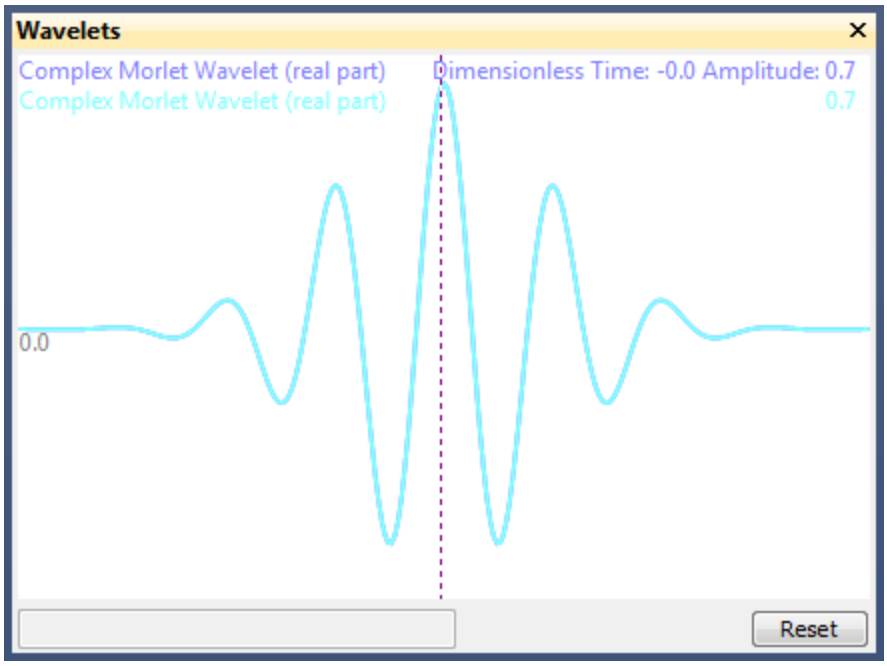




In this example, Beta (12) and Gamma (3) were adjusted to reproduce the Morlet waveform. This illustrates the flexibility of the Morse wavelets.

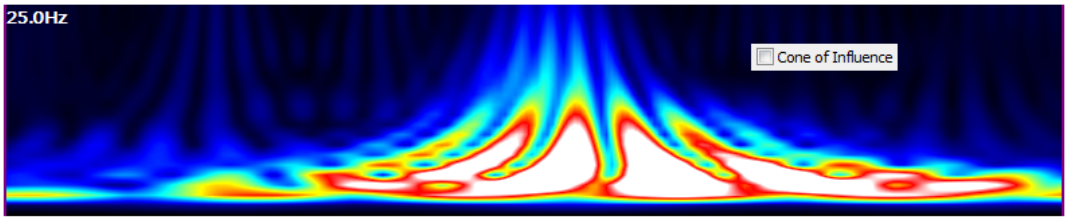


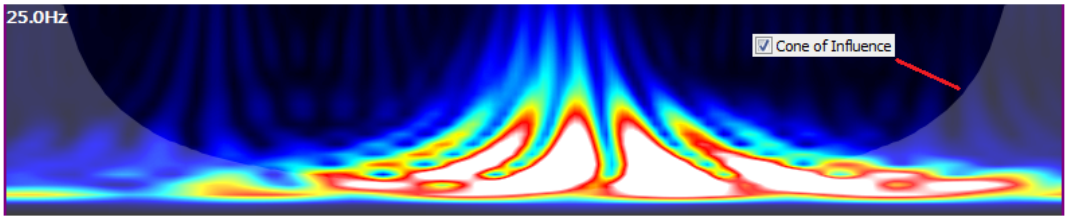
The Show Wavelet button lets you see the wavelet's waveforms.



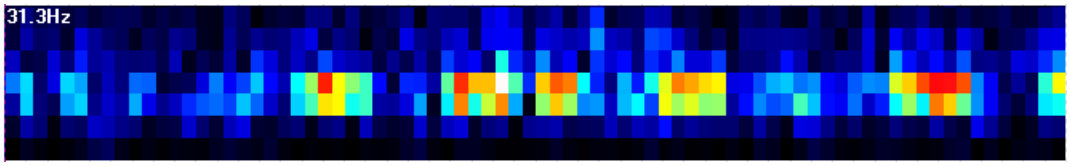
Autoscale. Autoscale will scale the display to whatever data are seen. In some cases, that may include large artifacts, which will cause the scaling to be inappropriate. In that case, uncheck Autoscale and a fixed scaling will be used.

Cone of Influence. The Cone of Influence shows edge effects due to zero-padding. It does not change the wavelet analysis result or remove edge effects. Colors that you see in the gray area should be treated with caution as they may be influenced by edge effects (seen at the beginning and at the end of the files, epochs, or averages). Colors outside of the gray area are clear to not be influenced by edge effects.

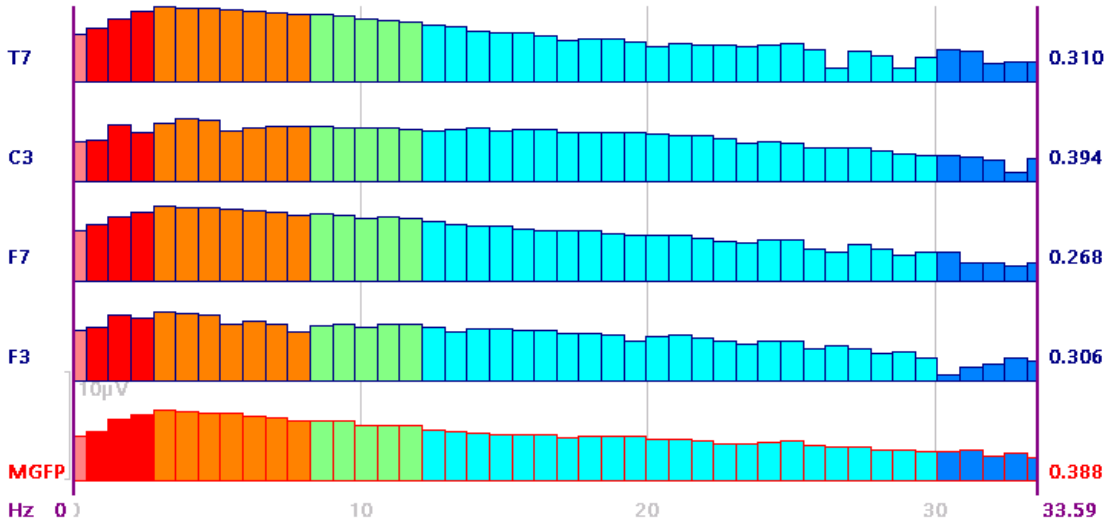




Interpolation. With Interpolation removed, the results for individual blocks may be seen.

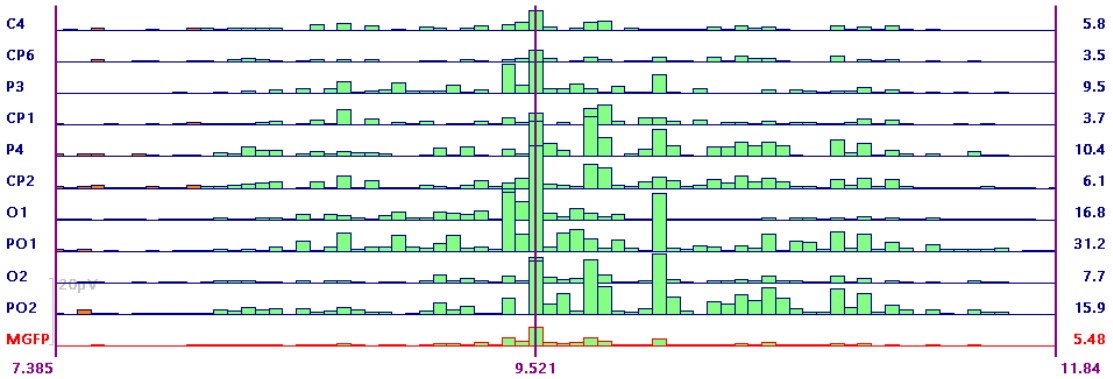


Display Options
Logarithmic. Enabling this option will display the **Spectra** data with a logarithmic scale. The adjacent field is the number of **Decades**. The greater the decade value, the better the lower power frequencies will be visualized.



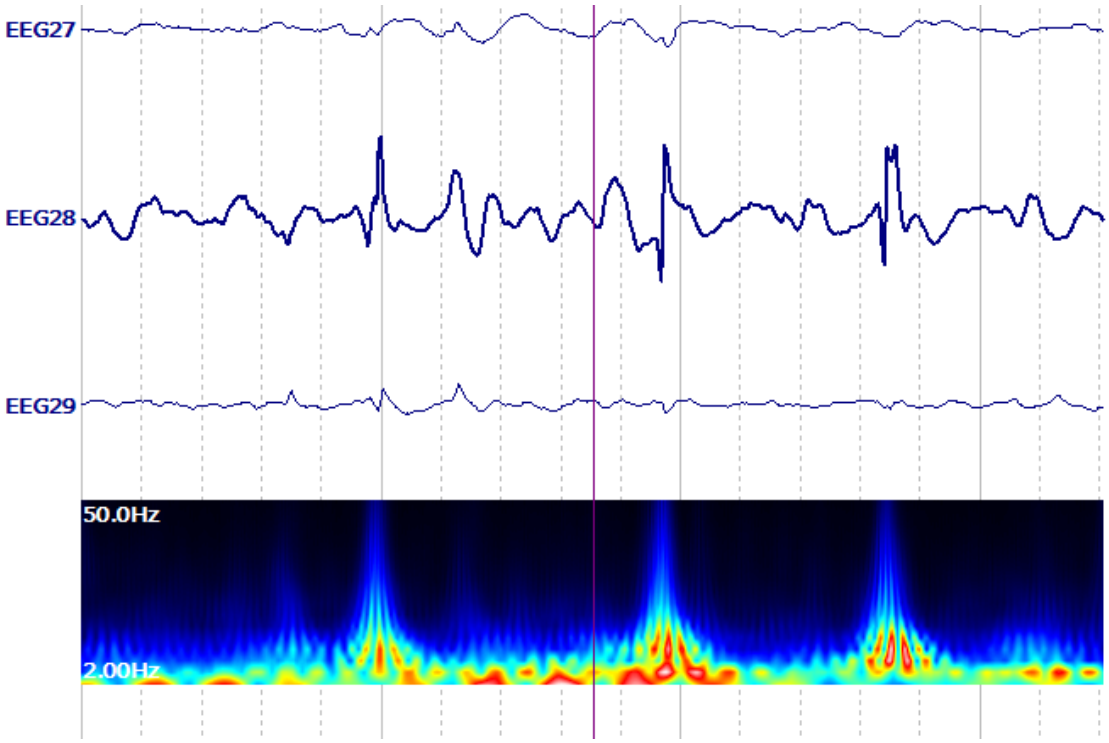
Energy Operators
Off. Displays the spectra without any energy operators.

Power. Enable this option to see the data scaled for microvolts squared (power). The Power option increases voltage greater than 1.0 and decreases voltages less than 1.0.

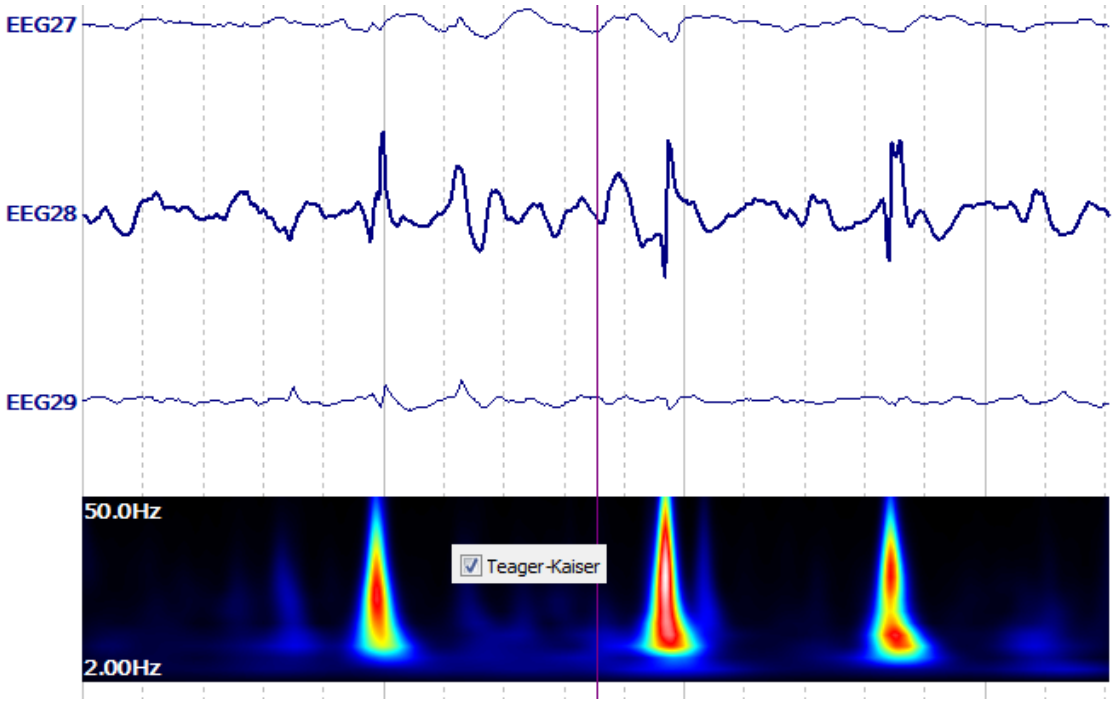


Teager-Kaiser. The Teager-Kaiser option applies a frequency-weighted, instantaneous, energy operator. It is available with the continuous Wavelets

(Morlet, Mexican Hat, Paul, and Morse). This accentuates the faster frequencies and suppresses the lower ones. The oscillations in the wavelet also disappear, which simplifies the display. This option is useful when exploring high frequency oscillations (HFOs). Be careful not to confuse the results with high frequency noise (and its harmonics).

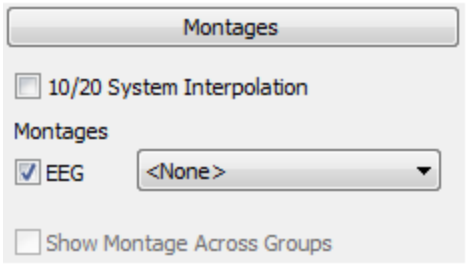


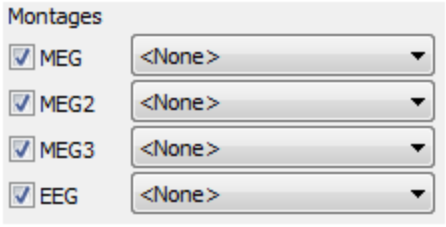
Above is with the option disabled, and below ids with the option enabled.



17.1.11 Montages

This panel is used to select the montage that you wish to apply or to access montage creation or editing. If you have multiple Active Channel Groups, you will see them as separate fields. Montages can be applied independently to groups.

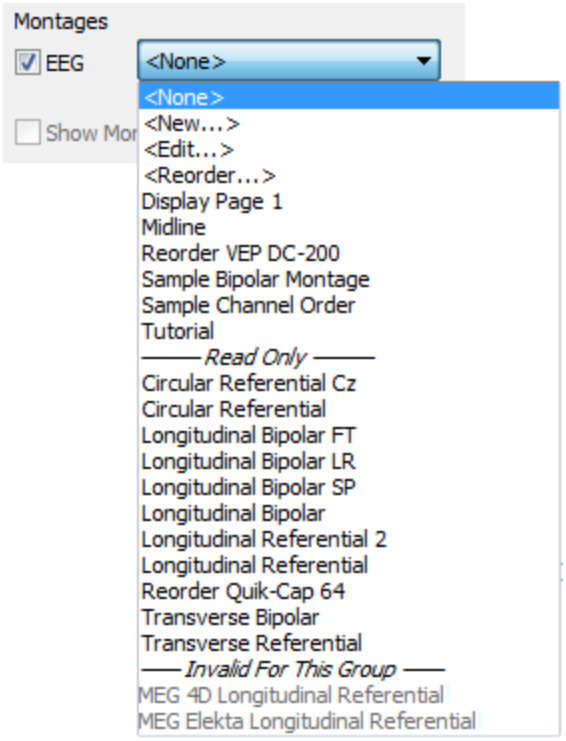




10/20 System Interpolation. This option is intended for use when you have a high-density EEG recording, and you want to see the data using only the 10/20 system. Enable the option and the interpolated channels will appear (many channels). This contains all of the 10/20 positions, as well as all of the intermediate positions. If desired, go to the **Montages** list and select **<New>**. Enter in a file name. You will then see the positions of all of the interpolated electrodes. You may then select a subset of desired electrodes, or create your own montage (e.g., double banana). Select that montage from the **Montages** list to see only the interpolated channels you selected.

As with all montages and interpolated channels, these are for display only. Any Mapping, Source Reconstruction, etc., will use the original data. If you want to save the interpolated data, you will need to select a Timerange and then, under Maps, select **Save → Save Interpolated Data**. You will need to select a positions file, as described in the **Interpolated and Extrapolated Channels** section.

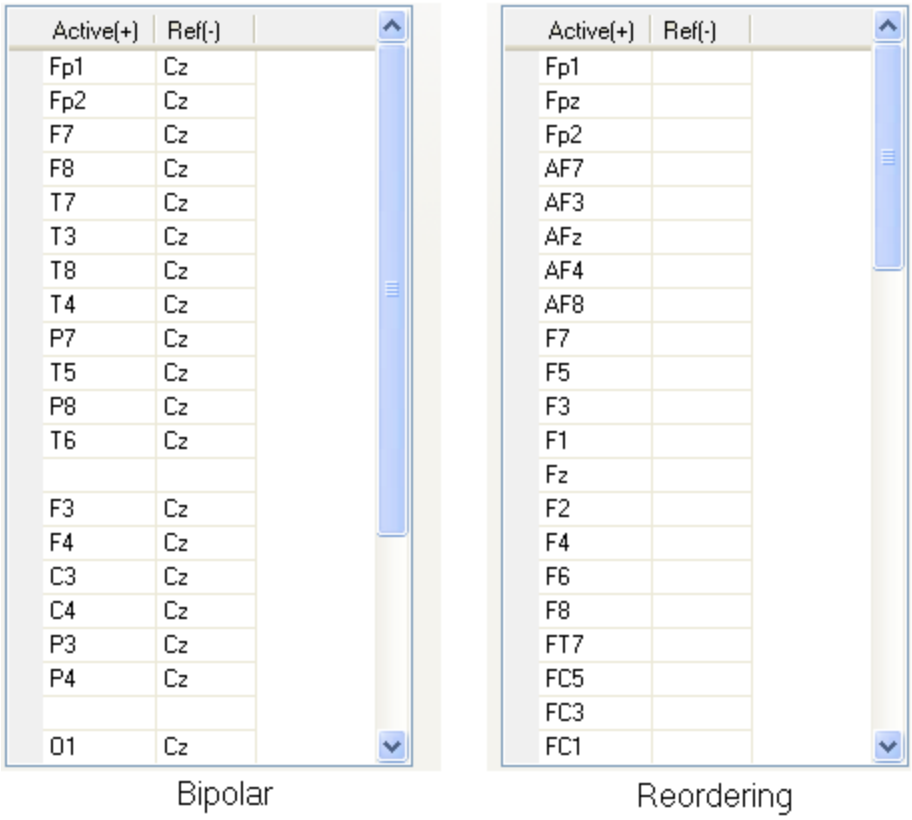
Montages. Select a montage from the drop-down list. Files above the *Read Only* line are user created; files in the *Read Only* section are supplied montages. Montages that do not contain any channels of the current device group are sorted out and placed in the *Invalid For This Group* section (so you can see directly which files can be meaningfully applied to a group). Click **<Edit...>** to access the Montage Editor (see **Configure montages** above). Click **<Reorder>** to access the Montage Editor in a form prepared for creating a montage to reorder the channels. Montages may be selected independently for Channel Groups.



Existing montages are accessed from the drop-down list (.xml files). Select a montage file and the new montage is seen immediately. Select ***<None>*** to remove it.

Montages affect the display only. For example, if you select a bipolar montage and then perform Artifact Reduction, the data that are used are the channels before you selected the montage. If you select a montage and then average the sweeps, you will see the selected montage, but when you remove it, the original channels will be there. Mapping uses the original data, not the montage data.

The montage files are saved as .xml files. There are two variations of .xml files, as shown below. Bipolar montages use the **Ref(-)** column; reordering montages do not.



Active(+)	Ref(-)
Fp1	Cz
Fp2	Cz
F7	Cz
F8	Cz
T7	Cz
T3	Cz
T8	Cz
T4	Cz
P7	Cz
T5	Cz
P8	Cz
T6	Cz
F3	Cz
F4	Cz
C3	Cz
C4	Cz
P3	Cz
P4	Cz
O1	Cz

Bipolar

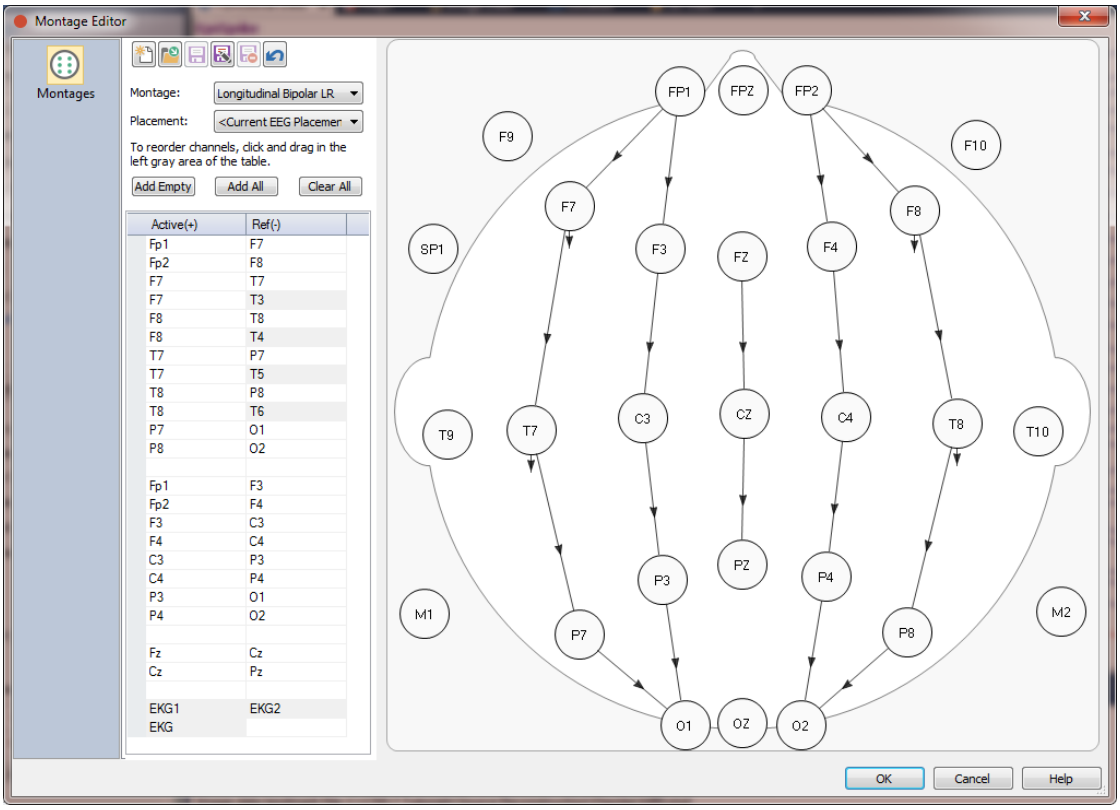
Active(+)	Ref(-)
Fp1	
Fpz	
Fp2	
AF7	
AF3	
AFz	
AF4	
AF8	
F7	
F5	
F3	
F1	
Fz	
F2	
F4	
F6	
F8	
FT7	
FC5	
FC3	
FC1	

Reordering

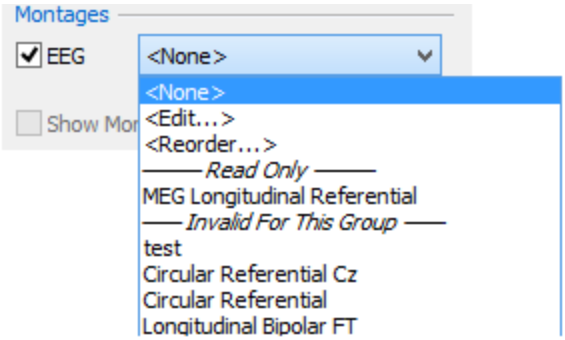
The first has pairs of electrode labels, and is used for bipolar montages where the second channel is subtracted from the first. The channel order you see will be the same as in the .xml file, so reordering is done at the same time as when you create the bipolar channels. The second variation has a single column of electrode labels, which will determine the displayed channel order. You can use these to create "Display Pages", as they existed in Scan. Select only the channels you want, in the order you want them. You can then go through several "display pages" to see the channels in selected groupings. This is especially useful with high density recordings.

Please see the **Target Folders for Windows 7** section for information about where the montages are saved.

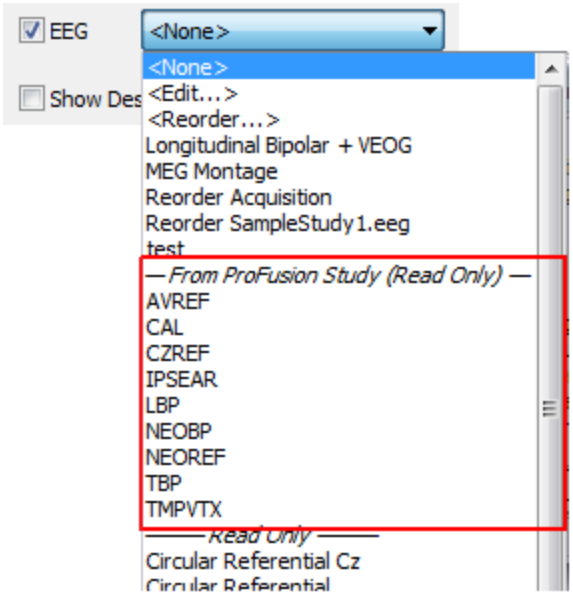
The Montage Editor can also be opened by selecting **Functional Data** → **Montage Editor** (or click the icon on the **Functional Data** Toolbar). It can also be used in the acquisition part of the program. The following display will appear (showing the last file used, or empty). If you have channels designated as "Other" channels, these will be seen in the lower part of the display.



Note the buttons at the top. If you open one of the supplied montages, you will see that the **Save** and **Delete** buttons will be grayed out. This prevents you from overwriting or deleting these files. Modify the file and use **Save As**. Files that you create can be overwritten and deleted. When you click on the **Montages** drop-down list, you will see several files. Again, files above the *Read Only* line are user created; files in the *Read Only* section are supplied montages. Montage files that do not contain any channels of the current device group are sorted out and placed in the *Invalid For This Group* section (so you can see directly which files can be meaningfully applied to a group).

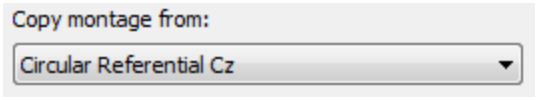


When loading a ProFusion (Compumedics clinical EEG software) study in CURRY, the montages contained in this study are now available in the montage selector.



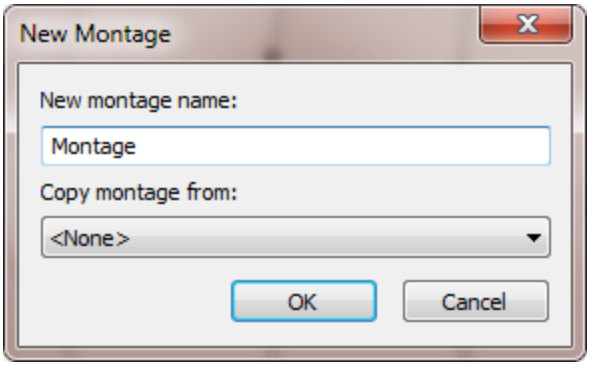
 **Create a new montage**. Click this to create a new montage. The following dialog will appear. Enter a name for the montage that you are creating.

If there is a similar montage already created that you wish to use to start with, select that montage from the **Copy montage from** list. Note that there is a special option for loading .mnt files: **<Load mnt files>**. Mnt files are montage files created in the Scan software. These can be selected in CURRY 8 and they will be converted automatically to .xml files. (The .mnt files themselves will not show up on the montage lists in CURRY 8, but the converted files will).

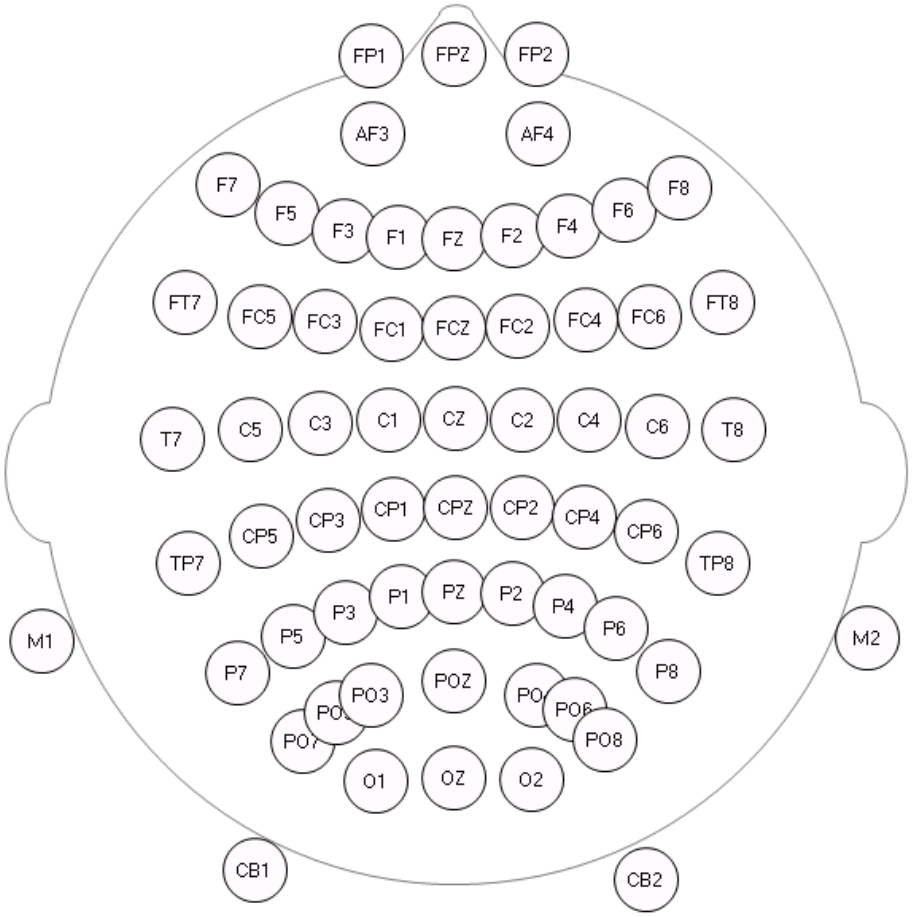


Otherwise, select a **Sensor Placement Scheme** from the list. To use the current file you have open, select **<Current EEG Placement>**

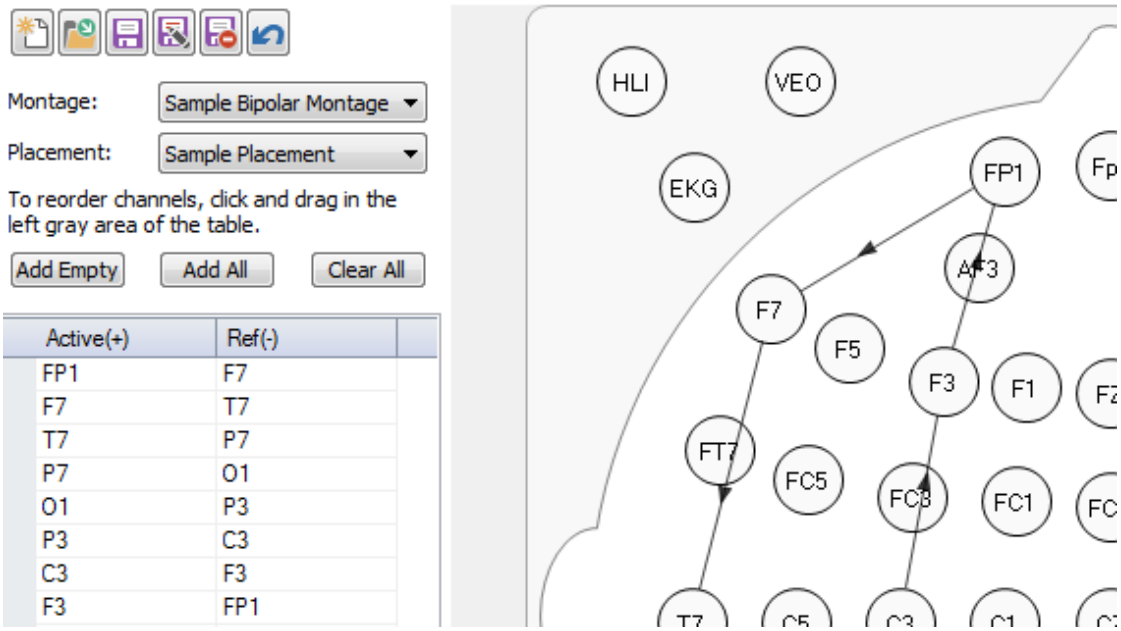
, or **Current MEG Placement**. Then click the **Create a new montage** icon and enter a file name for the montage.



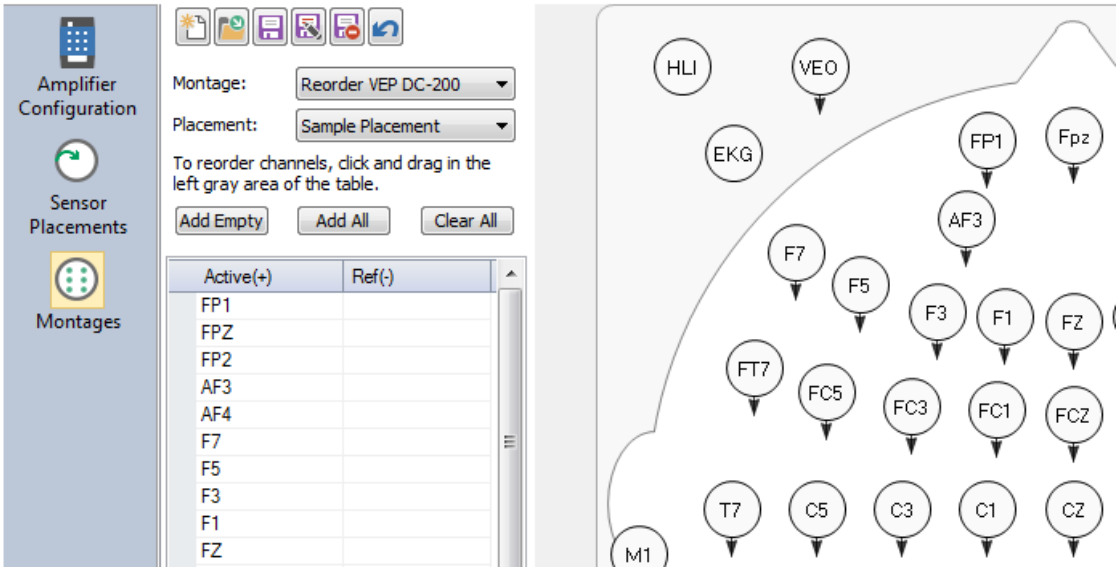
After clicking OK, you will see the electrodes in the display. You can then create the bipolar montage or reorder channels.



Create a bipolar channel by dragging/dropping a line from one electrode to another. The second one will be the subtracted channel. If you make a mistake, highlight that channel in the list and press the *Del* key on the keyboard.

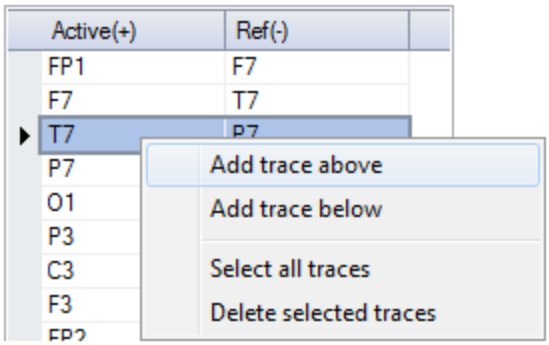


To create a montage that reorders the channels, you should either click **<Reorder...>** from the **Montage** drop-down list under **Options**, or go into the Montage Editor manually. If you use the **<Reorder...>** option, much of the work has been done for you. The name has been created automatically: "Reorder <Study Name>". The electrodes are already listed.



You can click Clear All to clear the list, and then Add All to list the electrodes. Then drag and drop them as desired. Or, click Clear All and just *double-click* on the electrodes in the order you want them to appear. Use Add Empty to create an empty line between groups of channels.

Right click on the list to see additional options. These are fairly self explanatory, but are described in the **Configure montages** section above.



 **Import a montage**. Montages with .mnt (from SCAN) or .xml (from Excel) extensions may be imported.

 **Save the active montage**. Be sure to save the montage before you exit the editor.

 **Save the active montage with a new name**. This opens a Save As dialog allowing you to save the montage with a different file name.

 **Delete the active montage**. Deletes the montage you have displayed.

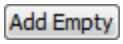
 **Undo all changes made to the current file since it was last saved**. Undo the changes you have made since last saving the montage file.

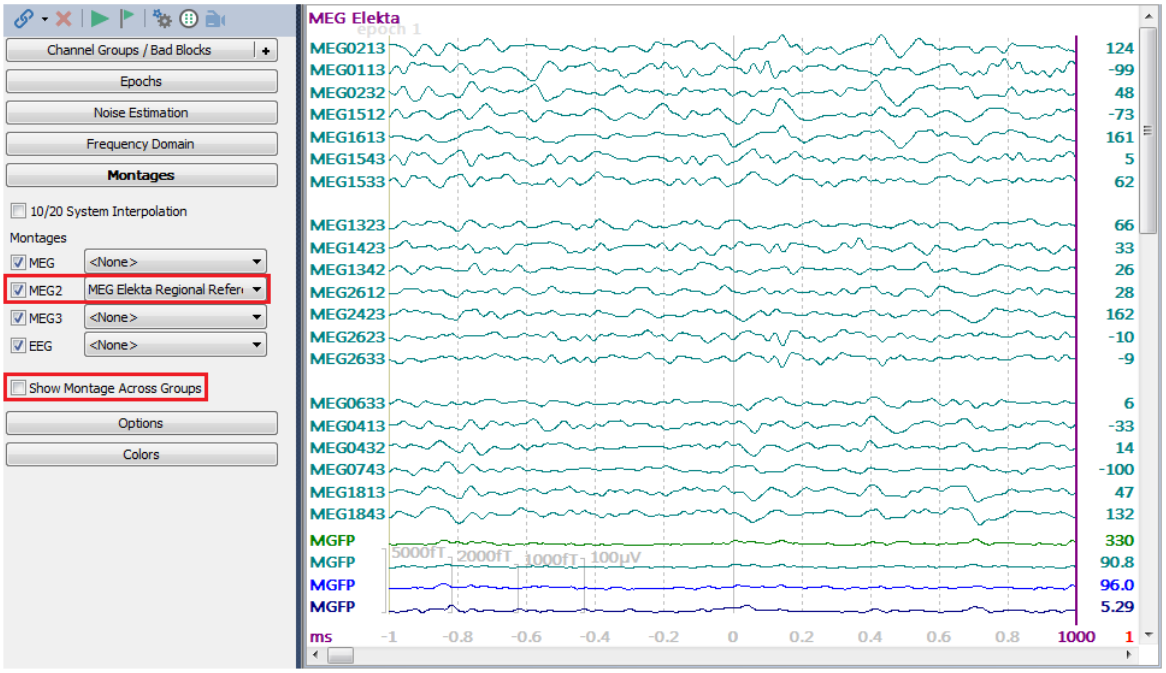
Add Empty  . Adds an empty line between groups of sensors.

Add All  . This option adds all channels from the currently selected sensor placement to the montage. If this placement is the **<Current Study Placement>**, then you will see a plain montage that you can use to reorder the channels of the current file you are working with. Just drag and drop the channels within the table.

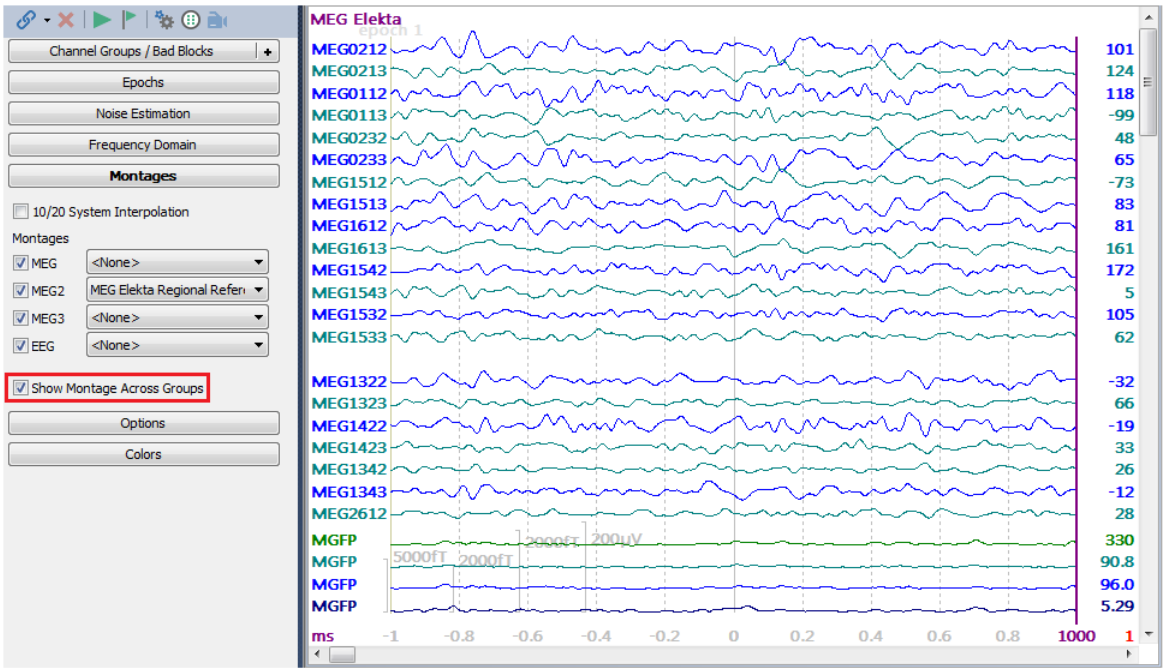
Clear All  . Deletes all existing channels from the montage list.

Please see the *Creating Montages* tutorial for a demonstration.

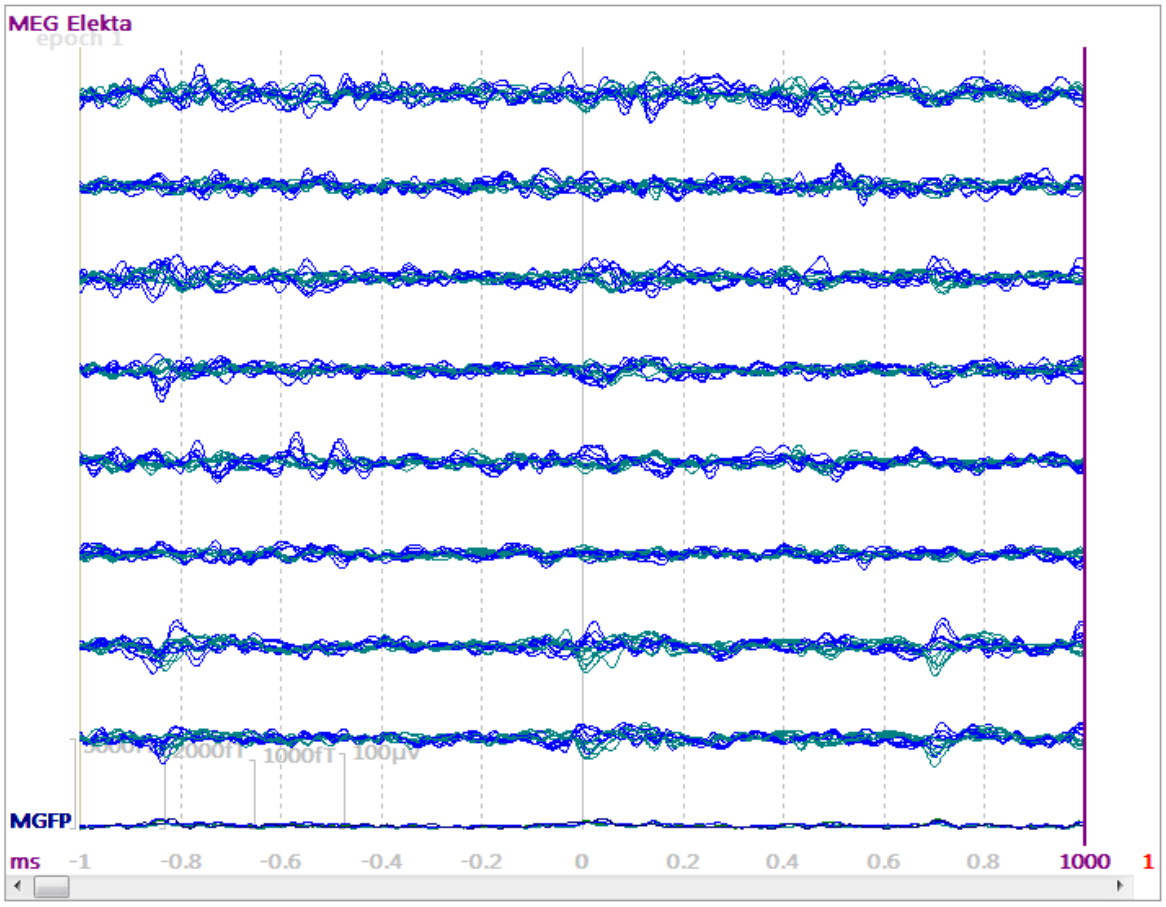
Show Montage Across Groups. This option is used when you have multiple Channel Groups (such as, several MEG channel groups). There may easily be too many channels to see them all at one time. You can create a montage file that includes selected channels from one group, as well as selected channels from another group(s). Then you apply that montage to the initial group. In this case there are now 56 channels, divided into 8 groups (using  in the Montage Editor to make the separations). **Show Montage Across Groups** is disabled.



Enabling **Show Montage Across Groups** will display the additional channels from the other Group(s) that were specified in the montage file. These are seen in blue since they came from the 3rd channel group, whose channels were all displayed in blue.

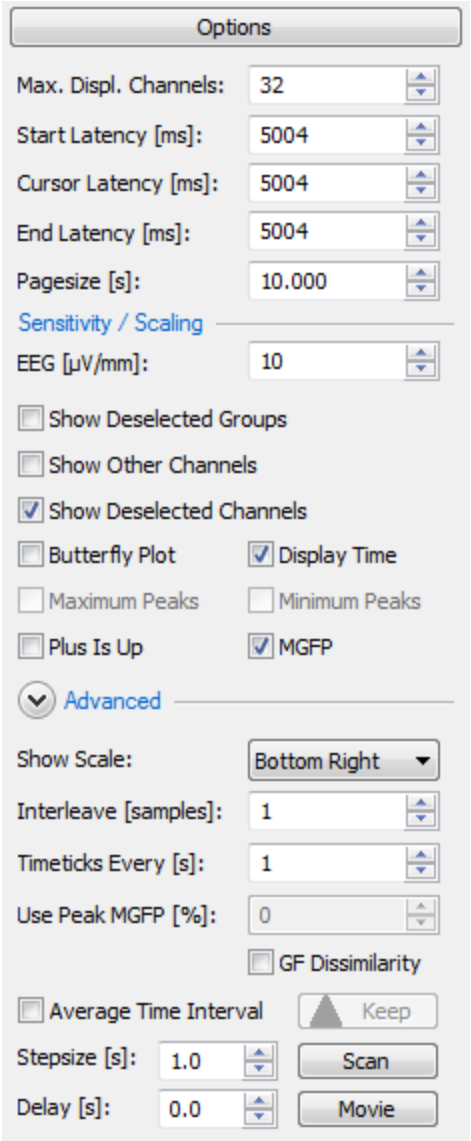


You can also select the **Butterfly Plot** from here and see all of the subgroups that have been defined.



17.1.12 Options

A variety of miscellaneous options are included in this section.



Max. Displayed Channels. This field is used to set the number of channels that are displayed (over all devices; grayed out in the Butterfly Plot display). If you set it for fewer than the actual number of channels, channels will be removed beginning at the bottom of the display. You can also position the cursor in the data display and use *Shift+mouse wheel* to change the number of channels displayed.

Start Latency [ms]. This is the time point position of the left vertical cursor (as seen in the Functional Data display). Set the cursor latency from this field, or drag the cursor to a new position and the field will be updated accordingly. Use *Ctrl+left* or *right* key to move it.

Cursor Latency [ms]. This is the time point position of the middle vertical cursor (as seen in the Functional Data display). Set the cursor latency from this field, or drag the cursor to a new position and the field will be updated accordingly. Use the *left* and *right* keys to move it.

End Latency [ms]. This is the time point position of the right vertical cursor (as seen in the Functional Data display). Set the cursor latency from this field, or drag the cursor to a new position and the field will be updated accordingly. Use *Alt+left* or *right* key to move it.

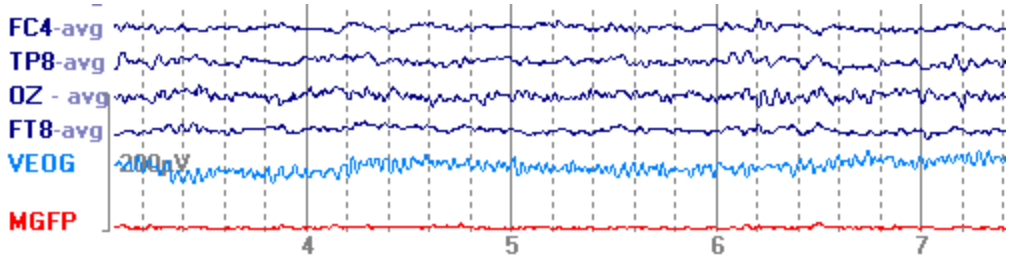
Note

There are some useful shortcuts for positioning the cursors. If you want to select the entire Timerange that is displayed, use *Ctrl+double click* in the data display. If you are in Tracking Mode, use *Shift+click* to exit Tracking Mode and position one outer cursor at the position you clicked. Use *double click* to return to Tracking Mode. Use *Shift+double click* to superimpose all three cursors.

Use *Ctrl+drag* to define an interval of interest. When you release the keyboard keys, you will see the two outer cursors at the edges you defined and the middle cursor will be midway between them.

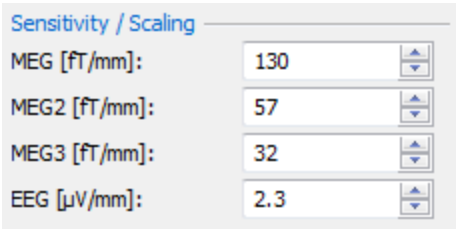
Timerange / Pagesize (s). This option displays the duration of the time span in the Data Display. If you have a continuous data file displayed, you will see **Pagesize(s)** instead of the Timerange. The number you enter is the number of seconds displayed. You can also position the cursor in the data display and use *Ctrl+mouse wheel* to change the number of seconds displayed (continuous data).

The value of 1.0 sec is a special case. When selected, you will also see vertical dotted lines every 200 ms. These are only seen when you have selected 1.0 sec. The color is set by the Vertical Lines field in **Colors** (white removes them, with a white background).



Sensitivity / Scaling. This option controls the display scale. Scaling can also be adjusted with the up and down arrows keys on the *keyboard* and the *mouse wheel* (a display screen must have the focus to scale the data) . If there are more channels than can be displayed on the screen, the *mouse wheel* will move the display up and down, rather than scale the data.

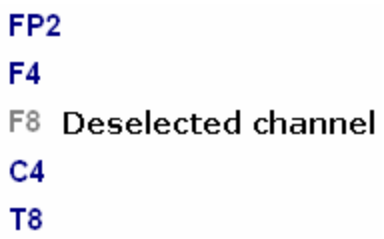
If you have MEG and EEG groups, you will see sensitivities for both, where MEG is scaled in (femo)Teslas per mm, and EEG is scaled in µV per mm.



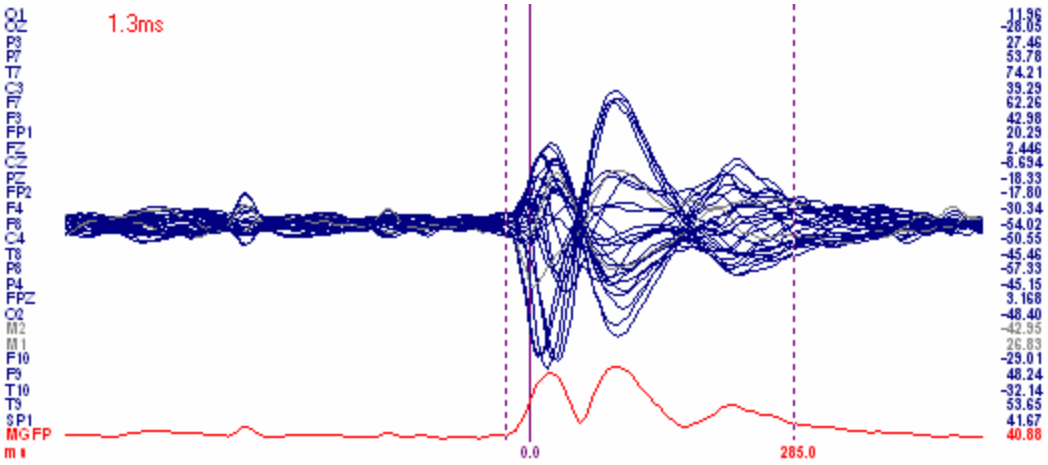
Show Deselected Groups. If enabled, the montage channels of deselected groups or devices will be displayed.

Show Other Channels. If you have channels designated as "Other" channels (such as artifact channels), you may display or hide these channels using the Show Other Channels options.

Show Deselected Channels. If you enable this option, Deselected channels will be displayed. You can set the color of the deselected channels under **Colors** (described above). Channels are selected and deselected by clicking on the channel label (use *Shift* to select a range of channels). Deselected channels are not used for further processing.



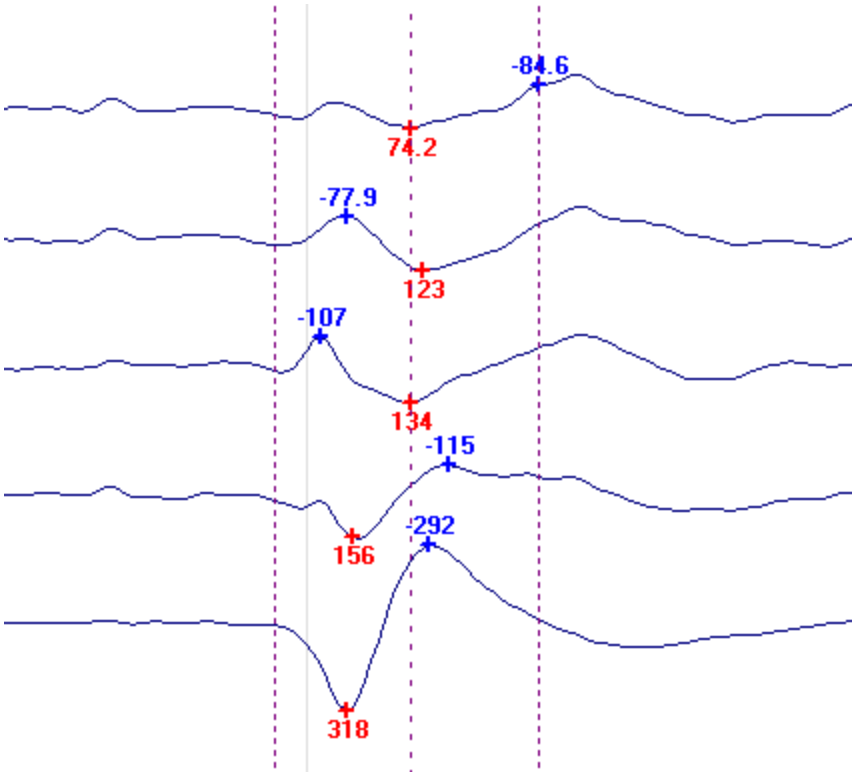
Butterfly Plot. Enabling this option superimposes all channels. The Butterfly Plot can be toggled on and off using the button on the **Functional Data** Toolbar (or *Alt+B*).



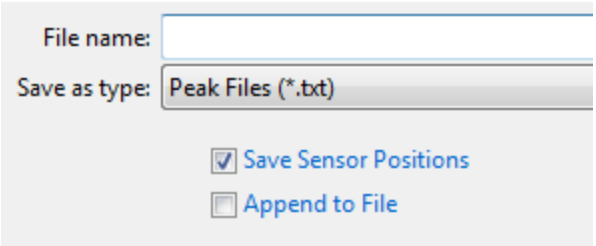
Display Time. The cursors of Studies (data files) with a valid start-time (wallclock time) can be displayed with timestamps. Otherwise, the time into the file will be displayed.

Maximum Peaks / **Minimum Peaks** (peak detection). The maximum and minimum voltage peaks within the selected Timerange (all file types) are displayed with red and blue plus marks, showing the amplitude. You need to display 10 or fewer channels to see the amplitude values. The detected values may be exported to an ASCII file using **Functional Data** → **Save** → **Save Peaks** (or use **Save Peak Detection** from the **Workflow**). If you have **MGFP** enabled, you will see the peaks for it as well. See also the *Peak Detection* tutorial. CURRY does not compute peak/trough differences, but

rather will export the values so that you may perform the additions/subtractions using Excel or other program.

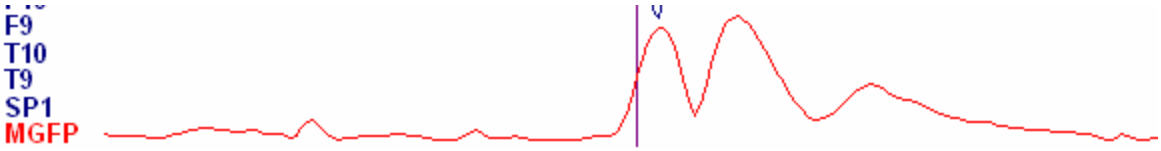


When you save the peak information, you will have the option to include the XYZ sensor positions, and to append the results to an existing file with prior results. If you have **MGFP** enabled, you will save the peaks for it as well.



Plus Is Up. When enabled, positive values will be in the upward direction. If not enabled, negative values will be in the upward direction (polarity setting).

MGFP. Enabling this option will display the Mean Global Field Power **of the active device** as a waveform at the bottom of the data display. The icon on the **Maps** Toolbar has the same function (or *Alt+G*).



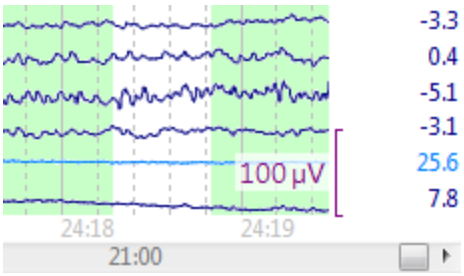
MGFP is defined as the standard deviation of the Common Average Referenced data D (n sensors, sensor index i) for each timepoint (t), measured signal of channel i at timepoint t: Mit, mean measured signal at timepoint t: Mt

Mt = SUM(i=1..n) [Mit] / n
CAR: Dit = Mit - Mt = Mit - SUM(i=1..n) [Mit] / n
MGFP(t) = SQRT ({SUM(i=1..n) [Dit^2] / n} = SQRT {SUM(i=1..n) [(Mit - Mt)^2] / n} = SQRT {SUM(i=1..n) [(Mit - SUM(i=1..n) [Mit] / n)^2] / n}

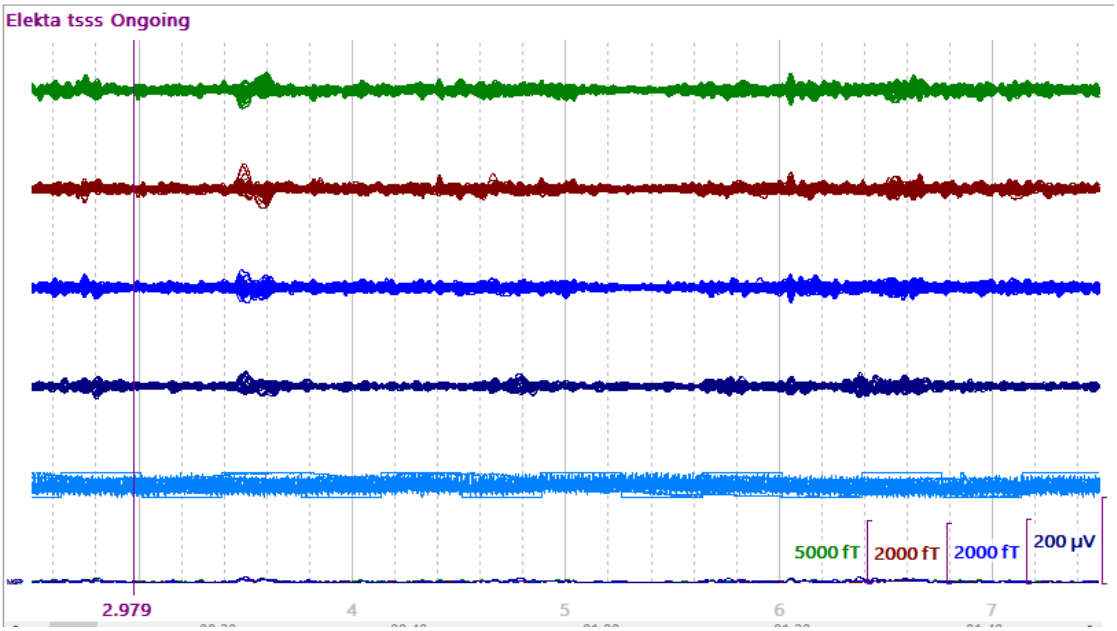
The MGFP of a single channel is always 0 due to the CAR, the MGFP is the standard deviation over all channels (zero mean by CAR).

Advanced

Show Scale. This option lets you position the Scale Tool in different corners of the display, or off.

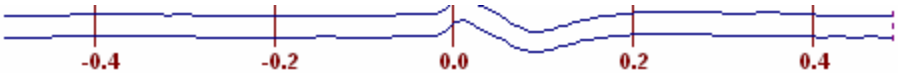


If you have multiple Device Groups (as with MEG data), the Scale Tool color will match the group color.



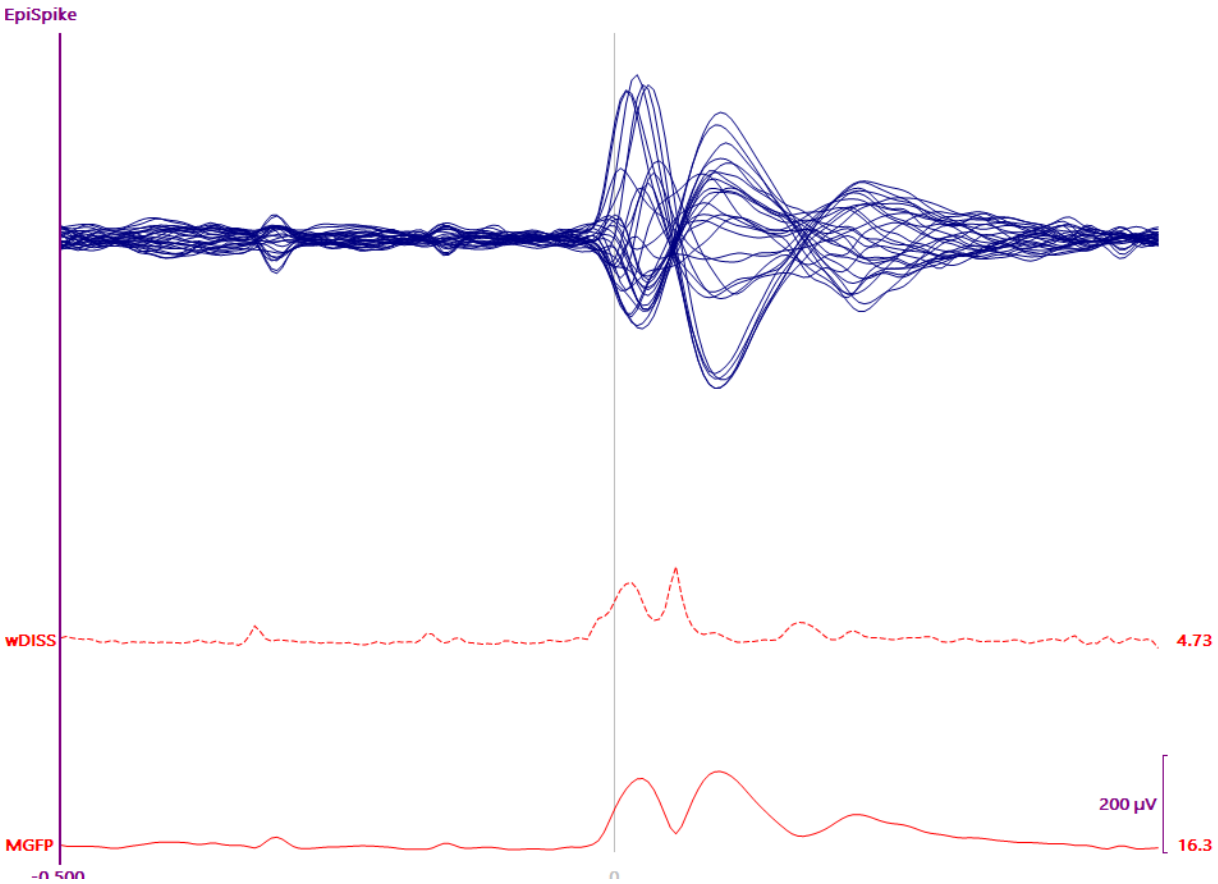
Interleave [samples]. This determines the number of data samples that will be used for source analysis, reducing the amount of data that enters, (e.g., a CDR method or a dipole fit), and reducing the temporal resolution of the computed result. Only every *n*th sample will be entered. For mapping purposes, every *n*th data point will be mapped. When using the keyboard commands to move the cursors, the cursors will jump to every *n*th data point.

Timeticks Every [s]. This option will place a time tick (vertical line with time label) every x secs, where x is the value entered in the field. The example below has timeticks every 0.2 secs.

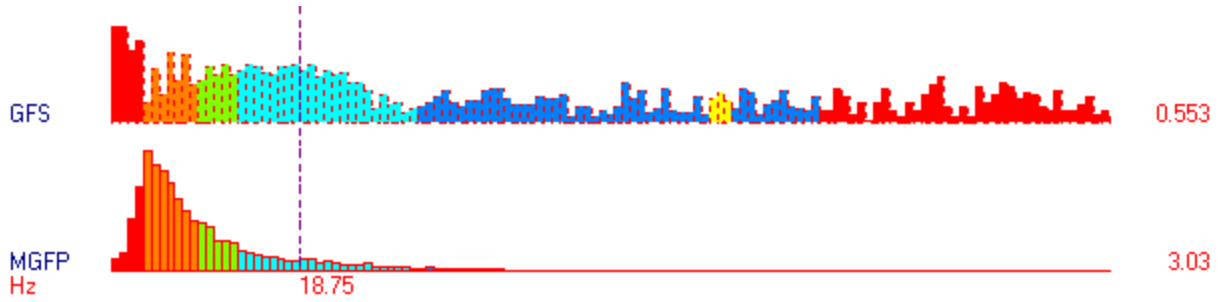


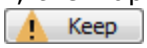
Use Peak MGFP [%]. You can use this option to identify peaks in MGFP in averaged or continuous data files. These peaks can then be used with source reconstruction, since dipoles are more likely to be present with MGFP peaks.

GF Dissimilarity. The Global Field Power Dissimilarity (dotted curve) and MGFP (solid curve) indicate the strongest changes in the *contour maps* over time **for the active device**.



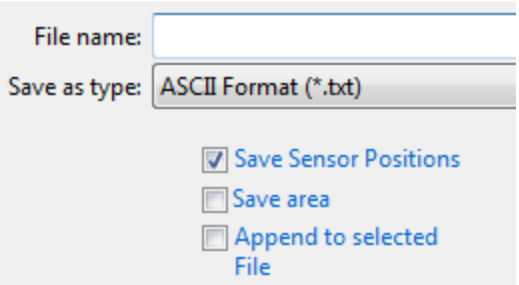
GFSynchronization (Global Field Power Synchronization). This option is seen when **Spectra** has been selected. It is based on the ratio of the differences of the singular values over the sum of the singular values, resulting in values between 0 and 1 (where 1 is perfectly in phase).



Average Time Interval (or **Average Freq. Interval** for frequency domain data). If you select a timerange (or frequency range with spectra data) and enable this option, the map that you see will be the averaged values for that interval. If you click 

, those results will be stored internally, and subsequent maps will be seen in relation to the first one (when you select **Normalized Maps** from the context menu).

If you look at the numbers in the column to the right in the data display, you will see them change (for both time and frequency domain data) when you select Average Time Interval. You are then seeing the average of the values in the Timerange or Frequency Range you select. If you want to save these values, go to **Functional Data → Save → Save Averaged Interval**. At the bottom of the Save As dialog, you will see options to Save Sensor Positions, Save the Area, and Append the results to an existing file (as opposed to overwriting it). A text file will be created with the values in it.



For time domain data, you will see a file similar to the following. The average for each channel across the -10 to 65ms Timerange is found in the column on the right.

```
# time domain
# channels, averaged samples
   28    15
# -10.0 ... 65.0 ms
# channel labels, [µV]
O1 - avg          15.893
OZ - avg         -22.083
P3 - avg          10.732
P7 - avg          84.218
T7 - avg         149.003
C3 - avg          23.067
F7 - avg         109.829
F3 - avg           6.727
```

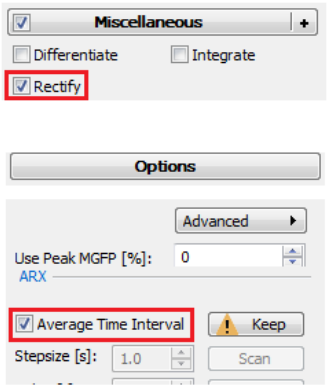
For frequency domain data, there are columns for each frequency band (delta, theta, etc.), showing the averages for each band, and the overall average in the far column on the right. In the example below, the cursors defined a frequency range of 0 to 70.4Hz. The numbers in brackets in the header are the number of frequency bins in each band, as well as the overall number of bins.

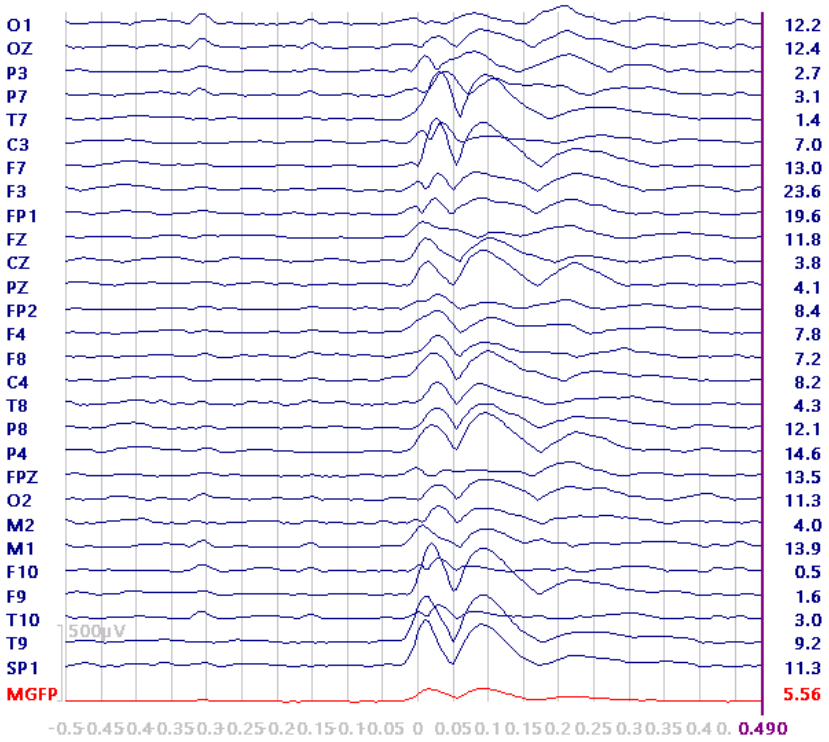
```
# frequency domain
# channels: 28
# averaged frequency ranges [bins]:
# 0.000...3.000 Hz [50]
# 3.000...8.000 Hz [83]
# 8.000...12.000 Hz [67]
# 12.000...30.000 Hz [296]
# 30.000...70.000 Hz [656]
# 59.000...61.000 Hz [33]
# averaged frequencies (cursors):
# 0.000...70.374 Hz [1154]

# channel labels, [µV]
FP1-avg    0.020      0.229      0.695      0.172      0.018      0.010      0.111
PZ - avg   0.018      0.286      1.474      0.255      0.013      0.005      0.179
FP2-avg    0.020      0.255      0.739      0.168      0.017      0.008      0.113
OZ - avg   0.013      0.251      0.710      0.172      0.015      0.007      0.112
F3 - avg   0.016      0.255      0.681      0.161      0.013      0.006      0.106
FC5-avg    0.012      0.170      0.571      0.137      0.012      0.003      0.087
F4 - avg   0.019      0.299      0.729      0.170      0.014      0.005      0.115
FC6-avg    0.013      0.197      0.615      0.139      0.011      0.004      0.091
C3 - avg   0.010      0.164      0.482      0.140      0.011      0.004      0.082
CP5-avg    0.012      0.174      0.520      0.142      0.011      0.005      0.085
C4 - avg   0.010      0.190      0.538      0.136      0.011      0.003      0.086
CP6-avg    0.010      0.173      0.474      0.150      0.011      0.004      0.084
P3 - avg   0.015      0.257      0.840      0.204      0.012      0.005      0.126
CP1-avg    0.012      0.197      0.631      0.188      0.012      0.004      0.106
P4 - avg   0.013      0.256      1.212      0.223      0.014      0.004      0.153
CP2-avg    0.012      0.203      0.914      0.198      0.011      0.003      0.125
O1 - avg   0.015      0.301      0.916      0.224      0.022      0.009      0.144
PO1-avg    0.018      0.347      1.388      0.280      0.015      0.005      0.185
O2 - avg   0.014      0.247      0.744      0.180      0.012      0.005      0.114
PO2-avg    0.016      0.300      1.442      0.230      0.014      0.005      0.171
```

Computing the Area. You can compute the area under a curve for time domain data, or for a frequency range with frequency domain data (averaged value times dwell time and number of point, or frequency bin width and number).

Time domain data. Change the Common Average Reference (CAR) to **Off**, as needed. Set the outer two cursors to define a timerange of interest. If the waveforms include positive and negative voltages, you will likely wish to **Rectify** the data first (found in the **Miscellaneous** panel) to convert the voltages to positive numbers, otherwise there will be cancellation when you compute the average across the time interval. Then enable the **Average Time Interval** option (in the current **Options** panel). The numbers that you see on the far right of the data display now show the average voltage across the Timerange for each channel. Note that the middle cursor has no effect when you have selected the averages.



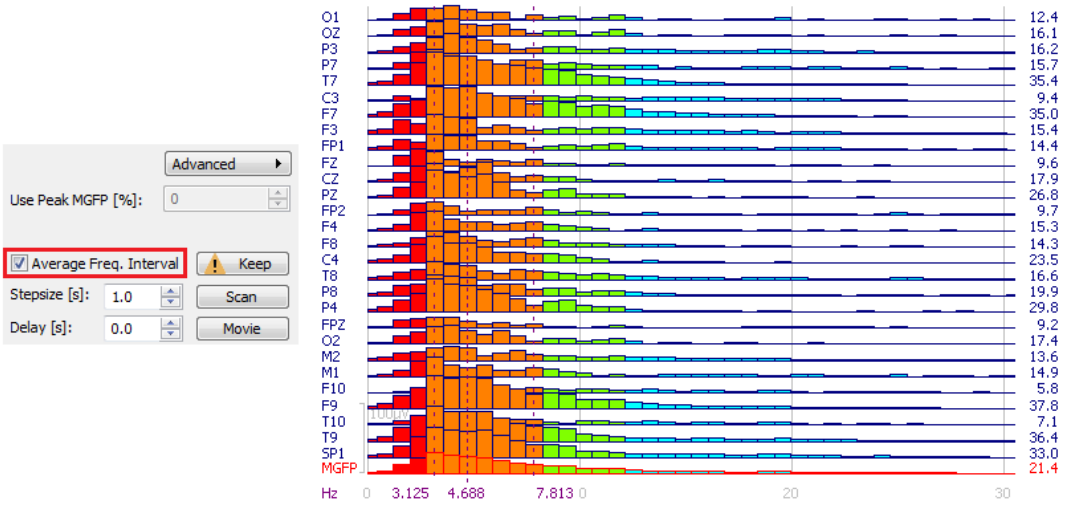


Save the values by going to **Functional Data → Save → Save Averaged Interval**. At the bottom of the Save As window, you will see an option to **Save Area**. The column on the far right contains the area values. It is not necessary to click the 

button. That has an additional function, described above.


```
# time domain
# channels, averaged samples, integrated area
   31      62   248.0 ms
# 1528.0 ... 1772.0 ms
# channel label, [µV], [µV ms]
FP1-avg          45.150        11197.212
F3 - avg         13.948         3459.145
C3 - avg         -1.050         -260.336
P3 - avg        -12.619        -3129.505
O1 - avg        -19.226        -4768.024
F7 - avg         25.425         6305.489
T3 - avg         -3.576         -886.739
T5 - avg        -16.819        -4171.162
FZ - avg          9.220         2286.568
FCZ-avg          -0.899         -223.074
CP3-avg          -8.106        -2010.304
FC3-avg           3.030          751.444
TP7-avg         -11.284        -2798.512
FPZ-avg          42.402        10515.750
```

Frequency domain data. Computing the area for a frequency interval is basically the same as for time domain data, although you do not need to **Rectify** the data. After saving, you will see a column on the far right that contains the area values.



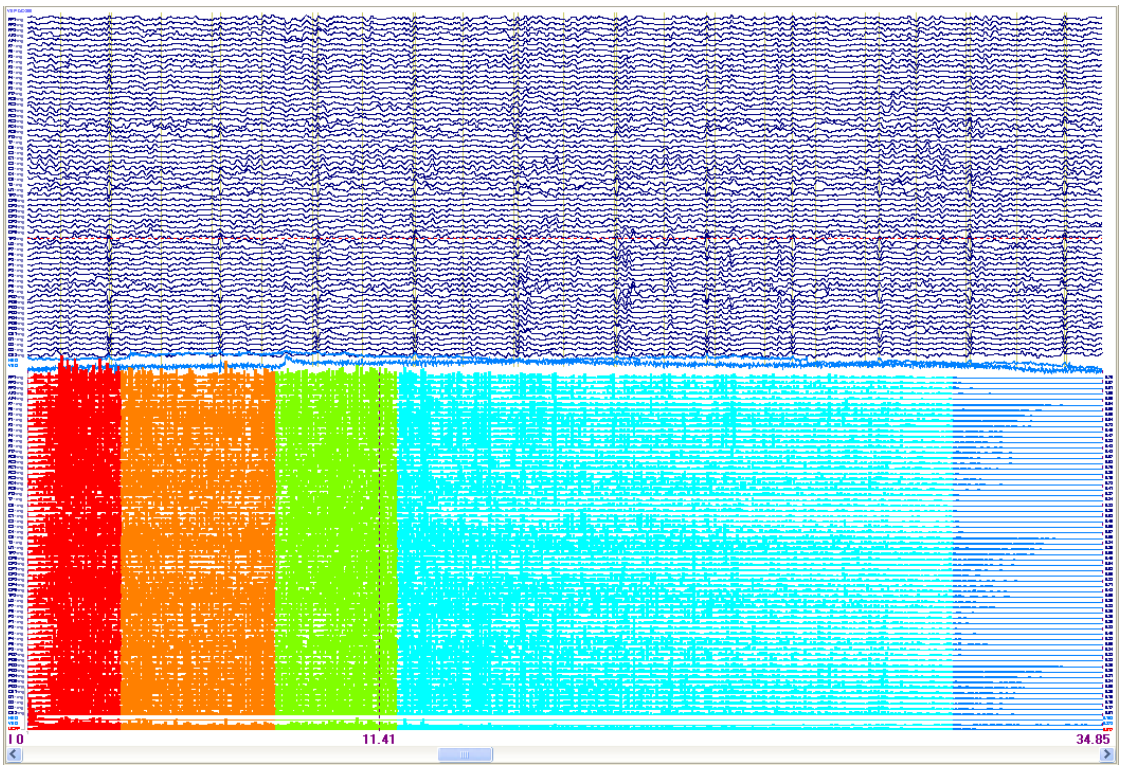
Stepsize [s] and Delay [s]. Click the Scan button to scan through the file automatically. You may select the duration of the steps that the replay will take, and the span of time between each step.

If you set Delay to 0, then you will see a continuous scanning of the file, where the rate is determined by the Stepsize Stepsize [s]: 2.0. The rate will also be affected by the file size (AD rate, number of channels, computer capabilities). Try different Stepsizes, including values less than 1.0. Press the *ESC* key to stop scanning, as indicated by the ESC -> Stop button.

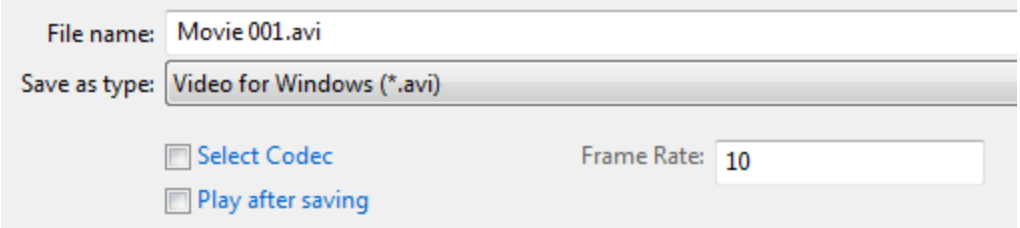
When Delay is set to a value other than 0.0, you will see the file advance is steps determined by the Stepsize, with a pause between steps determined by the Delay.

The middle cursor will be inactive when you have enabled Average Time Interval with either time or frequency domain data, as it is the average of the timerange that is being mapped, or used.

Movie. When selected, the file will be scanned and saved as an .avi file. Typically, it is used when you want to save and review waveform and spectral data. All windows in the data display will be saved.

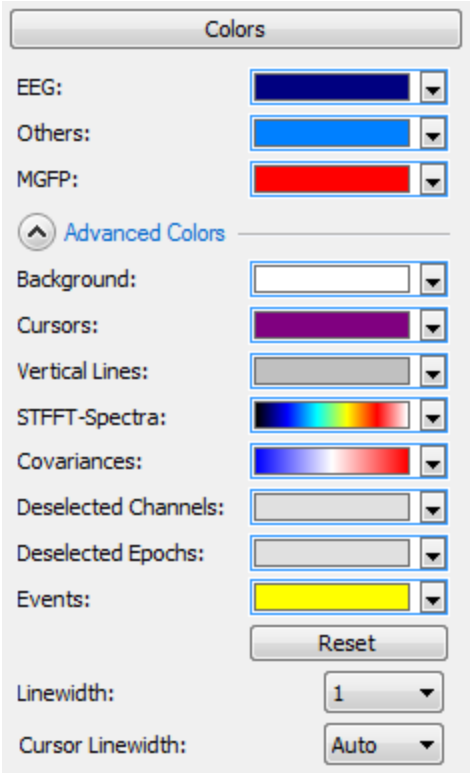


After clicking the **Movie** button, you will see a Save As window with additional options at the bottom for setting the **Frame Rate**, selecting a video compressor, and for playing the video automatically after the file is saved. If you enable the **Select Codec** option, you will be able to select which video compressor you want to use, depending on what has been installed on your computer (and this will be used in the future).



17.1.13 Colors

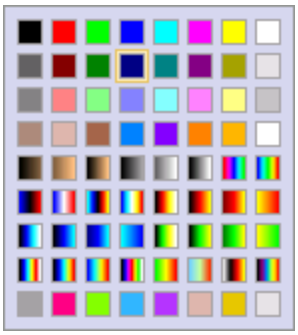
You may assign colors to the objects in the Functional Data display.



The Colors panel allows you to select the color of the waveforms for the various MEG and EEG data channels, as indicated, as well as the events in the file, deselected channels and epochs, the Mean Global Field Power waveform (**MGFP**), the cursors, vertical lines, the background of the display, the covariance matrix (seen in Noise Estimation), and the colors seen in the **STFFT-Spectra** displays. "Others" determines the color for all other channel waveforms. Click the Reset button to return the colors to their default settings. The **Linewidth** options are used to vary the width of the traces and vertical cursors (1, 2, or 3 pixels). If you select the Auto option, CURRY will adjust the line widths automatically. Few channels will have thicker lines; multiple channels will have narrower lines. Larger windows will have thicker lines for both waveforms and cursors.

Note
The color you set for **Vertical Lines** will also be used with the axes in the Waveboard.

When you click on one of the drop-down arrows, you will see a palette of colors from which to choose. Note that some are solid colors (top four rows), while others will apply a color spectrum. The new color will be applied when you select it. Not all colors are available with each object. See also **Edit → Options → Colors** for creating customized colors.



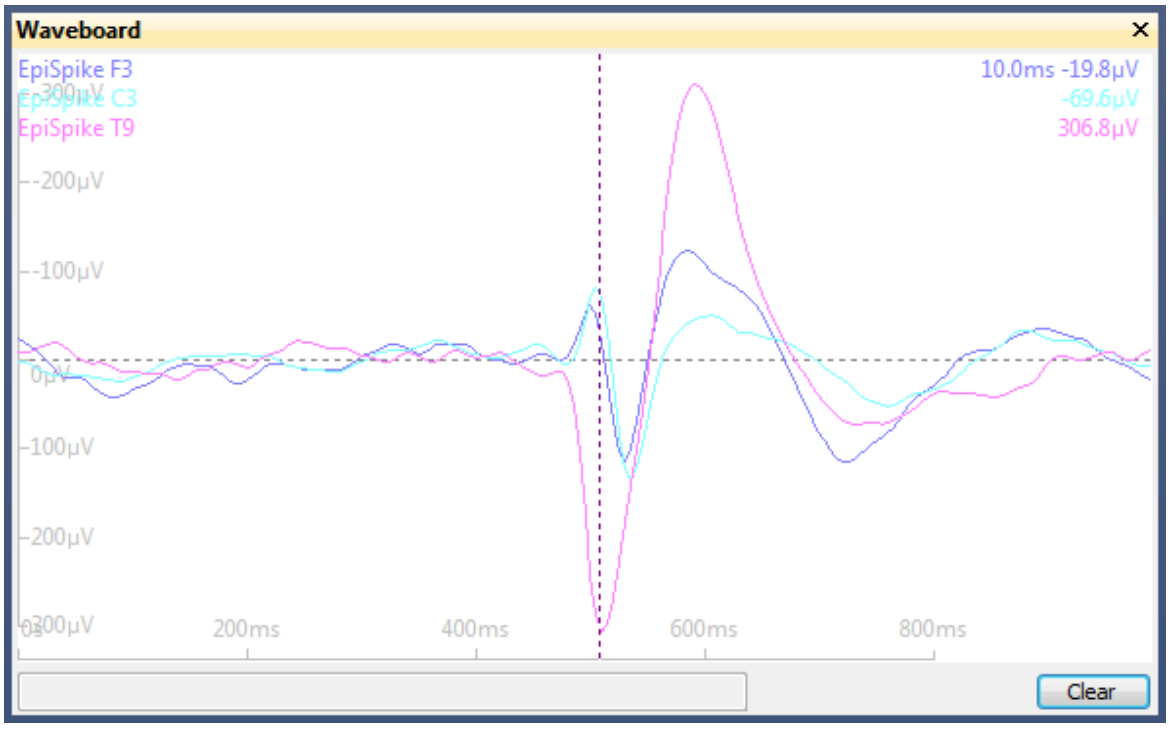
17.1.14 Waveboard

The Waveboard is a useful tool that appears in several places in CURRY. Its primary purposes are to let you extract one or more waveforms for closer examination.

To access the Waveboard, *right click* on one of the sensor labels in the Functional Data display, and select **Send to Waveboard 1** (or 2 or 3). You can have up to three Waveboards open and in use at a time.

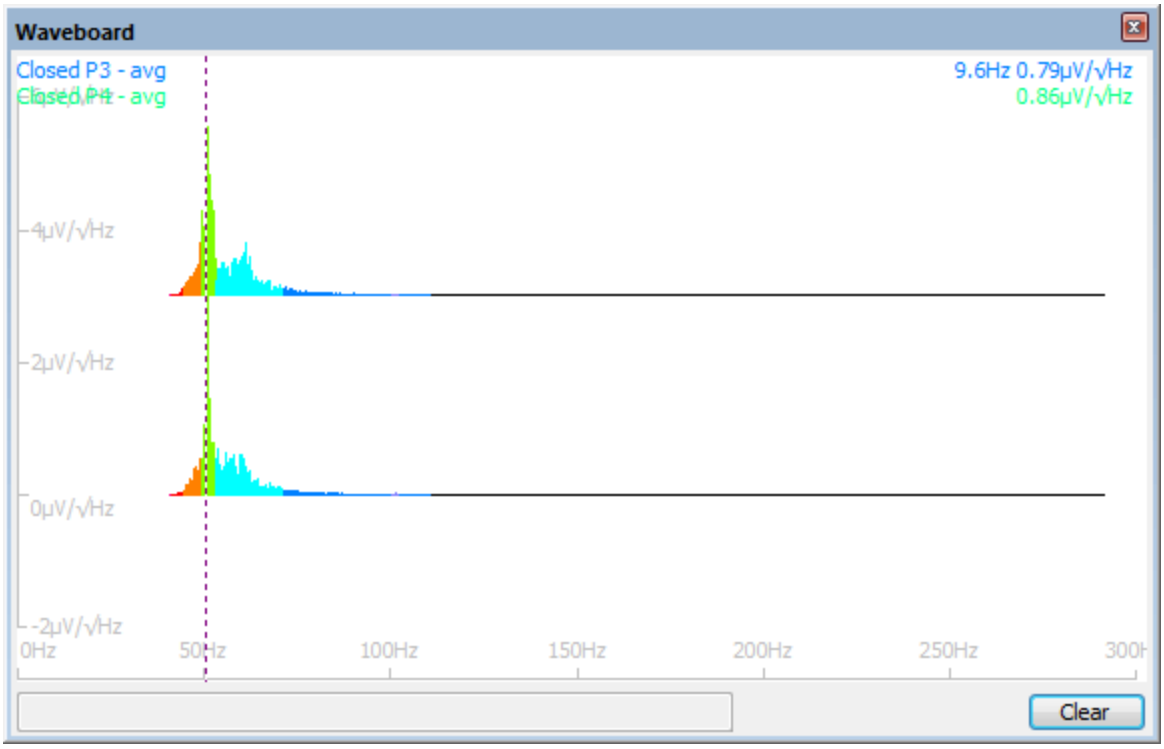
The horizontal dotted line is the zero voltage line for all waveforms, if the files are not stacked, and for the first waveform if they are stacked.

Right-click on the channel label to change the color of the waveform.



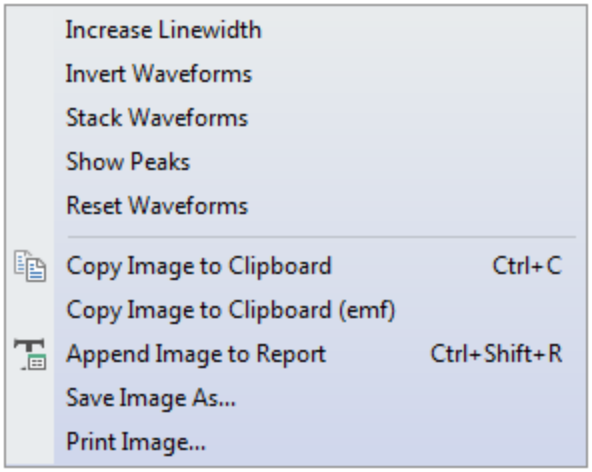
The latency and amplitude values associated with the cursor position are seen in the upper right for each channel. Click **Clear** to clear the Waveboard.

Spectral results may be sent to the Waveboard.



In the Waveboard display, use the *mouse wheel* for scaling. Use *Shift+mouse* wheel to expand or contract the display. Use *Shift+drag* to reposition the contents of the display. Use *Ctrl+mouse wheel* to separate the waveforms.

Right click in the display to access more options.

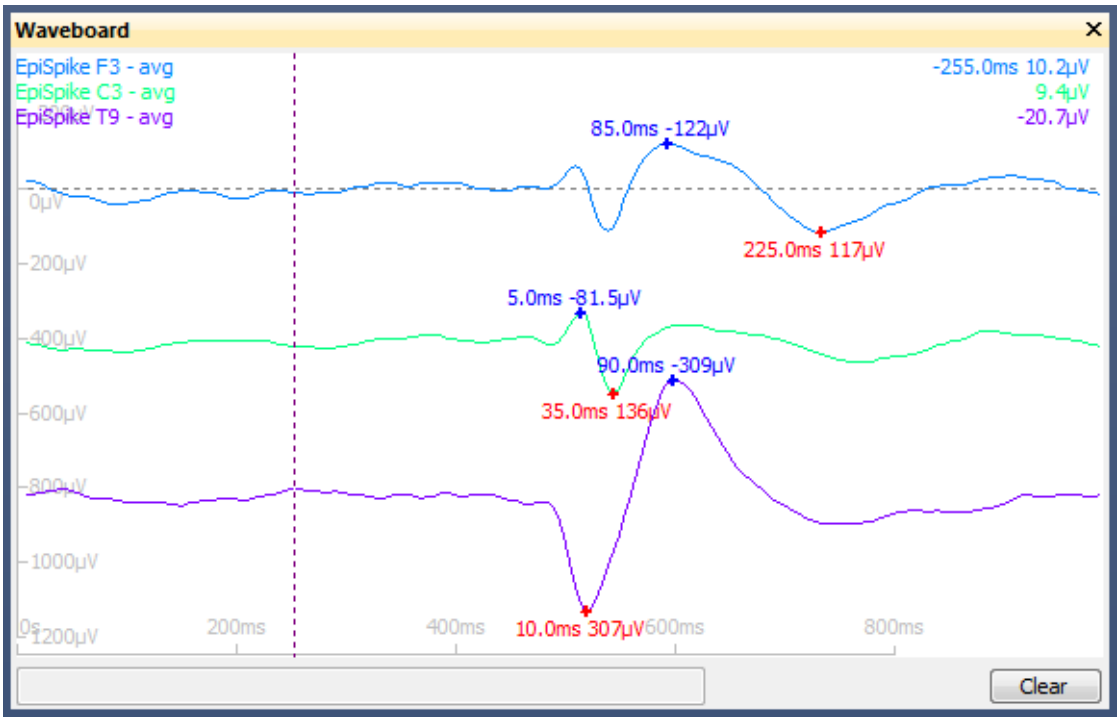


Increase Linewidth. Increases the pixel width of all waveforms.

Invert Waveforms. Inverts the polarity of the waveforms.

Stack Waveforms. Each time you click this option, the waveforms in the Waveboard will be separated a little more. It is easier to use *Ctrl+mouse wheel* to separate the waveforms.

Show Peaks. The minimum and maximum voltages for each waveform are displayed.



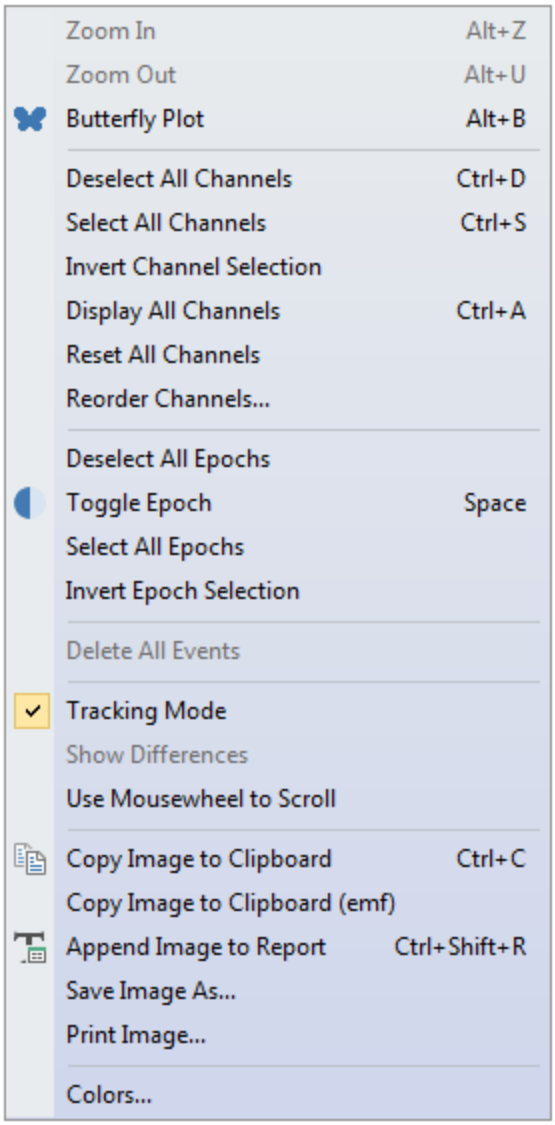
Reset Waveforms. Clears the Waveboard.

Note
The color of the axes and associated text can be changed in the **Colors** panel for **Functional Data** using the **Vertical Lines** option.

The remaining options are the same as those that appear in many other places in the program. Particularly useful are the options to Copy or Save the contents as an .emf (Enhanced MetaFile). You can then modify the individual components of the graphic file in Word or other applications.

17.1.15 Functional Data, Context Menu

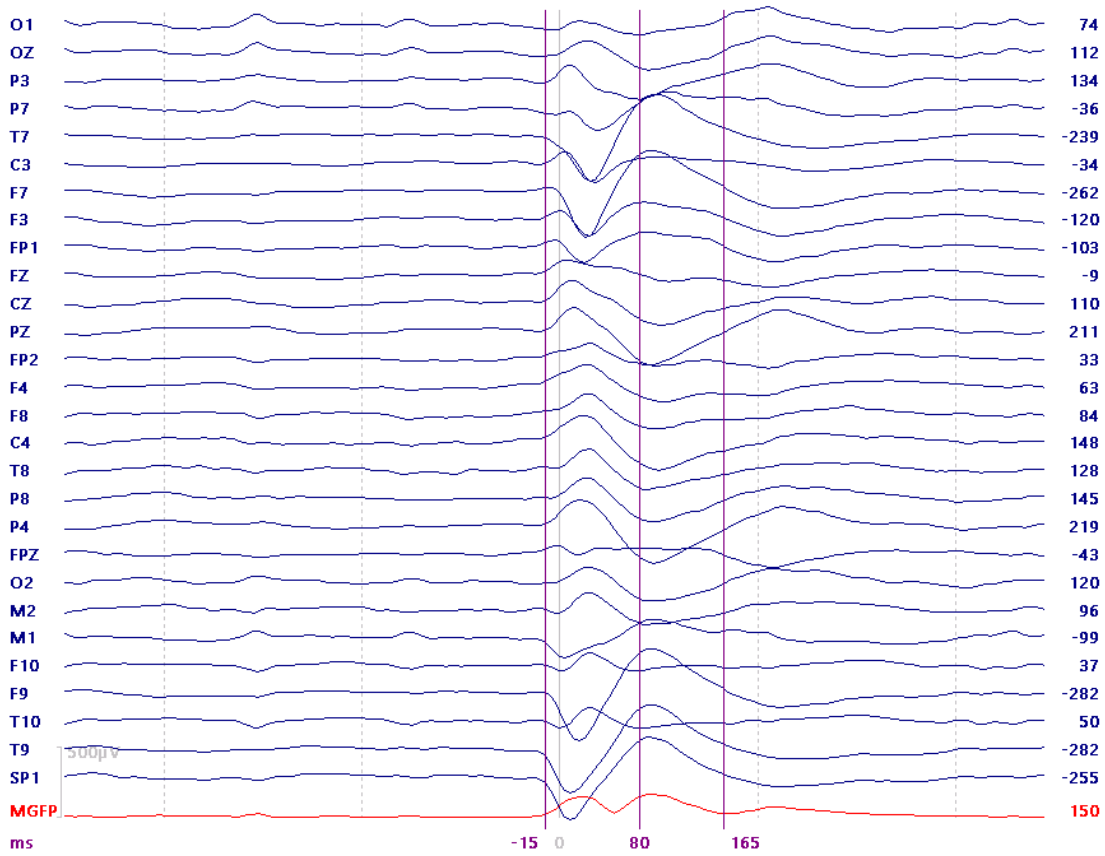
Click the *right mouse* button inside the Functional Data Display to access the menu list shown at the right. This is the same list of options found by selecting **Functional Data** on the **Main Menu** bar.



Zoom In (*Alt+Z*) **/ Zoom Out** (*Alt+U*). To Zoom In to a section of the displayed data, please complete the following steps.

1. Make sure **Tracking Mode** has been disabled by *right clicking* in the Functional Data Display and verifying that it is not enabled (or use *Shift+left mouse*). This will allow you to position the two outer vertical cursors.

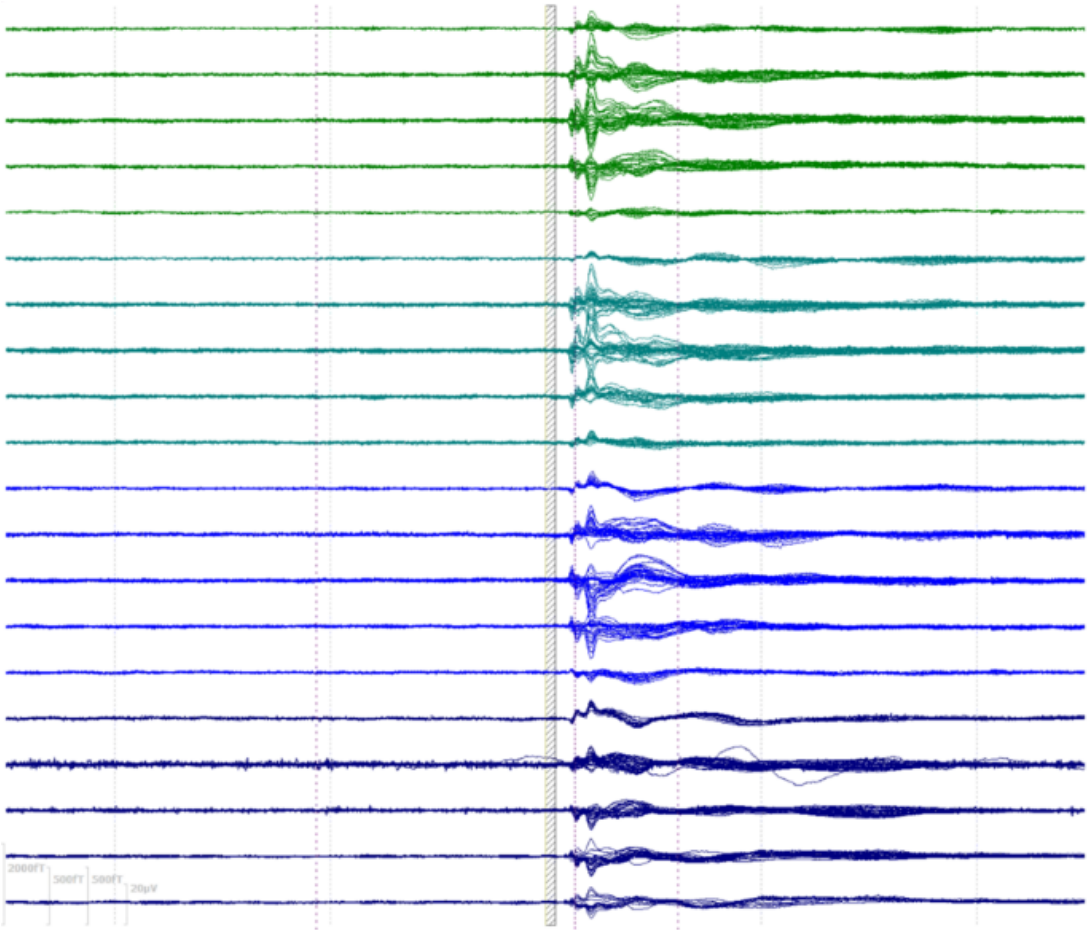
2. Position the two outer cursors (vertical lines) at the beginning and end of the section of data that you wish to Zoom into. This is done by either clicking the mouse on a position, which will cause the nearest cursor to jump to that position, or by grab-and-dragging a vertical cursor to the desired position.



3. *Right click* the mouse in the Data Display and select Zoom In . The display will then consist only of the span between the cursors.

4. *Right click* again in the Data Display and select Zoom Out to return to the original display.

Butterfly Plot. The Butterfly Plot display will superimpose all channels on a single X-axis, as shown above under Options (same as the button on the **Functional Data** Toolbar, or *Alt+B*). If you have multiple Channel Groups (EEG and MEG, or multiple groups of either), clicking Butterfly Plot will display butterfly plots for each channel group. In the Montage Editor, you can click the Add Empty button to add a blank space between subgroups of sensors. When you select the Butterfly Plot, you will see butterfly plots for each of the subgroups. In the figure below, there are 4 Channel Groups, and each one has five subgroups of sensors. Butterfly Plots are created for each.



Deselect All Channels (*Alt+D*) **/ Select All Channels** (*Alt+S*). You may toggle individual channels as Selected or Deselected by clicking the channel Label. To toggle the status for All Channels, select Deselect All Channels or Select All Channels. A channel range can be toggled by (de)selecting the last channel of the range and pressing the *Shift* key simultaneously.

Invert Channel Selection. Channels that were selected will become deselected, and channels that were deselected will become selected.

Display All Channels. Restores display of all channels.

Reset All Channels. Resets all channels to their original display parameters.

Reorder Channels. Opens the Montage Editor in reorder mode. See **Montages** under **Options** for details.

Deselect All Epochs / Select All Epochs. These options are active when you have retrieved a data file with multiple sweeps (such as a Neuroscan .eeg file). To toggle the status for All Epochs, select Deselect All Epochs or Select All Epochs.

Toggle Epoch. This option is used with epoched files to change the accept/reject state of the displayed sweep (same as the button or *Spacebar*).

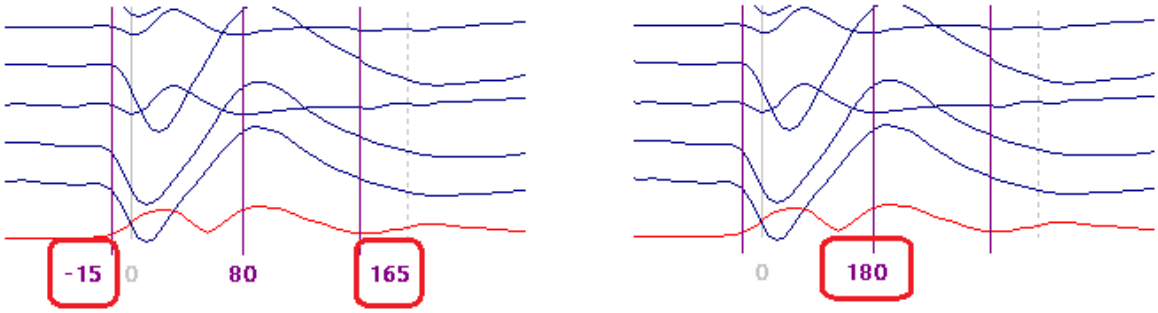
Invert Epoch Selection. Epochs that were selected will become deselected, and epochs that were deselected will become selected (manually selected/deselected epochs).

Delete All Events. This option is used with continuous data files, in which events have already been detected. Select the option to remove all events in the file.

Tracking Mode. When enabled, Tracking Mode, a single vertical cursor may be positioned by clicking the mouse on a position, or by grab-and dragging the cursor to a position. The voltages for each channel at the cursor position are displayed on the far right of the Data Display. *Shift+left mouse* also disables Tracking Mode; double-clicking the left mouse button enables it.

If you disable Tracking Mode, there will be three vertical cursors for positioning (see **Zoom In / Zoom Out** above). The two outer cursors are used to define the Timerange. The middle cursor defines the specific time point within the range. The Timerange is used for Noise Estimation, Source Reconstruction, Zooming, etc.

Show Differences. When disabled, you will see the latencies of the outer cursors displayed (left). Otherwise, difference in time between the two vertical cursors (right).



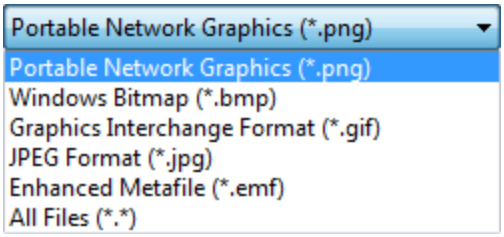
Use Mousewheel to Scroll. By default, the mouse wheel will scale the data up and down. If you enable this option, with continuous or epoched files, the mouse wheel can then be used to scroll through the file half a screen at a time (or one epoch at a time). Use *Shift+wheel* to step through one second at a time.

Copy Image to Clipboard. Copies the part of the data display having the focus to the Windows clipboard in .bmp format, where it may be pasted into another application. The option is also accessed from the **Standard** and **Report** Toolbar icon (*Ctrl+C*).

Copy Image to Clipboard (emf). When pasted into other Windows applications (such as Word), individual components of Enhanced Metafiles can be edited; whereas, .bmp files cannot. (In Word, *right click* on the pasted metafile, and select **Edit Picture**).

Append Image To Report. Copies the section of the data display having the focus to the Report. The option is also accessed from the **Report** Toolbar icon (*Ctrl+Shift+R*).

Save Image As. This option lets you save the graphic display in any of the formats shown.

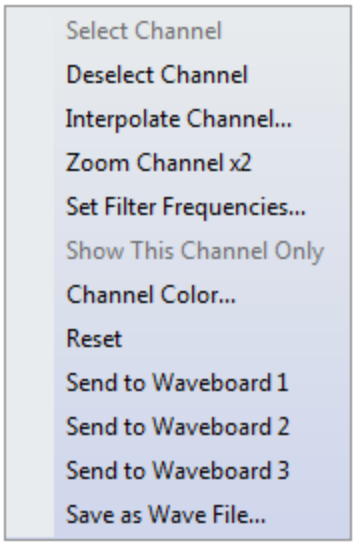


Print Image (*Alt+P*). The Functional Data will be displayed in the Windows Picture and Fax Viewer, where it can be viewed and printed.

Colors. Selecting this option displays the expanded **Colors** panel under **Functional Data** (described above).

Sensor Label Context Menu

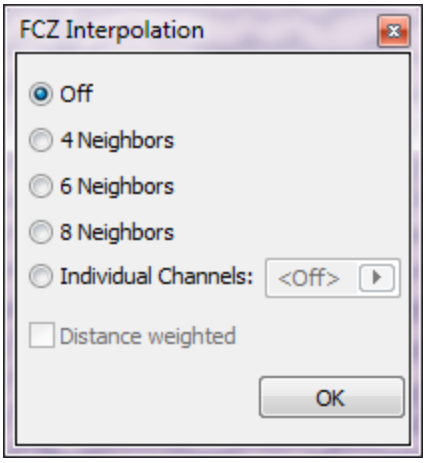
Right click on the sensor label for continuous data files to see the following context menu.



Select Channel / Deselect Channel. Use these options to select or deselect a channel (same as clicking on it). Deselected channels will change color (based on the color selection made in Colors under Functional Data). Disable Show Deselected Groups under Options (Functional Data) to hide the display of deselected channels. Deselected channels will be excluded from further analyses.

Interpolate Channel. This option is to reconstitute a bad channel based on the average of the N channels neighboring it (it should be used only as a last resort when you absolutely have to have data for that channel). The option will be grayed out if

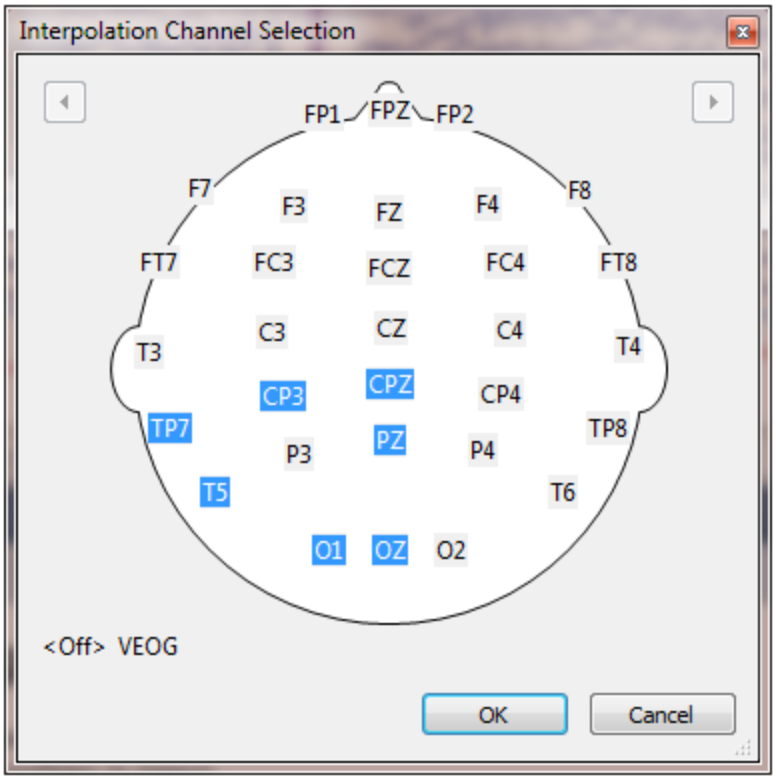
you have multiple files in the opened Study (otherwise the interpolation would be applied to all files in the Study). Selecting the option displays the following dialog (with the selected channel showing in the Title Bar).



Combining data files with interpolated channels in a single Study. The interpolated channels per data file are saved in the corresponding .dpa file when you close the study containing the individual file. This information is lost (same as other filter settings) when you save the data to another file, but the filtered and interpolated data are saved instead, and can be combined for statistics in another study. Thus, in order to have different interpolated channels per data file in a study with combined data files, the individual data file(s) have to be saved first (**Functional Data** → **Save** → **Save Data**...) with the bad channels interpolated. Otherwise, you will get a merging of the interpolated channels, and the channels will be interpolated over all files in the combined study. Similarly you should not use Study Parameters or add several Study Parameter files into the combined study, because then the last parameters will supersede the previous ones, and you might get some unexpected behavior for the combined study.

Neighbors. Select **4**, **6**, or **8** of the nearest sensors to be used in the interpolation. The sensors that are selected can be seen in the Output display (you must enable the **Debug** option from the Output context menu).

Individual Channels. Use this option to manually select the channels you wish to use. Select channels using *Ctrl+click*, or drag a box around a group of sensors to select them.

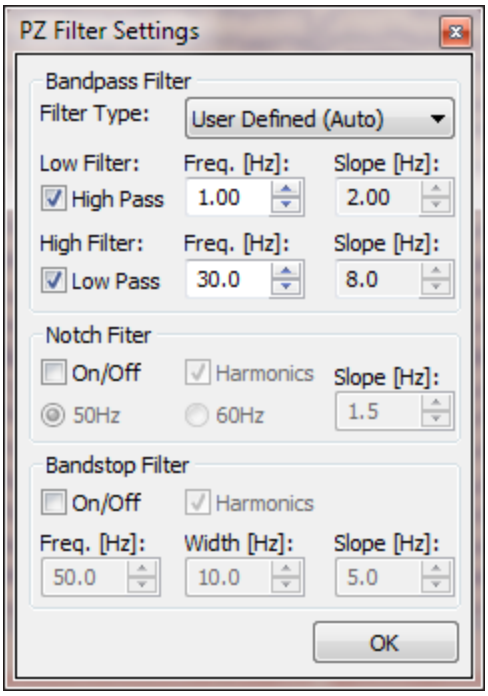


Distance weighted. When enabled, the interpolation will take into account the 3D distances from each sensor to the target one (to be replaced). If you have used Label Matching for importing the data file, the internal 3D distances will be used. If you used a 3DD or other sensor location file to import the data, then those 3D distances will be used. You will see the distances in the Output display.

Click the **Reset** option (below) to remove the **Interpolation**, or select **Off**.

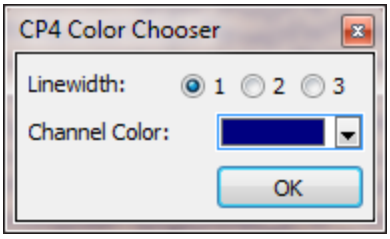
Zoom Channel x2. Click the option to zoom into the selected channel. Click the **Reset** option to return to the original display.

Set Filter Frequencies. This option allows you to select the filter parameters for an individual channel. Click **Reset** to remove the filtering. See the **Filtering** section above for details. If you change the filter parameters after performing a scan for artifact reduction (e.g., setting the parameters for the blink channel), it will be necessary to scan the data file again.



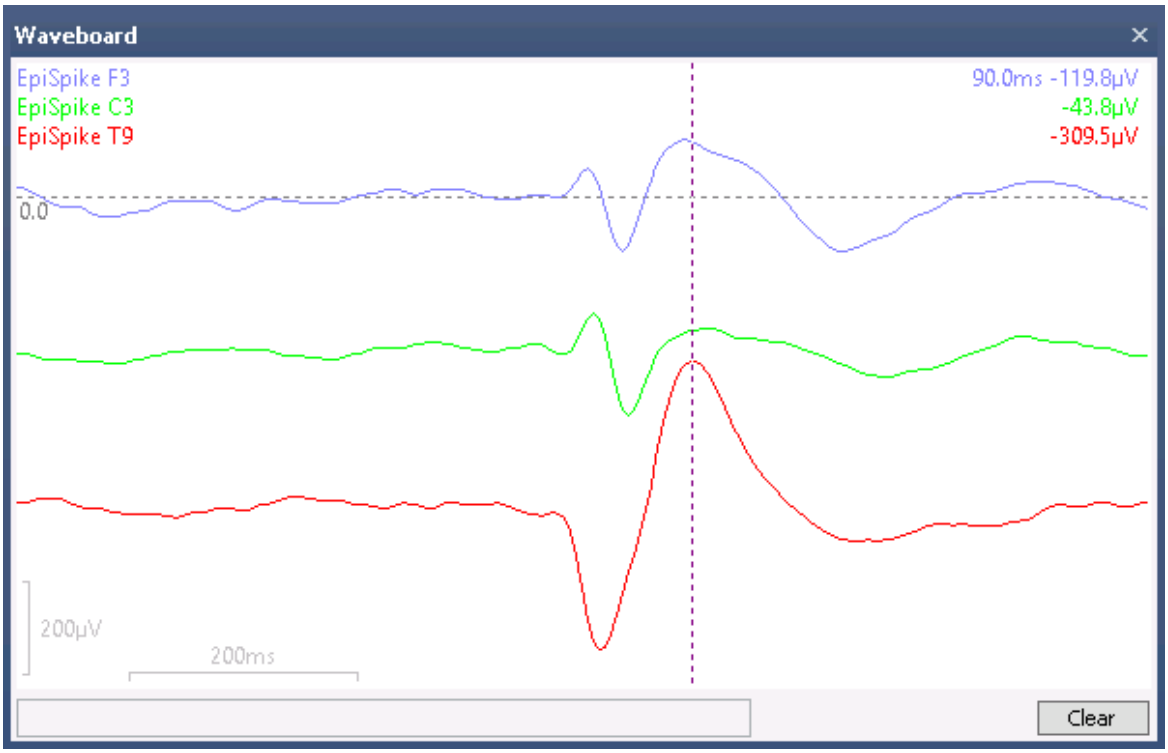
Show This Channel Only. Displays only the selected channel. Click **Reset** to return to previous channels displayed.

Channel Color. Select a color or line width for individual channels. Click **Reset** to remove it.

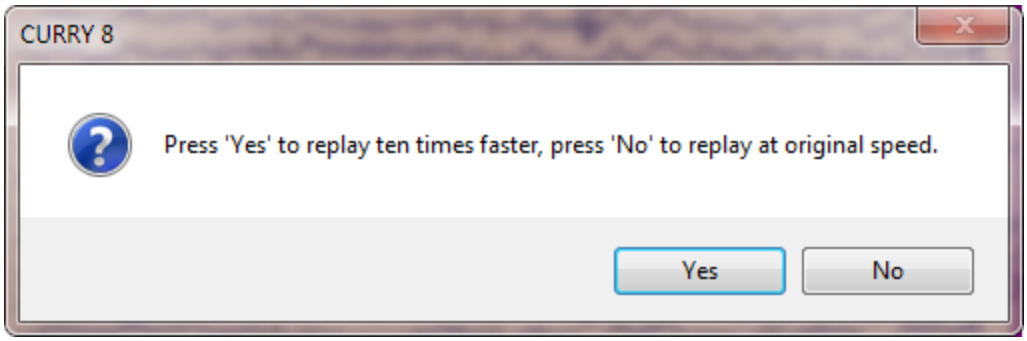


Reset. Restores the original parameters/settings to the channel or display.

Send to Waveboard 1 (2, 3). Select this option to send the channel to one of three Waveboards. As with all Waveboard displays, the *mouse wheel* will change the scaling, *Shift+mouse wheel* will expand/contact the display, and *Shift+drag* will reposition the contents of the display.

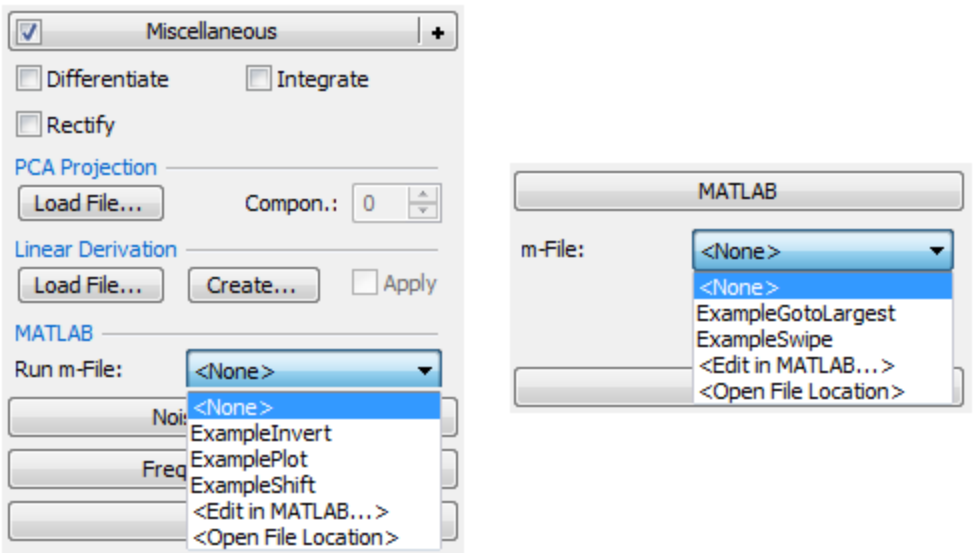


Save as Wave File. The purpose of this option is to allow you to hear changes in the EEG, such as seizures, line noise artifact, etc. When you select Save as Wave File, the selected channel will be saved as a .wav file. You will have the option to replay the file at 10x the normal speed (the pitch will increase accordingly), or at the original speed.

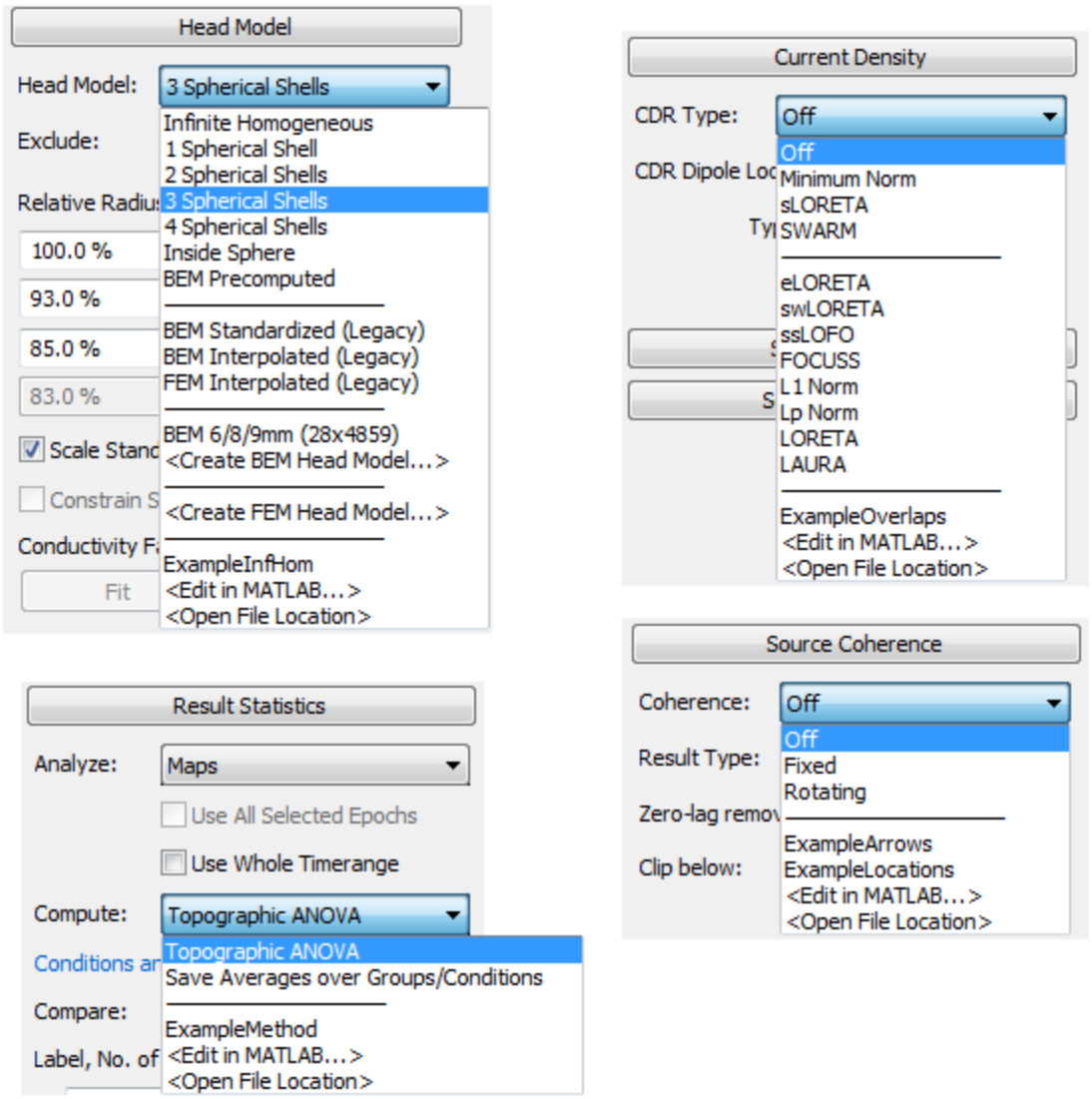


17.1.16 Interfacing with MATLAB

CURRY has been designed to have a very easy and fluid interface with MATLAB. (A 32 bit installation of CURRY needs a 32 bit installation of MATLAB; a 64 bit CURRY needs a 64 bit MATLAB). In various places within the CURRY software (**Miscellaneous**, the **MATLAB** panel under **Image Data**), you will see the MATLAB interface. If MATLAB is a separate option in the data flow, it will appear as a separate panel. A drop-down selector is used to select the m-file. If needed, such as in Image Data, a **Start** button will be provided.



If MATLAB is an alternative to algorithms already in CURRY, it will appear appended to an existing drop-down list. Examples are in the **Head Model**, **CDR Type**, **CDR Dipole Type**, **Source Coherence**, **Results Statistics**, etc. panels. In these instances, the MATLAB options are those below the horizontal line. The first two letters plus a number define in which drop-down list the m-file appears, e.g., SR2 (see list below).



Each MATLAB interface will have it's "code" (SR2, etc.), and there are example files in the Matlab folder that explain in their comments what data is passed down and what data can be passed back. The **<Edit in MATLAB...>** option in the drop-down lists opens the MATLAB editor.

A complete list of the codes is shown below.

Signal Processing (online and offline)
FD2: Artifact Reduction > Advanced > MATLAB > Run M-file (data filtering/modification)

This applies to the MATLAB interfaces in Functional Data and Acquire.

This data get sent from CURRY to MATLAB:

- indat: waveform data
- inlabels: list of channel labels
- insampleratehz: sampling rate of waveform data in Hz
- instartsample: absolute startsample of the current datablock

- inevents: list of events (sample number and event type) within current datablock
- inepochtype: event type of epoch (only used for epoched data)

These variables can be filled in MATLAB to send data back to CURRY:

- outdat: waveform data, must be of the same dimensions (number of channels and samples) as indat
- outevents: list of output events (sample number and event type) within current datablock; events will be merged with the existing event list in CURRY (only for contiguous data)

More detailed information about the data types can be found in the header of each FD2 example m-file.

Source Reconstruction
SR1: Source Reconstruction > Head Model > Head Model (leadfield computation)
SR2: Source Reconstruction > Current Density > CDR Type (CDR analysis)
SR3: Source Reconstruction > Current Density > CDR Dipole Type (CDR dipole analysis)
SR4: Source Reconstruction > Source Coherence > Coherence (Coherence analysis)

Image Data
ID1: Image Data > Matlab > m-File (image data analysis, cursor location)

Results
RE1: Result > Result Statistics > Compute (statistics)

The file names of the m-files that are displayed at these plugin locations start with the code; the remainder of their file name is shown in the drop-down.

Example files are provided in the *C:\Program Files\Neuroscan\CURRY 8\Matlab* folder. Please see the **Target Folders for Windows 7** section.

<Edit in MATLAB>. If an m-file was previously selected, and <Edit in MATLAB> is then selected, the file can be edited in MATLAB.

<Open File Location>. Opens the folder where the m-file resides using Windows Explorer.

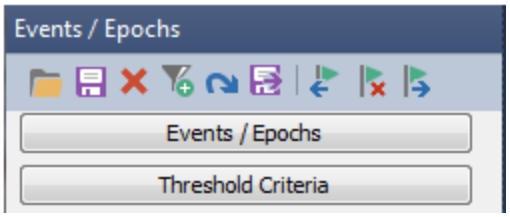
MATLAB During Acquisition

Note also the **Initialize MATLAB Interface** found under **Acquisition** on the Main Menu bar. This option can be used to start and initialize MATLAB manually if you plan to use it during acquisition. Otherwise, MATLAB will be initialized when it is needed, which might interrupt acquisition since it can take quite a while. This is especially the case with NuAmps where there is a danger of a buffer overrun. The option can also be used for troubleshooting to check whether the MATLAB interface is working correctly.

17.2 Events / Epochs

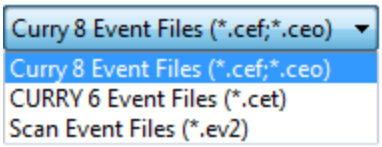
The Events/Epochs 

section is used to create averaged evoked responses or files containing the individual epochs. Conditional averaging may be applied. Epochs may be included or rejected on the bases of SNRs or voltage thresholds (time and frequency domains). The options are included in two parameter panels: **Events / Epochs** and **Threshold Criteria**.

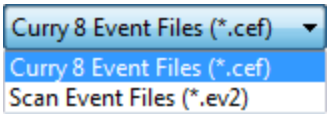


The icons at the top  are as follows.

Load Event File  . This option lets you select and load a previously saved event file (.cef). You can also load an .ev2 file. Ev2 files are created in the SCAN Edit program. They are text files that contain stimulus and response information. If you are using a stimulus presentation program other than Stim2, which does not output the response TTLs yet does contain the response information in a text file, you can create an .ev2 file that contains the response information and import that into CURRY 8.



Save Event List  . Saves a list of the events with corresponding event **Times** and **Annotations** in a text file (.cef and .ev2).



If it becomes necessary to modify the .cef file, you will find that this format is more complex than the .evt or .ev2 files used in EDIT (SCAN). For example, the sensor locations are included as well. If you need to make modifications that change the

number of events in the file, you will need to modify the `PointNrLocations` line, as well as the `ListNrRows` lines, which occur in three places (modify all of them).

Here is a more detailed explanation of all possible event types, their corresponding event codes (as they appear in .ceo, .cef, .ev2 files, or in data streams to MATLAB or over TCP/IP) and how they are displayed in CURRY:

Positive	0 - 49999	'0' - '49999'
Negative	50000 - 99999	'n0' - 'n49999'
Response	100000 - 109999	'r0' - 'r9999'
False Response	110000 - 149999	'f0' - 'f39999'
Accept	150000 - 199999	'a0' - 'a49999'
Manual	200000 - 299999	'm0' - 'm99999'
Threshold	300000 - 399999	'thr1' - 'thr100000'
Hypnogram	400000 - 599999	'hyp0' - 'hyp199999'
QRS	600000 - 699999	'QRS1' - 'QRS100000'
Bad Block	700000 - 799999	'bad' - 'bad99999'
Timebreak	800000 - 899999	'br0' - 'br99999'
Video	900000 - 999999	'vid0' - 'vid99999'
Audio	1000000 - 1099999	'aud0' - 'aud99999'
Microphone	1100000 - 1199999	'mic0' - 'mic99999'
Photic	1200000 - 1299999	'pho0' - 'pho99999'
Seizure	1300000 - 1309999	'szr0' - 'szr9999'
Seizure Free	1310000 - 1319999	'szrf0' - 'szrf9999'
Unknown	1320000 - ...	'un0' - 'un...'

You may specify "positive" events in the range 1 - 49999, "negative" events would be 50001 - 99999 (displayed as n1 - n49999).

Template Event codes are a special case:

All negative event codes appear as 'thr...' events. Template event codes can contain of up to 9 digits.

Example 1:
Event code: -1 1046 0883 (spaces added here for better readability).

The '-' indicates that this is a template event.
The last 4 digits (0883) represent the correlation 88.3% (= (10460883 modulo 10000) * 0.1).
The middle 4 digits (1046) represent the amplitude 104.6% (= (10460883 div 10000) * 0.1).
The first digit (1) represents the processing sequence number. The first sequence has the index 0, so this event shows up in CURRY as 'tmpl2'.

Example 2:
Leading zeros can be trimmed.
Event code: - 407 0920 (spaces added here for better readability).
The '-' indicates that this is a template event.
The last 4 digits (0920) represent the correlation 92.0% (= (4070920 modulo 10000) * 0.1).
The first 3 digits (407) represent the amplitude 40.7% (= (4070920 div 10000) * 0.1).

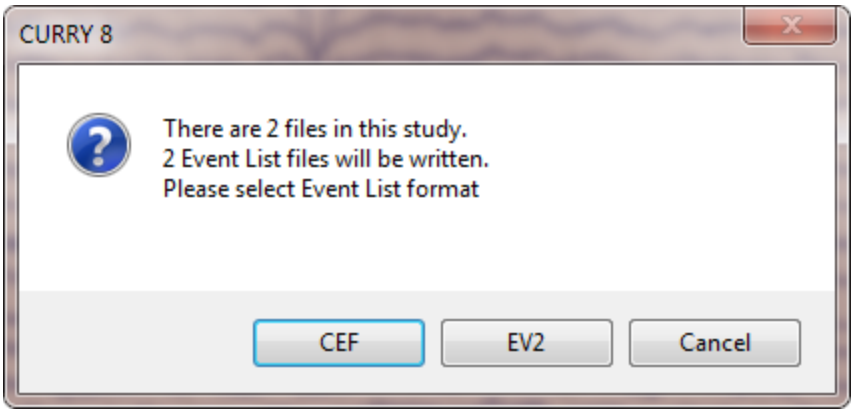
No 9th digit is available, so this threshold event is from the first processing sequence and thus appears in CURRY as 'tmpl1'

You may also encounter some unexplained events in your files:

br0 - these occur when you stop saving data to a file
br1 - these occur when you resume saving data to the same file
br2 - these indicate where files are concatenated together (the files must be at least 60s long for the br2 events to be inserted)

To return to the original continuous data, go to **Window** on the Main Menu Bar, and select the prior Study.

If you have more than one continuous data file in the same Study, such that the files are concatenated when the Study is opened, and you then click Save Event List, you will see a message similar to the one below. You have the option to save the event information as a CURRY .cef file, or the simpler SCAN .ev2 file format.



Delete Selected Event Type  . Deletes selected events (the selected Event Type) from the Event List.

Merge Behavioral Data File  . Dat files are text files created in the Stim2 program, and they contain stimulus and response information. The can be merged directly, or, when needed, you may edit the .dat file and then merge it with the data file. The .dat file reader will attempt to match responses to *existing* events; whereas, the *.ev2 reader creates a new event list from scratch.

In many cases you will not need to merge the .dat file. This was needed in EDIT for the Accuracy and Latency information it contained, so that you could then sort on correct or incorrect responses. In CURRY, the Conditions options, described above, let you select only those epochs where specified responses follow the selected stimuli. For example, if the correct response for stimuli type 1 is response type 1, you can accept epochs where the response type is r1 only. Or, if you wish to include correct responses that fall within a certain time range, you can specify the range under Conditions.

CURRY will detect incorrect responses in the .dat file, and label them as f1, f2, etc. For example, if the subject presses the 4th button, that will be seen initially as an r4 in the continuous data file. After merging the behavioral data file, that will remain r4 if it was a correct response, and be converted to f4 if it was an incorrect response (based on the 0's or -1's for responses in the .dat file). You can then sort to exclude "f" events under Conditions.

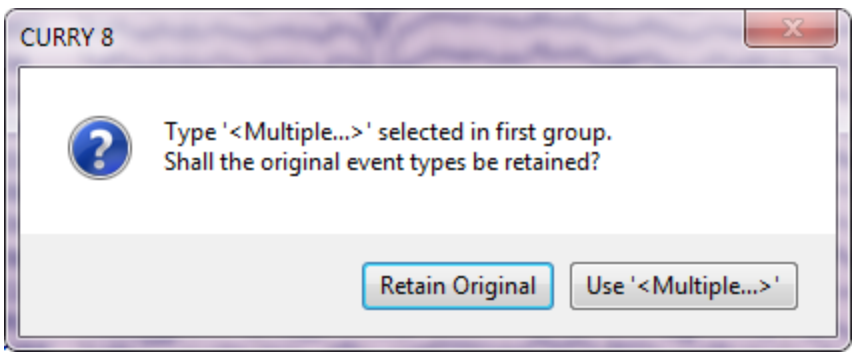
When you merge the .dat file with the continuous data file, CURRY will attempt to align the events between the two files. Always check the Output section to verify that all events have been merged. If you see that fewer that total number of events have been merged, that is a signal that there was an error in aligning the two files, or that there was some other disagreement between the events in the CURRY file and the .dat file.

If a stimulus line in a .dat file contains a response type and timing, then this response event will be generated in CURRY, if it doesn't already exist. If there is a separate response line in the .dat file, then this event is looked for in the existing event list and will not be created. In this case it is assumed that the response events were also sent to the amplifier and thus recorded in the file. During merging, incorrect responses will be changed to false responses.

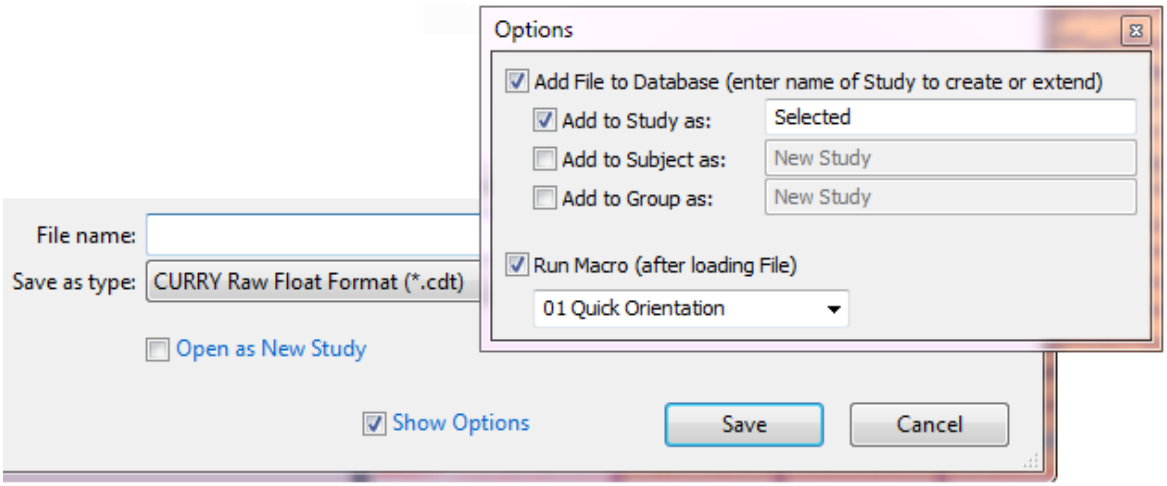
Reload Event List  . Reloads the currently stored event list.

Export Events  . This option will create a new file that contains all of the epochs are *for all event groups*. You can also select any single Event Group type, or combination of Event Groups, and create an average. For example, say you define 4 groups: Group 1 includes events 1-10, Group 2 includes event type 100, Group 3 includes events 21-30, and Group 4 includes event type 200. The epoched file that is created will have all epochs, with the type codes (Group Labels) in the upper right corner. If you select **Multiple**, you can choose which Event Groups you wish to combine. Select **All** to average all of them. Avoid using Group Labels that exceed 39 characters, as these may be dropped, truncated, or obscured in some places that display the strings. Instead, use the Group Label field to create shorter text strings.

If you have selected multiple event types (<All>, <Manual>, or <Multiple>), you will first be asked if you wish to retain the original event types. If you say **Retain Original**, each epoch will display the original type code in the upper right corner. This will allow you to average the epochs by event type. If you say **Use '<Multiple...>'**, each epoch will have "all" in the upper right corner, and you will not have the option to average the events by type.



A Save As window will appear, allowing you to select a folder, enter a file name, and select various options.



Two files will be saved (all with the same base name, but with different extensions). The .cdt file will contain the epochs, and the .dpa file contains the functional data parameters. The epoched file will be displayed automatically if you enable **Open File after saving**. Step through the file and reject any unwanted sweeps using the button on the **Functional Data** Toolbar (or the *spacebar*).

Previous Event, **Next Event**. Move to the Previous or Next Event (in continuous data files where events have been detected).

Erase Event (*Ctrl+E*). Removes the event from the continuous data file.

The **Events / Epochs** and **Threshold Criteria** panels are described in the following sections.

Change from CURRY 7

Users familiar with CURRY 7 will see that these sections have been reorganized to reduce redundancy. It will be necessary to see how the current reorganization affects the analysis flow. Please see the related tutorials as needed, as well as the information in these subsections. If you have macro files from CURRY 7, they should still function in CURRY 8.

These are the four main paths to go from continuous data to averaged data (time domain).

1. You can create in-place averages without applying any of the epoch rejection methods. No epoched file is created or saved. In this case you are simply averaging all of the epochs for each event type (relying on the Artifact Reduction methods to reduce artifact, if desired). The results are averages for each event group. This method gives the fastest results, although not necessarily the cleanest results.

2. You can create in-place averages using any of the epoch rejection methods. No epoched file is created or saved. Epochs may be rejected on the basis of voltage thresholds, FFT power thresholds, Noise Statistics (SNR), or any combination of the methods. The results are averages for each event group. This method gives you more control over which epochs are included in the averages.

3. You can create an epoched file excluding epochs that are rejected on the basis of voltage thresholds, FFT power thresholds, Noise Statistics (SNR), or any combination of the methods. The epochs are rejected prior to creating the epoched file. This gives you a clean file that may then be used for averaging or single file statistics. This method takes a little longer than the first two methods because another file is created and cleaned.

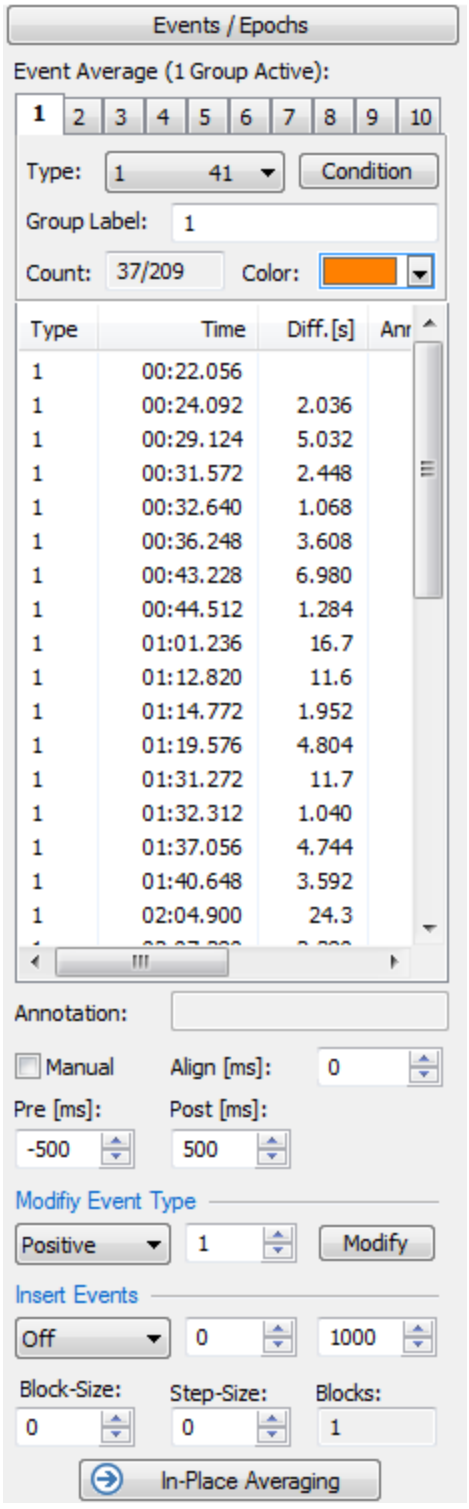
4. You can create an epoched file that contains *all* of the epochs. Open that file and then reject epochs on the basis of voltage thresholds, FFT power thresholds, Noise Statistics (SNR), or any combination of the methods. This gives you a clean file that may then be used for averaging or single file statistics. This method differs from the 3rd one in that you can see all of the epochs before rejecting any of them.

Within each of these are some minor variations. Please see the relevant Tutorials for details. Most of these are in the *Evoked Response Analysis* section.

With frequency domain analyses there are also some changes from CURRY 7. Again, please see the relevant tutorials for details.

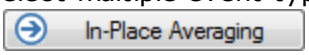
17.2.1 Events / Epochs

The **Events / Epochs** panel is used basically to create in-place averages or epoched files that may be saved. Epochs are created using trigger events, or from manually placed events.



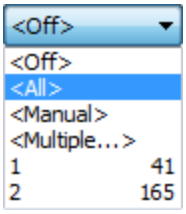
Event Average. You may create up to 10 averages at the same time. The averages can use different parameters, with the exception of the **Pre [ms]** and **Post [ms]** times, which must be the same across averages. Select Group 1, and enter the parameters, then select Group 2 and enter its parameters, and so on. When you

create the averages (or epochs), they will all be processed at the same time. (The parenthetical information tells how many groups have been prepared).

Groups do not have to contain single event types - events can be combined in the same average. You can, for example, select Type 1s in Group 1, Type 2s in Group 2, Type 3s in Group 3, Types 1-3 in Group 4, Types 1,3 in Group 5, etc. Use the **<Multiple>** option to select multiple event types. Averages will be created for each group when you select 

. The **<Manual>** option is selected automatically when you select the **Manual** option and insert number key events (see below).

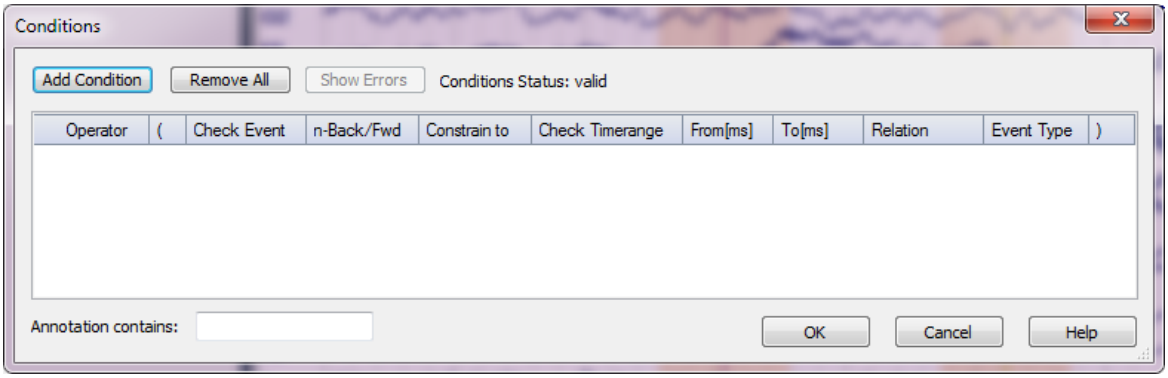
Type. This displays the list of all of the events in the file, or just the ones you select. Stimulus events are shown as numbers - the type code sent from Stim2 (or other similar system). Response events are seen as r1, r2, etc. Events that you enter manually (see **Manual** below) appear as stimulus events (the Length is the same as set in the Pre-Lat and Post-Lat fields). Events inserted as a result of the artifact reduction procedures are shown as *Thr* (Threshold), *QRS* (heart beat detection), and *temp* (Template matches). The 1 after Thr (Thr1) indicates this was the first Processing Sequence.



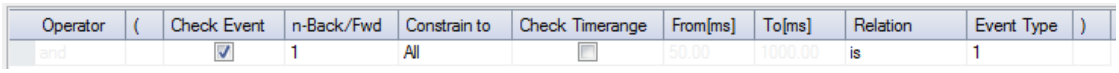
If you have a continuous data file from Scan with keyboard events, these will be read as m20 + event value. That is, if there is a keyboard event of 4, it will be seen as a 24.

Condition. The 

button accesses the **Conditions** dialog. This is used if you wish to impose conditional logic on the epochs that will be added to the average you are creating. You must select one or more events types in the **Types** field for the button to be active.

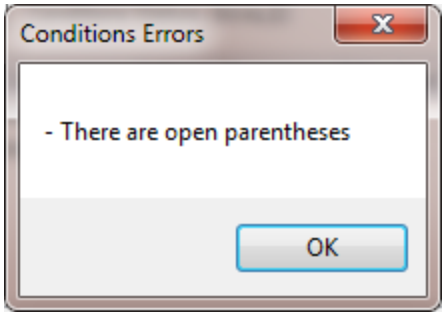


. Clicking **Add Condition** displays the initial line. Clicking it again adds more lines.



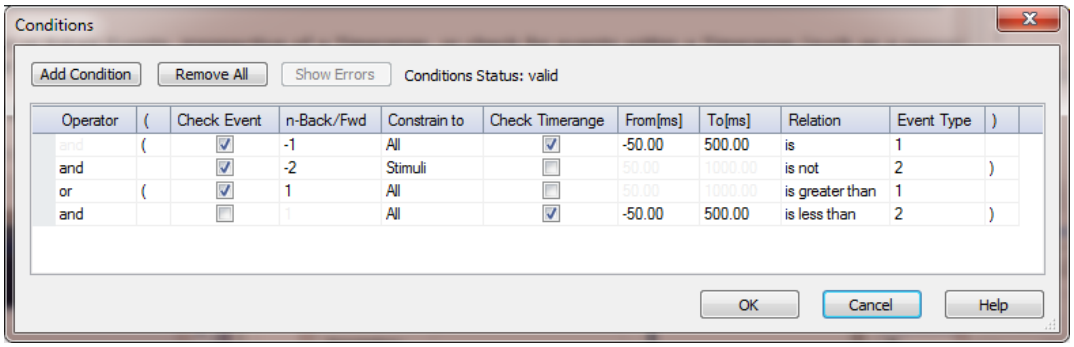
Remove All. Click to remove all lines. To remove a single or selected lines, highlight the line(s) (click box on far left), and press the *Del* key on the keyboard.

Show Errors. If there is an error in the conditional logic you have created, you will see Conditions Status: INVALID. Click **Show Errors** to see what the error(s) is.



Operator. After the initial line, additional lines can be connected using **And** or **Or**.

Open/Close Parentheses (). The Open and Close parentheses are used to combine and separate "terms" in the conditional statement. In the example below, the first two lines are combined within the parentheses, then there is an "or" operator, which connects the last two lines that are also combined within parentheses. "Nesting" (parentheses within parentheses) is not permitted.



Check Event. You must check for prior, current or future Events, irrespective of a Timerange, or check for events within a Timerange (such as a response event following a stimulus event). **Check Event** is associated with **Check Timerange** in the following ways.

If **Check Event** is enabled and **Check Timerange** is not, the Timerange is not considered.

If both are enabled, then the specified event *in the specified Timerange* is considered.

Not enabling **Check Event**, yet enabling **Check Timerange**, is illustrated in the following example.

If you have following events:

s1 r1 r2 s2

and the program is currently "considering" s1, it can check for an r2 event within a certain time range after s1. You do not have to care if you expect the event to be the next or next+1 event. You just look for events within a Timerange.

It is not valid to have both options disabled at the same time.

n-Back/Fwd. This field is used to define events before or after the current one, and is named for the n-Back paradigm. In a basic n-Back paradigm, the subject is presented with a sequence of stimuli, and the task consists of indicating when the current stimulus matches the one from *n* steps earlier in the sequence. The parameter *n* can be adjusted to make the task more or less difficult.

For example, a visual 3-back test might consist of the experimenter displaying the following list of letters, one at a time, to the subject:

A B C D E C r1 F G H I G r1 J K L M

The subject is supposed to indicate with a button press (r1) when a letter corresponds to the same letter that was seen three steps earlier, and otherwise not respond. Each letter would have a corresponding type code: A = 1, B = 2, C = 3, and so on. You want to create averages of the events where the third prior event was the same as the current event, and when the subject made a correct response.

The n-Back field determines how far back the program will search for a match. A value of -1 means the previous event, -2 means the event before that, and so on. In the 3-back design shown above, C has a type code of 3, and G has a type code of 7.

We also want the next event (n-Back = 1), to be a Response Type 1 event (r1), and further, we want the response to be between 100 and 2000 ms after the stimulus (100 to avoid impulse responding, and 2000 to limit the time there is to respond).

For the average you are creating for the Type 3's (the C's) the Conditions lines would appear as:

Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	)
and		☑	-3	All	☐	50.00	1000.00	is	3	
and		☑	1	All	☑	100.00	2000.00	is	r1	

The Type 3 epoch will be included in the average if the third prior event is also a Type 3, and, a Type r1 event must be found in the 100-2000 ms Timerange after the stimulus.

Similarly, for the average you are creating for the Type 7's (the G's) the Conditions line would appear as:

Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	)
and		☑	-3	All	☐	50.00	1000.00	is	7	
and		☑	1	All	☑	100.00	2000.00	is	r1	

In a different application, imagine a P300 paradigm where there are "oddball" and "standard" stimuli being presented randomly. By chance, there could be 2 or 3 oddball stimuli in succession. You may wish to exclude any oddball stimuli (Type 1's) that are preceded by another oddball stimulus. The conditions line would appear as:

Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	)
and		☑	-1	All	☐	50.00	1000.00	is not	1	

In this case, the -1 for n-Back is the preceding stimulus, and the Relation field is changed to "is not". The type 1's will be averaged if the previous event is not a type 1; those type 1's that are preceded by a type 1 will be excluded.

Constrain to. When set to Stimuli, or Responses, only stimulus, or response, events of the type specified in the Event Type field will be used. If All is selected, any event will be used.

For example, there are the following events in a sequence:

S1 r1 S1

The program is currently focusing on the second S1, and 1 is in the Event Type field. n-Back/Fwd is set for -1 (the previous event). If **Constrain to** is set to **Stimuli**, only the stimulus 1 events are recognized, and the previous event will be the prior S1 event. If Constrain to **All** is selected, the r1 event will be recognized as the previous event.

Check Timerange. Epochs of the current type will be added to the average if there is an event of the selected type occurring within the specified Timerange. A typical example of this is that you only want epochs to be added to the average of the responses to the "oddball" stimuli when the subject makes a desired response within a selected Timerange.

Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	)
and		☑	1	All	☑	50.00	1000.00	is	r2	

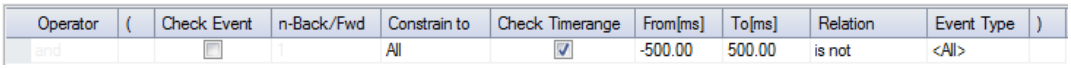
The epoch will be included in the average only if the next event is a Response Type 2 event that occurs form 500-1000 ms after the stimulus event.

From [ms]. The From and To fields determine the Timerange in which some other event must occur in order for the current epoch to be included in the average.

To [ms]. See **From [ms]**.

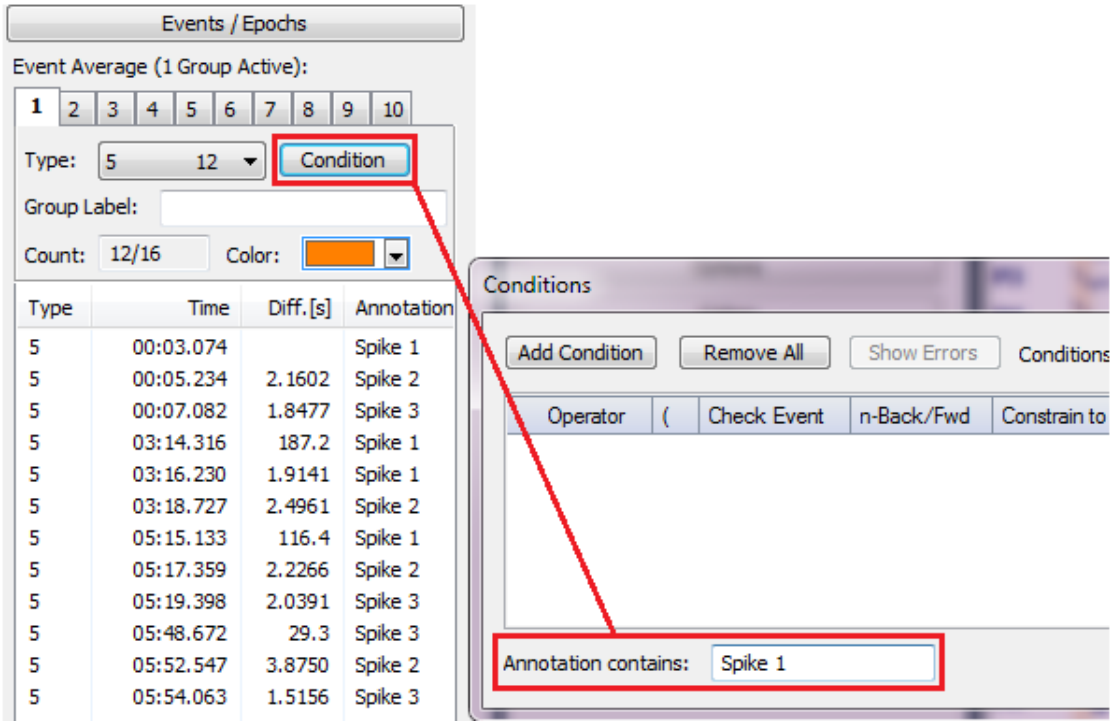
Relation. These are the conditional relationships that may be specified (**is**, **is not**, **is greater than**, and **is less than**).

Event Type. This is the event type code of the target event that is being tested. This can be a stimulus event or a response event. Notice also there is an **<All>** option. This is useful in instances such as the following. Template matching was used to identify blinks in the data file. You want to average them, but only the ones that do not overlap with any epoch intervals. That is, you do not want the blinks to contain any ERP components. With the templates selected in the Event List (tmpl1), click **Conditions**. Uncheck Check Event (since there no specific event order), select a **Timerange**, set **Relation** to **is not**, and select **<All>**. The tmpl1 epochs will only be included if there are no other events within +/-500 ms.



If you have a STIM2 system and have merged the behavioral data ( ) with the continuous data file, you will have access to the Accuracy information for the responses (correct or incorrect). The response events will be seen such as the following, where the 1's and 2's are stimulus events, the r1's and r2's are correct response events, and f1's and f2's are false or incorrect response events. If you want to include epochs where there are correct responses only (and these are always type 1's), select r1.

Annotation contains:. In some cases you may want to sort the epochs on the basis of the Annotations. In the example below, there are three types of spikes, and all have the same type code. To sort by Annotations, click the Condition button, and then enter the desired Annotation text in the **Annotation contains** field. When you click OK, only the epochs with Spike 1 will remain. You may then rename the Type for the selected events only, if desired. This option can be used in conjunction with the other conditional sorting options, where the settings are combined. In other words, whatever you type in the upper conditions (Operator, Check Event, etc.) and whatever you type in the Annotations field will both be applied (both have to be fulfilled in order for the epoch to be included).



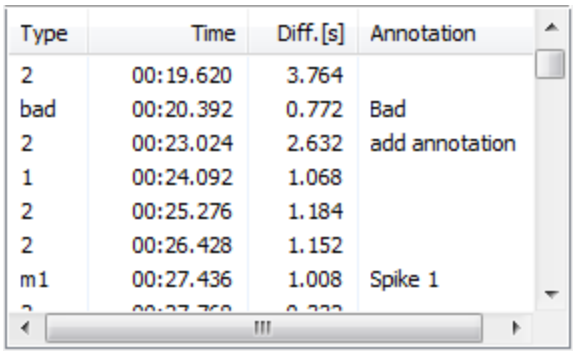
There is a tremendous amount of power in the conditional statements. See also the **Averages** section for using Conditions online.

Group Label. Use this field to simplify the label that will be seen to identify this group. For example, if you are combining events 1, 2, 3, 4, 5, 6, 7, 8, 9, and 10, you can simplify this to 1-10. You may also use text to identify the events, such as "Oddballs". The label will be carried through in later steps and files. Try not to use more than 19 characters. Strings beyond that will not be seen, or seen completely, in all subsequent text fields. If you will be performing Statistics, the text strings you enter here will be used to label the cells automatically.

Count. Displays the number of events detected in the file for the selected Type(s) over the total number of events in the file.

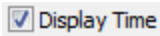
Color. The different groups will be highlighted with different colors in the continuous data file.

Event table. The list will display all of the selected event types. The columns are described below.



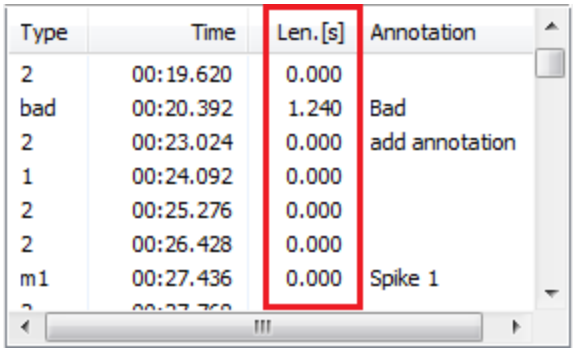
Type	Time	Diff.[s]	Annotation
2	00:19.620	3.764	
bad	00:20.392	0.772	Bad
2	00:23.024	2.632	add annotation
1	00:24.092	1.068	
2	00:25.276	1.184	
2	00:26.428	1.152	
m1	00:27.436	1.008	Spike 1

The **Type** column displays the selected event Types.

The **Time** column shows the time point in the file where the event occurs. This can be either the time into the file, in seconds, or the clock time from the data file, if it exists. To change it, go to **Options** under **Functional Data** and select (or deselect) **Display Time** 

. *Double-click* on an event to go to that part of the continuous data file.

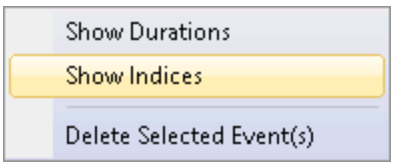
The **Diff.[s]** field shows the time difference between successive events. *Right click* on the field and select **Show Durations** to see the durations of bad blocks, thrN events, etc. instead of the differences.



Type	Time	Len.[s]	Annotation
2	00:19.620	0.000	
bad	00:20.392	1.240	Bad
2	00:23.024	0.000	add annotation
1	00:24.092	0.000	
2	00:25.276	0.000	
2	00:26.428	0.000	
m1	00:27.436	0.000	Spike 1

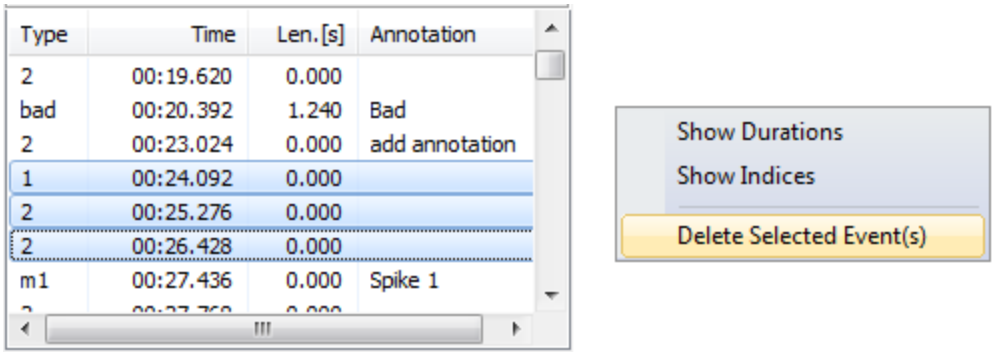
The **Annotation** column displays the Amplitude and Correlation (%) for each template event, or other labels, or nothing. Text can be added or modified in the Annotation field for any type of event by highlighting it and typing the text in the **Annotation** field below.

Right click in the list and select **Show Indices** to see the event number in the first column.

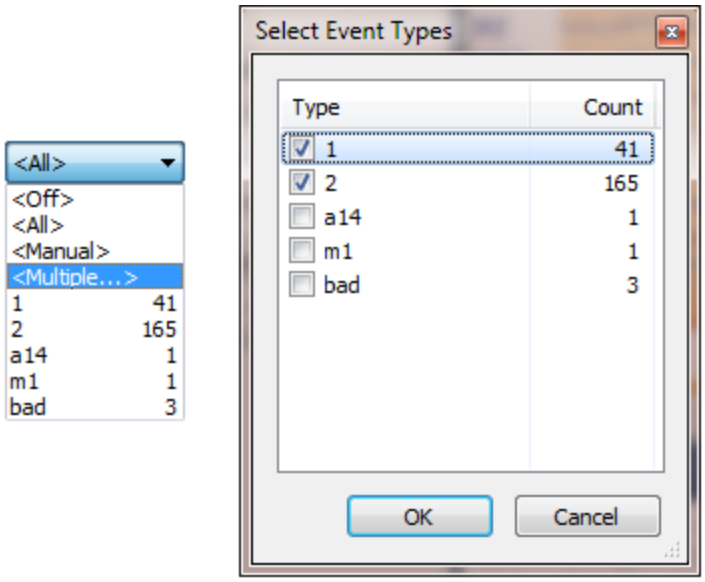


If you wish to select specific events from the list, use *Ctrl+click* (use *Shift+click* to define a range to be selected) to highlight the items. To delete those events, *right click* and select **Delete Selected Event(s)** from the context menu (or the *Delete*

key). You may also change the event type using **Modify Event Type** (described just below).



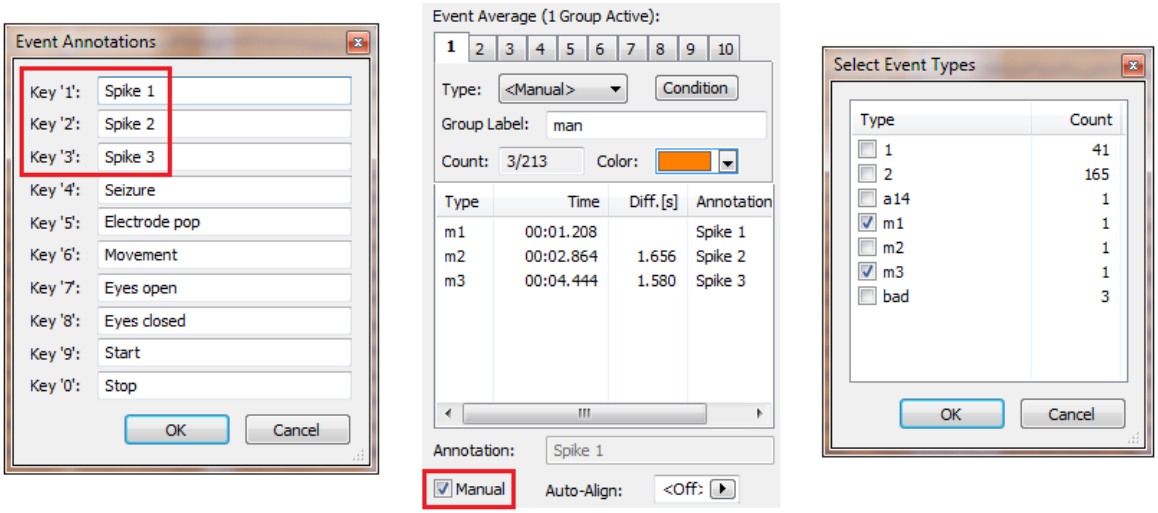
The drop-down list lets you select which events to display, and how many there are for each type. Note that there is an option for **<Multiple...>** in the list. Clicking this displays the **Select Event Types** window. Select the events to be included.



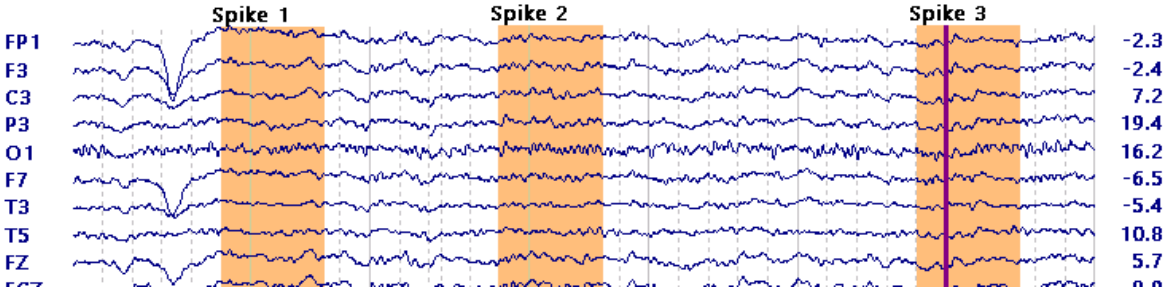
Annotation. This list displays annotations associated with the events. Highlight an Event in the list and type in a new Annotation in the field, as desired.

Manual. If you want to manually insert event codes (0-9), or Annotations with event codes, at specific positions in the continuous data file, enable **Manual**, position the middle cursor at the desired point, and click a number key (0-9) from the keyboard to enter that event. Events are distinguished by an "m" before the number, and these may be selected in the Type field, like other events. (If you are in **Tracking Mode**, all three cursors will be close together and move as a single unit - it is still the middle cursor that defines the point where the event is placed). Click the Previous Event or Next Event button to see the list of events entered.

To insert Annotations, you must first define the text you want to enter. Go to **Functional Data → Edit Event Annotations**. Enter the desired text for the *0-9* keys. Enable the **Manual** option in the **Event List** panel. This will automatically select the **<Manual>** option for **Type**. You will see the events added to the list as you insert them in the continuous data file. When you select In-Place Averaging or **Save All Event Groups as Epoched File**, all manual events will be processed. To include only selected events, select them using the **<Multiple>** option under **Type** (example on the far right). You may relabel the events in the Annotation field.



You will see the annotations in the data display when you position the mouse and click the corresponding number.

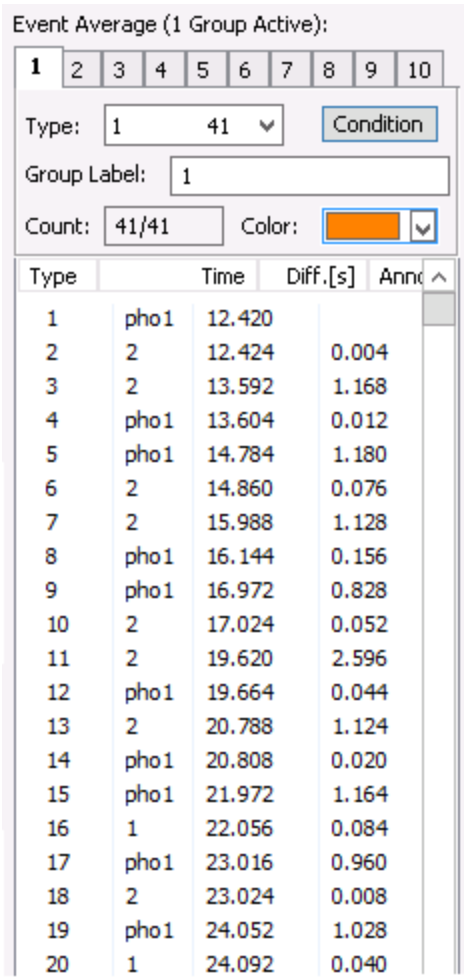


To save the manually inserted events, click the **Save Event List** button at the bottom of the Event List. If you save the .cef file in the default location that appears, you will see the events when you subsequently open the Study. If you save the .cef file elsewhere, you will need to use the **Load Event File** button to select the file. Or, you can save the entire file using **Functional Data → Save → Save Data**. If you forget to save the events, upon closing the Study you will be asked if you want to save them.

Align[ms]/Auto-Align. **Align[ms]** is an option used only with the StimTracker system. Briefly, you will see pairs of events for each auditory or visual stimulus. The numbered events come from STIM2. The other event in the pair will be a "pho1" or an "aud1". These are generated in the StimTracker, based on direct measurement of the

sound or light levels. The StimTracker events are therefore more accurate than the events originating in STIM2. The **Align[ms]** option will adjust the STIM2 events so they are aligned with the StimTracker events.

Consider the following example using visual stimuli. These are fabricated events with exaggerated differences. Generally, the photic events (pho1) will occur just a few ms after the STIM2 (numerical) events. The first two lines show that the type 2 event came 4ms after the corresponding pho1 event. In the next pair, the pho1 event came 12ms after the corresponding type 2 event. And so on. If we look down the Differences column, the maximum difference is 156ms (which is far greater than you will encounter).



Type		Time	Diff.[s]	Anno
1	pho1	12.420		
2	2	12.424	0.004	
3	2	13.592	1.168	
4	pho1	13.604	0.012	
5	pho1	14.784	1.180	
6	2	14.860	0.076	
7	2	15.988	1.128	
8	pho1	16.144	0.156	
9	pho1	16.972	0.828	
10	2	17.024	0.052	
11	2	19.620	2.596	
12	pho1	19.664	0.044	
13	2	20.788	1.124	
14	pho1	20.808	0.020	
15	pho1	21.972	1.164	
16	1	22.056	0.084	
17	pho1	23.016	0.960	
18	2	23.024	0.008	
19	pho1	24.052	1.028	
20	1	24.092	0.040	

In the Align[ms] field, we therefore entered a slightly larger number - 160 ms. We then see that the latencies of the STIM events have been changed to the pho1 latencies, thereby aligning them.

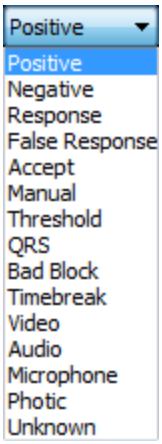
Type		Time	Diff.[s]	Anno
1	pho1	12.420		
2	2	12.420	0.000	
3	2	13.604	1.184	
4	pho1	13.604	0.000	
5	pho1	14.784	1.180	
6	2	14.784	0.000	
7	2	16.144	1.360	
8	pho1	16.144	0.000	
9	pho1	16.972	0.828	
10	2	16.972	0.000	
11	2	19.664	2.692	
12	pho1	19.664	0.000	
13	2	20.808	1.144	
14	pho1	20.808	0.000	
15	pho1	21.972	1.164	
16	1	21.972	0.000	
17	pho1	23.016	1.044	
18	2	23.016	0.000	
19	pho1	24.052	1.036	
20	1	24.052	0.000	

You can then perform epoching/averaging, etc. with the STIM2 numerical events, as usual. To revert to the original events, enter 0 in the Align[ms] field. To save the changes permanently, click on the button at the bottom row of buttons, and overwrite the existing .cef file.

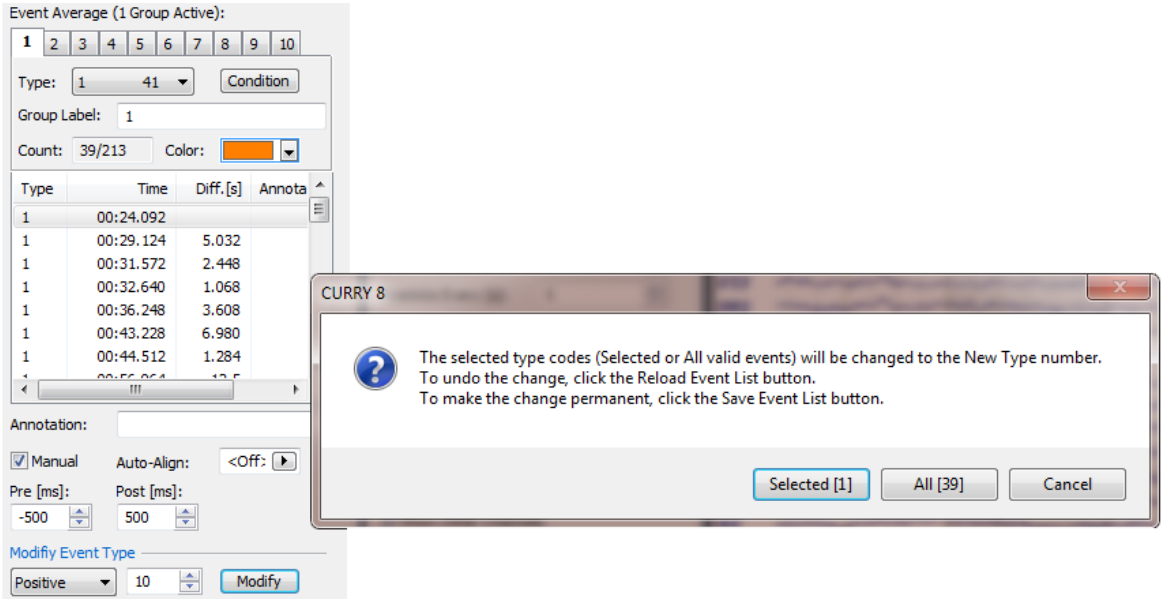
When **Manual** is enabled, this option will change to **Auto-Align**. You will need to select one or more channels to use. The program will automatically set the actual time cursor to the (relative) maximum of the selected channel in the vicinity (+/- 50 ms) of the selected timepoint at the time you insert the event.

Pre [ms]/Post [ms]. Establish the Timerange in relation to the event latency. For example, if you are analyzing evoked potential data, where you wish to create epochs from -100 ms before the zero point (time of stimulation) to 500 ms afterward, enter -100 and 500 ms. It is necessary to increase the **Pagesize** (**Options**) to encompass the entire epoch duration before creating the epoched file.

Modify Event Type. This option is used to change the event type(s) in whichever Event Group has the focus. The list displays all of the event types that can be modified.

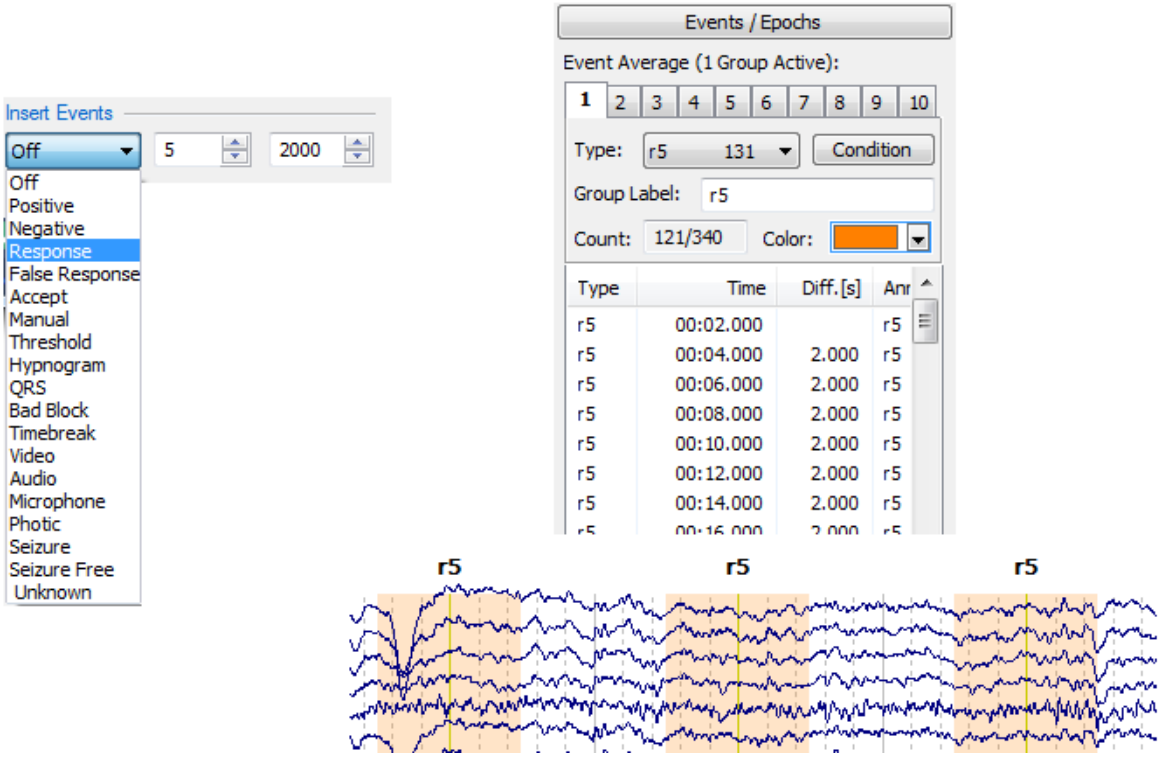


Example. If Event Group 1 has type codes of 1, and you wish to change them to 10, select **Positive**, enter **10**, and click the **Modify** button. In this case, one line in the list was highlighted, and so you will be asked if you want to change that one line or all of the Type 1's.



Click the **Reload Event List** button to restore the original events. To make the change permanent, click the **Save Event List** button.

Insert Events. This option allows you to insert events into the continuous data file. For example, if you want to insert event type "r5" (response type 5) every 2000 ms, enter **2000** first, then the **5** and then select **Response** from list. You may wish to then select the r5's for the **Type**. The r5's will be seen in the data display. Save the new event file if you want to make the change permanent.



Block-Size. This option is used to create a sequence of averages based on blocks of N epochs, when using In-Place Averaging only. A Block-Size of 50, therefore, will create averages of 1-50 epochs, 51-100 epochs, and so forth, with the final block consisting of whatever epochs are left (less than 50). The **Blocks** field will display how many averages will be created. A Block-Size of 0 means to include all epochs in the average.

Step-Size. Step-Size in used in conjunction with Block-Size to create averages with overlapping blocks of epochs, when using In-Place Averaging only. For example, if Block-Size is 50 and Step-Size is 25, averages will be created for epochs 1-50, 26-75, 51-100, 76-125, 101-150, 126-175, and so on. A Step-Size of 0 means no overlapping blocks of epochs, and therefore only Block-Size will be used.

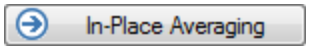
Blocks. The Blocks field shows the number of averages (based on blocks of epochs) that will be created.

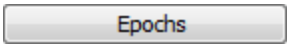
In-Place Averaging In-Place Averaging. This will create *averages* for the event groups you define (e.g., Type 1, Types 5-10, etc.). The averages for multiple groups will be seen as separate epochs. You can save the averages and go on to perform source reconstruction, etc. No individual epochs are created. If you have created averages using the In-Place Averaging button, you may return to the original continuous data by deselecting the In-Place Averaging button.

If you are rejecting epochs before you average, use Threshold Criteria before averaging.

The averages are seen with the original event codes in the upper right corner, with the number of epochs in parentheses 

.

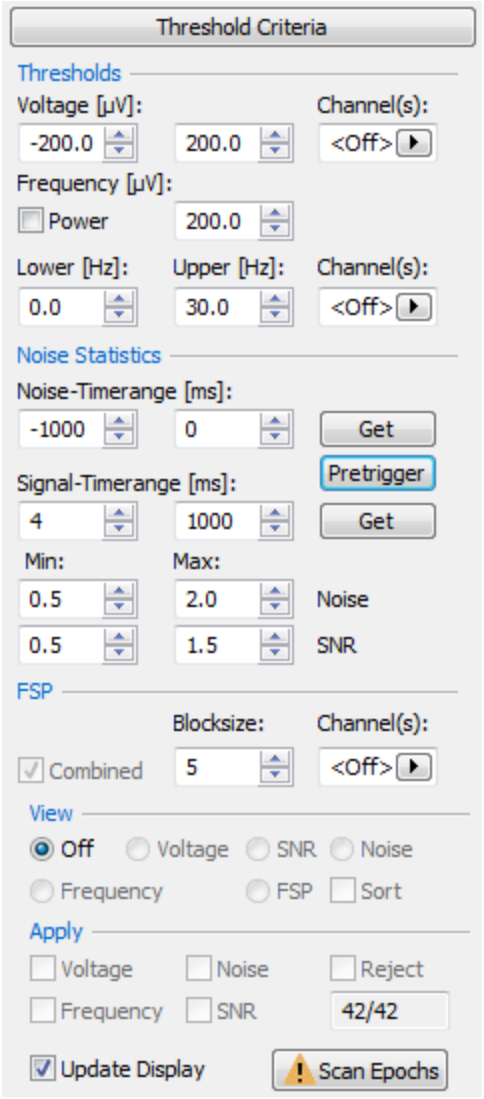
In most instances you will use the 

button, with either continuous or epoched data. In some cases with epoched data, you may want to use the **Average** button under 

. For example, that method will allow you to select blocks of epoch to average, such as 1-50, as opposed to all of them. See the **Epochs** section for details.

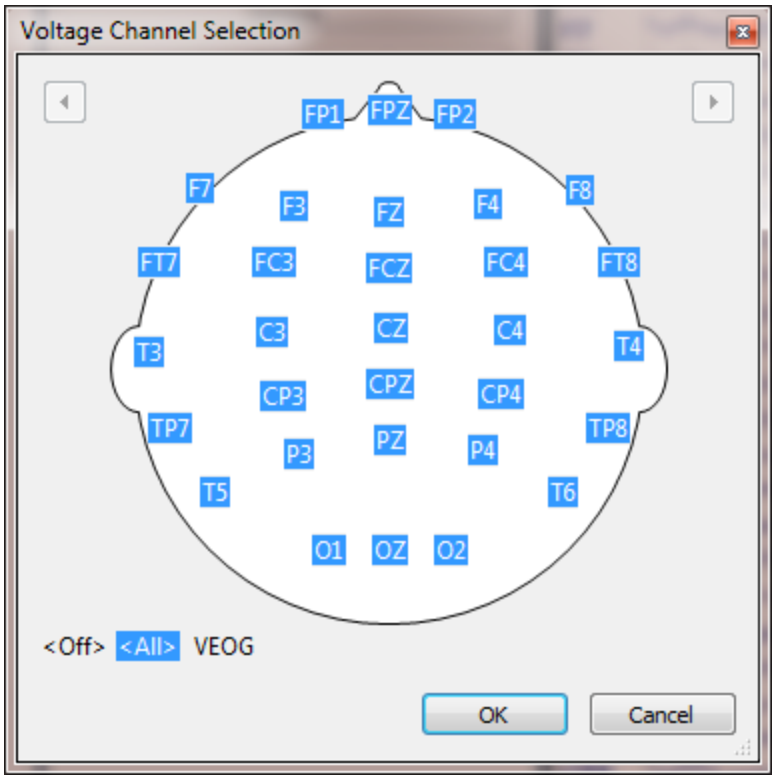
17.2.2 Threshold Criteria

The process of averaging within CURRY can be performed using minimum and maximum Voltage threshold criteria, Frequency interval thresholds, or the SNR or Noise estimates of each sweep as the criteria for accepting/rejecting the epochs. The methods can be used alone, or in any combination. In all cases, the thresholds are not applied when you Scan the Events - they are applied afterward when you change the thresholds and apply the selected corrections.



Thresholds. There are two options for rejection using a voltage threshold - time domain and frequency domain. The time domain method (**Voltage**) allows you to deselect epochs where the voltage (or fT values for MEG) at any of the selected channels exceeds the thresholds (positive and negative) you set (values are in microvolts). The **Frequency** domain option will reject epochs where the FFT results are greater than the thresholds you set, using the channels you select.

Voltage [µV]. Set the negative and positive thresholds, and an epoch will be rejected if either of the thresholds are exceeded, from any of the selected channels.
Channel(s). Select the channels to be monitored by clicking on them. Use *Ctrl+click* to select multiple channels, or, drag a rectangle around the desired channels. Set **Channel** to **Off** to disable the function. Clicking **<All>** uses all of the channels except "Other" channels.



Frequency [μV]. This option allows you to deselect sweeps in an epoched file where the amplitude or power of the selected channels exceeds the **Lower** and **Upper Thresholds [Hz]** you set (values are in microvolts; enable the **Power** option to use μV squared). Select the channel(s) to be monitored as above. If you select multiple channels, the average of the selected channels is used. Set **Channel(s)** to **<Off>** to disable the function.

Noise Statistics. The Noise Statistics represent a different approach to the selection of epochs that are to be used in creating the final average. In previous versions of EDIT, you typically defined selected channels as being Artifact Rejection channels, and set minimum and maximum voltage criteria. Any voltage that exceeded the criteria in the monitored channels would result in the rejection of that epoch.

With the current method, you may use SNR levels (signal to noise ratios), or noise levels, to exclude epochs (all channels are included in the analysis). The rationale is that epochs with abnormally high SNRs or noise levels contain artifact that should not be included in the average. SNRs or noise levels that are too low may also indicate something unusual in the epochs and these may be excluded also. The result will be an average based on high SNR or low noise epochs, which should then also have a higher SNR or lower noise level, and thus be a truer representation of the actual phenomena of interest (and better source reconstruction results due to decreased confidence ellipsoids).

The noise Ni of a channel i for a given time-range (timepoints t=1...m) is the standard deviation of the signal over time (zero mean):

Mi = SUM(t=1..m) [Mit] / m

Ni = SQRT {SUM(t=1..m) [(Mit - Mi)^2] / m} = SQRT {SUM(t=1..m) [(Mit - SUM(t=1..m) [Mit] / m)^2] / m}

The average noise N of all n sensors is:

N = SUM(i=1..n) [Ni] / n

The average signal is computed accordingly for the signal time-range.

Noise Timerange [ms]. "Noise" is typically defined as that part of the epoch where there is no signal of interest, such as the pre-stimulus interval. If no prestimulus interval is available, you may define another Timerange with no or minimal signal, or else use the entire epoch interval. The fields set the Timerange to be used for estimation of noise. Pressing the Get button transfers the latencies of the outer cursor positions, or you may enter the values manually or use the Pretrigger button.

Pretrigger. The Pretrigger button automatically selects the interval from the beginning of the sweep to the 0 ms time point. It also selects the first point after 0 ms to the end of the file for the Signal Timerange.

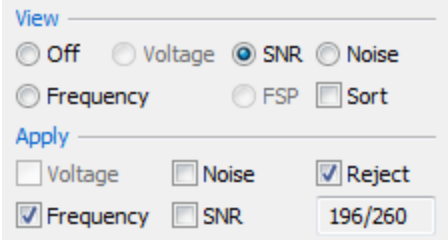
Signal Timerange [ms]. A measure of the "signal" is needed as well as a measure of the "noise" in order to compute the SNR. The "signal" interval is typically defined as that section of the epoch that contains the evoked responses, or the spikes. It often coincides with increases in MGFP. Pressing the Get button transfers the latencies of the outer cursor positions.

Min, Max for Noise. These values set the threshold criteria for the Noise calculation.

Min, Max for SNR. These values set the threshold criteria for the SNR calculation.

In Use

You can use none, any, or all of the epoch rejection methods. Set the parameters as desired, and click the Scan Epochs button. Once you scan the epochs, the following fields become active (and the Scan button will change to Scan Epochs). The first set of options lets you **View** the results in the Waveboard display. The lower set of options **Apply** the thresholds to the method(s) you select. Enable the Reject option and look at the accept/total field 196/260 to see how many epochs remain. When the desired epochs have been accepted, select Average (in the Epochs panel) to see the averaged epochs.



FSP

If the brain potential you are interested in has a particularly low signal-to-noise ratio (SNR), then you will need to collect a large number of sweeps. For example, extraction of the auditory brainstem response (ABR) usually requires thousands of sweeps. This situation presents two related problems: (1) the SNR can vary considerably between recording sessions, so that the same number of sweeps may yield averages of different quality; and (2) the SNR can vary considerably within a recording session so that a "bad" block of sweeps can potentially degrade the average which is building.

The first problem (between-session SNR variability) could be handled by collecting sweeps until a prespecified SNR in the average is achieved — if there were a way of estimating the SNR as the average is building. A statistical approach to solving this problem was detailed by Elberling and Don (1984) who proposed use of the Fsp ("single point F") statistic. Please refer to the above mentioned article for complete details. Briefly stated, the Fsp is essentially a ratio of two variances: the estimated variance of the signal between two time samples, divided by the estimated variance of the noise at a single point. If certain assumptions and approximations are made, the sampling distribution of the Fsp statistic can be computed. For each target SNR that one wishes to achieve in an average, there is a critical Fsp value such that one can state with confidence p that the actual SNR equals or exceeds the target value. This critical Fsp value can be used as a stopping criterion for averaging. All averages obtained in this way — though they be constructed from differing numbers of sweeps — will have about the same quality of SNR.

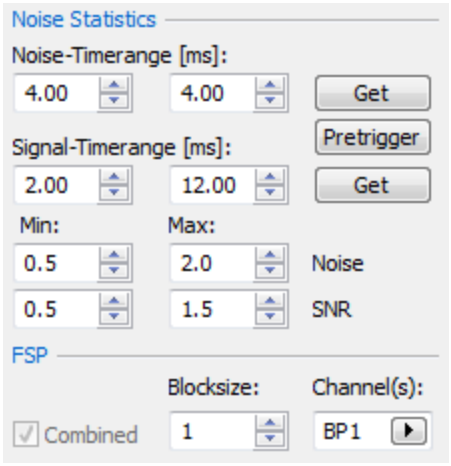
In CURRY, you do not necessarily need a single point for noise estimation. You can use either a single point, or an interval defined by the Timerange.

The Fsp statistic is computed for blocks of sweeps.

Perhaps of greater significance for offline analysis is a solution to the second problem of within-session variability of the background noise. If the total number of collected sweeps is divided into several blocks, a single point estimate of the background noise (i.e., variance about the mean) can be computed for each block. By "single point" it is meant that a fixed point in time for each sweep is chosen for this computation (or Timerange). There may be considerable variability in the background noise estimates for the different blocks of sweeps. Ordinary averaging would give each block an equal weight. Intuitively, however, one would prefer to assign a higher weight to blocks of sweeps with lower background noise. This intuition is fulfilled by a Bayesian weighting scheme: The total average is constructed by weighting each block average by its reciprocal single point variance, divided by the sum of all block reciprocal sp-variances (Elberling & Wahlgreen, 1985).

Thus, the Fsp average is a Bayesian weighted average with computation of the Fsp statistic for each block, and for each sensor.

The following fields are used.



FSP. The **FSP** option will become active after you Scan the events. If you change the parameters that will affect these values, you must rescan the file. (Deselect any channels you wish to exclude before you Scan for the SNRs or Noise estimates).

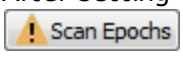
Noise-Timerange. These fields are used to select the single point, or interval for analysis.

Signal-Timerange. The Signal-Timerange is used to specify the range of the ABRs, such as **2-12**ms. It is important that this interval be at least 10 ms long in order to capture a complete cycle of the ABR components (which is typically about 100 Hz).

Combined. The **Combined** option averages the selected channels together. If deselected, you will see individual results for each channel.

Blocksize. The analyses are performed across blocks of data, typically with 100-200 sweeps for **Blocksize**.

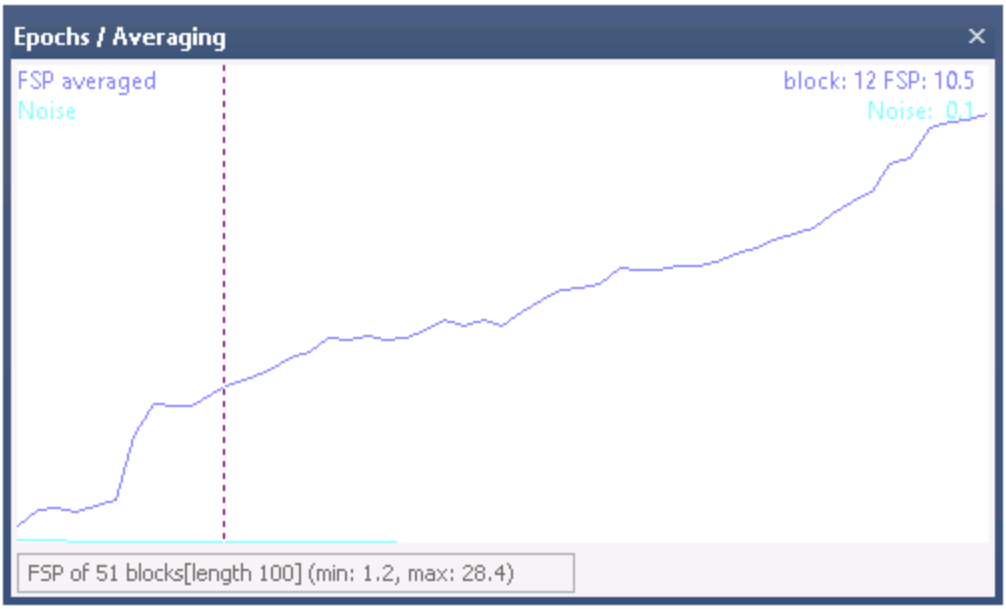
Channel(s). Select the Channel(s) that you wish to use (). Use *Ctrl+click* to select multiple channels, or drag a rectangle around a group of channels.

After setting the parameters it is necessary to scan through the data file. Click the 

button (this may take a while).

After the scan has completed, select the 

option for **View**. You should see the ascending F values and the descending Noise values (rescale to see the Noise function).

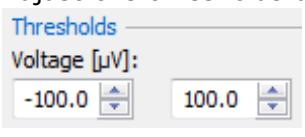


To see the ABRs, click the Average option in the Events / Epochs panel.

See the *Fsp Averaging* tutorial for an illustration of FSP averaging.

View

Off. Closes the Events / Epochs dialog.
Voltage. The Waveboard window displays the results of the Voltage Thresholds. Adjust the thresholds using the **Voltage** fields for Thresholds



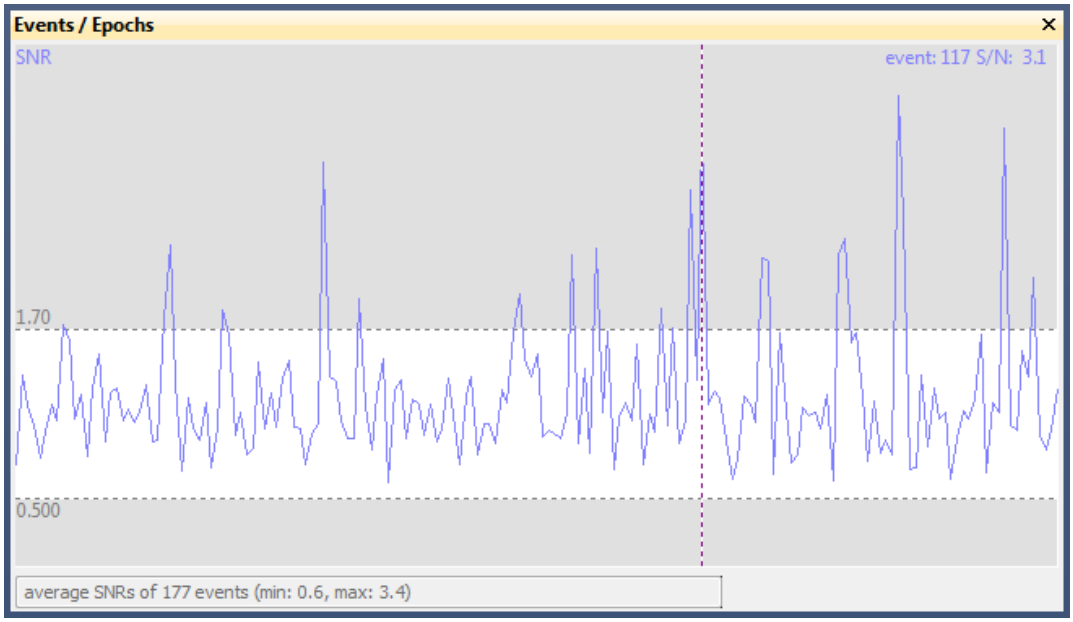
.

In all of these displays, the white area is the accept region within the thresholds; the gray regions are the reject regions outside of the thresholds. The epoch number and maximum/minimum voltages *for the cursor position* are shown in the

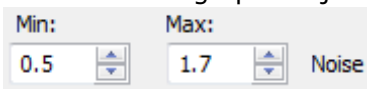
upper right. The maximum values (positive and negative) across sweeps are shown below the waveforms. *Double-click* at any point to view that particular epoch. Use the *mouse wheel* to rescale the display. Use *Shift+mouse wheel* to expand/constrict the display. Use *Shift+drag left mouse* to reposition the entire display within the window.

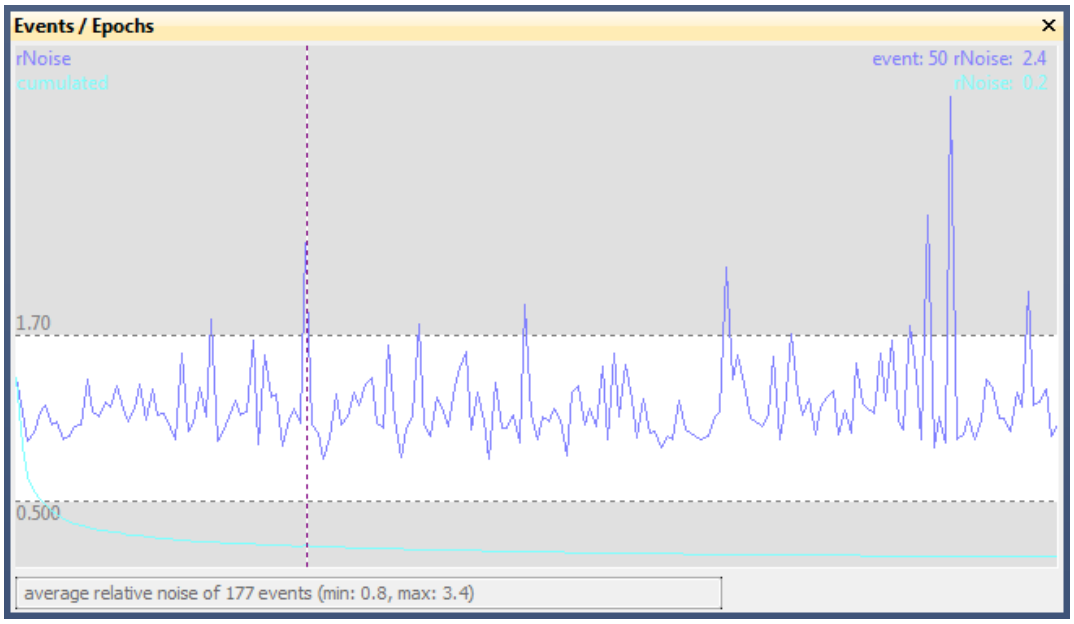
SNR. The SNR values across epochs are displayed. Adjust the thresholds using the **Min** and **Max** fields for **SNR** 

.

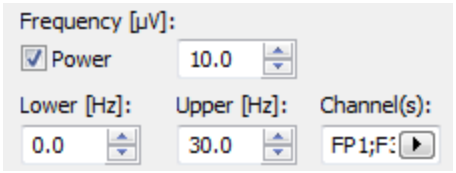


Noise. The Noise values across epochs are displayed. The accumulated noise values are shown in the lower graph. Adjust the thresholds using the **Min** and **Max** fields for **Noise**





Frequency. The Frequency option will reject epochs when the amplitude of the FFT exceeds the threshold you set, using the channels you select.

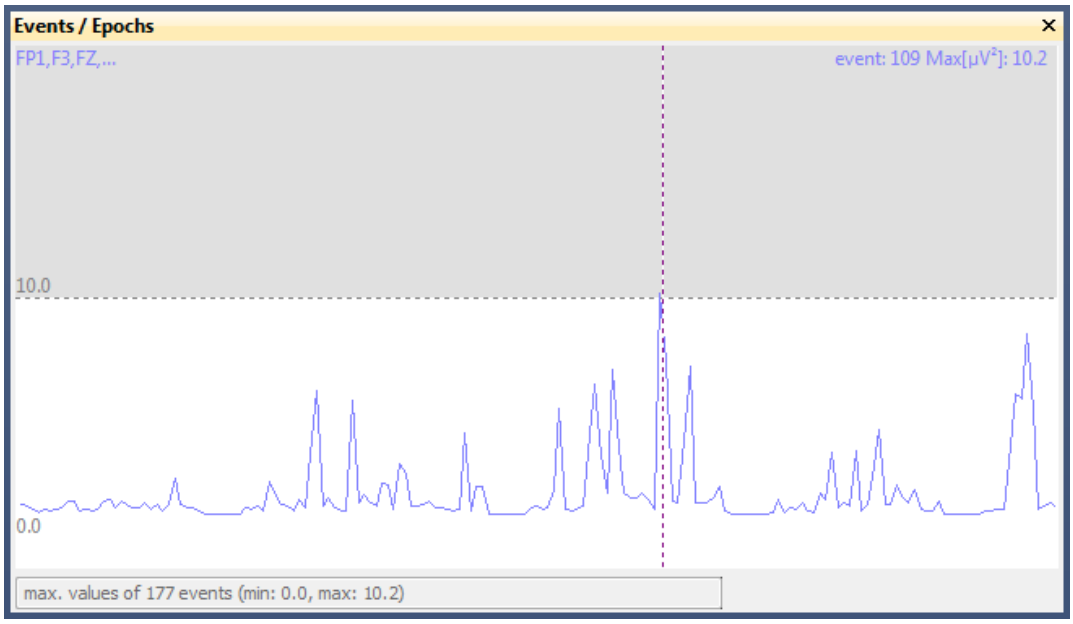


Power. You have the option of using Power (microvolts squared) or not. The field adjacent to the Power option is the threshold.

Lower [Hz] and Upper [Hz]. These fields define the frequency range that will be computed.

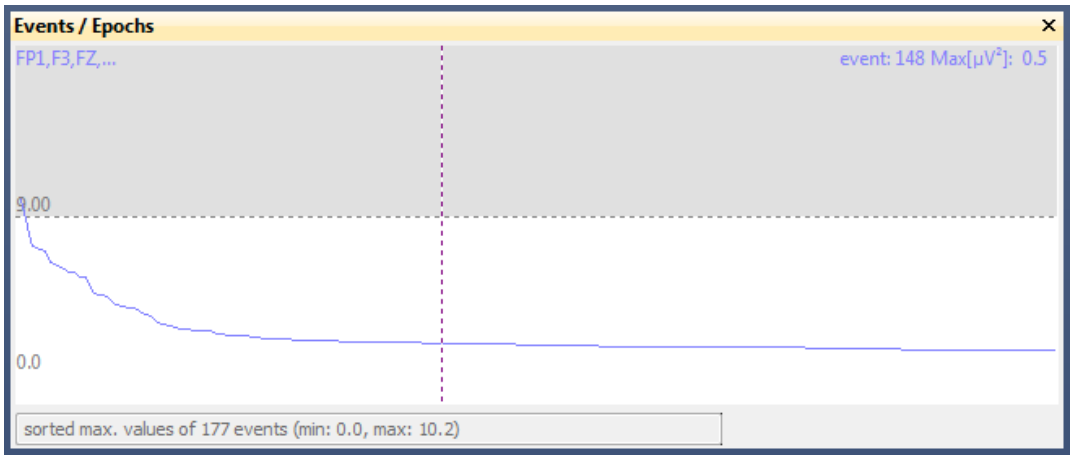
Channels. This is the same Channel Selection display that is used elsewhere.

After scanning the epochs and selecting the **View Frequency** option, you will see the results in the Waveboard display. Adjust the threshold using the field adjacent to **Power**.

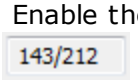


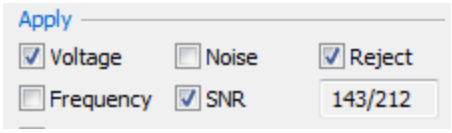
Fsp. See the Fsp section just above. You will see the ascending F values and the descending Noise values (rescale to see the Noise function) in the waveform display.

Sort. After selecting one of the results to View, click **Sort** to see those results in descending order.



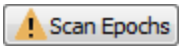
Apply

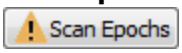
The **Apply** fields let you selectively apply the reduction results (**Voltage**, **Noise**, **Frequency** and/or **SNR**). Enable the Reject button to see how many epochs remain, as shown in the  field.

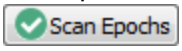


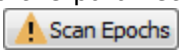
After Applying any of the criteria, you will see the rejected epochs as shaded regions in the epoched file, like the bad blocks in continuous data files.

Update Display. When enabled, you will see the waveforms in each epoch as the epochs are scanned. This gives you a quick review of the epochs, although it can be time consuming. If you are sure the epochs are good and you want the scan to go faster, disable Update Display.

Scan Epochs 

. Once you have the threshold criteria set, click 

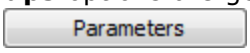
to scan the epoched file, applying the criteria. After scanning, the button will change to 

. letting you know the file has been scanned. If you make any changes to the parameters that could affect the data inn the epochs, the button will revert to 

, letting you know you should rescan the file.

17.3 Maps

As an alternative to SVD decomposition in earlier versions, CURRY offers PCA and ICA decomposition. The **Maps** options are generally associated with the 

display (clicking it opens the 

panel).

Principle Component Analysis (PCA) and Independent Component Analysis (ICA) are statistical techniques akin to factor analysis that are used to (1) to reduce the number of variables and (2) to detect structure in the relationships among variables.

PCA generates patterns and loadings that are orthogonal to each other. After the first factor is extracted (by fitting a regression line to a scatter plot), the second factor is extracted from the remaining variability, and so on until there is essentially no variance left. The resulting components are orthogonal to, or uncorrelated with each other (1st order decorrelation). It has been argued that PCA may not be the most appropriate method for use with physiological data.

ICA generates patterns and loadings using a stricter criteria for statistical independence (requires that all second order and higher correlations are zero). The generality of ICA lies in the simple principle that different physical processes tend to generate statistically independent signals. Given that scalp-recorded EEG is the summation of signals from multiple sources, ICA computes individual signals that are statistically independent, and which are therefore likely to have been generated by different physiological processes. ICA has been asserted by some to be the preferred method for use with physiological signals.

Principle of ICA

The ICA decomposes the data not into orthogonal components - as does the PCA - but into mutually independent components. (CURRY 8 uses a Fast ICA algorithm).

Mutual independence here is a statistical concept. Suppose the data of one component are known, this component is mutually independent of a second one, if no information about the second component can be derived from the first one and vice versa. In this context, orthogonality is already a kind of information.

Because such mutually independent components can only be identified if the data are covariance free, the first step of an ICA analysis is pre-whitening the data using a PCA. The PCA is also used to estimate the number of mutually independent components to be found in the following ICA iteration. Components with an SNR in excess of approximately 1.0 are appropriate for the ICA. This implies that the result of noise estimation affects the number of ICA components that are found.

Because a typical number of components above noise level are three to six, the ICA effectively decomposes a 3x3 to 6x6 matrix only. The number of components used is written in the Results section of the Output window. CURRY will not allow you to use more than 10 components (more than 10 can be displayed).

In order to have a good statistical measure for the independency, there should be at least three times as many samples as channels.

Results of ICA

The results of the ICA analysis are presented in a way that is very similar to the results of the PCA: There are a number of measured data patterns, each associated with a time course (“loading”) and a weight. The weights are provided in SNR units. The original data can be represented as the superposition of all patterns, weights, and loadings. The ICA components are not mutually orthogonal; the PCA components are - also with respect to the ICA components. This type of presentation of ICA results makes it possible to assess each component with its relative significance.

ICA-based Filtering

The ICA can be used for filtering in a similar way as the PCA: a number of components can be selected, and the data that enter source reconstruction are assembled from these components only. Because a major application of the ICA is artifact detection (e.g., eye-blink detection), ICA filtering provides the opportunity to exclude an arbitrary artifact component from the data.

In General Use

As you use PCA and ICA, you will notice several differences between their operations. When you select PCA and set a Timerange in the data waveforms, all loadings are computed (there cannot be more loadings than there are sensors or data samples). Rarely do more than about 3-6 loadings, at most, represent anything other than noise, and these later ones can be disregarded.

When you select ICA, the program attempts to determine a transformation for the subspace of the PCA results (in a mathematical sense, or, in other words, the number of components you select), such that the components are as independent from each other as possible. If you could select only one ICA component, there is nothing for ICA to do, so the result is the same as the first PCA loading. Therefore, you do not have the option to select only one ICA component - there will always be at least two.

With ICA, you can independently select components to be filtered (such as, retain components 1 and 3 while filtering out component 2). With PCA, since the extracted

field patterns are orthogonal to each other, it is generally not appropriate to remove the leading or distinct non-noise components because this will have no effect on the trailing components. It is appropriate, however, to remove the trailing noise components. In fact, you will find that CURRY does not let you selectively filter leading PCA components. Whenever you deselect a PCA component, all trailing components are also deselected.

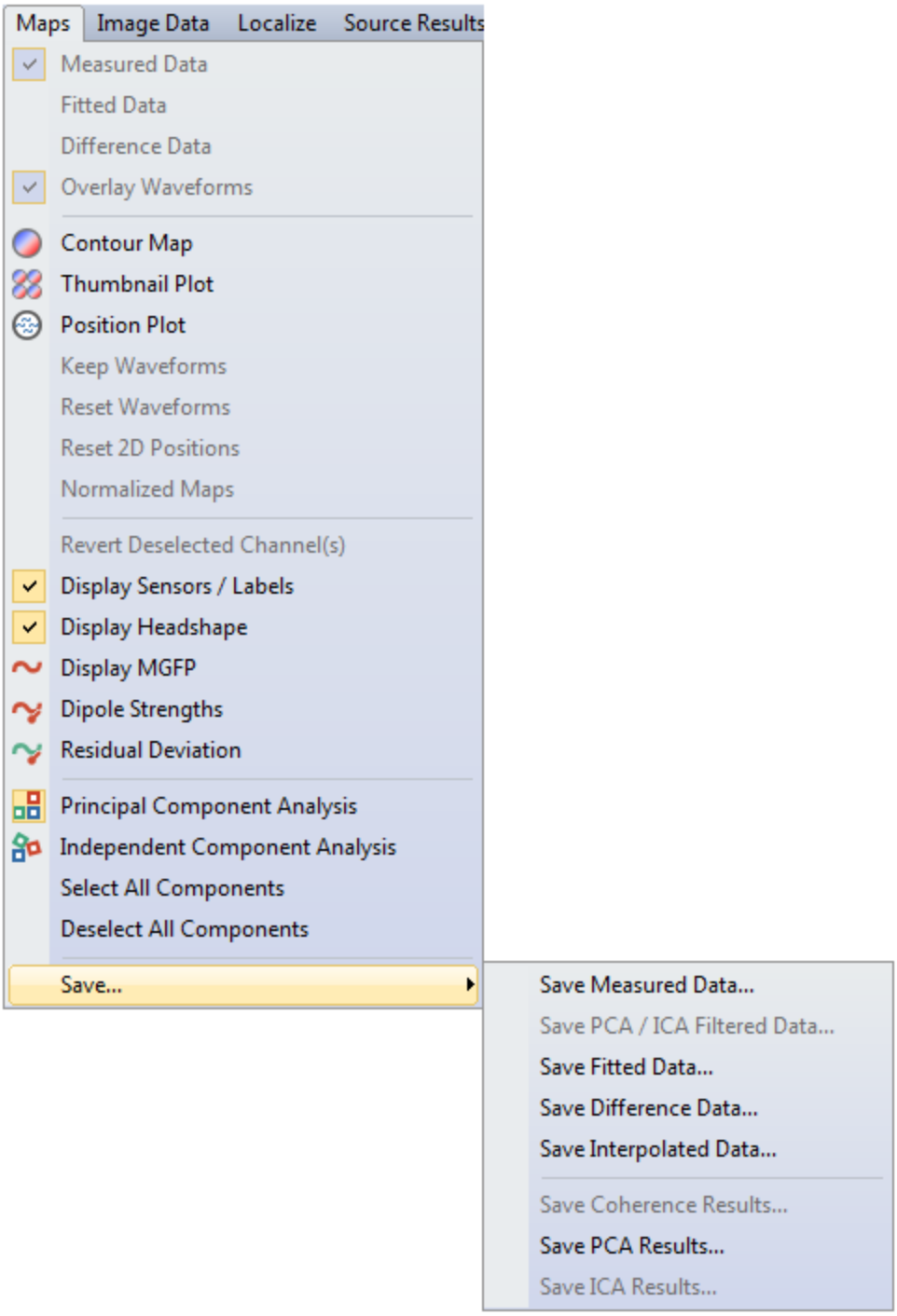
Note
CURRY 8 always uses an internal CAR (Common Average Reference) data when computing PCA and ICA in Maps, even if you have turned off the CAR option in Functional Data. If you are using the PCA results from Maps to project artifact from your data in the **PCA Projection** option under **Artifact Reduction**, you should enable CAR to see the expected effect.

Operation

The **Maps**, **Parameters** panel is used to modify the Sphere/Projection Center coordinates and radius; display and modify the contour maps; and to perform PCA and ICA decomposition. It is generally used in conjunction with the Maps display tab (clicking it displays the expanded **Parameters** panel).

Some of the options pertaining to Maps and PCA/ICA are found on the Main Menu Bar.

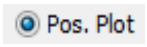
These options are used to select different displays in the Maps display, select PCA or ICA analyses, or export Measured, Fitted, Difference data or PCA/ICA results. Position Plot, PCA, ICA, MGFP, Dipole Strengths, and Residual Deviation are only possible if a Timerange is selected (not possible for a single timepoint). These are discussed in more detail in later sections.



Many of these options can be accessed from the Toolbar icons  that are above the **Maps** parameter panels, and also seen when you position the mouse in the upper left area of the  display.

Measured Data. This is the actual data in its original form.

Fitted Data. Fitted Data are those that are generated by the best fit dipole reconstruction.

Difference Data. Difference Data are the differences between the Measured and Fitted data. These can be viewed either as 2D contour maps or as waveforms using the 

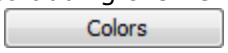
option.

Overlay Waveforms. This option allows you to overlay Measured, Fitted, and Difference waveforms.

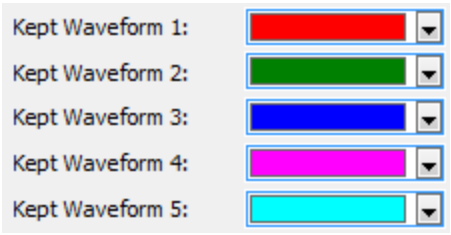
Contour Map  . Displays a single contour map corresponding to the position of the middle cursor in the Functional Data display (or *Alt+C*).

Thumbnail Plot  . Displays the maps in a series of Thumbnails (the number of thumbnails is set in the **Parameters** panel under **Maps**; or *Alt+T*).

Position Plot  . Select this option to display the data on a 2D head shape (or use *Alt+P*).

Keep Waveforms. Select this option to "keep" the current waveforms seen in the Position Plot view. Make a change, such as, apply a filter or move to a different epoch, and the new display will be superimposed on the kept one. This allows you to compare the effects of an operation you have applied. It is also used to compare multiple average files or epochs (up to 5). For overlaying multiple displays, click **Keep Waveforms** each time prior to adding the new display. The colors are assigned automatically, as seen in the 

panel for **Maps**. The most recent waveform - not yet "kept" - will always be the color you have selected for the EEG (or MEG) waveforms.



Reset Waveforms. Removes "kept" waveforms.

Reset 2D Positions. If you have changed any of the sensors in the Position Plot (repositioned or resized), clicking this option will restore the original positions and sizes.

Normalized Maps. This option is used in conjunction with the **Average Time Interval** option, found under **Options**, under **Functional Data**. If you select a Timerange and click the **Save** button, the **Normalize Maps** option will become active. If you click it and move to another Timerange, the 2D Maps will show the difference with respect to the "saved" maps.

Revert Deselected Channel(s). If you click on a channel(s) from the Maps display to deselect it, the channel(s) will disappear (and be removed from the maps computations). Clicking this option will restore the deselected channel(s). The last deselected channel will be restored if they were deselected individually. If you deselected channels by dragging a rectangle around them, all of those will be restored. If you want to have all channels selected, use **Select All Channels** in the Functional Data context menu (or *Ctrl-S*).

Display Sensors / Labels. Toggles the sensor or sensor labels on and off.

Display Headshape. Toggles the display of the background headshape on and off.

Display MGFP  . Display the Mean Global Field Power (*Alt+G*).

Dipole Strengths  . Display the dipole strengths (*Alt+D*).

Residual Deviation  . Displays the residual deviations (*Alt+R*).

Principle Component Analysis  . Select PCA (or *Ctrl+A*).

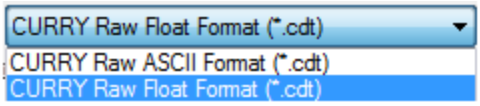
Independent Component Analysis  . Select ICA (or *Ctrl+I*).

Select All Components. All components will be selected.

Deselect All Components. All components will be deselected.

Save...

Save Measured, **PCA / ICA Filtered Data**, **Fitted**, or **Difference Data**. These options may be used to export the measured, PCA/ICA filtered, fit or difference data to a float-format or ASCII-format .dat file (Export Fit and Export Difference are active after a source reconstruction has been performed). Parameters and sensor locations are written to the accompanying .dpa file.



Save Interpolated Data. If you have data files that have, for example, different numbers of channels, yet you wish to combine them into a grand average, you can use the sensor positions from one file to interpolate and extrapolate the channels in the first file to match those in the second file (with more channels). Obviously, this is a fairly drastic thing to do, since you are changing data on existing channels and creating new channels that did not exist. This option should only be used with care. The required steps are explained in the following sub-section **Interpolated and Extrapolated Channels**.

Save Coherence Results. The Coherence results, including sensor positions, are saved to an ASCII file (.coh extension). These .coh files are not interchangeable with the .coh coherence files created in Scan's EDIT program.

```
# frequency domain
# sensors frequencies
   28    11
# 8.972 - 10.254 Hz
# sensor positions[mm] [x y z]
   29.00  -106.50    32.90
   -0.00    55.00   141.30
  -29.00  -107.50    32.80
   -0.00    94.50    70.40
   51.00   -81.50    86.10
   77.00   -44.30    69.30
  -53.00   -82.30    84.00
  -77.00   -44.20    68.30
   71.00    17.60   116.70

   85.00    -6.50    38.50
  -84.00    -8.50    38.30
   74.00    51.60    49.30
  -73.00    50.60    49.20
   -1.00   -23.30   156.40
   -0.00   -92.60   112.00
# coherence matrix
1.000 0.250 0.967 0.704 0.920 0.871 0.904 0.870 0.665 0.016 0.6
0.250 1.000 0.268 0.120 0.144 0.283 0.198 0.260 0.197 0.196 0.0
0.967 0.268 1.000 0.726 0.879 0.798 0.939 0.918 0.629 0.020 0.7
0.704 0.120 0.726 1.000 0.828 0.583 0.858 0.711 0.614 0.133 0.8
0.920 0.144 0.879 0.828 1.000 0.877 0.914 0.772 0.754 0.033 0.6
0.871 0.283 0.798 0.583 0.877 1.000 0.766 0.682 0.793 0.026 0.4
0.904 0.198 0.939 0.858 0.914 0.766 1.000 0.921 0.666 0.045 0.8
0.870 0.260 0.918 0.711 0.772 0.682 0.921 1.000 0.524 0.053 0.8
0.665 0.197 0.629 0.614 0.754 0.793 0.666 0.524 1.000 0.084 0.4
0.016 0.196 0.020 0.133 0.033 0.026 0.045 0.053 0.084 1.000 0.2
```

Save PCA Results. Select this option to export the PCA results to a text file (.pca extension). The file contains the number of sensors, number of data sample points in the Timerange, the number of patterns, their weights, and the normalized results (shown in part below). The PCA ASCII file can be read by **Functional Data** → **Artifacts and Baseline** → **PCA Projection** for artifact suppression.

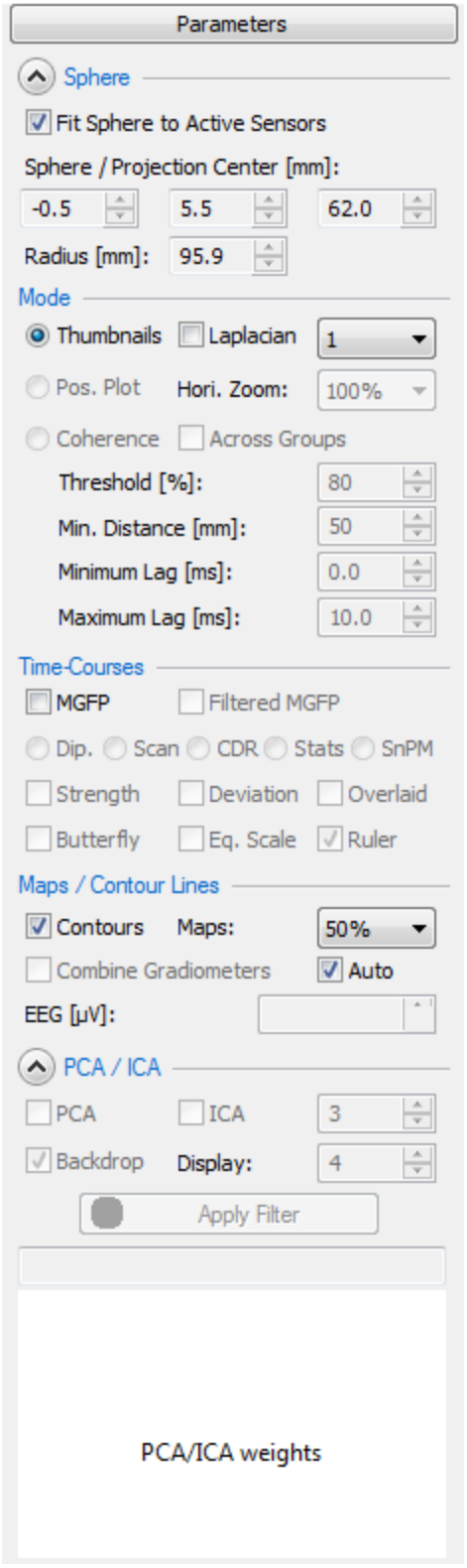
```
# sensors samples
   28    15
# selected patterns
  1   2   3
 PCA PCA PCA
# weights
   148.851    58.6908    30.2899
# normalized patterns [SNR]
 -0.008332  -0.065820  -0.048511   0.126843   0.410721   0.053407   0.276939   0.047862   0.080806
-0.140650  -0.130257  -0.135422  -0.182963  -0.216449  -0.170724  -0.211995  -0.140648  -0.152823
-0.186454  -0.063362  -0.110865  -0.105570   0.132416  -0.061023   0.357499  -0.057831   0.404430
0.298778
```

Save ICA Results. Select this option to export the ICA results to a text file (.ica extension). The file contains the number of sensors, number of data sample points in the Timerange, the number of patterns, their weights, and the normalized results (shown in part below).

```
# sensors samples
   28    15
# selected patterns
  1   2   3
 ICA ICA ICA
# weights
   135.155    73.2262    58.6704
# normalized patterns [SNR]
  0.008562  -0.055202  -0.018730   0.159422   0.421678   0.053415   0.245966   0.026375   0.043786
-0.161477  -0.133521  -0.126659  -0.195367  -0.230175  -0.171509  -0.216405  -0.134325  -0.142888
-0.181933  -0.099141  -0.102812  -0.093167   0.152253  -0.049550   0.330275  -0.044492   0.415267
0.300355
```

17.3.1 Parameters

The Parameters let you select your own parameters for fitting the sphere to the sensors. You can switch between **Position Plots**, contour maps of single latencies or latency ranges (seen as **Thumbnails**), **Principal (PCA)** or **Independent (ICA) Component Analyses** of the selected Timerange, and source results (**Strength** and **Residual Deviation**). **PCA** or **ICA** patterns can be switched on and off for spatio-temporal filtering purposes. **Coherence** can be computed.



Sphere

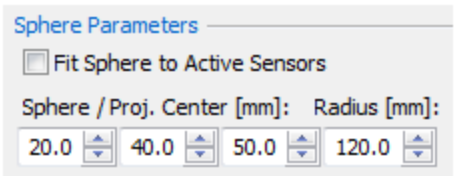
Fit Sphere to Active Sensors. If this option is activated, a sphere is fitted to all selected channels of the selected device. Selecting or deselecting channels will

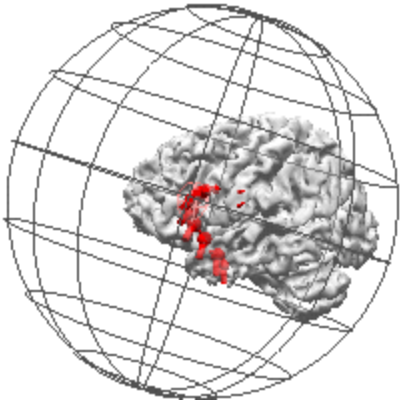
modify the projection center of the contour lines and the sphere center of the head model, and thus lead to an automatic update of all results. If this option is deactivated, the sphere parameters are kept fixed and/or can be adjusted manually.

Sphere / Projection Center [mm]. These fields display the fitted sphere center in the selected coordinate system, if **Fit Sphere to Used Sensors** is activated. If **Fit Sphere to Used Sensors** is deactivated, the sphere center can be manually adjusted (e.g., if the sphere fit fails in the case of planar MEG-systems).

Radius [mm]. If **Fit Sphere to Used Sensors** is activated, this field displays the fitted sphere radius. If **Fit Sphere to Used Sensors** is deactivated, the sphere radius can be manually adjusted (e.g., if the sphere fit fails in the case of planar MEG-systems).

You can see the effects by displaying, for example, the segmented cortex within the out sphere of a three shell head model. Disable **Fit Sphere to Used Sensors** and change the Center coordinates and Radius to see the changes.



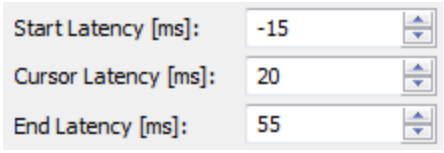


Note
The sphere / projection center is used as the head model center and as the projection center for contour maps. It is *not* used for the projection of sensors onto surfaces, e.g., during BEM setup (where the closest location in the closest triangle is used).

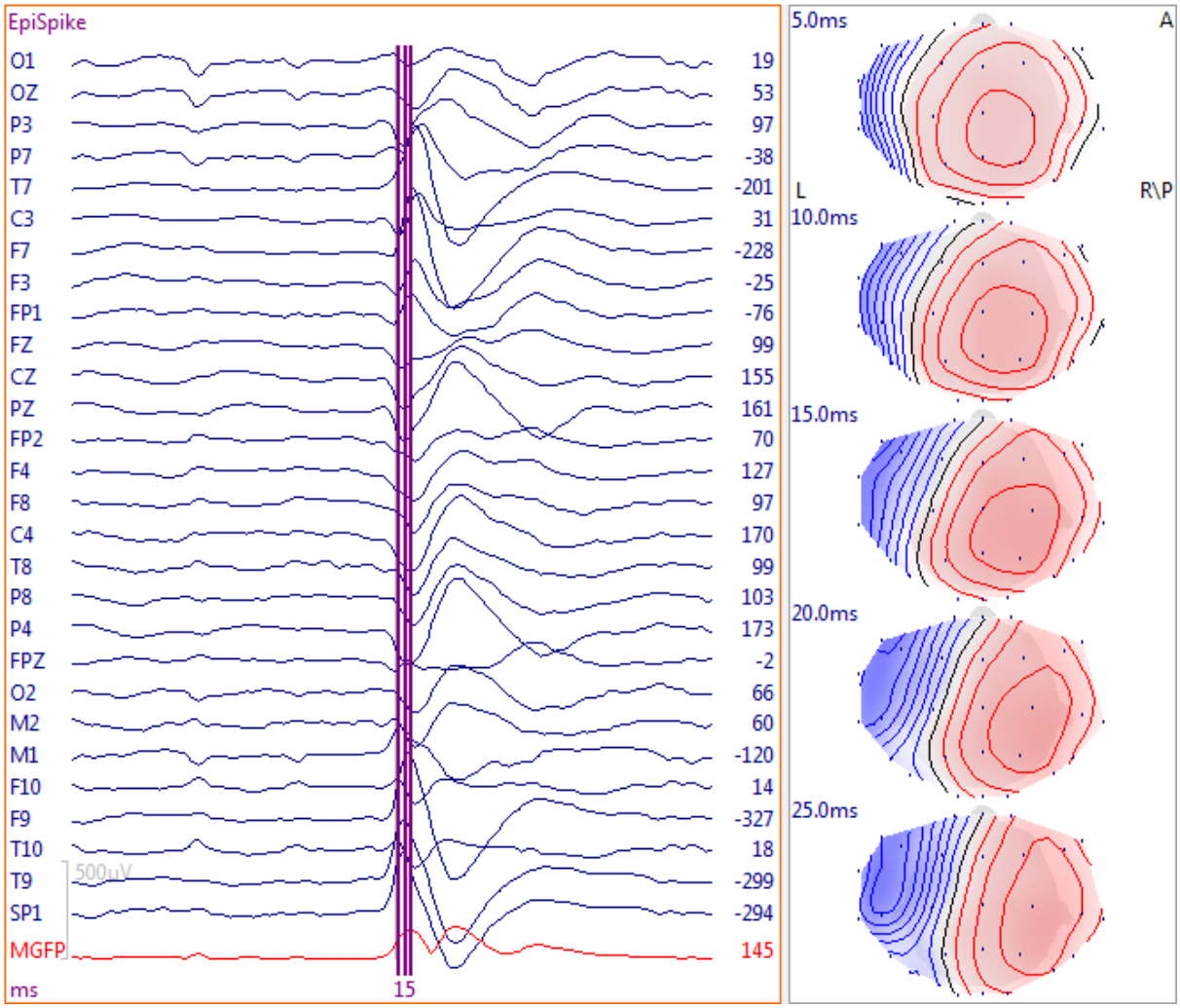
Mode

Thumbnails. If you enable Thumbnails, or click the tab on the **Maps** Toolbar (or *Alt+T*), you will see 2D maps for time points in the Timerange.

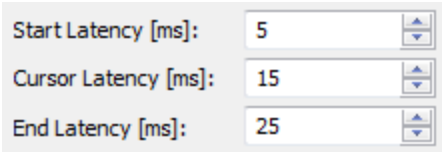
There is a relationship among the three vertical cursors in the Functional Data display, the **Start**, **Cursor**, and **End Latencies** (in the **Options** panel under **Functional Data**), and the number of Thumbnails you select for display.

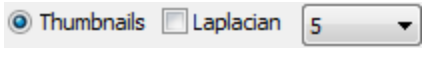


When you first load a Study and the functional data are displayed, you may see three vertical cursors superimposed on each other, or you may see three separate cursors. The relationship between the cursors and the 2D maps is most easily understood if you select the FD, Maps display.



Initially, in this example, the **Start Latency** is **5.0**ms, the **Cursor Latency** is **15.0**ms, and the **End Latency** is **25.0**ms. The corresponding positions are seen in the Functional Data display.



Thumbnails was set to **5** 

, and five 2D maps are displayed in the range from 5 to 25ms, including 0 ms (the AD rate was 200 ms, yielding data samples every 5ms; the outer cursors will be ±2 data samples from 0.0 ms). If you leave Thumbnails set to 5, and increase

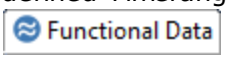
the interval to -5ms to 35ms (by moving the cursors using the Start and End Latency fields), there are still five 2D Maps displayed. If you move the Cursor Latency, the five maps will bracket the middle cursor (until it approaches an outer cursor). If you select **All** for **Thumbnails**, there will be a 2D map for each timepoint in the Timerange.

Initially, 

is invoked. *Right click* in the Functional Data display and deselect Tracking Mode (or use *Shift+left* mouse). You can then position the outer cursors independently by dragging them with the mouse, using the keyboard, or the Start and End Latency fields. If you return to Tracking Mode, there will be the three cursors.

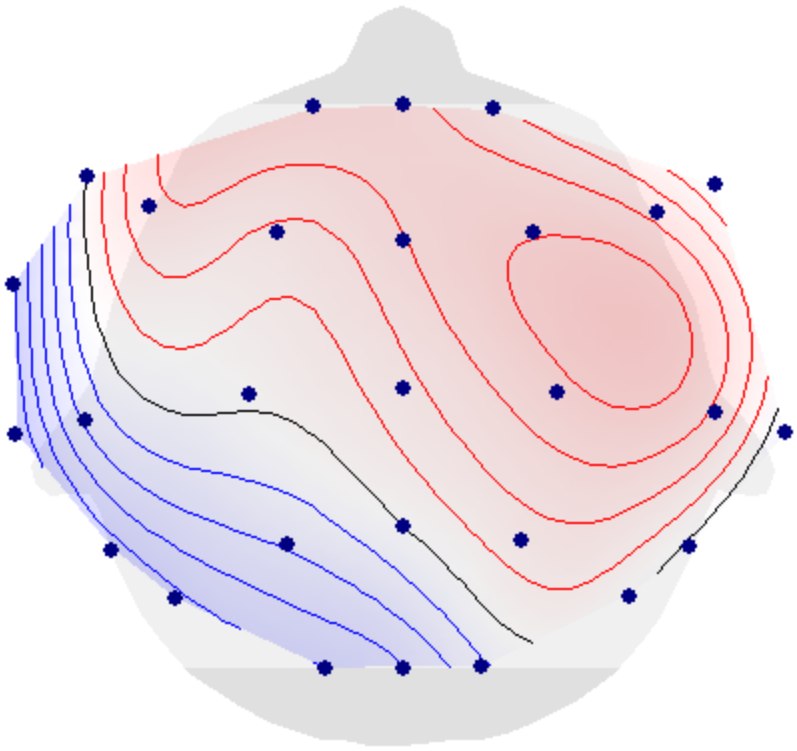
You can select All maps, or a selected number of them using the 

field. Use the **Interleave (samples)** option in the **Options** panel to map every *n*th data point, where *n* is the Interleave value.

You may display contour maps for the Measured, Fitted, or Difference data (dipoles must be computed first, then *right click* in the display and select which set(s) you wish to display). Contour maps are created for each point within the defined Timerange (defined by the positions of the vertical cursors in the 

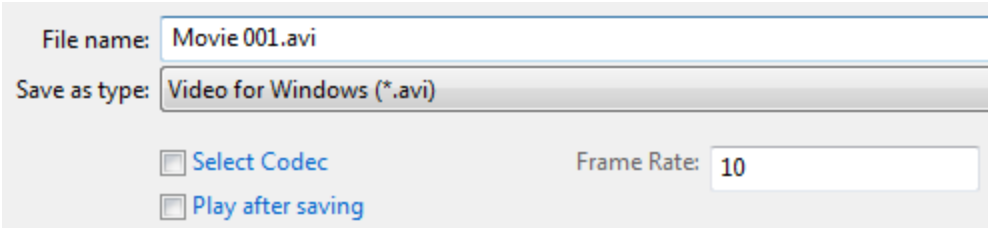
display). If you select fewer maps than there are samples in the Timerange, the maps that are displayed are those that bracket the middle vertical cursor.

Red contour lines display positive voltages; blue contour lines display negative voltages. The black line is the line of zero voltage (the color scheme can be changed under **Colors**).

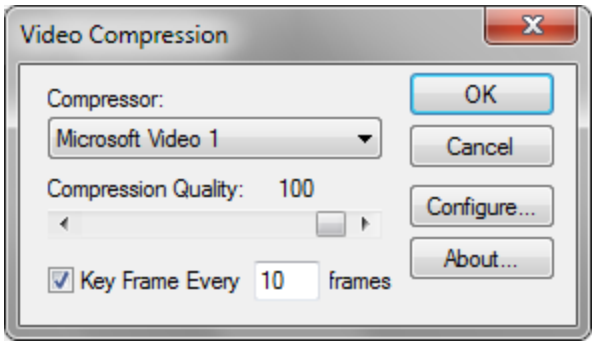


To play a movie of the maps, click the Contour Maps icon on the **Maps** Toolbar, and click the Show Movie icon on the **Standard** Toolbar. Save the movie as an .avi file by *right clicking* and selecting **Save Movie As**.

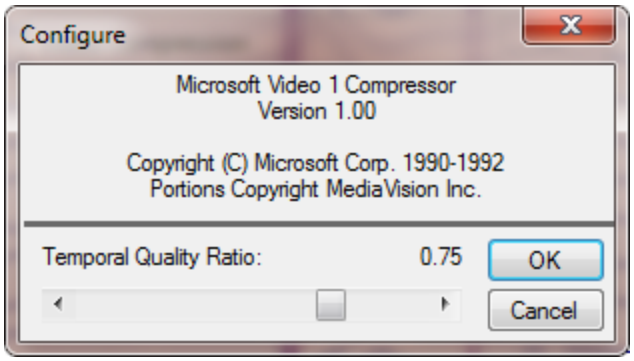
When you save the .avi file, you will see options at the bottom of the Save As window allowing you to set the Frame Rate, select video compression, or to play the video after saving the file.



If you select video compression, you will see more options. These will vary depending upon what is installed on your computer. Compression is recommended for space reasons; the Full Frames (Uncompressed) option can result in very large .avi files, depending on the number of frames. With some of the options, you can select the **Compression Quality** using the sliding bar.



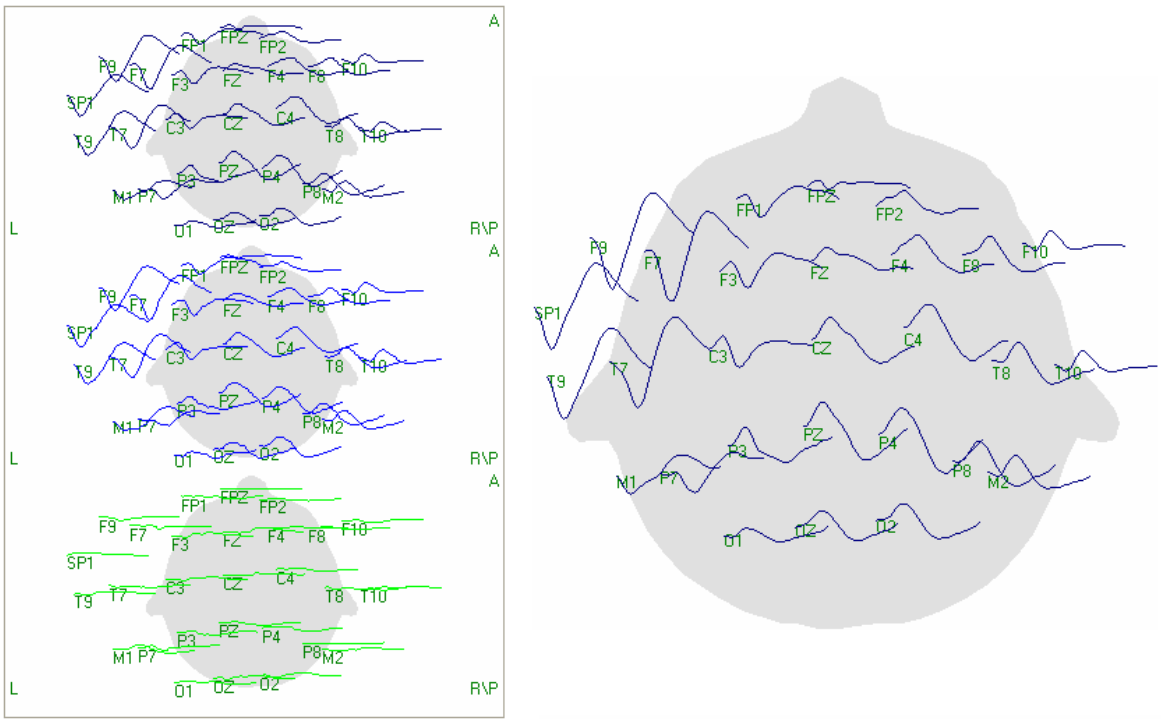
The Configure... button will become active with some of the codecs. The configuration screen(s) varies depending on the codec selected.



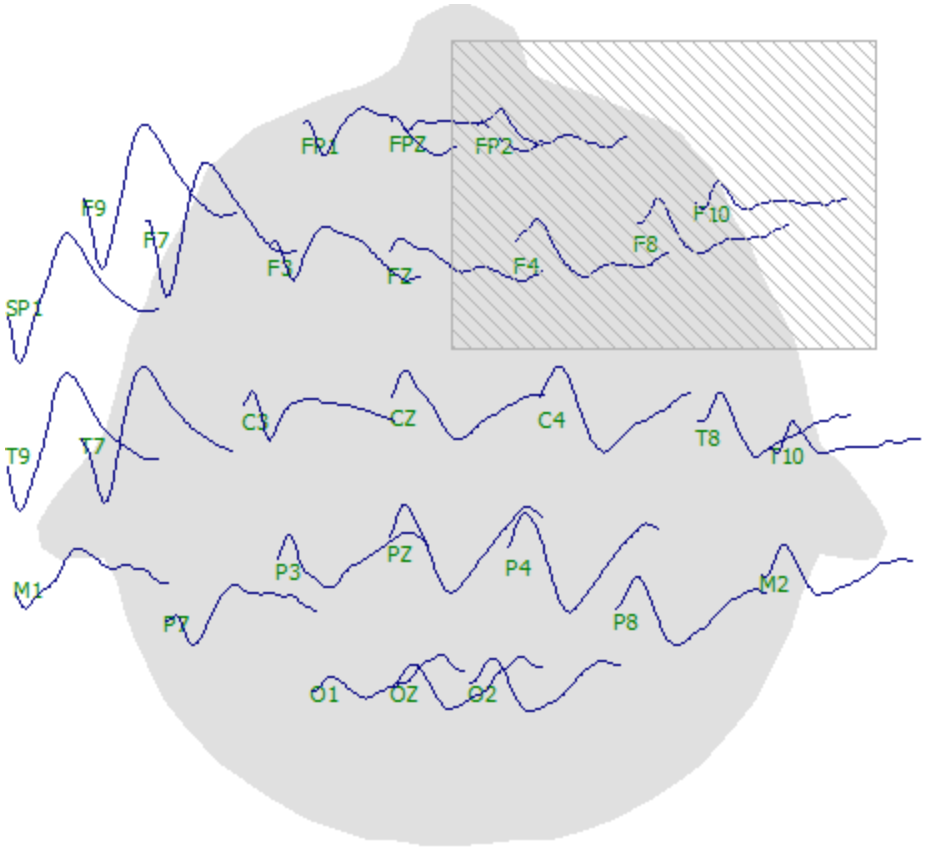
Laplacian. A Laplacian transform provides an alternative to source reconstruction (same as current source density). Potentials are computed everywhere, with an analytic solution based on the second derivation, and not just the weighting of the neighboring sensors. This is a very resource demanding operation - you may see some performance loss when used online.

Perrin, Pernier, Bertrand, Echallier, Current Source Density (CSD) transformation based on spherical spline / surface Laplacian. Electroenceph Clin Neurophysiol 1989, 72, 184-187; Corrigenda, Electroenceph Clin Neurophysiol 1990, 76, 565. See also appendix of Kayser J, Tenke CE, Clin Neurophysiol 2006, 117, 348-368.

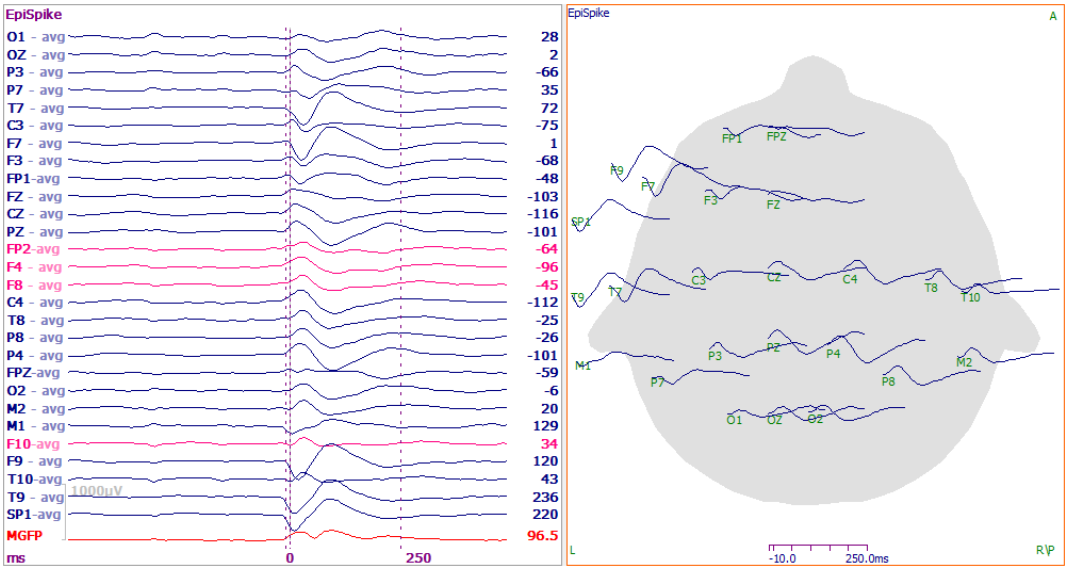
Position Plot. Enable this option, or click the button on the **Maps** Toolbar (*Alt+P*), to display the Measured, Fitted, and/or Difference data in spherical projection positions (Fitted and Difference Fields become active after performing a source reconstruction). Only the selected Timerange is displayed.



You may **Deselect** groups of sensors from the **Position Plot** display. Drag a rectangle around the sensors to be deselected.



They will disappear and the deselected channels will be seen in pink in the **Functional Data**. *Right click* in the **Functional Data** and click **Select All Channels** (*Ctrl*+*S*) to reselect them.



Horizontal Zoom. Select a different value to compress and expand the waveforms in the Position display.

Coherence. EEG Coherence is selected with this option. Coherence is computed with continuous, epoched, and averaged data, throughout the Timerange you select (outer two cursors). Since Coherence is performed on time domain data (raw waveforms), a complex demodulation is computed, and the results you see in the **Maps** display are based on all possible frequencies.

CURRY uses its own implementation where the coherence of the selected timerange is computed (maximum shift is +/-50% of the selected timerange). FFTs of the zero-padded waveforms are computed, their correlations are determined and finally the (signed) lags of the maximum overlaps are searched.

If you want it to be constrained to a certain frequency range you have to filter the data accordingly before the computations. The results are the lags (time-shifts) of maximum overlap between the waveforms. Clipping of the results is done by the user interface settings; however, the saved coherences are not clipped. The results are always in the time-domain (only the internal computations are done in the frequency domain).

The coherences Cxy are computed from the cross-spectral densities Gxy and auto-spectral densities Gxx and Gyy of the channels x and y:

$$Cxy = (Gxy * Gxy) / (Gxx * Gyy)$$

The channels signals are zero-padded, FFT-transformed, correlations are computed, back-transformed, normalized, and searched for the lags of the maximum overlap (see above). The direction comes from the sign of the lag

with the maximum overlap.

The coherences are computed for all lags before the maxima are determined, but only the maxima are displayed.

Across Groups. If you have MEG and EEG data, or two EEG groups, you may compute Coherence Across Groups. The links will be displayed in the **3D View**. Control the groups that you wish to include by enabling the desired fields in the **Channel Groups / Rereferencing** panel (under **Functional Data**).

Threshold [%]. Coherence values greater than or equal to the Threshold percentage (coh x 100) are displayed. Adjust the threshold using the up and down arrows, by entering a desired value, or using the *mouse wheel*. If the focus is in the Maps display, you can also use the mouse wheel to change the Threshold values. Changes to the Threshold are seen in the 3D View also.

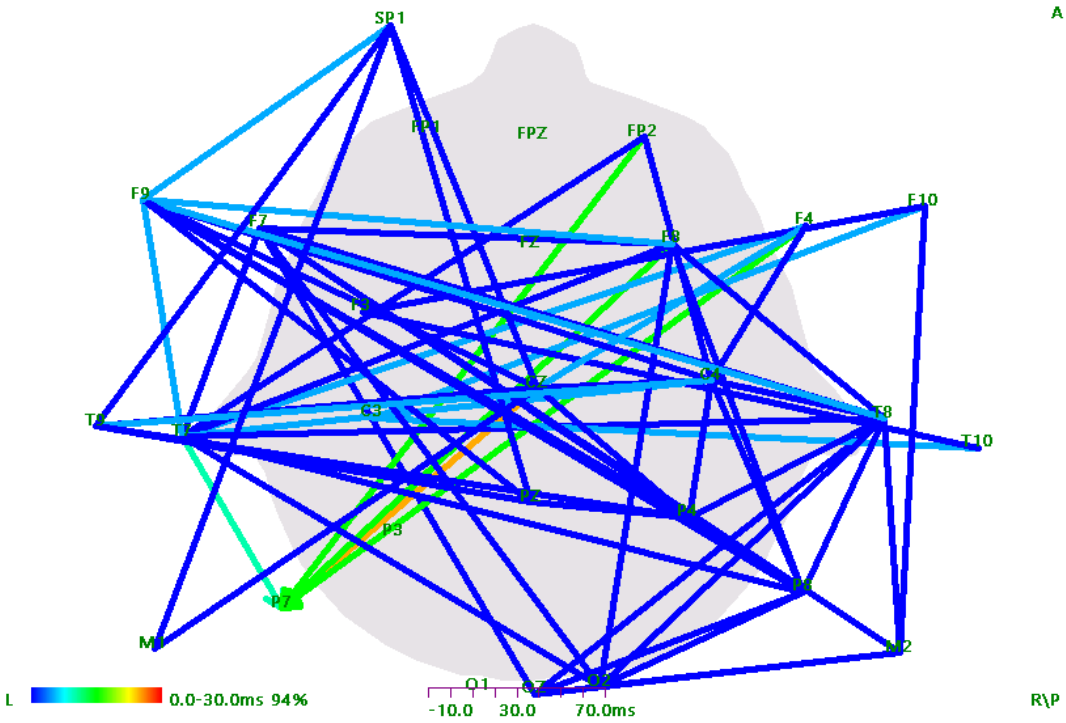
Min. Distance [mm]. Select the minimum distance between sensors. Generally, the closer the sensors are together, the higher the coherence between them, due at least in part to volume conduction. By setting a larger distance between sensor sites, these artificially large coherence links are not displayed.

Minimum Lag [ms]. Phase relationships are displayed in terms of the "lag" between the waveforms at two sites. If you select **0**, all links will be displayed, regardless if any phase shift. If you select **1**, then links where the lag is within 1 sampling point will be displayed, and so on. The values that are available will be determined by the AD Rate. If you have an AD Rate of 500 Hz, the steps will be in 2ms increments.

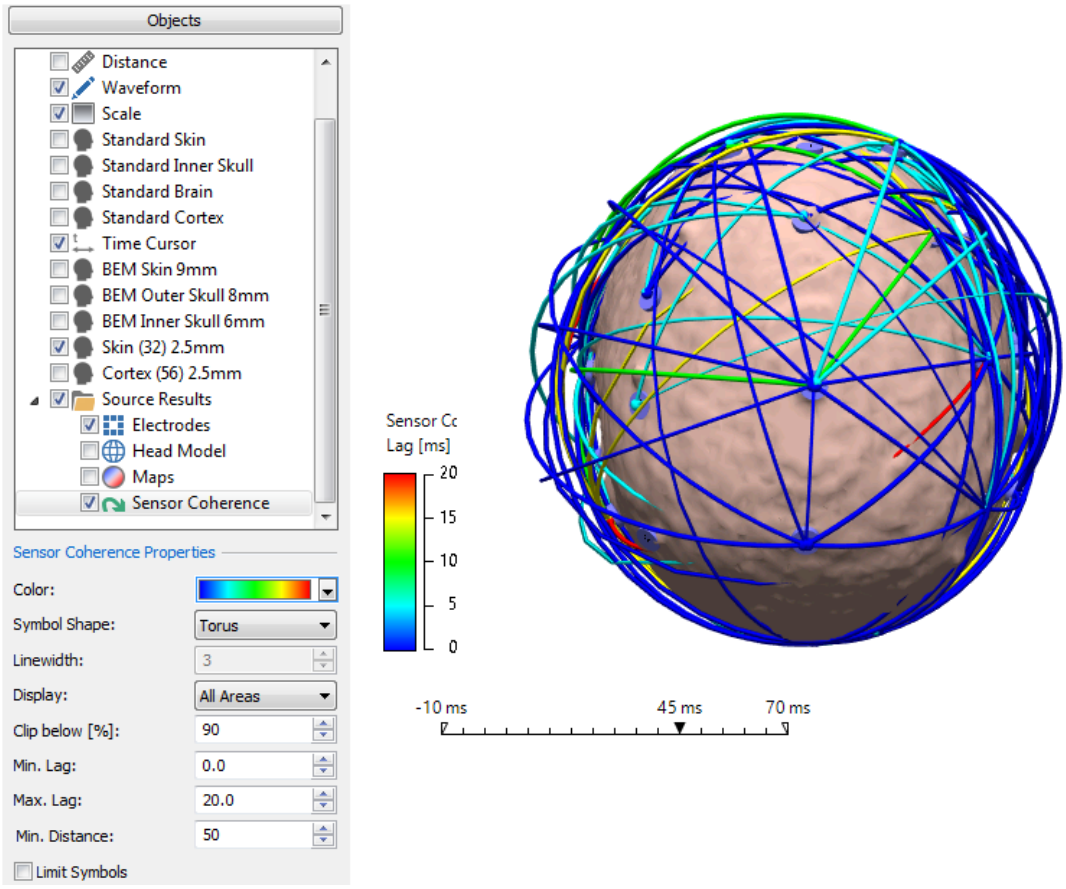
Maximum Lag [ms]. Maximum lag, along with Minimum Lag, lets you define a range of lag values. If you define a range of, for example, 5-10 ms, then the links will be seen if the signals are in phase, within 5-10 ms.

Changing any of these values will have the same effects in the **3D View** display (and the values in the Sensor Coherence Properties will change accordingly).

Note that an arrow will appear at one end of the link between sites (unless the Minimum Lag and the Maximum Lag are set to 0, or if the Minimum Lag is 0 and the Maximum Lag is the next point). This indicates the direction of the phase relationship. The origin of the arrow indicates the leading sensor.

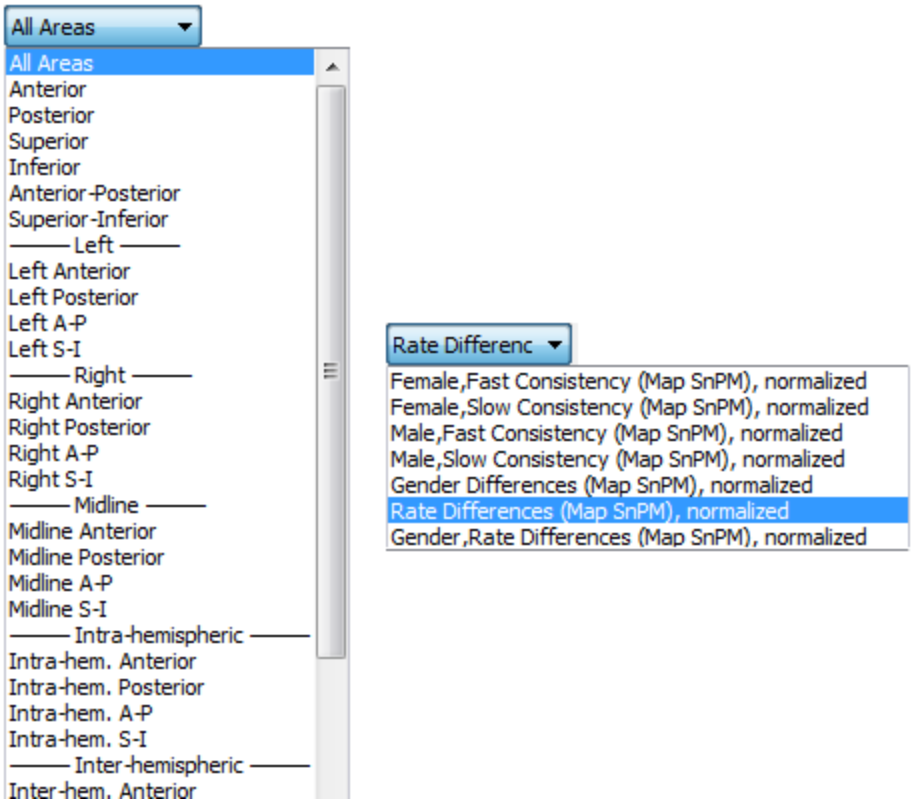


The Coherence results can also be viewed in the 3D View display. **Clip Below**, **Min. Lag**, **Max. Lag**, and **Min. Distance** affect the **3D View** display only.



In the **Sensor Coherence Properties**, there are options for under **Display as** for plain curved lines (**Line**), shaded 3D lines (**Torus**), and straight lines (**Pointer**).

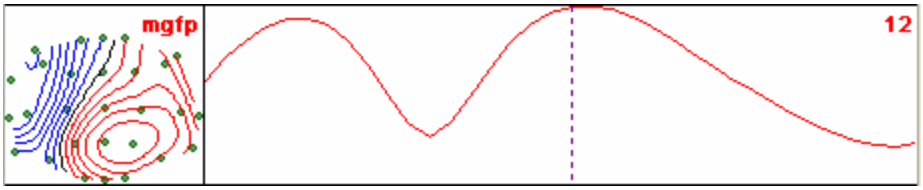
In the **Display** option, you may choose to display only certain coherence links by anatomical areas. You can constrain the regions by using only the **Segmentation Result**, or by using **Stop Markers**, **Pass Markers**, or both **Stop-Pass Markers**.



Coherence results may be saved from **Maps** → **Save** → **Save Coherence Results**, or from the Workflow list Save Coherence Results .

Time Courses

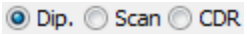
MGFP. Enabling this option MGFP, or clicking the button on the **Maps** Toolbar (*Alt+G*), will display the MGFP (mean global field power) beneath the ICA/PCA components. MGFP is a commonly used measure to obtain a quick overview of the measured EEG time courses, since it collapses the information of all sensors into a single channel.



As the name suggests, the MGFP is an average of the (common average re-referenced) data. The MGFP is an averaged measure for the signal strength (and thus the Signal to Noise Ratio, or SNR). One can easily distinguish latency ranges with meaningful signal from noise or background activity periods. Estimating the SNR from the MGFP together with the Deviations percentage can tell you if the chosen source model is at least able to explain the signal part of your data.
The MGFP is computed as follows. Let Si be the measured data (i = 1...n {n sensors}, for a given timepoint). The common average C is: C = 1 / n * Sum

(Si), the re-referenced measured data Ri = Si - C. MGFP = Sqrt [1 / n * Sum (Ri * Ri)].

Filtered MGFP. Enabling this option will show the global effects of filtering on the MGFP channel prior to applying the filter to the data.

Dipoles, Scan, and CDR. These buttons 

will become active after you have performed a Dipole, Deviation Scan, or Current Density Reconstruction. Select the one you wish and the **Strength** and Residual **Deviation** options beneath will be displayed depending on the type of reconstruction you have selected.

Stats. This option 

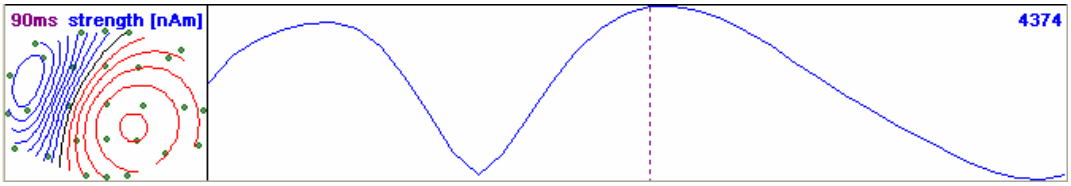
is used to display the statistics obtained from 

. See the **Result Statistics** section below for details.

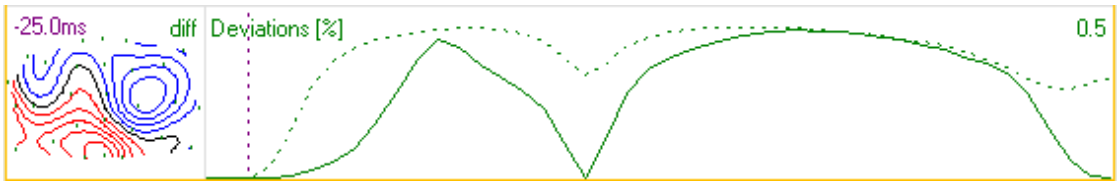
SnPM 

. Statistical non-Parametric Mapping. These are the time-resolved p-values for Statistics' SnPM results (analogous to their TANOVA counterparts that are referenced as "Stats") as selected in the respective 3D View display setting. When computing an SnPM, Curry should automatically switch into a display mode where this option becomes activated.

Strength. This option, or the  button on the **Maps** Toolbar (*Alt+D*), displays the dipole strengths (and fit field contour maps) of the selected Timerange. It will become active after you have performed a source reconstruction. Strength for CDRs with **CDR Dipoles** enabled will show the strengths for each dipole over the Timerange.



Deviations. This option, or the  button on the **Maps** Toolbar (*Alt+R*), will become active after you have performed a source reconstruction. The Residual Deviation (D) is a measure for the fit quality (how well the source model explains the measured data). Typically, you should disable **Autoscale** under **Contour Interval** (described below) when looking at the Residual Deviation. The solid line is the "achieved" goodness of fit, and the dotted line is the "expected" goodness of fit, that is, the maximum achievable fit quality without fitting noise. In a perfect world without noise, that would be a straight line at 100%. The closer together the two lines are, and the higher they are, the better. You may alternate between Deviations [%] and Deviations (original) [%] using the **Color coding** options for **Dipoles** in the **Objects** list for the **3D View**.



D is the root mean square of the difference between measured (Ri) and calculated signals (Fi):

$$D = \mathrm{Sqrt}[\,1 / n * \mathrm{Sum}((Ri - Fi) * (Ri - Fi))] / MGFP$$
$$= \mathrm{Sqrt}[\mathrm{Sum}((Ri - Fi) * (Ri - Fi)) / \mathrm{Sum}(Ri * Ri)]$$

normalized for the measured field (MGFP), which corresponds better to the Signal-to-Noise ratio (SNR) than variances.
The residual (or "rest") variance V is simply the square of the standard deviation:

$$V = D * D = \mathrm{Sum}((Ri - Fi) * (Ri - Fi)) / \mathrm{Sum}(Ri * Ri)$$

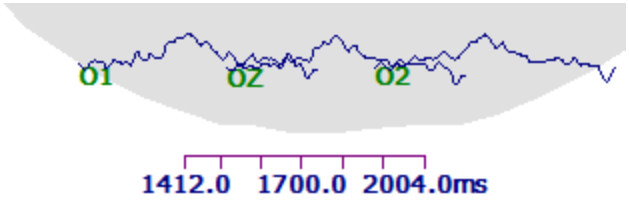
The explained variance is 1 minus the residual variance: EV = 1 - V.

Overlaid. This option overlays the Deviations and the Strength.

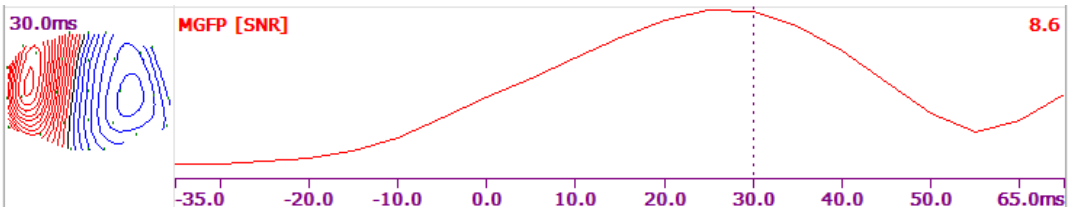
Butterfly. This is used in conjunction with the Dipole Simulation feature, in the Localize parameter panel. Please see the **Dipole Simulation** section for more details. Briefly, the option overlays two or more dipole loadings or statistical group results (with **Strength** and **Deviation** enabled).

Eq.Scale (Equal Scale). Comparing, e.g., dipole traces in Maps can be misleading if their timecourses vary in magnitude. "Equal Scale" renders all timecourses in the same y scale (obtained from the largest result).

Ruler. Enabling the **Ruler** option will display tick marks at the bottom of most of the displays in Maps (MGFP, Position Plot, Coherence, etc.). The distance between the tick marks will vary with the width of the Timerange and the AD Rate.



If the zero time point is included in the Timerange, it will have a tick mark and the 0.0 label.

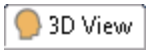


Note

The **Dipole Strength**, **Residual Deviation**, and **MGFP** functions are useful in helping you determine if the dipole solution is a valid one. Loosely stated, the Dipole Strength shows the strength and Timerange of the dipole(s). The Residual Deviation function displays the residual standard deviation through the Timerange. MGFP is a composite measure that indicates the strength of the signal against the noise background. For a valid dipole, you would expect to see, during the approximate same time course, a strong dipole (peak in the Dipole Strength), low residual or unexplained standard deviation (displayed as a peak in the Residual Deviation function), and a good signal to noise ratio (peak in the MGFP function). In other words, you would expect to see approximately concurrent peaks among the three measures. There are no hard and fast rules as to how strong the dipole must be, how low the residual standard deviation must be (less than 10% is good), or how high the SNR (from MGFP) must be. This becomes a subjective determination, influenced also by the physical location of the dipole solution(s), and by your *a priori* expectations. Obviously, a source located outside the head is not a valid solution. Similarly, an occipital lobe solution for an early SEP component is not valid. Solutions based on Label-Matching and the generic MR head shape will not be as precise as those with measured sensor positions and the subject's own MR images.

Maps / Contour Lines

These fields allow you to control the 2D Map contour increments. Selecting **Maps** displays the color maps; enabling **Contours** adds the contour lines. The Maps percentage field changes the transparency of the maps (and intensity of the colors). The color scheme is selected from **Contour Lines** under the **Colors** panel.

Maps can also be overlain on the surface in the 

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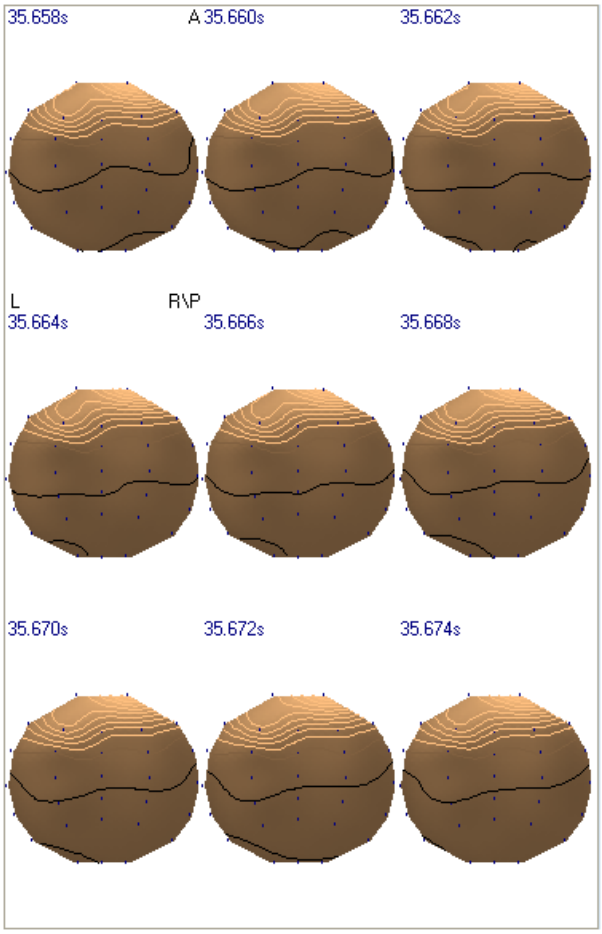
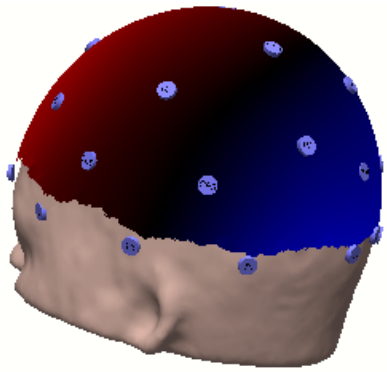
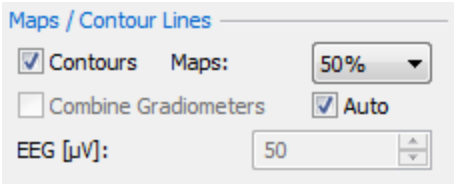


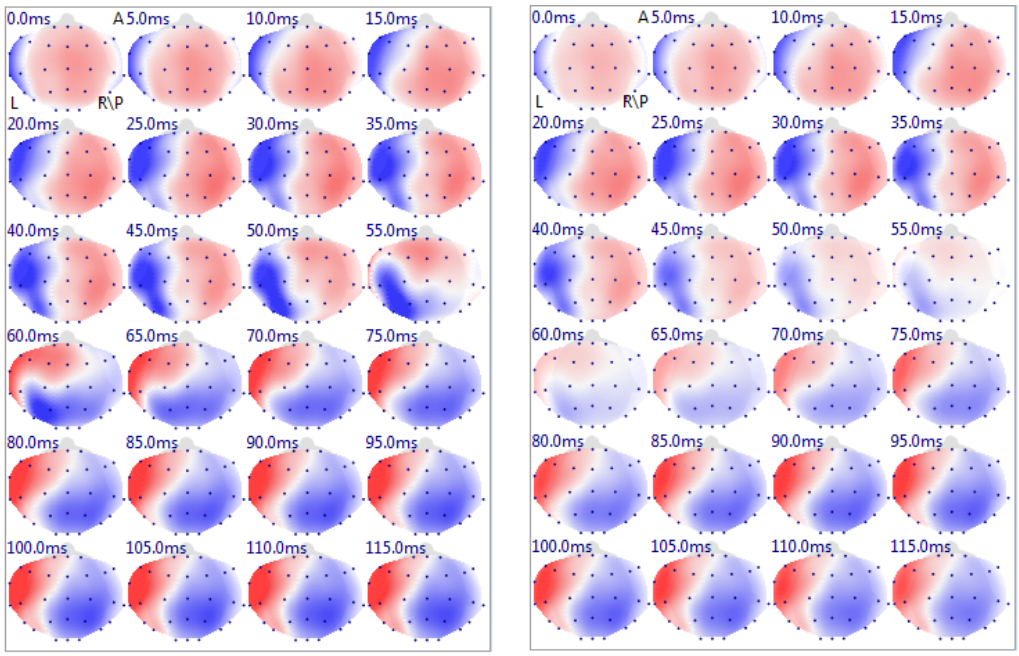


The  button on the **Maps** Toolbar will autoscale the contours.

If you enable **Auto**, CURRY will automatically set the increments between contour lines. You can override the interval by rotating the *mouse wheel* (making sure the 2D display has the "focus"), or with the up and down arrows on the *keyboard*. If you disable Auto, you may change the size of the **EEG [µV]** increment using the *mouse wheel*, the up and down arrows, or by entering a value from the *keyboard*.



Disabling **Auto** also has an effect on the maps. When **Auto** is enabled, all maps will be scaled to maximum and minimum values *for each time point individually*. When disabled, the maps are scaled to the maximum and minimum values found *in the entire Timerange, across channels*. Disabling **Auto** lets you compare the maps to each other.

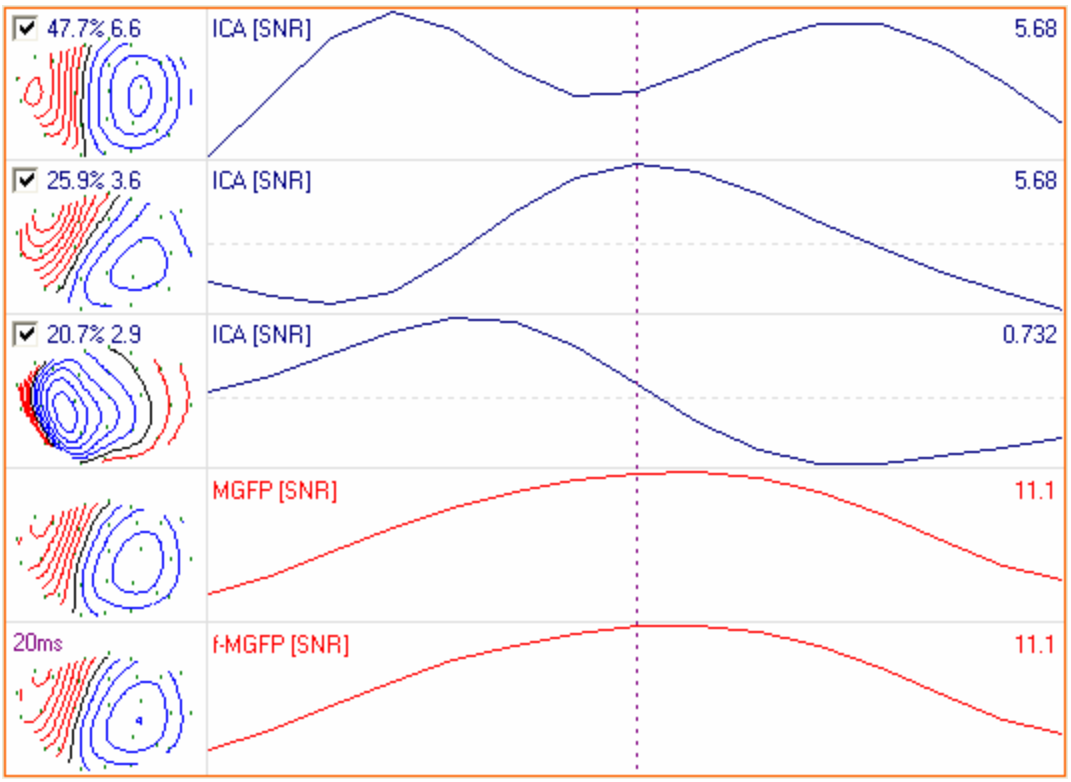


Auto enabled Auto disabled

Combine Gradiometers. This option is grayed out unless you have Neuromag data with crossed gradiometers. In that case, there will be three devices and three maps. Enabling this option combines them into a single map.

PCA/ICA

PCA (*Alt+A*) and **ICA** (*Alt+I*) **Decomposition**. PCA (principal component analysis) and ICA (independent component analysis) are performed using the selected Timerange (sensor positions are required). The decomposed waveforms are shown on the right. The patterns with their explained field percentages (measured field strength) and overall SNR values are displayed on the left.

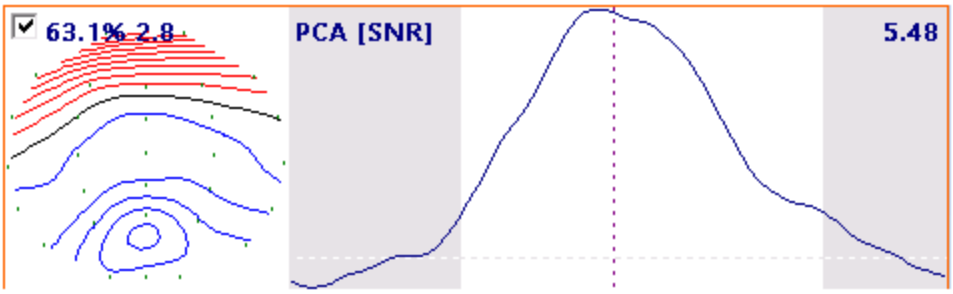


PCA PCA results in orthogonal (no overlap) maps (patterns) and orthogonal timecourses (waveforms), so in general the patterns or waveforms are not correlated to source patterns or waveforms.

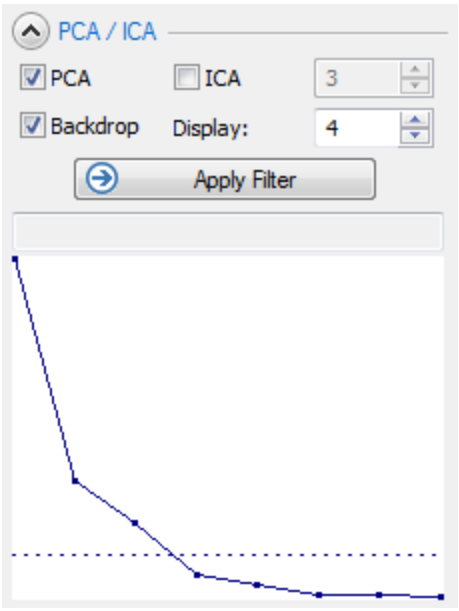
ICA ICA results in temporally as independent as possible timecourses (waveforms). In general, the corresponding maps (patterns) are not orthogonal to each other, and with independent enough sources there is more correlation to the source patterns and waveforms than **PCA**. Thus single patterns can be selected for spatio-temporal filtering and source reconstruction. In order to have a good statistical measure for independency, there should be at least three times as many samples as channels.

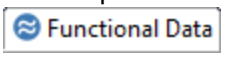
The percentages you see in the contour maps displays are derived from amplitude values (corresponding to the SNRs which are also amplitude based). In the PCA-case, 100% represents the sum over all singular values available (minimum of the number channels and samples) in the singular value decomposition (SVD) that is performed for the PCA. For the ICA a similar measure is given; however, since only a partial ICA decomposition is performed (only the signal-space is decomposed, specified be the number of ICA-components in the UI), these values are only a qualitative measure and should only be used to compare the significance of the ICA-components relative to each other.

Backdrop. When enabled you will see those intervals, in white, where the SNR value is greater than 1.0.



Display. The number of PCA or ICA components that are computed. The trailing (PCA) components (with average SNRs that should be below 0.9) are treated as noise-subspace and are not considered in the ICA. The number of ICA components to be computed is generally based on the number of valid PCA components (the number of PCA components with SNR≥1 typically is the number of ICA Components that should be computed). You may increase it with caution; increasing the number of components will ultimately result in invalid ones.

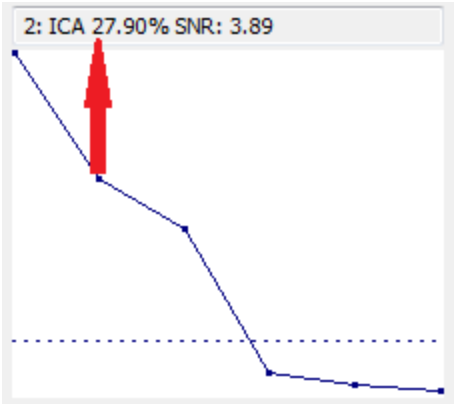


Apply Filter. Spatio-temporal filtering of the measured data in the selected Timerange if a **PCA** or **ICA** decomposition is performed and patterns are deselected. Filtered waveforms are displayed in the 

window. Applying the PCA/ICA Filter 

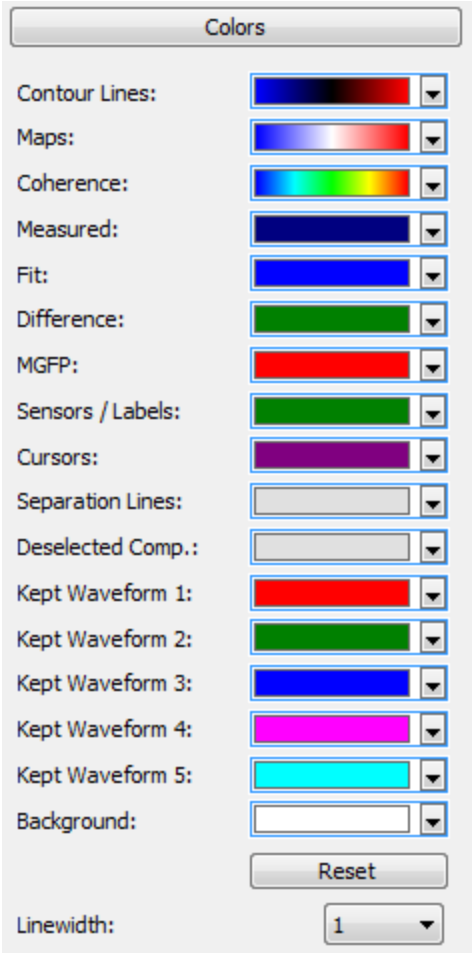
will remove the deselected components from the measured data. The ICA results will identify two or more independent components in the Timerange. You may wish to remove the contributions of all but some of the components. For example, you might find two components that are clearly associated with the evoked potential feature of interest, while a third component is associated with eye blink artifact. The Filter will let you select which component(s) to exclude from the source reconstruction (see the steps below). See the *PCA and ICA Analysis* Tutorial for more information.

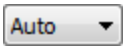
The PCA and ICA component percentages and SNRs are displayed in a line graph at the bottom of the Parameters panel. Position the mouse cursor over one of the points to see the values. The horizontal dashed line displays the SNR value of 1.0.



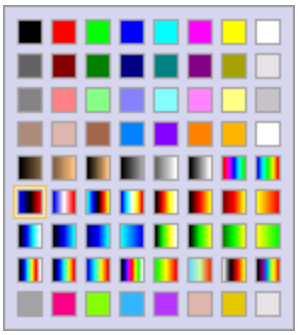
17.3.2 Colors

The **Colors** panel allow you to assign colors to various components in the display. Clicking the drop-down arrow displays the color palette from which you may select the solid color or color spectrum to apply.



You can select separate colors for the **Contour Lines**, and **Measured** and **Fit** data, and the **Difference** between them. You can also select colors for the **MGFP**, **Coherence**, **Sensors/Labels** and **Cursors**. **Separation Lines** are the lines separating the ICA components and contour maps regions in the display. The Separation Lines color also defines the color of the headshape. **Deselected Comp.** are the deselected components in the PCA/ICA. You may select the color for each of the **Kept Waveforms**. **Background** in the background color of the display. Click the **Reset** button to return the colors to their default settings. **Linewidth** changes the thickness of the traces (1, 2, or 3 pixels). If you select the 

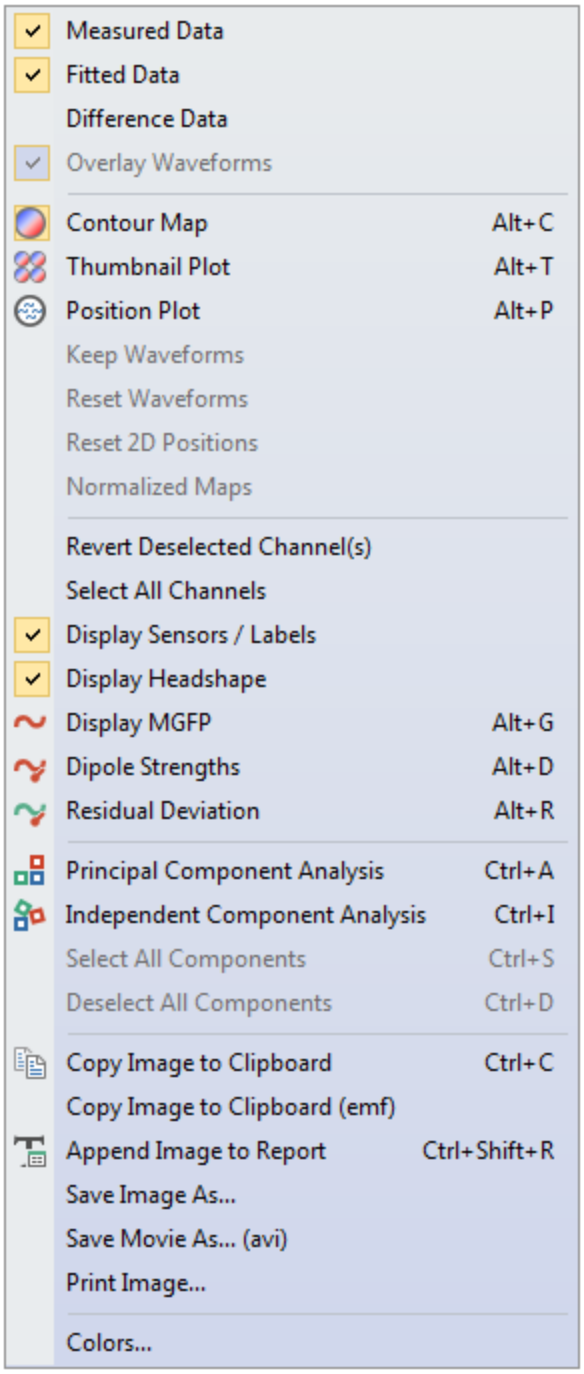
option, CURRY will adjust the line widths automatically. Few channels will have thicker lines; multiple channels will have narrower lines. Larger windows will have thicker lines for both waveforms and cursors.



17.3.3 Maps, Context Menu

If you *right click* in the 

display, you will see the following options. Most of these are the same as those seen if you click **Maps** from the **Main Menu** bar; some have icons on the **Maps** Toolbar, as indicated.



Measured Data. This toggles the display of the measured data on and off.

Fitted Data / **Difference Data**. These options will become active after you have performed a dipole reconstruction. The Measured Data are the original data; Fitted Data are those that are generated by the best fit dipole reconstruction; and Difference Data are the differences between the two. These can be viewed either as 2D contour maps or as waveforms using the 

option.

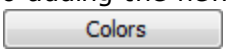
Overlay Waveforms. This option allows you to overlay Measured, Fitted, and Difference waveforms. You may also select it from the Parameters panel 

.

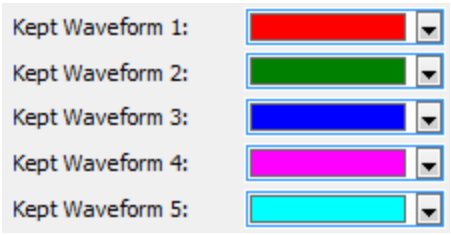
Contour Map  . Displays a single contour map corresponding to the position of the middle cursor in the Functional Data display (or *Alt+C*).

Thumbnail Plot. Enabling this option, or clicking the  button from the **Maps** Toolbar (or *Alt+T*), will display the contour maps in the selected Timerange as a series of thumbnail maps.

Position Plot. Enabling this option, or clicking the  button from the **Maps** Toolbar (or *Alt+P*), will display the waveforms on a 2D spherical projection.

Keep Waveforms. Select this option to "keep" the current waveforms seen in the Position Plot view. Make a change, such as, apply a filter or move to a different epoch, and the new display will be superimposed on the kept one. This allows you easily to compare the effects of an operation you have applied. It is also used to compare multiple average files or epochs (up to 5). For overlaying multiple displays, click Keep Waveforms each time prior to adding the new display. The colors are assigned automatically, as seen in the 

panel for **Maps**, where they can be changed, as desired. The most recent waveform - not yet "kept" - will always be the color you have selected for the EEG (or MEG) waveforms.



Reset Waveforms. Removes "kept" waveforms.

Reset 2D Positions. Selecting this option restores the waveforms to their original positions and size.

If you position the mouse over an sensor label in the **Position Plot**, the cursor will change to a finger. You may then grab-and-drag the sensor to other positions. While the finger is displayed, you may rotate the *mouse wheel* to increase/decrease the size of the waveform.

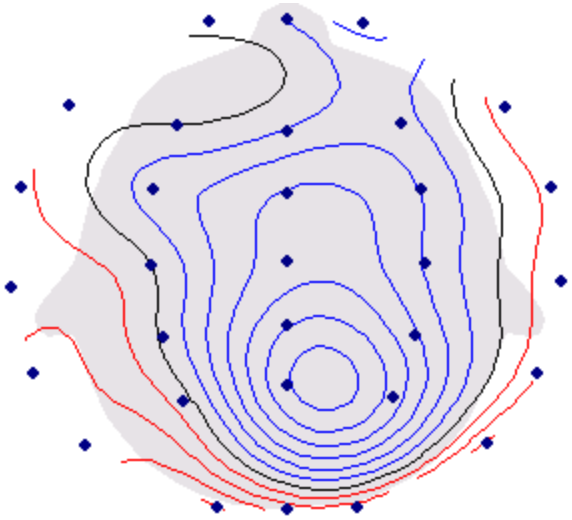
Normalized Maps. This option is used in conjunction with the **Average Time Interval** option, found under **Options**, under **Functional Data**. If you select a Timerange and click the **Save** button, the **Normalized Maps** option will become active. If you click it and move to another Timerange, the 2D Maps will show the difference with respect to the "saved" maps.

Revert Deselected Channel(s). If you click on a channel(s) from the Maps display to deselect it, the channel(s) will disappear (and be removed from the maps computations). Clicking this option will restore the deselected channel(s). The last

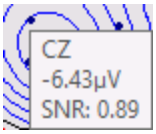
deselected channel will be restored if they were deselected individually. If you deselected channels by dragging a rectangle around them, all of those will be restored. If you want to have all channels selected, use **Select All Channels**.

Select All Channels. Use this option to restore all deselected channels.

Display Sensors / Labels. Enabling this option will display the sensor positions on the contour displays (seen as the black dots on the figure below).



If the mouse is moved over a sensor symbol in a single contour map display, the corresponding label, signal amplitude, and Signal-to-Noise-Ratio (SNR) are displayed (if you have **View** →**Show Tooltips** enabled).



Display Headshape. This option toggles the display of the background headshape on and off.

Display MGFP. Enabling the option, or clicking the button on the **Maps** Toolbar (or *Alt+G*), displays the MGFP waveform. This has the same function as MGFP in the **Parameters** panel.

Dipole Strengths. Enabling the option, or clicking the button on the **Maps** Toolbar (or *Alt+D*), displays the Dipole Strength waveform. This has the same function as Strength in the **Parameters** panel (see the **Parameters** section above).

Residual Deviation. Enabling the option, or clicking the button on the **Maps** Toolbar (or *Alt+R*), displays the Dipole Residual Deviation waveform. This has the same function as Deviation in the **Parameters** panel (see the **Parameters** section above).

Residual Deviation is rDev = 1 - [goodness of fit].

The explained variance is eVar = 1 - rDev * rDev, so for 10% rDev (=90% explained field) this gives 99% explained variance.

Principle Components Analysis. Selecting this option, or clicking the  button on the **Maps** Toolbar (or *Ctrl+A*), sets the Mode to PCA Decomposition  . You must define a Timerange for the option to be active.

Independent Component Analysis. Selecting this option, or clicking the  button on the **Maps** Toolbar (or *Ctrl+I*), sets the Mode to ICA Decomposition  . You must define a Timerange for the option to be active.

Select All Components. This selects all PCA/ICA components for spatio-temporal filtering purposes (or *Ctrl+S*).

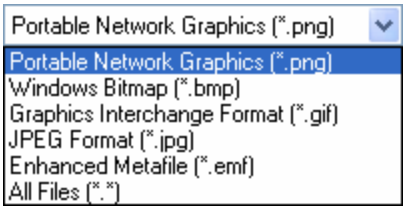
Deselect All Components. This deselects all PCA/ICA components for spatio-temporal filtering purposes (or *Ctrl+D*).

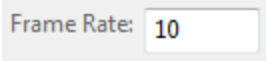
Copy Image to Clipboard  . This copies the data channel display (.bmp format) to the Windows clipboard (or *Ctrl+C*), from which you may Paste it into other Windows applications.

Copy Image to Clipboard (emf). When pasted into other Windows applications (such as Word), individual components of Metafiles can be edited; whereas, .bmp files cannot. (In Word, *right click* on the pasted metafile, and select **Edit Picture**).

Append Image To Report  . Copies the section of the data display having the focus to the  (or *Ctrl+Shift+R*).

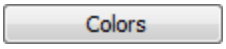
Save Image As. This option lets you save the graphic display in any of the formats shown.

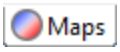


Save Movie As. This option lets you save the Movie in .avi format. The Save As window contains an option to set the speed of the replay of the movie: 

. Higher Frame Rates will replay the movie faster.

Print Image. The Functional Data will be displayed in the Windows Picture and Fax Viewer, where it can be viewed and printed.

Colors. Clicking this options displays the 

panel under 

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18 Image Analysis

This section of CURRY will allow you to import image data, perform manual and automatic segmentation, co-registration of different image data sets, localize depth electrodes, and display the results (assuming your license allows it). Specifically, you will have access to the Image Data, Localize, Results, and 3D View parameter panels.

General Parameters for MRI and CT Image Data

For MRI and CT, make sure that the full head is scanned, including features such as nose, ears, and skin, preferably extending below the chin.

For MRI, a 1.5T scanner is preferable to a 3T scanner, because the latter is more prone to produce an artifact referred to as RF inhomogeneity, shading artifact, or intensity non-uniformity. In any case, you will need a good white matter/gray matter contrast. For MRI, a matrix size of 256x256 is sufficient, with a slice thickness of 1 to 1.2mm. The **Bias Field Correction** (*Step 5* in the **Image Data Parameters** windows) improves the image intensity distribution. It can be useful for MRIs obtained from high-Tesla scanners where cortex segmentation quality varies among brain regions.

For CT, a matrix size of 512x512 with a slice thickness of approximately 0.5mm is superior for localizing implanted electrodes, but 256x256 and 1mm should work as well.

For more details, please see **Appendix B**.

18.1 Loading Image Data

Introduction

Image data are used for various purposes:

- overlay with source reconstruction results.
- the setup of realistic head models (BEM).
- the derivation of source space models (cortex).
- In addition, CURRY can manipulate and process image data in a very flexible way which makes the image processing part of the software a tool that is open for a wide range of applications.

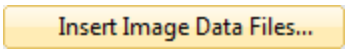
Up to five separate image data sets may be loaded at a time (many more are possible with a customized layout file). All are inserted into the same Study. When they are successfully read in, you will see additional display tabs allowing you to switch among the data sets (see **Switching Between Image Modalities** below). You can drag and drop image data in the Database within the same Study to change the order (the parameters will remain with the file when you move it).

CURRY's image processing options are described shortly. This chapter is dedicated to the process of retrieving image data parameters, loading images, and defining basic image properties such as landmarks and thresholds.

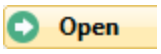
Entering Image Data into the Database

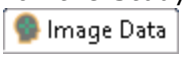
This section describes the process of entering image data into the Database. If no image data are loaded, CURRY will use the averaged MR data set. Loading an individual's MR data is somewhat analogous to loading the Functional Data.

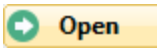
For example, say the image data are contained in a single .dat file.

1. Right click on the Study in the Database, select 

, and retrieve the .dat file.

2. If you *right click* on the Study in the Database, select 

(or click ), and then click the 

display tab, you will instead see the **Image Data Parameters** windows (described below). This is roughly analogous to the **Functional Data Parameter Wizard** for functional data. It is used to enter/detect parameters of the image data set, and then create a .imd file that contains the parameters. The next time you load the image data set, load the .imd or the .nii file (for example) and the image data will load automatically (when you click 

), assuming you have both files in the same folder.

Accessing an Image Dataset for the First Time

When image data are accessed for the first time, image-related parameters have to be defined. This procedure consists of the following steps, which are described in more detail in following sections:

1. Entering the image data into the Database.
2. Entering the **Image Data Parameters** windows.
3. Autodetecting the image data file format.
4. Supplying the missing parameters for reading image data.
5. Reading the image data.
6. Estimation of segmentation thresholds.
7. Definition of landmarks that determine the internal coordinate system.
8. Setting the boundaries for Talairach conversion

Image Filenames

Image data are identified by a filename (if all images are in one file), or by a folder name (if images are single files in this folder). This filename - including the path, but not the extension - is referred to as the image basename. If the filename is D:\xxx\image.ext, the basename would be D:\xxx\image, and the file would be referred to as basename.ext.

Derived Files

There is a whole family of files whose names are derived from the image basename. These are files whose contents directly refer to the image data. Examples are:

- image parameters	extension .imd
- surface meshes	extensions .s00...99
- segmentation results	extensions .bo0...99
- lists of points	extensions .sp0...9
- BEM models	extensions .bd0...29, .bt0...29
- FEM models	extensions .fd0...29, .ft0...29

The parameter file is used to store parameters that describe the image data, anatomical landmarks, segmentation thresholds. The other files can be seen as results of image processing operations.

All Images are Stored in a Single File

CURRY can read data files in which all of the images are stored in a single file (regardless of the extension). A parameter file is created with an .imd extension. In the example below, the data file has an .img extension (.img is typically accompanied by an .hdr file, which would be the Analyze/SPM file format).

Example

After CURRY has successfully read in the images, there are (assuming the original file name is basename.img)

- basename.img
- basename.imd

After some image processing has been performed, there are e.g.,

- basename.img
- basename.imd
- basename.s10
- basename.s11
- basename.s12
- basename.bo3
- basename.sp5

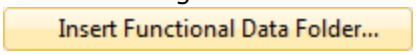
Separate Image Files in One Folder

When CURRY reads image files that are in a single folder, it scans the contents of the folder and groups the files that were found. If DICOM files are found, DICOM series are presented. If no DICOM files are found, files are grouped by their file size and ordered lexicographically. The number of files in a folder that CURRY considers can be enlarged by including the contents of subfolders and/or restricted using file name masks. Examples of masks are:

- *	all files in the folder
- ***.img**	all files with extension .img
- **img***	all files beginning with img

Care

If an image dataset consists of multiple files in a folder, insert the *folder* in the **Image Data** folder, not one of the files. After the files are read, CURRY will create an .imd file and place it in the same folder that contains the subfolder with the image files.

For example, say you initially have a folder "A", with a subfolder "B", where B contains the individual image files. In the Database under **Image Data**, load the B *folder* by selecting 

from the Image Data folder *right mouse* menu. After you go through the **Image Data Parameters** windows, described below, CURRY will create the parameter file "*B.imd*", and place it in the *A* folder. Do not place the .imd file manually in the same folder with the individual MR slice files; it should be in the folder "above" it.

18.1.1 Image Data Parameters Windows

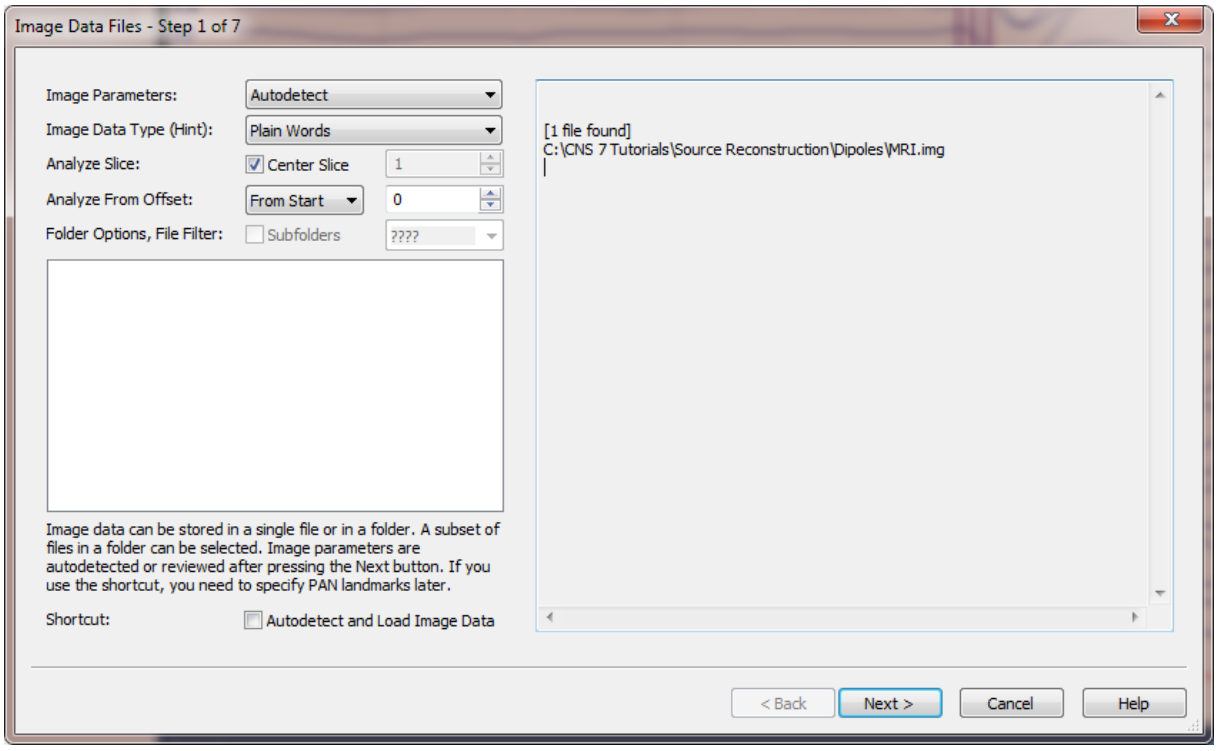
As described above, the *Raw Image Data Files* screen (the start of the Image Data Parameters windows) will appear when you first attempt to load/display raw MR data. It can also be accessed from **Image Data** → **Image Data Parameters**, or **File** → **Image Data** → **Image Data Parameters**, or from

in the Workflow list. This assumes you have already loaded the image data, and wish to access the parameters again. As with functional data files, image data files must be loaded into the Database before they can be accessed in CURRY; the only way to load the files is from the Database.

The **Image Data Parameters** windows are used in the following ways:

- File specification and autodetection hints, where you may supply basic information to help autodetection.
- Image parameters, which describe how a slice is stored in an image file and which are the basic slice parameters. Most of these can be autodetected.
- Target image parameters, which control how a slice is transformed into the iso-image cube.
- Image cube parameters, which control how slices are stacked and interpolated when they enter the cube.
- Determine segmentation thresholds that are used later with BEM Geometry.
- Determine the landmarks for coregistration and boundaries for the Talairach system.

Step 1. The **Image Data Files** screen is seen in Step 1.



If you are loading multiple MR slice files or if you have multiple folders containing different image data sets, you will see them listed. Your file structure may be more complicated than this, with levels of subfolders. CURRY will generally display the folder with the greatest numbers of files in it, as this will likely be the one you will want to use. Different ones may be selected manually by clicking on them.

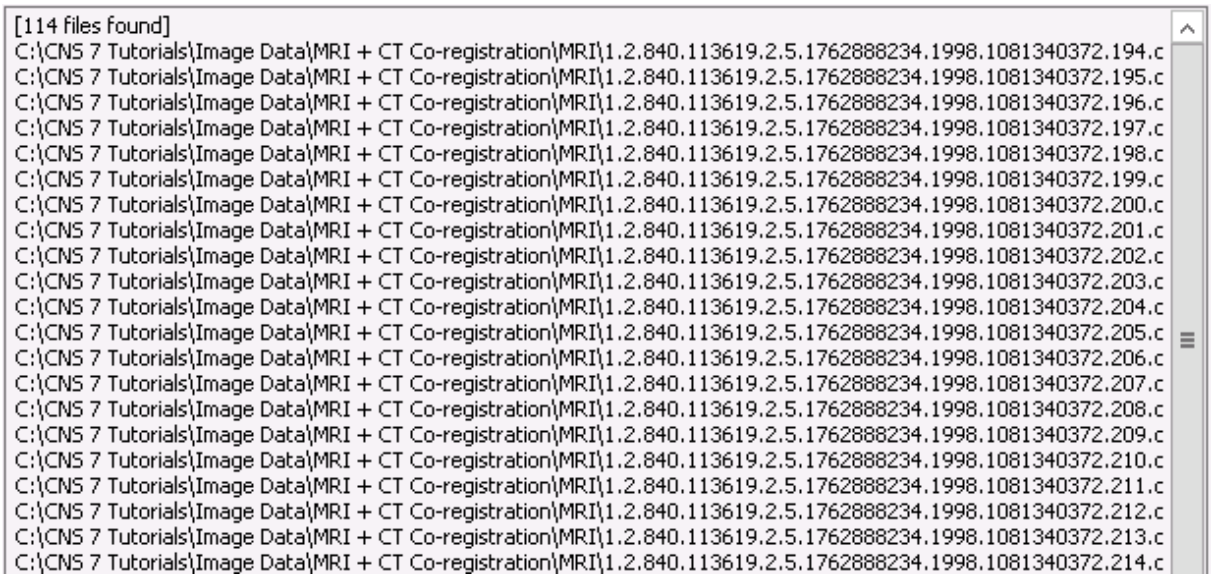
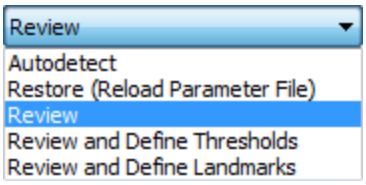
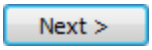


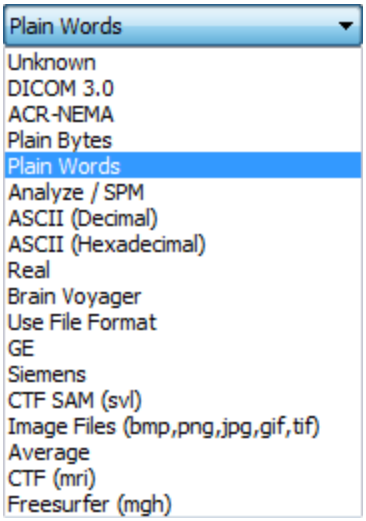
Image Parameters. Select to **Review**, **Autodetect**, or **Restore** parameters.



If you select Autodetect, CURRY will attempt to find the image parameters. This occurs when you click the 

button, and the results are seen in the next dialog screen. If you have already created a parameter file in CURRY (.imd), you can **Review** the parameters, or use the parameters contained in that file by selecting **Restore (Reload Parameter File)**. Selecting **Review and Define Thresholds** will take you directly to **Step 5** where you can review, modify, or define the segmentation Thresholds. Selecting **Review and Define Landmarks** (available only if image data parameters are already present) takes you directly to **Step 6** where you may review, modify or define the Landmark locations.

Image Data Type (Hint). Provides a hint that specifies the file format when **Autodetect** has been selected for **Image Parameters**. **Autodetect** uses this hint to detect the exact format and as many parameters as possible. Select the file format you are using.



Unknown. Autodetect tries to find the image type by itself.

DICOM 3.0. DICOM 3.0

ACR-NEMA. ACR-NEMA

Plain Bytes. Calculates number of slices assuming 1 byte per pixel, if all data are stored in a single file.

Plain Words. Calculates number of slices assuming 2 bytes per pixel, if all data is stored in a single file.

Analyze / SPM. Analyze / SPM

ASCII (Decimal). ASCII files in a folder containing image intensities as whitespace separated decimal numbers.

ASCII (Hexadecimal). ASCII files in a folder containing image intensities as whitespace separated hexadecimal numbers.

Real. Binary files in a folder containing image intensities as 4-byte real (floating point) numbers.

Brain Voyager. Brain Voyager

Use File Format. The file format is used as a hint.

GE. General Electric

Siemens. Siemens

CTF SAM (svl) / CTF (mri). CTF SAM (svl) and CTF (mri)

Image Files (bmp, png, jpg, gif, tif). Image data are sometimes stored in a folder with one bmp, png, etc. file per slice.

Average. Each image file in the folder is itself a 3D image data that has been previously exported by CURRY (in CURRY's iso/imd format). CURRY will then average these 3D images.

CTF (mri). These are the file formats for CTF (MEG manufacturer) result files (extension .mri) which typically contain functional SAM (synthetic aperture magnetometry) result images.

Freesurfer (mgh). These are the file formats for Freesurfer images (extensions mgh or mgz, where mgz is simply a compressed version of mgh with smaller file sizes).

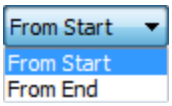
Analyze Slice. This option determines the properties/file to be analyzed. Sometimes the very first images in a dataset have formats different from the rest, e.g., if they contain planning slices.

When enabled (recommended), the slice/file that is analyzed will correspond to the central slice of the image data set.

Note

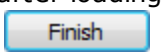
The first few slices of some data sets are planning slices. The slice orientation and/or pixel dimensions (or field of view) of such slices typically differ from the values for the slices in the 3D image data set that is acquired. By analyzing a slice from the middle of the stack, the correct values for the stack can be obtained. If a planning slice is analyzed, a **Warning** window will report a problem with the pixel size(s), whenever a slice from the stack is displayed.

Analyze from Offset. This option makes it possible to skip information at the beginning or ending of an image file. Enter the offset in bytes in the adjacent field to be skipped before searching for image information.



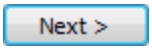
Folder Options, File Filter. The options let you filter the selected folder for all files (*), files with an .img extension (.img), or files with .img in the file name (img*). Enable the Subfolders options if there are additional files in subfolders. Up to three levels of subfolders are supported.

If it is known that this type of image data can be read successfully, **Autodetect and Load Image Data** will directly load the images using the autodetected parameters. Obviously, this does not include correctly set landmarks and the **Define landmarks** task will be highlighted after loading. Click the 

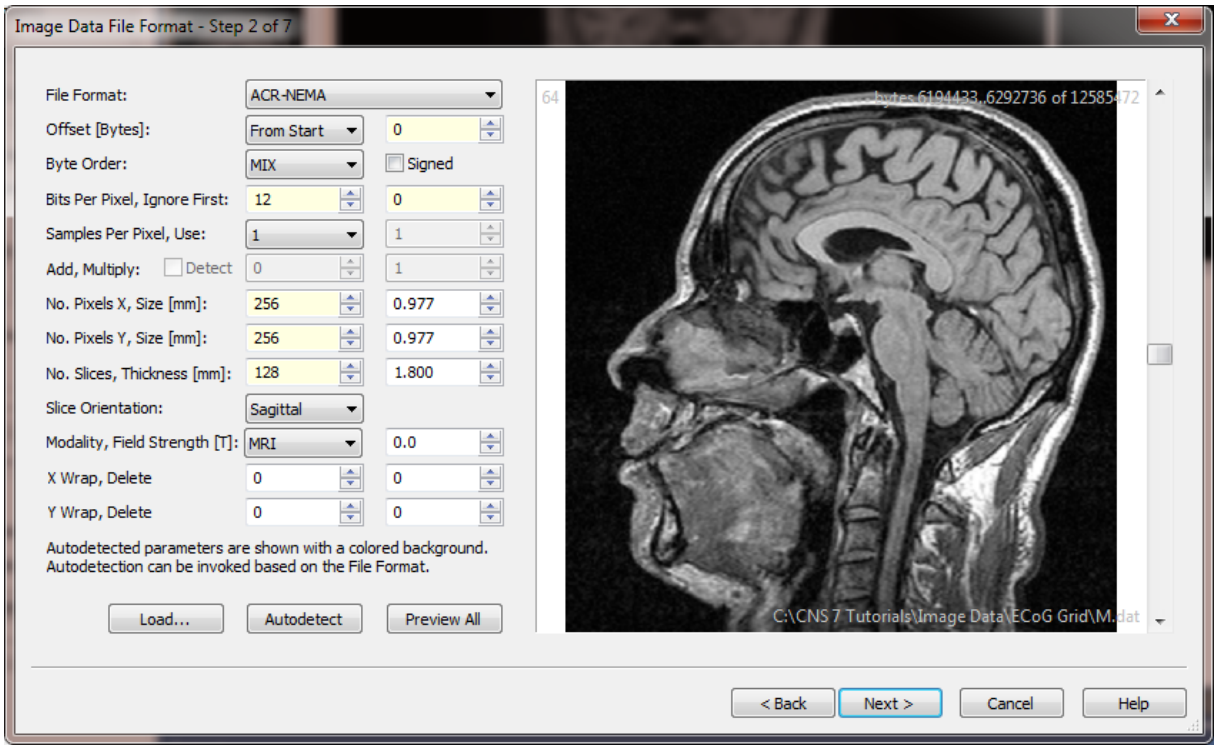
option and the 

button to bypass the subsequent steps and load the image data after autodetection of the parameters.

Folder Contents. The contents of the image data folder are analyzed and presented here, based on their DICOM header information (if available). Select one of the entries and the list of files to the right will change to reflect this selection.

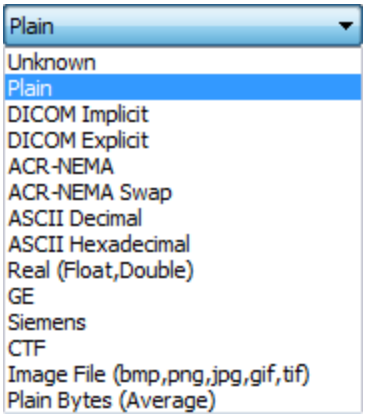
Step 2. Click the 

button to display the **Image Data File Format** screen. These parameters determine the file format for a 2D slice. If you selected Autodetect on the previous screen, the settings in yellow were the ones that were found. Autodetection can be invoked on the basis of File Format.



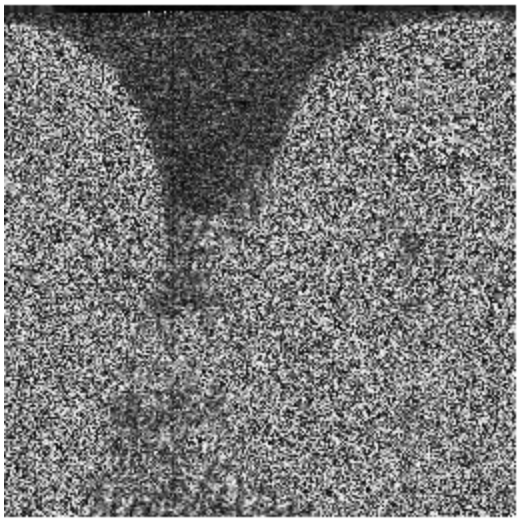
The detected parameters are displayed in yellow. Corrections can be made to any of the fields if they contain incorrect information. In this file, the pixel **Sizes** are **.997**. not the default value of 1.0. This is information you must provide. Similarly, the slice **Thickness** is **1.8mm**, not the default 2.0mm. Be sure to enter the correct parameters.

File Format. Typically, this parameter is autodetected. Select **Unknown** if the format is totally unknown. If autodetection fails, the file format is often **Plain**. Then try the different Byte Orders (MIX, LSB, MSB, etc.).



In the case of **ASCII** files, the format can be detected by opening the file in an editor. There are two sub-types, **Decimal** and **Hexadecimal**. **ASCII Decimal** files in a folder contain image intensities as whitespace separated decimal numbers. **ASCII Hexadecimal** files in a folder contain image intensities as whitespace separated hexadecimal numbers.

If you do not see a clear image, as in the example shown, you will need to try different formats and byte orders until you do see the image. Enter as much information as you know, and then try Autodetect.



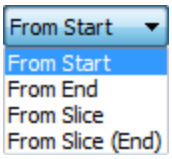
Note
The file size may help in determining raw data parameters if the file is in **Plain** format:

Example 1
The file size is 65,576 bytes (per image). The image dimensions are probably 256x256, which is normally the case. As 256x256 + 40 = 65,576, there is reason to believe that the image format is **Plain**, and there is a header or a trailer of 40 bytes in the image file. The header can be skipped using the **Offset** text field.

Example 2
All images are stored in one file with a size of 13,107,240 bytes. As 256x256x200 + 40 = 13,107,240, we probably either have 100 slices and a **Plain Words** file format, or 200 slices in **Plain Bytes** in the file. Again, the header size is 40 bytes.

Offset [Bytes]. Each slice of the image data often contains a header of a defined size (e.g., ACR-NEMA data). The set number of bytes will be skipped. The size of the header can in most cases be calculated from the file size S, where the size of one slice s = S / No._of_Slices [Bytes]. Header size (per slice) H = s - No._of_Horizontal_Pixels * No._of_Vertical_Pixels * Bits_per_Pixel / 8).

For example, say a slice is 152,244 bytes (use the file properties to get this value). This means that with the typical image size of 256x256 pixels, there are 2 bytes (16 bits) per pixel (256x256x2=131,072 bytes) plus a header of 152,244-131,072 = 21,172 bytes.



Options other than **From Start** are normally used when loading image data in plain format, and determine which part of the image data file is actually read. **From Slice** and **From Slice (End)** are only needed if all slices are contained in a single file.

o Offset
x data
| start of slice
. ignored

From Start. Read image data starting from the offset. If all images are contained in one file, slices are assumed to be contiguous (no gaps between slices).

ooooo|xxxx|xxxx|xxxx|xxxx|....

From End. Start reading image data at the given number of bytes before the end of the file. If the offset is smaller than the amount of data to be read, data are read so that no trailing bytes remain. If all images are contained in one file, slices are assumed to be contiguous (no gaps between slices).

.....|xxxx|xxxx|xxxx|xxxx|

From Slice. If images are individual files in a folder, this option behaves the same as **From Start**. If all images are contained in one file, the specified offset is ignored before each individual slice is read.

ooxxxx|ooxxxx|ooxxxx|ooxxxx|.....

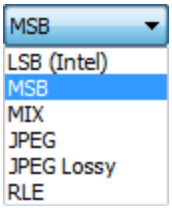
From Slice (End). If images are individual files in a folder, this option behaves the same as **From End**. If all images are contained in one file, the specified offset is ignored before each individual slice is read, and an initial offset is used to make sure that the end of the last slice is the end of the image data file.

.....|ooxxxx|ooxxxx|ooxxxx|ooxxxx|

ACR-NEMA or DICOM headers should not need to be overread. In these cases, an **Offset** of **0** will normally be appropriate.

Byte Order. This specifies how the pixel data is stored on a bit level. Typically, **LSB** is correct if files stem from a PC, while **MSB** is correct for workstations. **MIX** only occurs with ACR-NEMA or DICOM images. For Plain files, try switching between **LSB** and **MSB** to see if high-intensity regions are clipped or not. JPEG, JPEG Lossy, and RLE are alternative and increasingly common ways in which the data may be contained in a DICOM file. **JPEG** is a lossless variant of the well-

known jpg compression, **JPEG Lossy** is recognized but **not** supported (read) by CURRY. **RLE** stands for run length encoding and is another (less sophisticated) lossless compression scheme.



Signed. Sometimes the number format of image data is Signed, most often with fMRI maps, but also for anatomical images. This can be autodetected from all but Plain file formats.

Bits per Pixel, Ignore First. This is the bits per pixel. Eight bits are one byte. In rare cases, it is necessary to ignore the first few bits (if they contain noise).

Image data can be stored with one byte (8 bits), one and a half bytes (12 bits), or two bytes (16 bits) per pixel. Each pixel contains the gray level information of one 2D image point (pixel). The **Bits per Pixel**, Number of Significant Bits (NSB), and the Most Significant Bit (MSB) are transformed into a mask which is laid over the image data:

$$Mask = (2^{MSB} - 1) xor (2^{MSB - NSB} - 1)$$

Examples
If there are 16 **Bits per Pixel**, bits are numbered 15 to 0, which means that the first bit is bit 15 and the last bit is bit 0. If 10 bits are significant and the **Most Significant Bit** is bit 15, the following bits (marked with an x) are read: (15) xxxxxxxxxxoooooo (0).

If the **Most Significant Bit** is bit 14, bits (15) oxxxxxxxxxxoooooo (0) are read.

If there are 8 **Bits per Pixel** and the **Most Significant Bit** is bit 7, and there are 8 significant bits, all bits are read: (7) xxxxxxxx (0).

Note
Using these settings, most unknown data file formats can be read. Image data is usually located at the end of an image file, and the dynamic range per pixel is rarely larger than 12 bits. For example, the proprietary GE Signa scanner file format can be read using an offset of **7904** bytes in the **Plain** format, **MSB** mode. The number of valid bits is usually **12**.

Samples Per Pixel, Use. Sometimes there are three samples per pixel, meaning that each pixel is stored three times. Usually this is the case for RGB images. If the number of samples per pixel is > 1, you may choose which of the samples to read (e.g., the red, green, or blue channel). Various RGB options are available.

Add, Multiply. Multiply applies mostly to float images (typically these stem from fMRI) because CURRY internally stores a pixel in 16bits, while a float number has 32bits. Usually these are **0** for **Add** and **1** for **Multiply**. **Detect** will find the largest and smallest entries of all slices and return values that represent this range.

Add is also used in the **Signed** case (see above) and determines which negative values are visible. If Add is **0** and there are negative values, these are all cut off and appear as black.

No. Pixels X, Size [mm]. The number of pixels in the X dimension is normally 256, but may be different in some cases. Rectangular images can be processed as well. The **Size** relates to the **Raw Image Size** and the field of view of the raw images by the following formula: field of view [mm] = **Raw Image Size** [pixels] x **Pixel Size** [mm].

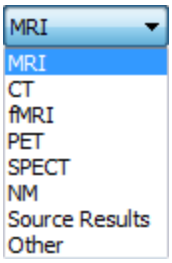
No. Pixels Y, Size [mm]. The number of pixels in the Y dimension is normally 256, but may be different in some cases. Rectangular images can be processed as well. The **Size** relates to the **Raw Image Size** and the field of view of the raw images by the following formula: field of view [mm] = **Raw Image Size** [pixels] x **Pixel Size** [mm].

 **Care**
Although non-quadratic pixels are supported, they hardly ever occur.

No. Slices, Thickness [mm]. The number of slices is shown as well as the thickness. The **Slice Thickness** *including the gap* is the distance between the voxel centers of consecutive slices. Often this value is incorrect even if it was autodetected. If this parameter is wrong, the iso-image will look stretched or squeezed along the axis perpendicular to the plane of the raw slices.

Slice Orientation. The **Slice Orientation** (**Sagittal**, **Coronal**, or **Axial**) can be determined easily by visual inspection. On the subsequent screens, Left, Right, Anterior, and Posterior markers are plotted with the slices. If these make no sense, the slice orientation is wrong. Select the orientation that matches the displayed image.

Modality, Field Strength [T]. The Modality setting influences how **Automatic** intensity functions (Step 3). For all but MRI, intensities are adjusted so that they are mapped linearly onto the 0..255 range used for segmentation. For MRI, the highest 1% collapse into the 255 intensity. **NM** in the list refers to Nuclear Medicine and is a modality that can be contained in a DICOM file (rarely encountered). **Source Results** is selected, for example, when reading .svl (CTF SAM) result images. Field Strength [T] is only available, autodetected (from DICOM), and evaluated for MRI-type image data files (as opposed to CT, fMRI, etc), and is the fieldstrength (in Tesla) of the scanner. If this value is larger than 1.5, Bias Field Correction will be offered.



X Wrap and Y Wrap, Delete (Pixels). Wrapping can be used to remedy MRI folding artifacts where, for example, the nose is visible at the back of the head. Deleting a positive number of pixels closes a gap by ignoring trailing pixels, while negative numbers cause leading and trailing pixels to be ignored. Increase or decrease X or Y as needed. If **Delete** is greater than **0**, some pixels are deleted, and if **Delete** is less than **0**, the same number of pixels is deleted on both sides. These values are never autodetected.

Load... . If you have already created an image parameter file in CURRY (.imd), clicking this button will restore those parameters. You may also load parameters from another data set's .imd file.

Autodetect . The upper part of the **Image Data File Format** window is devoted to the general image data description upon which autodetection relies. The Autodetect button is used if not all of the image parameters were detected from the first dialog screen, or, if you made changes to the settings and wish to restore the autodetected ones.

Care
If the first few slices are planning slices, they must be skipped.

Click the button to start autodetection. As a result, one of the following things will or may happen:

- Detected image parameters are entered in the fields. All autodetected parameters have a yellow background, while undetected parameters have a white background. All other parameters are *not* subject to autodetection. Autodetected parameters have to be checked by the user. Unrecognized and unmarked parameters have to be provided by the user.
- Image information is written to the **Output** field.
- A popup box may appear and give further advice, e.g., to refine the **Image Data Type**. This occurs if images are suspected to contain data only and no header information that CURRY can understand.

  Partially corrupted headers are also indicated by a popup box.

After autodetection, parameters must be checked and missing parameters must be supplied. The preview window helps determine image parameters. It shows the processed raw images, reflecting the entered/selected parameters.

Note

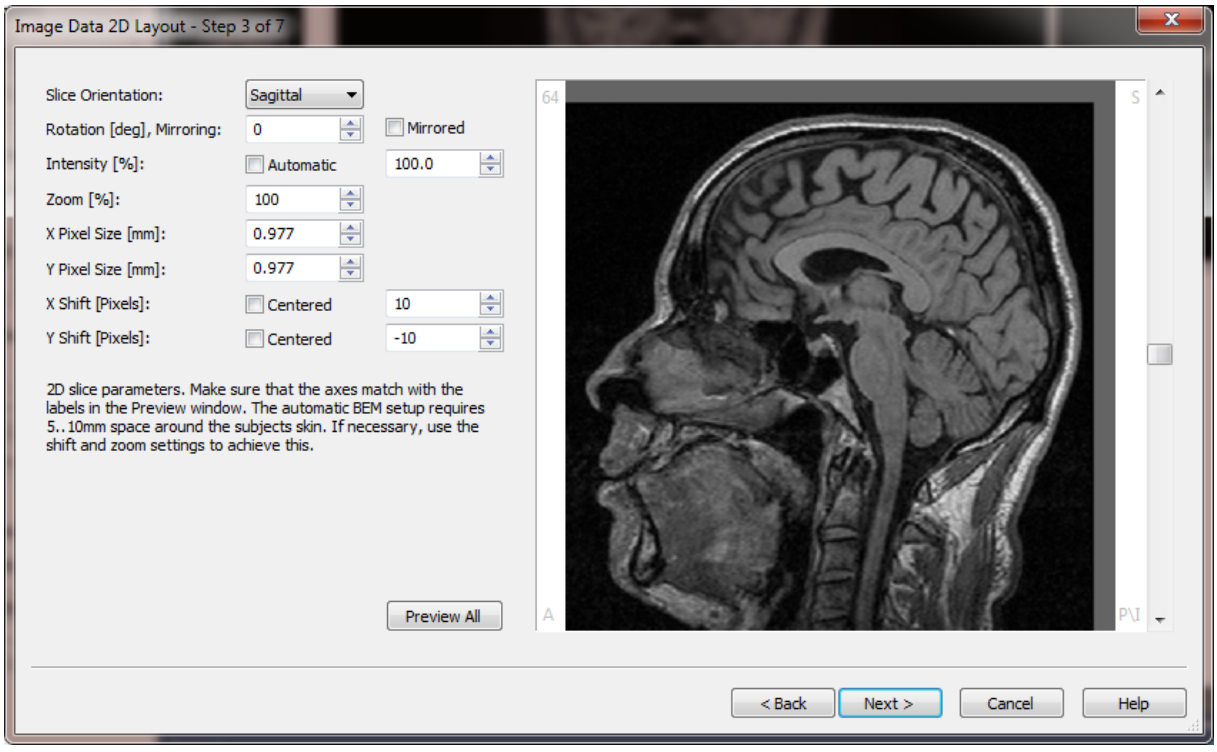
If autodetection fails and no hint has been given, but the images are in fact in **Plain** or **ASCII** format, try to give this as a hint and repeat autodetection.

Care

The parameter that is the most difficult to autodetect, even for DICOM headers, is the **Slice Thickness**. The reason is that this is a true 3D parameter: it defines the spatial relation *between* slices and *not* the slices themselves.

Preview All. Click this button to preview all of the slices. This will include the planning slices that may not appear as the rest of the MR slices.

Step 3. Click the Next > button to see the **Image Data 2D Layout** dialog screen. These are the 2D slice parameters. Make sure that the axes (Slice Orientations) match with the labels (**A**, **P**; **R**, **L**) in the Preview window. The automatic skin and BEM setup requires 5-10mm of space around the subject's skin. If necessary, use the **Shift** and **Zoom** settings to achieve this. In this example, **Intensity** was decreased to **100**, and **Centered** was disabled to allow an **X Shift** (**10** pixels) and a **Y Shift** (**-10** pixels).



The target image parameters control how single slices appear in the image cube. A target image has a size of 256x256 pixels, as this is the size of a slice in the iso-image cube.

- The image **Intensity** percentage can be adjusted to achieve saturation (use Automatic if you are uncertain).
- The image **Intensity** can be inverted if necessary by using negative percentages.

– The images can be shifted, in order to guarantee a minimum distance of about 10 mm between the skin and the image borders. Such a minimum distance is a prerequisite of many segmentation procedures. *Actually, this is the only parameter that might need to be adjusted for DICOM files, where everything else can be detected from the header. Everything else on the prior pages rarely needs to be adjusted.*
– The images can be zoomed or shrunk, in order to make them fit well into the available 256x256 pixels. Zooming or shrinking images can degrade image quality.
– The images may be rotated and mirrored, so that the image contents coincide with the anterior, posterior, left, and right marks that appear in the **2D Preview** window.

 **Note**
If nothing can be seen in the **2D Preview** window, increasing the **Intensity** factor significantly may be the key.

 **Care**
For axial and coronal slices, it can be difficult to tell left from right. Nevertheless, it is crucial that these are known and that rotation/mirroring are used to assign them correctly.

Experience shows that often, if rotation is 180deg, mirrored needs to be checked.

Slice Orientation. Select the view that matches the MR orientation in the display. Left, Right, Anterior, and Posterior markers are plotted with the slices. If these make no sense, the slice orientation is wrong.

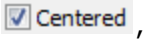
Rotation [deg], Mirroring. Adapt the slice so that the Left, Right, Anterior, and Posterior markers are correct, and up is up. Enable the Mirrored option to reverse the image.

Intensity [%]. Increasing the percentage increases the intensity of the images. Very often, the Intensity must be increased significantly, before the images in the preview window become visible. Intensity factors of **1000**% are common. Negative values invert intensities. Click the 

option to have CURRY determine the best intensity.

Zoom [%]. This can be used to increase or decrease the Zoom percentage (size of the image). Some space should be left around the subject's skin in order to enable CURRY's automatic BEM setup.

X Pixel Size [mm] / Y Pixel Size [mm]. Use these options to vary the pixel size along the x or y axes. The Field Of View is defined as (No. Pixels) x (Size).

X Shift [pixels] / Y Shift [pixels]. Use these option to reposition the image along the x-axis or y-axis in the screen. If you enable 

, CURRY will center the image automatically. Some space should be left around the subject's skin in order to enable CURRY's automatic BEM setup.

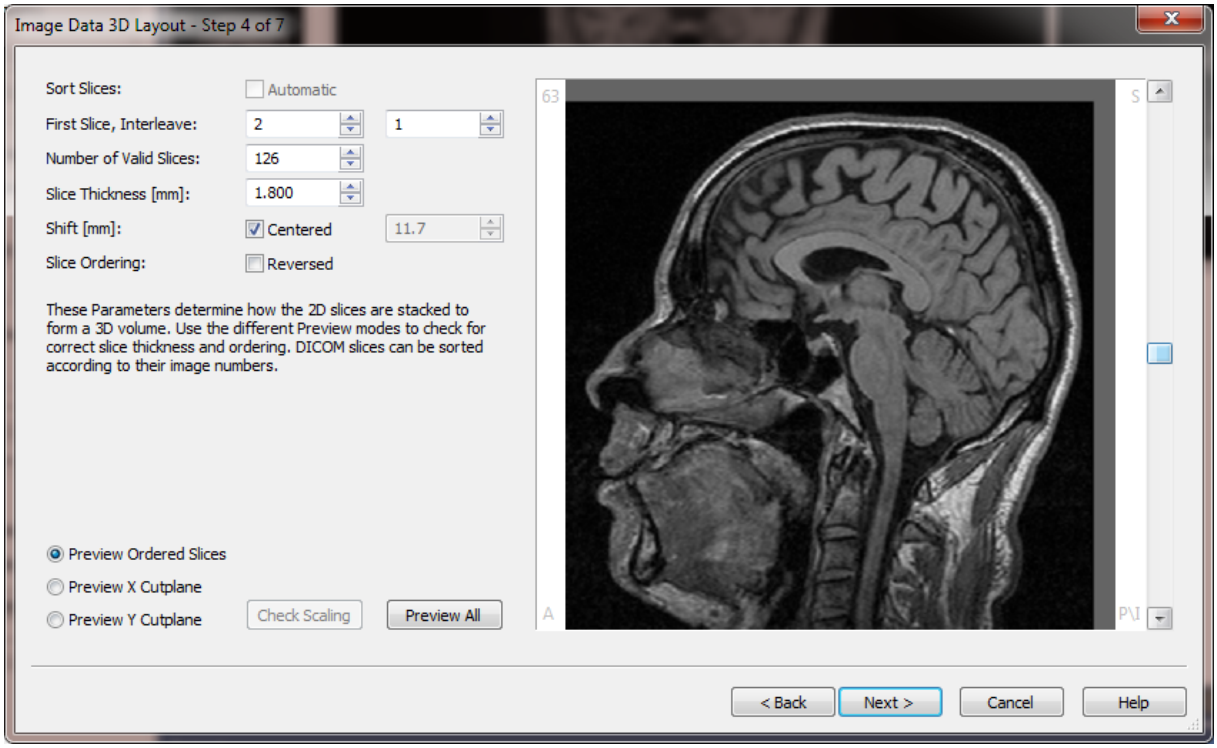
Note

As mentioned above, the X and Y Shift parameters are often the only ones that might need to be adjusted for DICOM files, where everything else can be detected from the header. Everything else on the prior pages rarely needs to be adjusted.

Click the Preview All button to scan through the images.

Step 4. Click the Next > button to display the **Image Data 3D Layout** dialog screen. These parameters determine how the 2D slices are stacked to form a 3D volume. Use the different Preview modes to check for correct slice thickness and ordering.

In this file, the **First Slice** was set to **2**, and there were **126 Valid Slices**. Again, these parameters will depend upon your particular file.



When the target images in the **2D Preview** window look reasonable, they have to be arranged in the image cube.

Care

It is crucial to distinguish correctly between left and right sagittal slices. Markers should be used during MR acquisition to alleviate this task.

Sort Slices. In folder mode (where there is one file per slice), for ACR-NEMA and DICOM, image files contain series and image numbers that imply an ordering of slices that does not need to be the same as the lexicographic ordering that

is determined by the first page, if "All slices" is selected. Use **Automatic** to sort the slices automatically.

First Slice, Interleave. An interleave larger than one means that slices are skipped. Normally, slice **1** is the first slice, and the interleave is **1**. A First Slice of **30** will disregard the first 29 slices. An Interleave of **2** will omit every 2nd slice.

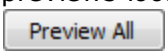
Number of Valid Slices. This is the number of slices to be read. Typically, this parameter is equal to the number of slices. If there are **100** slices in the dataset and the first three are bad, the **First Slice** would be **4** and there would be **97** Valid Slices.

Slice Thickness [mm]. This is the slice thickness, including the gap. Ensure that the Slice Thickness is correct.

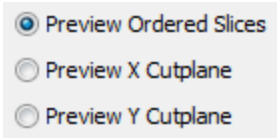
 **Care**
Even if the **Slice Thickness** is automatically detected, its value may be incorrect! This is the most difficult parameter to determine, and it is not always correctly stored in the file headers.

Shift [mm]. This determines the start of the slices in CURRY's internal image cube. Normally, **Centered** is the best option.

Slice Ordering. Adapt the Slice Ordering so that the Left, Right, Anterior, and Posterior markers are correct and up is up. Use the **Reversed** option if needed.

Previewing. In the **Orthogonal Cut** previews, the stacking of slices can be controlled. Adapt the Slice Ordering so that the Left, Right, Anterior, and Posterior markers are correct and up is up. Some space should be left around the subject's skin in order to enable CURRY's automatic BEM setup. If the previews look stretched or compressed, review the **Slice Thickness**. Click the 

button to scan through the images.



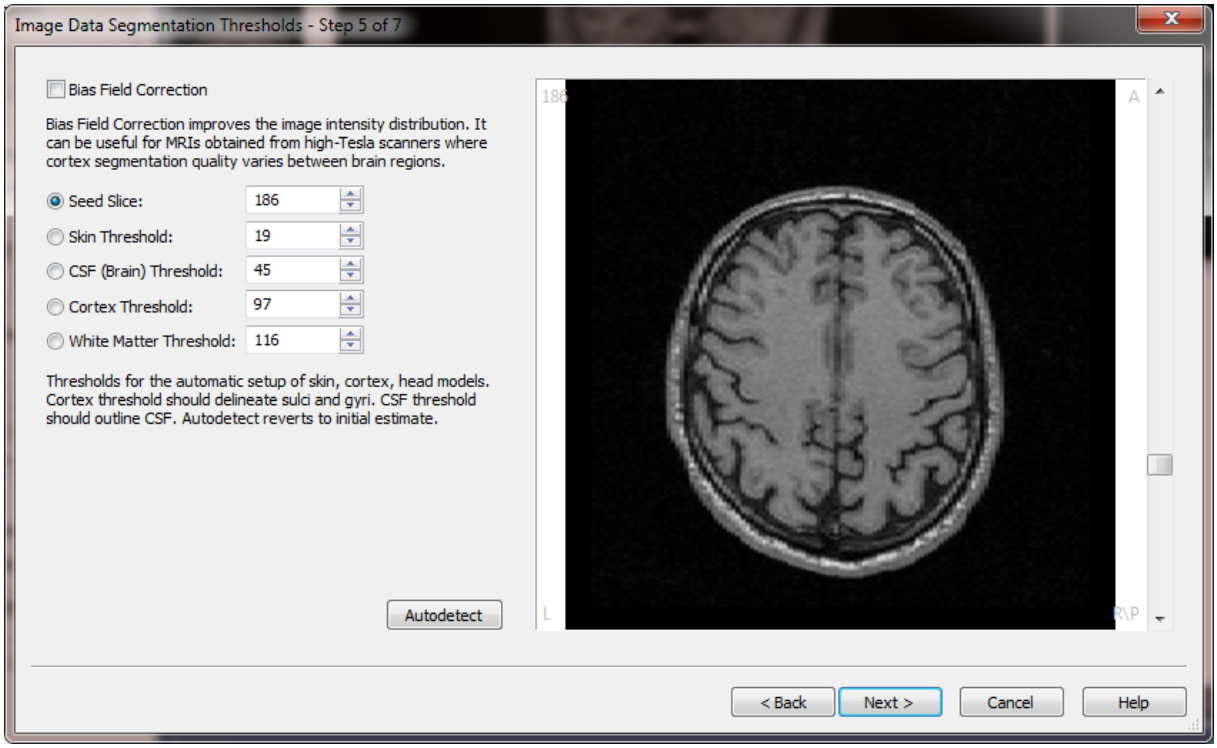
Check Scaling. When loading Image Data 2 (after a first image data set is already loaded), the image data can be matched using a procedure called volume-based coregistration. This is used in Step 6 when you select **Autodetect** in order to derive landmarks locations from Image Data 1 without needing to enter them manually. The **Check Scaling** button is active for Image Data 2 (or 3) only, and is another way of employing the same algorithm, this time in order to see whether the voxel size is specified correctly. When this button is pressed, there will be an extensive message if any errors or problems are detected. In general use, this option is rarely needed. It is used only when you have reason to suspect the voxel dimensions (FOV) in either data set are incorrect.

Step 5. Click the Next > button to see the **Image Data Segmentation Thresholds** dialog screen. These are the thresholds used for the automatic setup of the skin, cortex, and BEM models. The Cortex Threshold is generally the most important one. It is what later determines the shape of the cortex created by BEM Geometry (automatic segmentation). If this value is too high, the cortex will look atrophic (eroded). In such a case, the cortex threshold will appear more like a white matter-gray matter boundary: the automatically detected value should be lowered. When lowering the cortex threshold, make sure that sulci are not filled as this will exclude them from the resulting triangle net. The autodetected cortex threshold is sometimes too high but hardly ever too low.

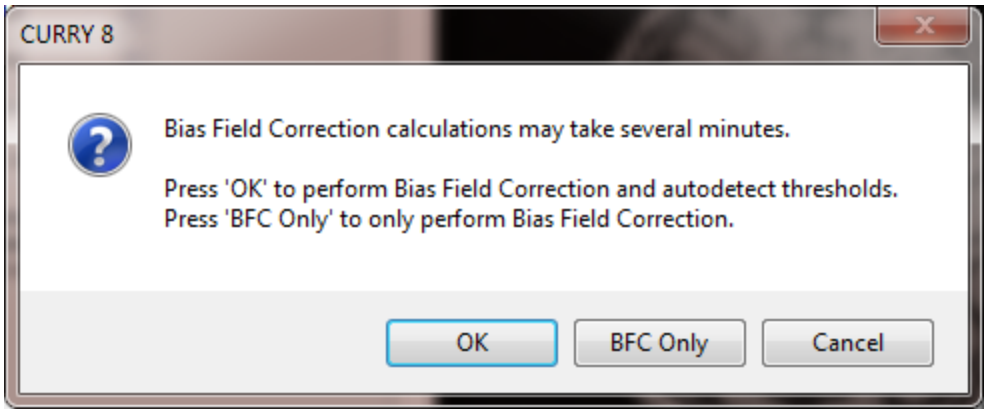
The white matter threshold is an uncritical parameter; it should simply show some contrast anywhere within the white matter and hardly ever needs to be adjusted.

The values shown are the Autodetected thresholds, which are usually good estimates. The **Seed Slice** is shown first. Click **Next**.

Use Autodetect to obtain an initial estimate.

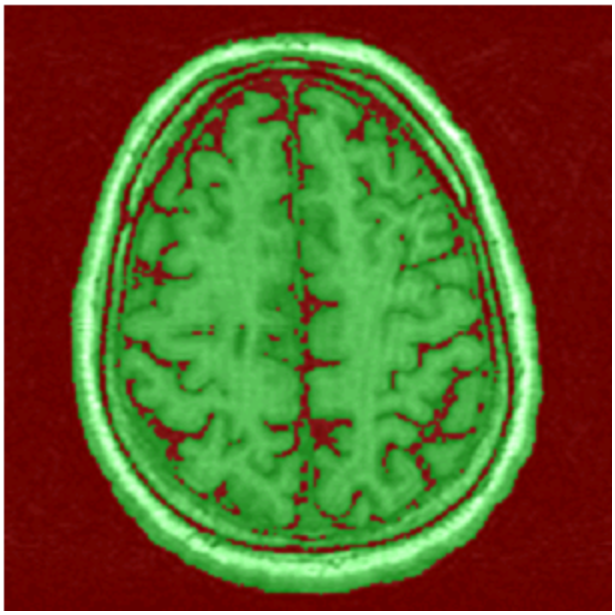


Bias Field Correction. Bias Field Correction improves the image intensity distribution. It can be useful for MRIs obtained from high-Tesla scanners where cortex segmentation quality varies among brain regions. Enabling the option displays the following screen. As it explains, press OK to perform Bias Field Correction and autodetect thresholds (same as Autodetect). Select BFC only to perform only the Bias Field Correction. You may then set the thresholds manually or by using Autodetect.

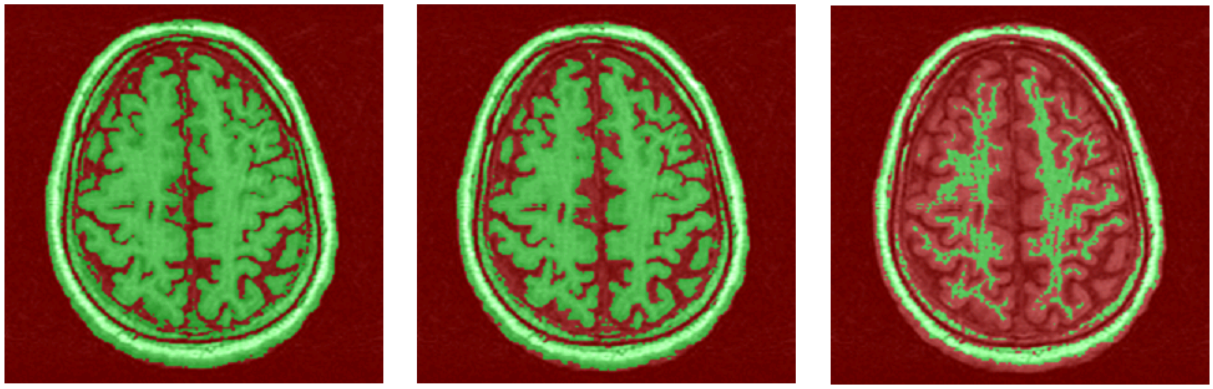


Seed Slice. This is the number of the slice used for the seed for segmentation. This should be a slice slightly above the eyes, containing no other structures than brain, skull, and skin. This slice is not used for autodetection, it is rather used for starting automatically seeded segmentation.

Skin Threshold. This will be a number that clearly differentiates the Skin from the exterior (make sure that Skin structures are visible while background noise is suppressed). For example, click the **Preview** button for **Skin Threshold**. The **Stop Markers** are in red (dark red), and the **Pass Markers** are in green. For the Skin Threshold, there should be a separation between the skin (pass) and the exterior (stop).



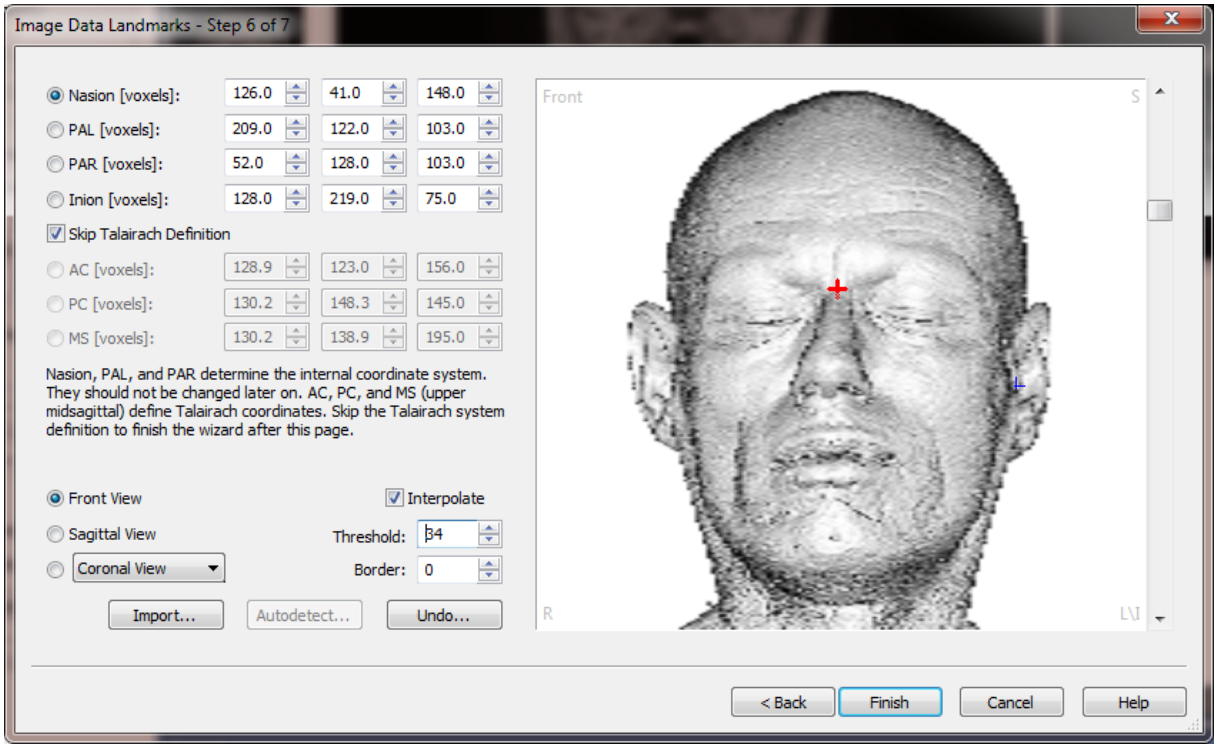
Similarly, the **CSF (Brain)**, **Cortex** and **White Matter Thresholds** should clearly differentiate their respective boundaries, with little or no "bleeding" across the boundaries. If possible, the **Brain Threshold** should encompass all brain structures, including the dura. The **Cortex Threshold** should be set to expose the center of the gray matter layer. All cortical gyri and sulci should be delineated. The **White Matter Threshold** should include the white matter structures without the gray matter.



CSF (Brain) Threshold | Cortex Threshold | White Matter Threshold

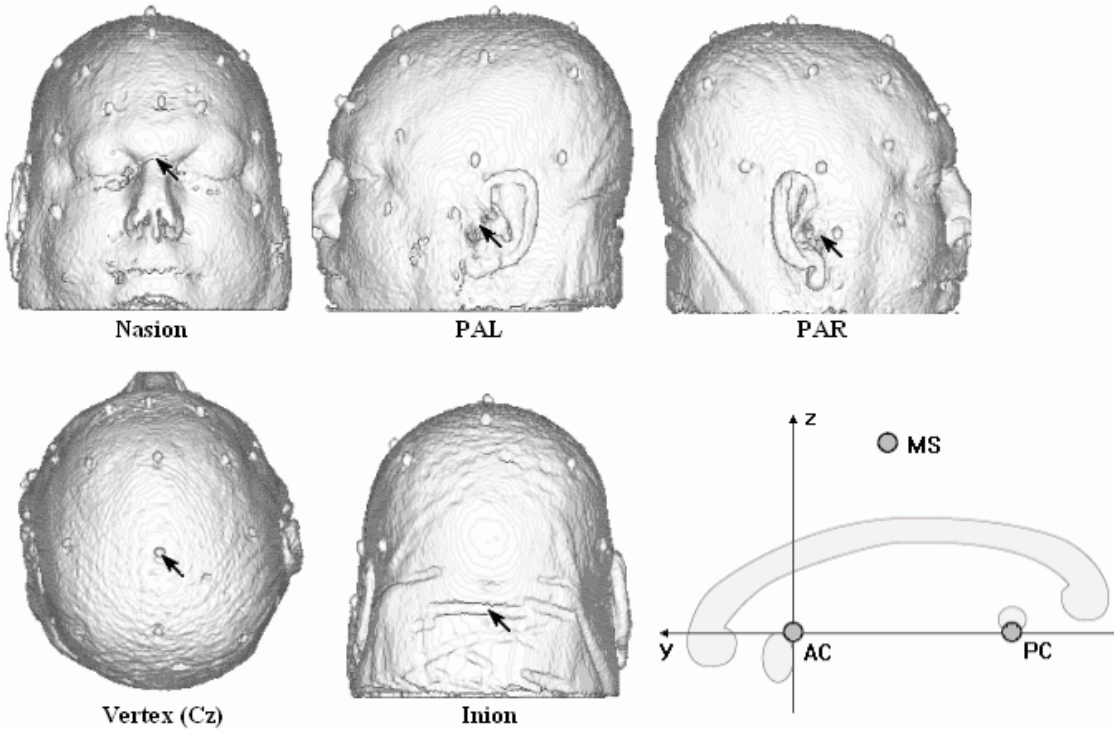
Autodetect. Click this button to start CURRY's automatic threshold estimation.

Step 6. Click the Next > button to see the **Image Data Landmarks** dialog screen. Use this display to set or review the landmarks: Nasion, Preauricular left (PAL), Preauricular right (PAR), and Inion. If you will be defining the Talairach coordinates, you will also need to define the Anterior Commissure (AC), Posterior Commissure (PC) and Upper Midsagittal (MS). AC and PC locations in the mid-sagittal view are shown below. The midsagittal position is directly along the longitudinal fissure.

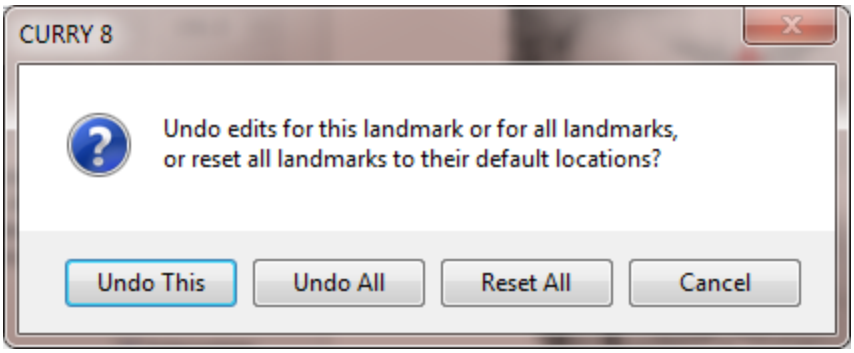


Care

As discussed earlier, the image data landmarks should be defined as early as possible. When you initially load the MR data, the crosshair positions of the landmarks will be incorrect. Reposition these carefully, as they will be used for co-registration with the Functional Landmarks. If you change PAL, PAR, and Nasion at a later time, results you may have already obtained become invalid. The other landmarks may still be changed at a later time.



Clicking the Front View and Sagittal View buttons, along with the Coronal View views, will display different orientations to allow you to set/verify the landmarks. The Front View is the one in which the landmarks can best be identified. This view is depth-buffered, which means that by clicking or dragging, the landmark is defined in all three axes. Grab-and-drag a crosshair to reposition it, as needed. The Interpolate option (same as is Step 7) provides a slightly more "blended" or smoother view of the images. The Next > and < Back buttons will step through the landmarks. If you have the positions already stored in an .imd parameter file, you may use the Import... button to retrieve and apply the positions. The Undo... button allows you to undo edits you have made. You may undo the most recent edit (Undo This), undo all edits, or reset all edits.



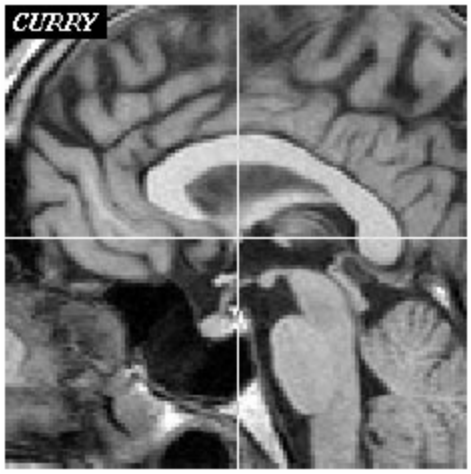
Increase or decrease the Threshold: 34 as needed if the images are noisy or frayed. The Border: 0 option sets the depth starting from where the image is rendered. This is used to remove objects in the images (e.g. a stereotaxic frame in CT images) in order to see the ears for entering the PAL/PAR landmarks.

The Skip Talairach Definition is enabled by default. If you wish to skip this step, just click the Finish button and to see the image data displayed in CURRY. Deselect the option to define the additional landmarks, shown below, and then go to Step 7 to define the Talairach boundaries.

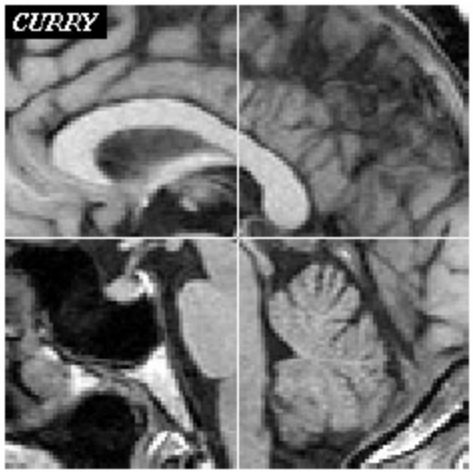
Care
You may decide to use other definitions of PAL and PAR landmarks that might be used in your lab's electrode digitization protocol. However, the built-in standardized and interpolated (non-individual) BEM and FEM models work best with the landmark definitions shown here.

Care
If you are going to use the Talairach system. it is especially important that you define the AC, PC, and MS positions carefully.

The AC and PC as seen in a midsagittal slice are shown below. The AC is the origin of the Talairach coordinate system. The negative Talairach y axis goes through the PC. When defining AC and PC, make sure you are placing them in the interhemispheric plane, which is best done by switching to an Axial view.

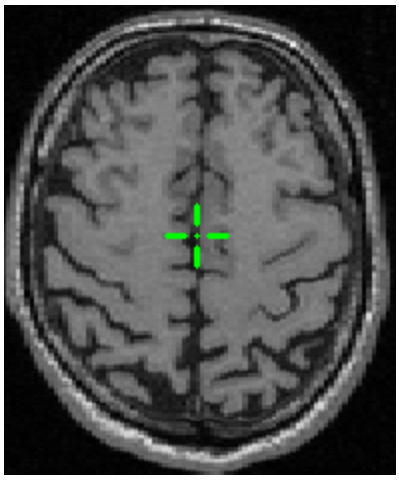


anterior commissure



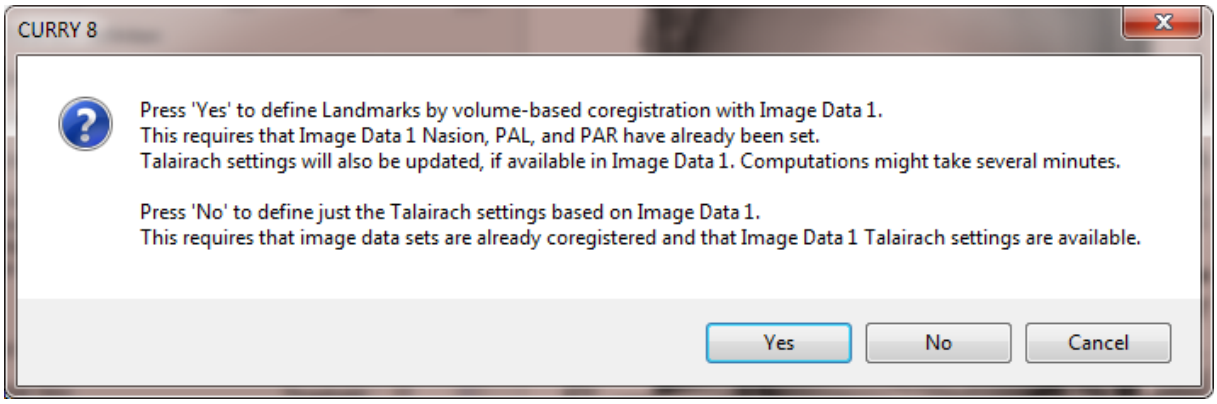
posterior commissure

The MS position is a midsagittal point in the interhemispheric fissure. The Talairach (y,z) plane will go through this point.



Volume based coregistration. If you have two (or three) image data sets together, you can use "volume based coregistration" to avoid having to define the landmarks manually in the second (and third) sets (although at least crudely setting the Nasion, PAL and PAR in the second, and third, sets will help). Volume based coregistration is a form of landmark autodetection, in which the spatial relation (coregistration, transformation) between a second (or third) image data set and the first image data set is computed by means of a method called "maximization of mutual information". The landmarks are then set accordingly, and you do not need to enter the landmarks manually. This is accessed by clicking the 

button. It is only available for the second (or third) image data set because it needs an existing Image Data 1 with its PAL, PAR, NAS landmarks set.



In most cases where you have, for example, MRI and CT data sets, the recommended procedure is:

1. The MRI data should appear above the CT data in the Study in the Database (so Image Data 1 is the MR, and Image Data 2 is the CT data set).
2. Define the Nasion, PAL and PAR for the MR data.
3. Return to the **Image Data Parameters** windows after selecting the CT data, and go to Step 6.
4. Click the **Autodetect** button to see the above message (**Skip Talairach Definition** should be enabled).
5. Click **OK** and then Finish the **Image Data Parameters** windows.

If the resulting coregistration delivers nonsensical results (rare), then the Nasion, PAL, and PAR should be set manually and approximately (crudely) for Image Data 2 before pressing Autodetect.

Step 7. The final step for importing the image data is to set the boundaries for the extent of the brain in relation to the AC and PC. These are used in the conversion to Talairach coordinates, and so should be set carefully.

Anterior-AC. The distance between AC and anterior border of the brain.

Posterior-PC. The distance between PC and posterior border of the brain.

Superior-AC. The distance between AC and superior border of the brain.

Inferior-AC. The distance between AC and inferior border of the brain.

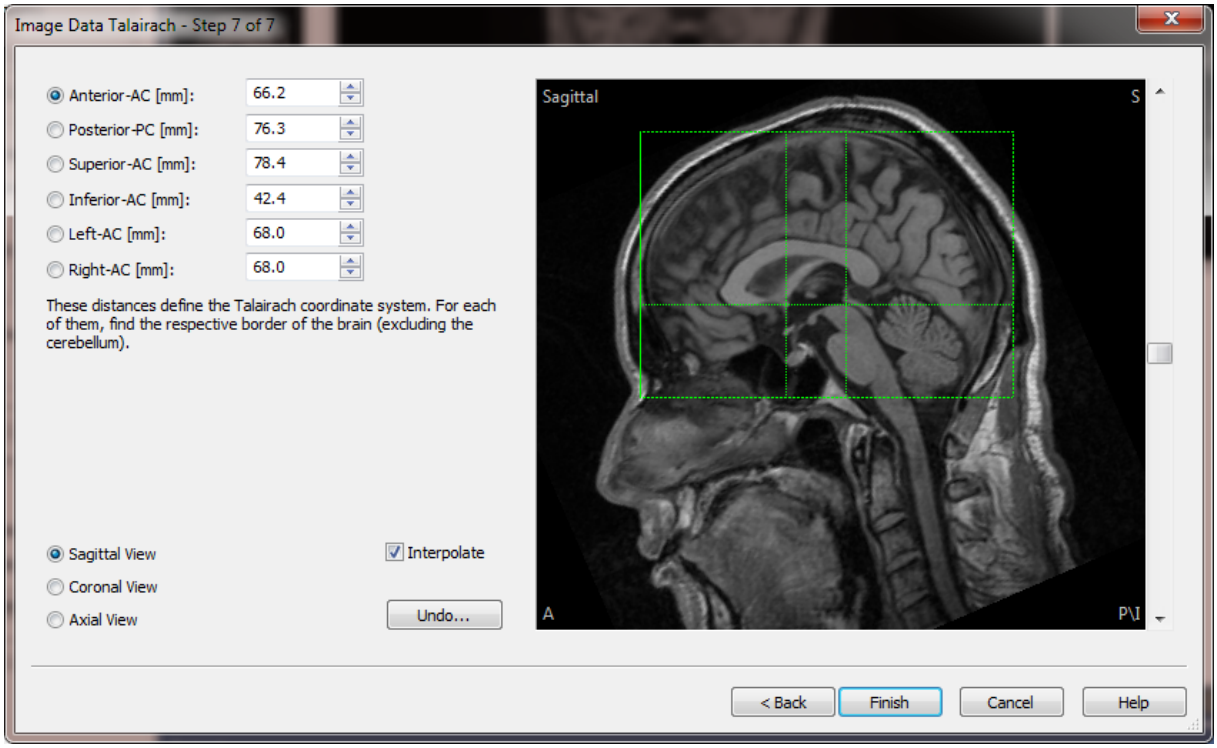
Left-AC. The distance between AC and left border of the brain.

Right-AC. The distance between AC and right border of the brain.

View (Sagittal, Coronal, Axial). The displayed cutplane (aligned to the Talairach axes defined by AC, PC, and MS) through the image data.

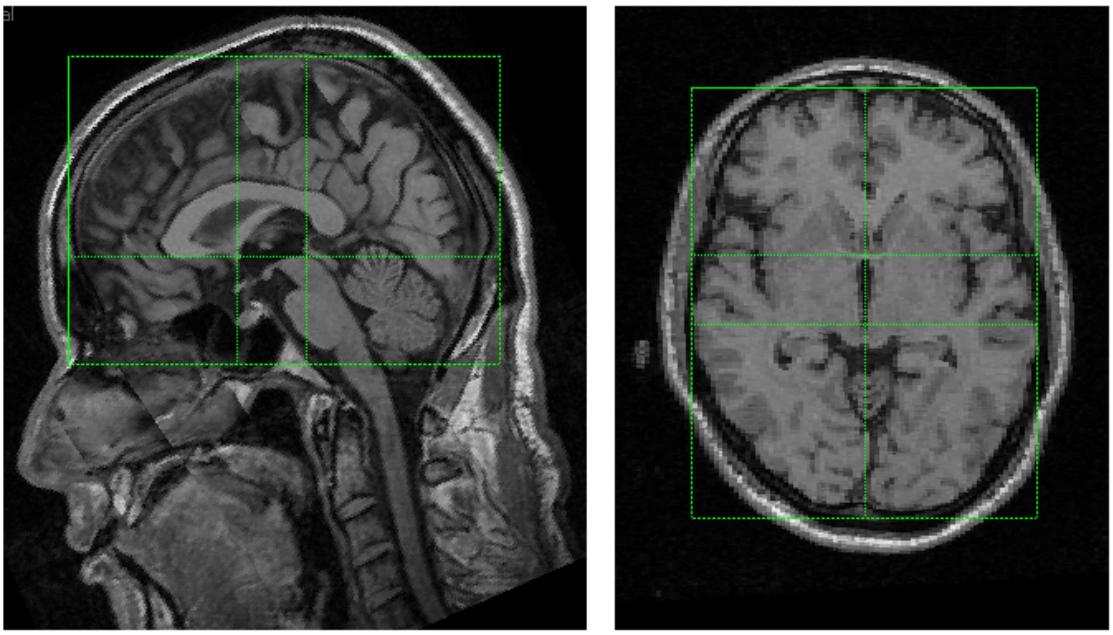
Interpolate. If selected, image data are interpolated for a smoother image (same as in Step 6).

Undo. Brings up a selection that allows to change the edited distance back to the value it had when this page was first displayed, or to change all distances back to the values they had when this page was first displayed, or to reset all distances to their defaults.

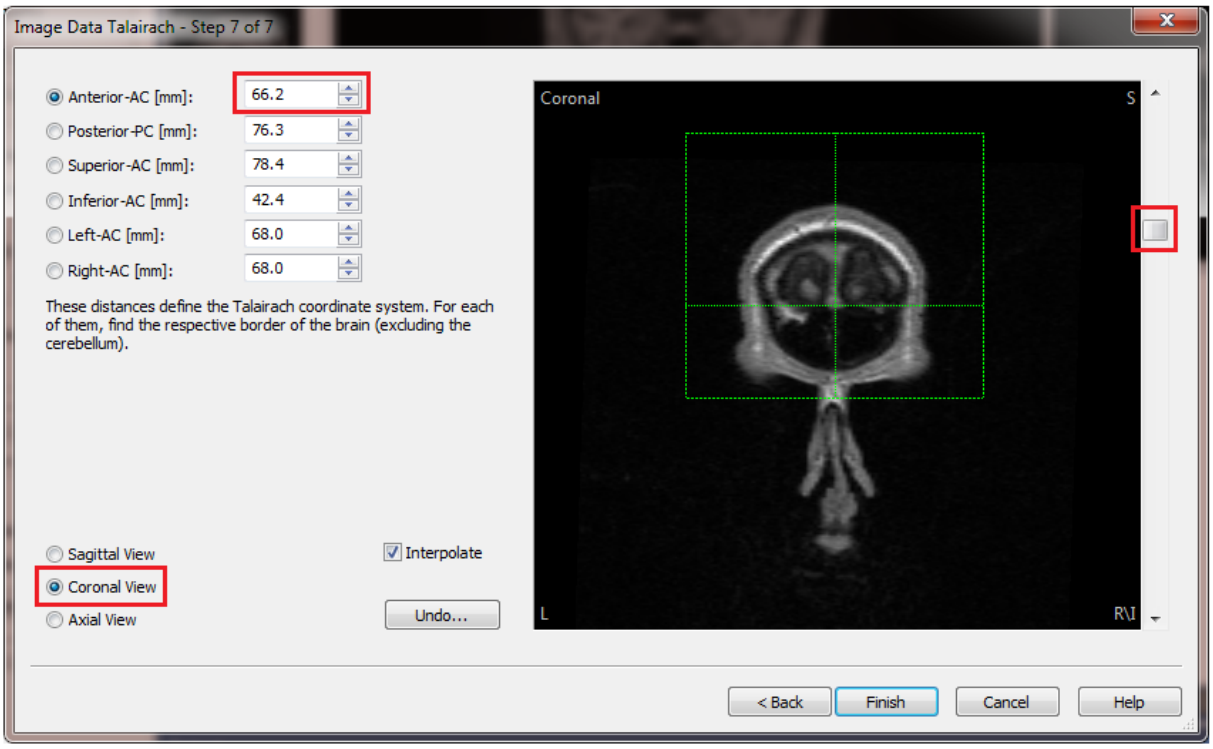


The numerical fields display the mm distance from either the AC or PC position set in Step 6 to the various boundaries. Use a slice that best displays the extent of the brain, and then position the edges of the rectangle to encompass the brain. Do not allow the brain to extend beyond the boundaries. For the lower extent (inferior-AC) use the temporal lobes, not the cerebellum.

The interior lines seen in the boundary boxes illustrate that a 12-compartment (2 layers of 6 regions) method is used in converting the images to Talairach space. The exterior lines define the outer planes of the rectangular box. The inner planes go through the AC and PC, horizontally and vertically. The compartments are fitted individually, which makes for a more accurate conversion.

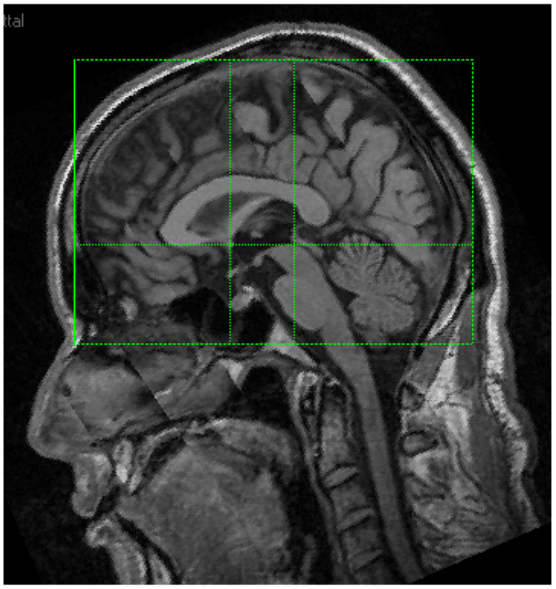


Note that you can change the view using the Sagittal, Coronal, and Axial View options to help in the placement of the boundaries, if needed. For each measurement, one of the three Views is tied to the boundary position. For example, if you select the Anterior-AC [mm]: measurement, the Coronal View is tied to the frontal boundary. That is, if you select both of those options, you can then use the sliding bar to the right of the image display to move through the frontal slices. By viewing the images, you can see where to position the boundary by seeing where the brain no longer appears in the MR images. That position is transferred automatically (continuously) to the Anterior-AC measurement.

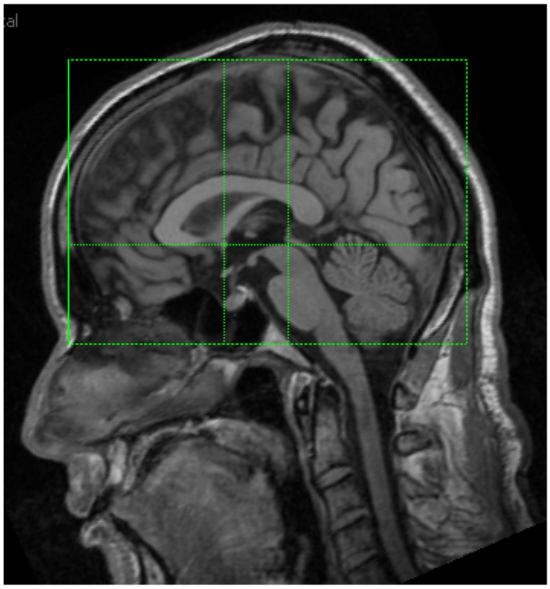


The View that is linked to the measurement field varies depending on the boundary you have selected, but one View will always be linked. This provides an additional way to determine the boundary placements.

The Interpolate option  can be enabled to provide smoother appearing images.

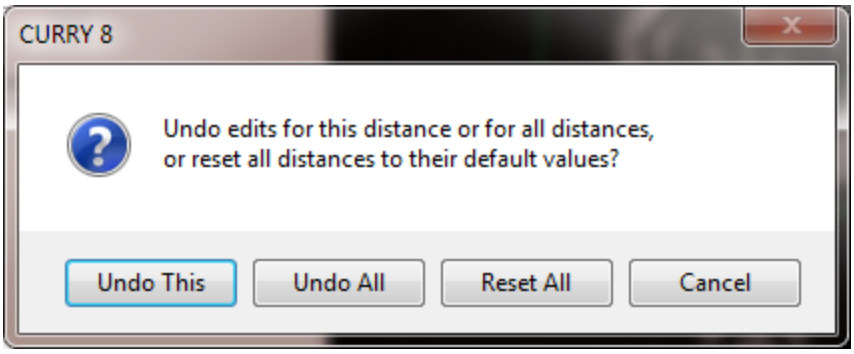


Uninterpolated

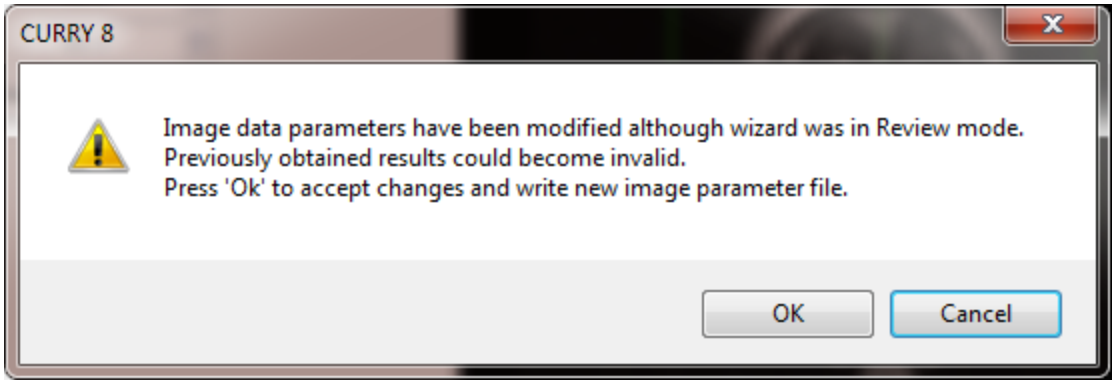


Interpolated

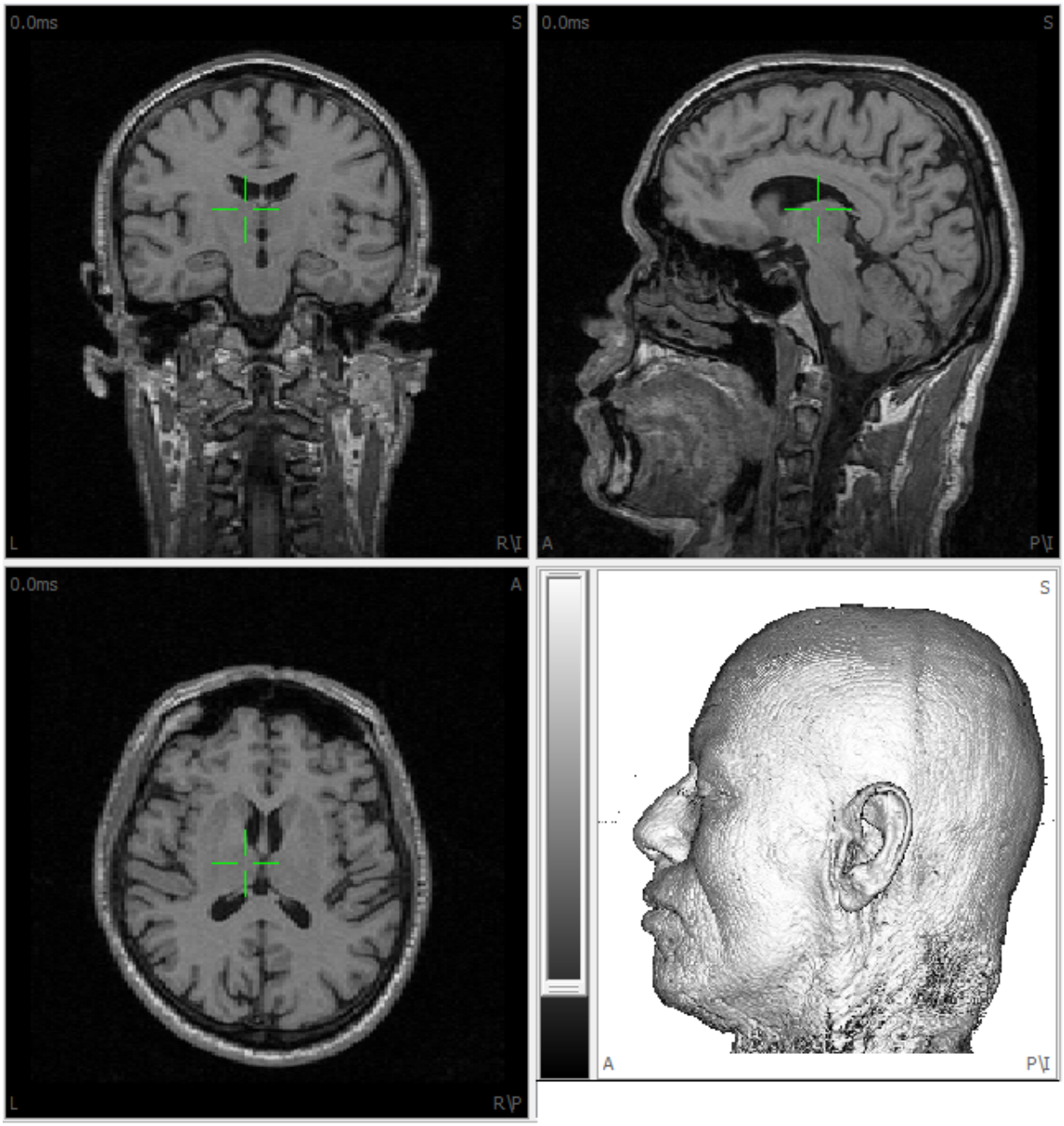
The Undo... button allows you to undo changes to the selected landmark (that is, the one that is currently selected: Anterior-AC [mm]:), undo changes to all landmarks, or revert to the default landmarks.



When you have set/reviewed all of the landmarks, the Next > button will be replaced with the Finish button, and you will see a Warning for any changes that were made (if you are reviewing previously loaded data).



Click OK to the message, realizing that prior results may be invalid. The image data are now loaded (and the anatomical landmarks are written to the .imd file).



Carefully check the appearance of the images in the window, especially with respect to slice spacing (the **Slice Thickness** parameter) and orientation of the axes (left/right, anterior/posterior).

18.1.2 Coordinate Systems

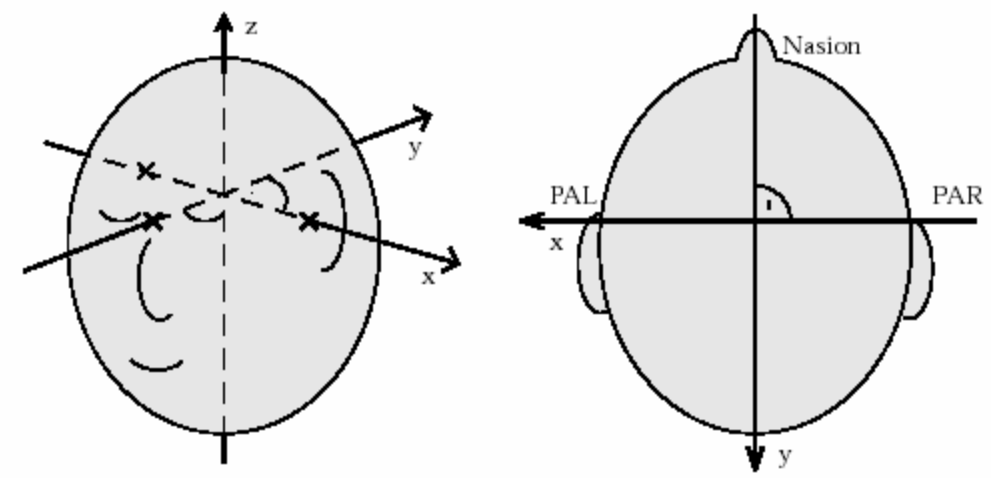
CURRY represents locations and orientations in an *internal coordinate system*. File or user interface input and output of locations and orientations is performed in a coordinate system that has been chosen by the user, the *display coordinate system*.

The display coordinate system may be changed at will (described below). After changing the coordinate system, all user interface elements and all files and logs that are written use the new coordinate system.

Internal Coordinate System

The internal coordinate system is a PAN system. This means that it is defined via the preauricular points and the nasion of the subject.

- Its positive x axis goes through PAL (left preauricular point).
- Its negative x axis goes through PAR (right preauricular point).
- Its negative y axis goes through the nasion.
- Its z axis is 90 degrees from the intersection of the x and y axes.



Such a landmark-based internal coordinate system has been chosen in order to facilitate the comparison of results between subjects (see below).

Care

The internal coordinate system depends on the image data landmarks: PAL, PAR, and Nasion. If any of these are changed, all segmentation results including triangle nets and anatomical landmark files, and all source reconstruction results will become invalid.

Display Coordinate Systems

Once landmarks have been defined and saved, the coordinate system which CURRY uses for input and output can be freely chosen using the **Coordinates** options in the **Results Properties** panel under Results, or from the Main Menu Bar.

18.1.3 Switching Between Image Modalities

The **Image Data** windows can display and process image data from up to three data sets. This can be useful for a variety of purposes:

- comparison of image data sets across subjects,
- comparison between individual and gross average image data (gross average image data comes with CURRY),

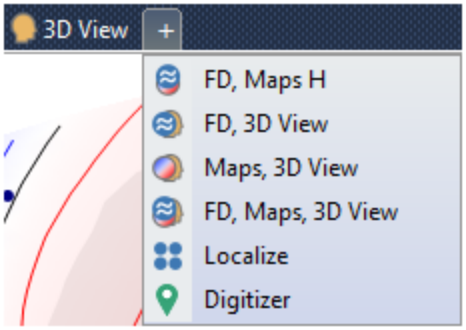
- more exact head models using the skull shape from CT,
- comparison between source reconstruction results and functional imaging such as fMRI, PET, or SPECT, and
- constrained source reconstructions incorporating information from functional imaging.

The additional image data sets are loaded just like the first one: insert the data sets in the **Image Data** folder in the Database. When you open the Study, you will see additional display tabs: 

, allowing you to switch among MR data sets. When you select the 

display, you will see additional tabs at the bottom allowing you to switch among sets.

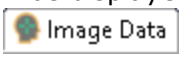
If you do not see the display option you are looking for, click the + sign at the end of the options to additional display options.



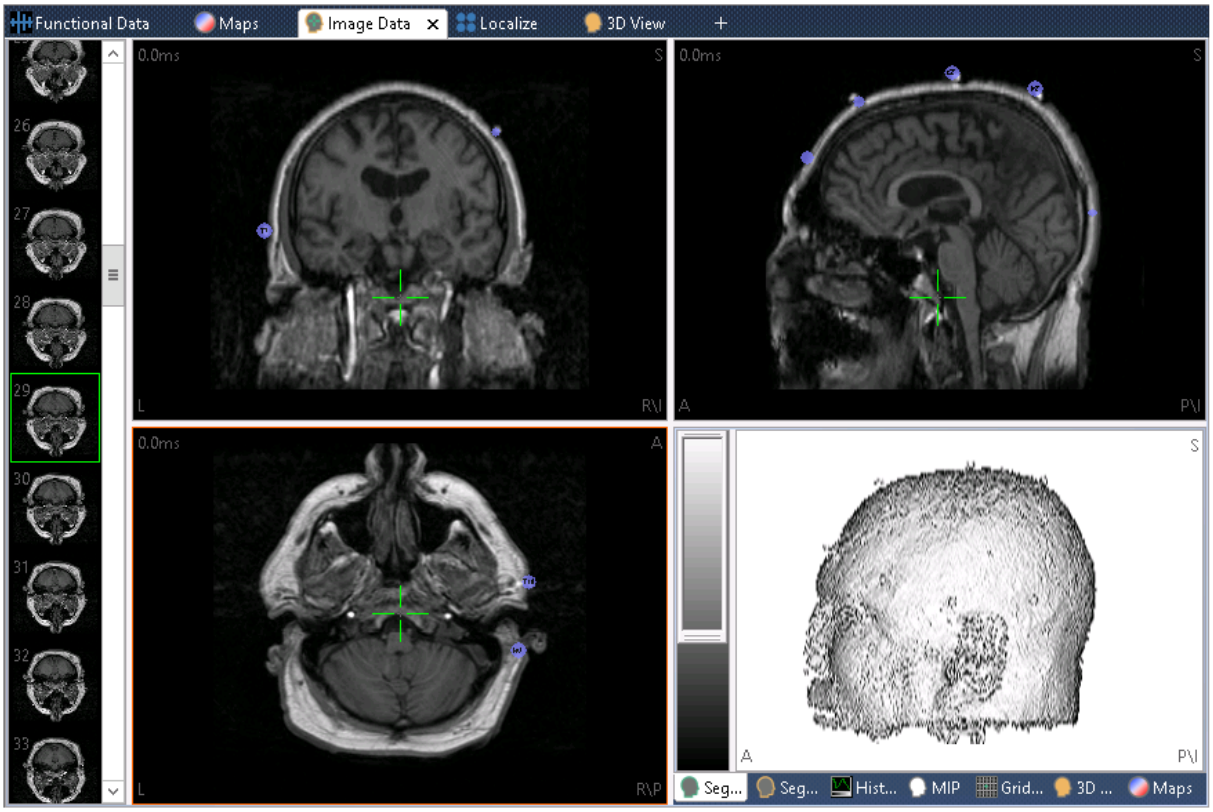
18.2 Image Data (Processing)

This chapter describes CURRY's image processing features (and these will vary depending upon the license you have). These include the display and segmentation of images, the manipulation of segmentation results and the generation of triangle nets for visualization, BEM modeling, and anatomically constrained source reconstruction.

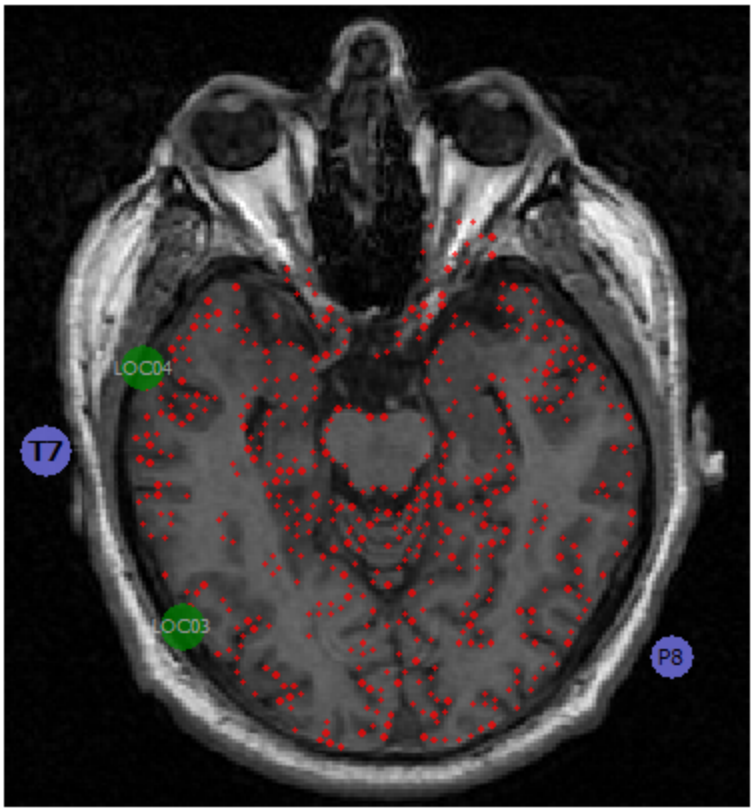
Image Data Display

Once image data have been loaded, they can be displayed in a variety of ways. The upper left, upper right, and lower left areas in the 

window provide the basic views, while the lower right area can show a selection of special displays.



Electrode labels (blue), surface points (red), and Localize labels (green) will be seen in the Image Data display, assuming these have been selected and sized in the 3D View.



Filmstrip. The Filmstrip on the left side shows the individual slices in their original orientation. A tooltip displays the slice number. Clicking on a slice will select it in the orthogonal display.

Image Data Cursor

The **Image Data** windows each have its own cursor that defines a position within the iso-image. Changing the cursor changes all related views. The cursor is displayed as a cross-hair in the orthogonal sections. A red border will outline the area that has the focus.

Mouse Controls

Left click - changes the location of the 3D cursor. In **Edit Markers** mode (crosshair mouse pointer), a marker is drawn.
Drag - changes the location of the 3D cursor. In **Edit Markers** mode (crosshair mouse pointer), connected markers are drawn.
Mouse wheel - changes the slice number. Depressing the mouse wheel or pressing **Control** results in a finer resolution.
Right click - displays the context menu.

Selectable Fourth View

The lower right view is used to display several special views using the tabs below it. For more information, see the **Image Data, Context Menu** section below.

Segmentation Preview. This is the depth-buffered segmentation preview display. Depending on the selected view, the surface matching the segmentation thresholds is rendered. Using depth-buffering, the surface locations can still be retrieved.

Segmentation Result. This is the depth-buffered segmentation result display. Depending on the selected view, the segmentation results are rendered. Using depth-buffering, the surface locations can still be retrieved.

Histogram. Image data intensity histogram display, together with the segmentation thresholds. In the color scale below, the color lookup table for the image data can be changed (Hounsfield scaling, level-and-window).

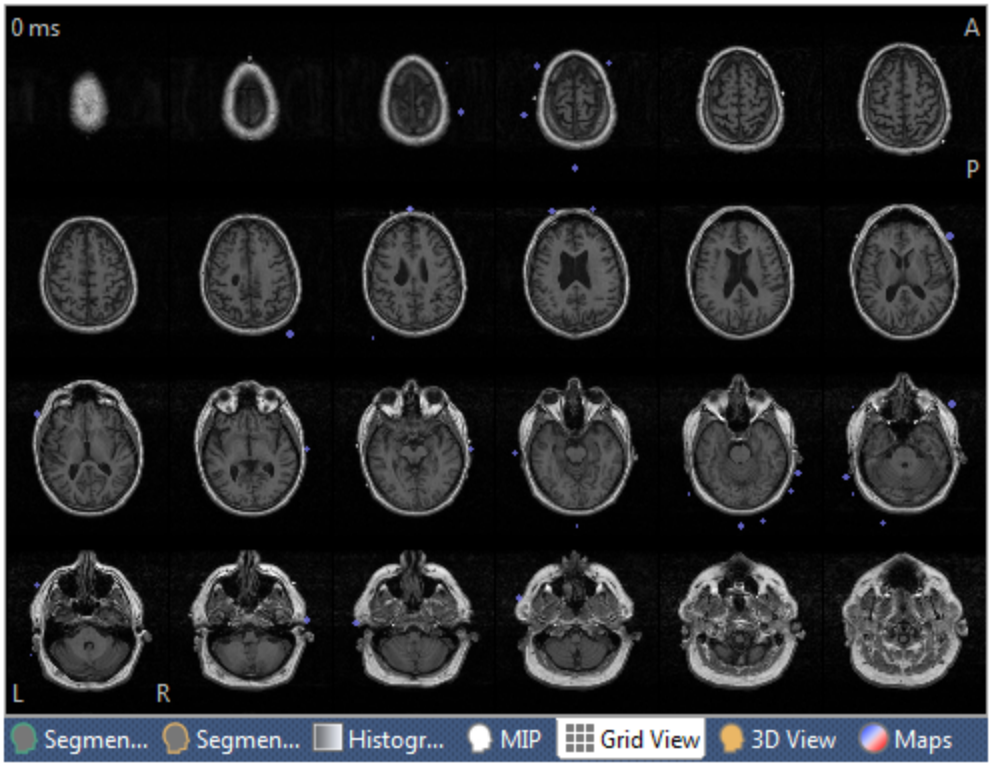
Maximum Intensity Projection (MIP). This is the depth-buffered maximum intensity projection display. Depending on the selected view, the voxels with the largest intensity are projected onto the view plane. Using depth-buffering, the locations of the maximum intensity voxels can still be retrieved. In the color scale on the left, the color lookup table for the MIP can be changed (Hounsfield scaling, level-and-window).

3D View. This shows the 

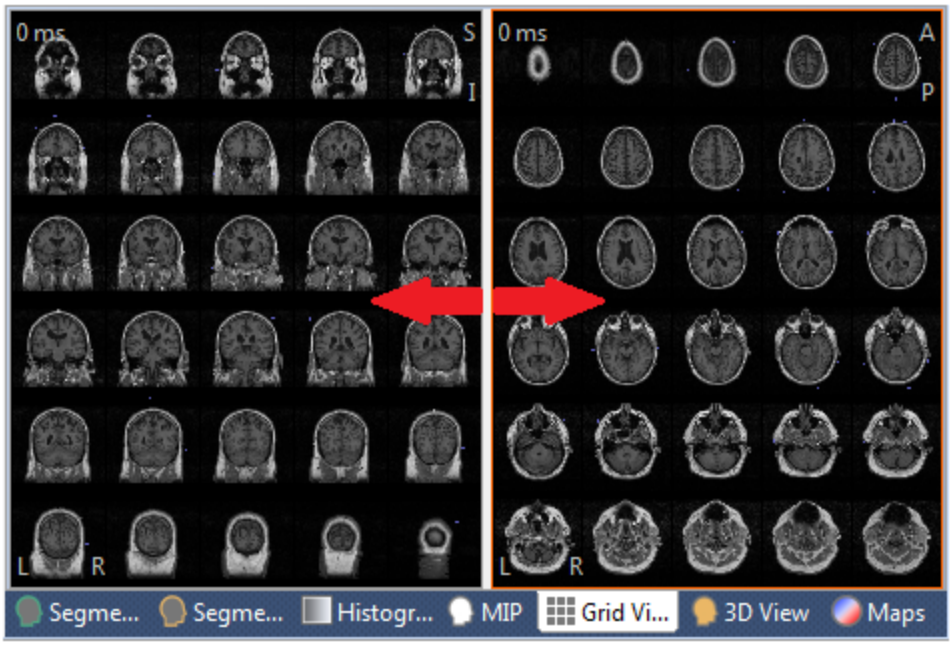
display.

Grid View. This displays the 

. Use the *mouse wheel* to vary the number of slices displayed.



Drag the divider to see the Dual Grid view.



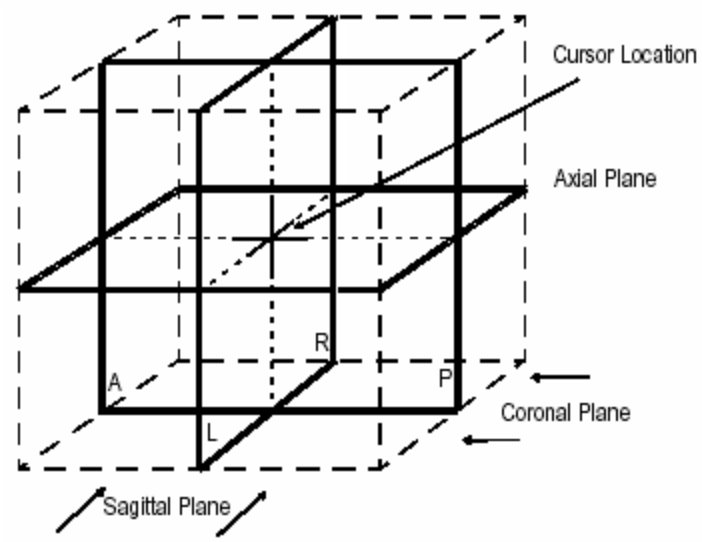
Maps. This shows the Maps display.

Orientation

The raw anatomical data series contains a stack of 2D slices all having the same orientation. In the Image Data window are shown three orthogonal cross sections through this stack of slices, as shown below.

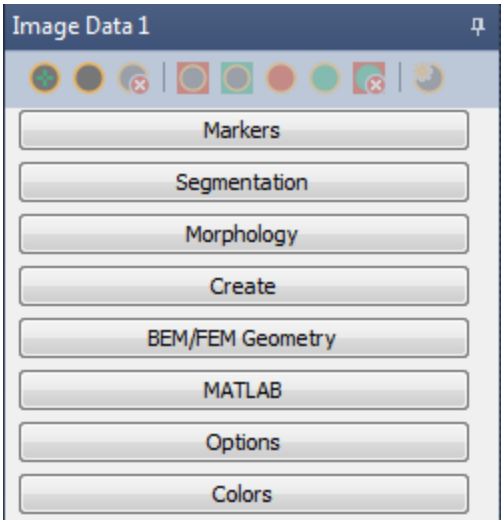
The sagittal, coronal and axial views are related to each other and show a cross sectional view through a loaded anatomical data set. All three views have cross hairs that can be moved manually. This changes the other cross sectional views. In the lower and right corners of each view there are letters. These letters display the orientation of the image. A: Anterior, P: Posterior, L: Left, R: Right. The contents of the lower right hand image can be selected. It shows a Maximum Intensity Projection (MIP), a segmentation preview, a surface rendering of the segmentation results, a histogram of the image intensity, or the same view as seen in the 3D View or Maps display.

Below is a schematic representation of the relation between image slices and the three orthogonal planes shown in the Image Data window.



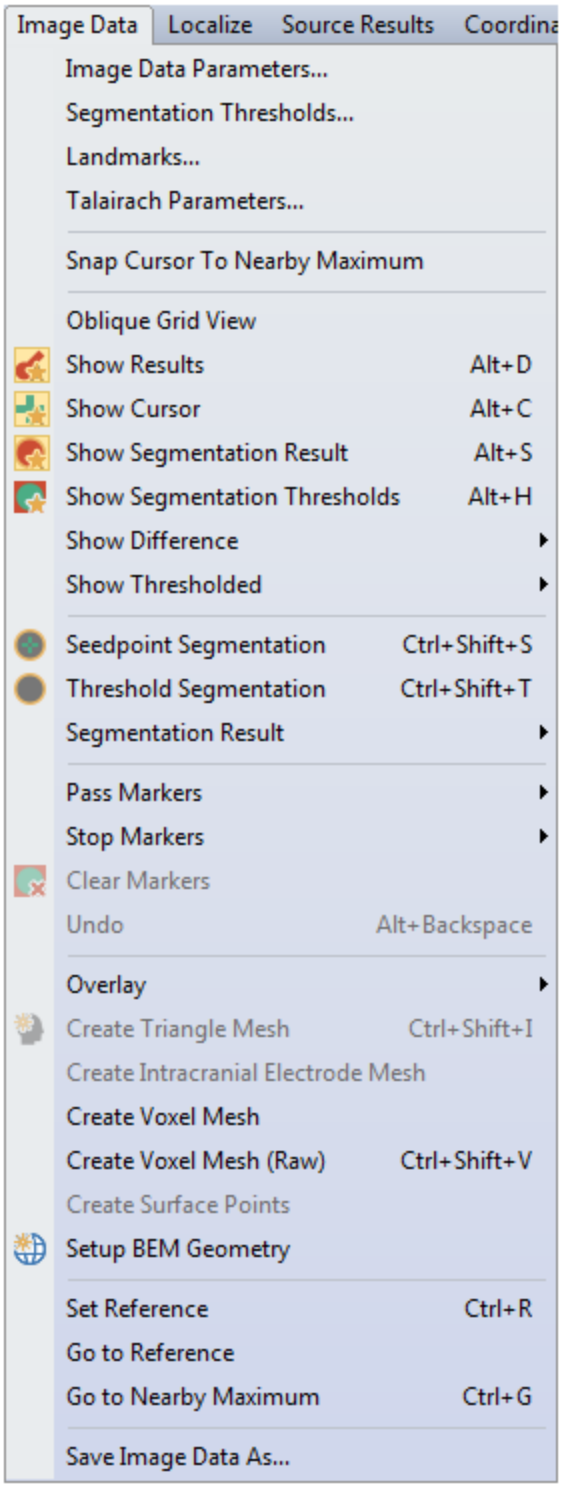
The Image Data window provides three orthogonal views. Each view shows the image data, along with the cursor location and markers for left, right, anterior, and posterior. By selecting a different slice (mouse click or *mouse wheel*), the **Image Data** cursor is moved.

Image Data Parameter Dialogs



The Image Data display and **Image Data** options allow reading, inspection, processing, and segmentation of anatomical data such as MRI, CT, fMRI, PET, and SPECT. It is these features that give CURRY its unique multi-modal capability by allowing anatomical data to be incorporated into source reconstruction. (Press *F10* to display the **Image Data** panels).

Many of the options you will need are found under **Image Data** on the Main Menu bar, and in the **Image Data, Context Menu**. These options are used to import raw MR data, perform segmentation, and additional options. Fewer items will be seen if you do not have the advanced analysis license.



Many of these same options can be accessed from the Toolbar above the **Image Data** parameter panels, and in the top left corner of the iso-image displays and the context menus.

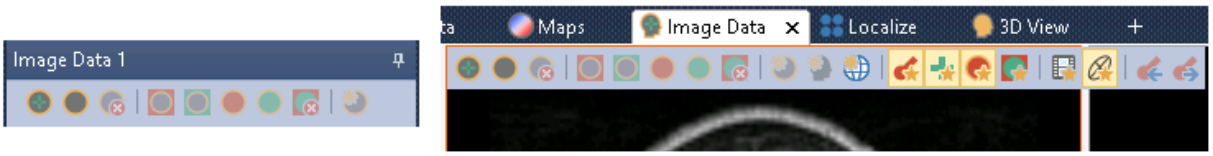


Image Data Parameters. This option opens the **Image Data Parameters** windows (described below).

Segmentation Thresholds. **Step 5** from the **Image Data Parameters** windows is accessed, allowing you to review or modify the segmentation thresholds.

Landmarks. **Step 6** from the **Image Data Parameters** windows is accessed, allowing you to review or modify the anatomical landmarks.

Talairach Parameters. Click this option to review or modify the anatomical landmarks (AC, PC, and MS) and the brain region boundaries as related to defining the Talairach parameters (**Steps 6** and **7** of the **Image Data Parameters** windows will appear).

Snap Cursor to Nearby Maximum. This feature, when enabled, will move the image data cursor to a nearby intensity maximum after clicking in the image data. It is, in a way, a sibling feature to the "magnetic cursor" that can be enabled for manual event marking. It is typically used for defining electrode locations in CT data that are usually rendered as small bright dots.

Oblique Grid View. This option allows you to apply the oblique view you set in the iso-images to the Grid View as well. The Oblique Views are described in the **Image Data Context Menu** section.

Show Results. This option toggles the display of the source localizations on the Image Data display. It is also accessed by the icon on the **Image Data** Toolbar (or *Alt+D*).

Show Cursor. This option toggles the display of the cross-hair cursor on the Image Data display. It is also accessed by the icon on the **Image Data** Toolbar (or *Alt+C*).

Show Segmentation Result. This option toggles the display of the segmentation results on the Image Data display. It is also accessed by the icon on the **Image Data** Toolbar (or *Alt+S*).

Show Segmentation Thresholds. Toggles on and off the display of the segmentation thresholds. It is also accessed by the icon on the **Image Data** Toolbar (or *Alt+H*).

Show Difference. If you have more than one set if image data opened, you may subtract, for example, Image Data 2 from Image Data 1.

Show Thresholded. The option is used to superimpose the image data from one set upon another. It will be active after you load at least two image data sets. If you select it from one data set, you will have the option to select either of the other data

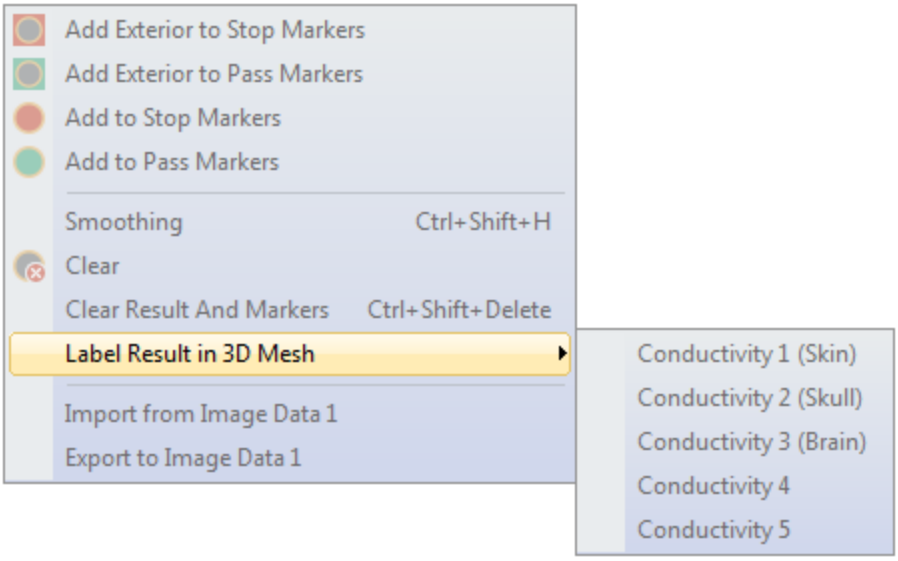
sets for superimposition. Note that only the portions above the threshold set in the modality to be added are shown.

This option may also be used to superimpose DTI data on the MR data (from the same subject). Load the MR data first in the Database. Make sure the MR data has the focus, then select **Image Data 2** to display the DTI data on the MR data. The same result may be obtained by selecting the **Threshold** option from the **Options** panel. Use the **Transparency Atlas** option to adjust the transparency.

Seedpoint Segmentation. This option performs **Region Growing** segmentation from the current cursor position. Clicking it has the same function as clicking the Start button in the **Segmentation** panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+S*).

Threshold Segmentation. This option performs **Threshold** seedpoint segmentation, which is independent of the current cursor position. Clicking it has the same function as clicking the Start button in the **Segmentation** panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+T*).

Segmentation Result. This accesses a secondary menu with the following options. Pass Markers are generally seen in green, and Stop Markers are in red (you can change the colors in the **Colors** panel under **Image Data**). Most of the same options are seen in the **Segmentation** panel after clicking the Result button.



Add Exterior to Stop Markers. Exterior regions will be filled with Stop Markers (regions will turn red). It is also accessed by the icon on the **Image Data** Toolbar.

Add Exterior to Pass Markers. Exterior regions will be filled with Pass Markers (regions will turn green). It is also accessed by the icon on the **Image Data** Toolbar.

Add to Stop Markers. Click this option to include the segmented region with the Stop Markers (regions will turn red). It is also accessed by the icon on the **Image Data** Toolbar.

Add to Pass Markers. Click this option to include the segmented region with the Pass Markers (regions will turn green). It is also accessed by the icon on the **Image Data** Toolbar.

Smoothing (*Ctrl+Shift+H*). This option is meant to be used to obtain a quick Smoothing result, and so always uses a **12mm Dilation**. Use the **Morphology** panel options for any other parameters, and its **Start** button to apply them.

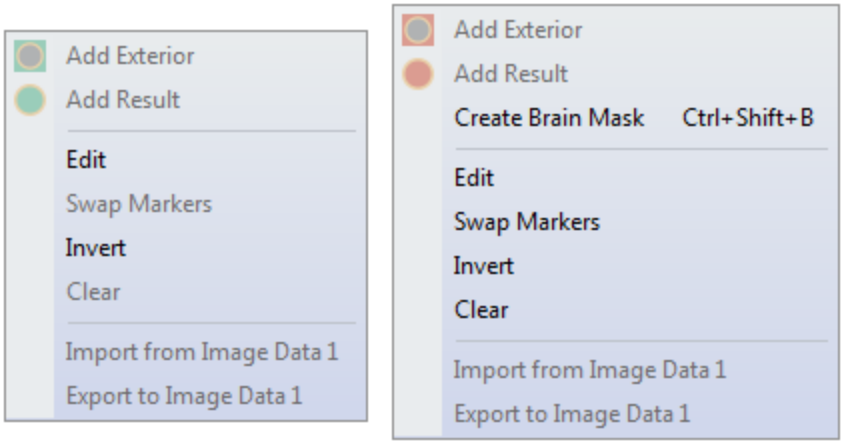
Clear Segmentation Result. This clears the segmentation result. It is also accessed by the icon on the **Image Data** Toolbar

Clear Result and Markers. This clears the segmentation result and markers.

Label Result in 3D Mesh. This feature is related to the creation of FEM models. Between creating a tetrahedra/cube mesh and exporting it in CAUCHY format (which can be done from the context menu in Results), one might wish to "label" tetrahedra with respect to which tissue type they represent. This is based on the segmentation result currently in **Image Data**. Because compartments enclose each other, the program starts with the skin, then the outer skull, then the inner skull, overwriting in each step the labeling for the enclosed tetrahedra.

Import from Image Data 1/Export to Image Data 1. You must have two (or more) image data sets loaded to use these options. The second or third data set can import results from the first, or export results to the first.

Pass Markers/Stop Markers. Pass and Stop Markers determine the boundaries or regions used in segmentation.



Add Exterior. Adds the complement of the segmented volume to the markers of the selected **Marker Type**. It is also accessed by the icon on the **Image Data** Toolbar.

Add Result. Adds the segmented volume to the markers of the selected **Marker Type**. It is also accessed by the icon on the **Image Data** Toolbar.

Edit. Selecting this option expands the Markers panel, and sets the **Edit Mode** to **Pass/Stop Markers**.

Swap Markers. Swaps Stop and Pass Markers.

Invert. Inverts **Pass/Stop Markers**.

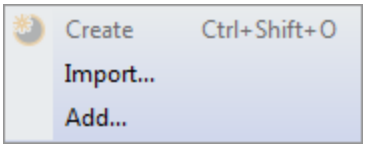
Clear. Clears all **Pass/Stop Markers**.

Import from Image Data 1/**Export to Image Data 1**. You must have two (or more) image data sets loaded to use these options. The second or third data set can import markers from the first, or export markers to the first.

Clear Markers. Select this option to clear the Stop and Pass Markers (same as the button on the **Image Data** Toolbar).

Undo. The most recent step is undone.

Overlay. The options are used to Create, Import, or Add overlays. Overlays store segmentation results and markers for later use.



Create. This creates an overlay of the most recently segmented surface(s). It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl*+*Shift*+*O*).

Import. This selects the Doubleclick: Import Overlay mode in the **Properties** panel under Results. Import Overlay shows all Overlays (segmentation results) that can be imported to **Image Data**. Creating a new overlay will *replace* an existing one. Double-click an overlay to import it.

Add. This selects the Doubleclick: Add Overlay mode in the **Properties** panel under Results. New overlays will be *added* to the list. Double-click an overlay to import it.

Create Triangle Mesh. After segmentation, click this option to create a quick triangulated mesh surface, using a fixed **Dilation** of **12mm**. The results will appear in the **Properties** panel as Surface**#** (where # is the number of the next available Surface). The results are displayed in the 3D View. The option is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl*+*Shift*+*I*). Use the parameter fields in

the Create panel for other settings, and then click its **Start** button to apply them.

Create Intracranial Electrode Mesh. This is a convenience option that is only available for CT data with depth electrodes, saving you from performing the steps manually. It consists of the following operations.

1. Create brain mask.
2. Find thresholds suitable for intracranial electrodes.
3. Creates a voxel mesh (raw).

The result in the **3D View** Objects list is called Electrode Mesh, and displays the segmented depth electrodes.

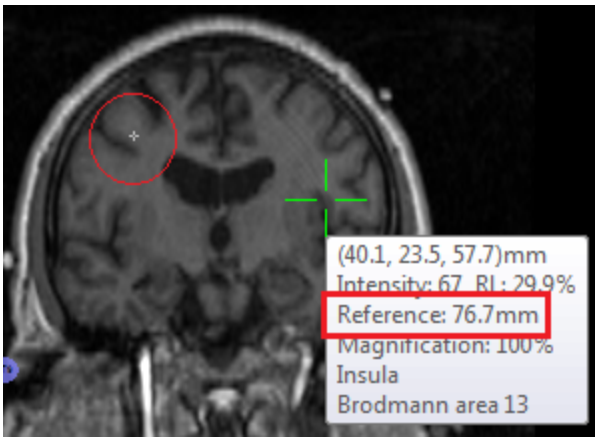
Create Voxel Mesh. A voxel mesh is created (see also Create).

Create Voxel Mesh (Raw). This feature is similar to the Create Voxel Mesh command, which transforms the yellow segmentation result into a voxel mesh and therefore has an inherent resolution of 256x256x256 (the resolution of markers and segmentation result). However, especially for CT, the raw image resolution may be higher, usually 512x512x512, and the "raw" voxel mesh will have the resolution of the raw image data, not using the segmentation result at all, but simply including all voxels that satisfy the threshold (and marker) criteria into the voxel mesh. This results in higher-quality 3D View renderings of e.g., intracranial electrodes.

Create Surface Points. After segmentation, click this option to create a surface consisting of points (see also Create). The results will appear in the **Properties** panel as Points**#** (where # is the number of the next available set of points). The results are displayed in the 3D View.

Setup BEM Geometry. This is a shortcut to the BEM/FEM Geometry panel for using the automated BEM Realistic Head Model algorithm. It is also accessed by the  icon on the **Image Data** Toolbar.

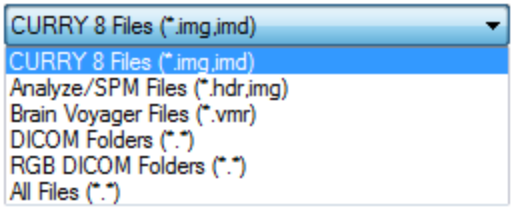
Set Reference. Click this option (or *Ctrl+R*) to set the reference point at the current cross-hair cursor position. A small star will appear, with the color determined by the **Text** color setting under Colors. The distance from the cursor to the Reference is displayed in the Tooltip and in the **Options** panel.



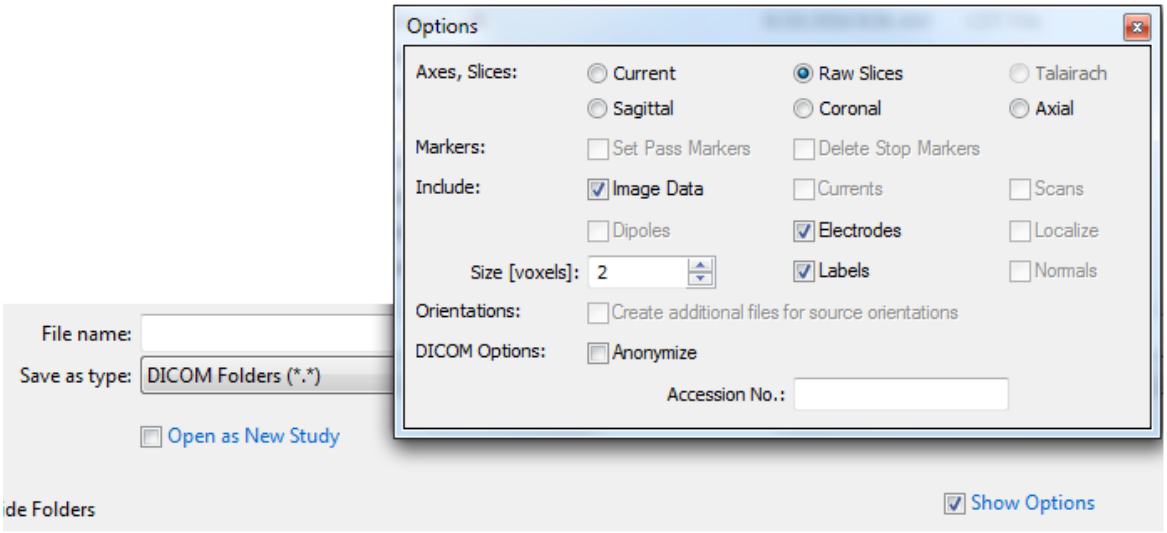
Go To Reference. Select this option to return the cross-hair cursor to the reference point in all three iso-images.

Go To Nearby Maximum (*Ctrl+G*). This is used for finding the exact center of bright dots in an MRI or CT, such as vitamin E markers or ECoG electrodes. "Nearby" translates to a 5mm radius, wherein the center-of-mass is computed. A similar routine in Localize performs the operation for all Localize locations. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, the **3D View**, click the border of the bright area, and this functionality brings the cursor to its center (this can be applied repeatedly).

Save Image Data As. This option allows you to save the MR images in one of several forms:



In the **Show Options** part of the Save As dialog are additional options that you may use. Click **Show Options** to see them.



Axes, Slices. If you have changed the axes or resliced the image data, you have the option to save the **Current** axes and slices, or the **Raw Slices**. The **Talairach** option will be active if you have selected the Talairach coordinate (**Coordinates → Talairach (R,A,S)**). If **Raw Slices** is not selected, a 256x256x256 image cube will be exported.

Markers. If you have included Pass Markers and/or Stop Markers, you can save these. Pass Markers will be seen in white if you select **Set Pass**. Stop markers will be seen in black, unless you enable **Delete Stop Markers**.

Include. Dipole results (etc.) can be exported to surgical navigation system with or without **Image Data** (enabled by default). You can include the **Currents** (thresholded current densities exported as high-intensity markers in 3D images), **Scans**, and **Dipoles** results, the **Electrodes**, any **Localize** points you have created, and the **Normals**. You can vary the **Symbol Size** (in voxels).

For whatever components (Dipoles, Localize, Electrodes) are visible in Image Data (controlled by the respective checkbox in **3D View**), the respective checkbox in the Save Image Data dialog becomes active.

Orientations. This option is used when saving CDR results in SPM (image) format. Three additional images for the normal components are created. If not checked, only the strengths are saved.

DICOM Options. Generally speaking, CURRY 8 includes the following meta-information (read from the original image data file) when writing DICOM: modality, field strength, patient name, gender, birthday, age, series description, and study description. The exported information may be modified as follows.

Anonymize. The Anonymize option results in patient name and birthday not being written to the DICOM files.

Accession No. The accession number is a way to store an additional, manually entered 16-character string (usually a number) with the written DICOM files.

Open as New Study. If you enable **Open as New study**, the .imd file will be added to the Database as an unfiled Study, and this image data-only study will be opened.

Exporting results to surgical navigation systems (e.g., Stryker). Please follow the steps below to export the image data and other results to surgical navigation software.

1. Make sure **Show Results** has been enabled  (Toolbar or Image Data context menu).

2. The **Save Image Data As** dialog shows checkboxes for including Dipoles, Electrodes, and Localize (or any) locations in the saved MRI. Formats can be DICOM, etc. (select under **Save as type**).

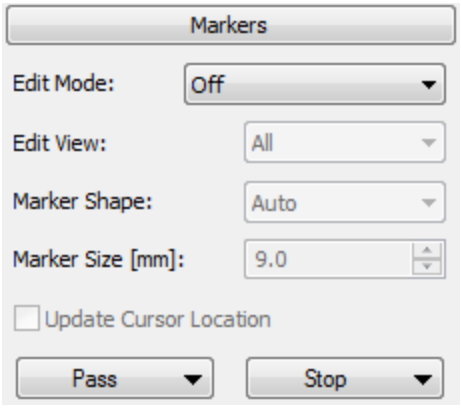
3. The items that are checked are included with the saved structural MRI as high-intensity markers (their size can also be selected).

4. No overlays are necessary, and coregistration is not an issue.

5. If a second version of the image without markers is desired, resave the image data without the items being checked. The navigation system needs to be able to deal with two 3D images (one with structural data only, one with additional bright spots where the CURRY results are).

18.2.1 Markers

Markers are used for constraining segmentations: Volumes containing Stop Markers are always excluded from segmentation, while volumes containing Pass Markers are included, regardless of the segmentation thresholds used. If marker editing is enabled (from the orthogonal views context menu or the **Mode** setting of this dialog), clicking or dragging with the mouse in one of the orthogonal views adds or deletes markers of the type and shape selected.



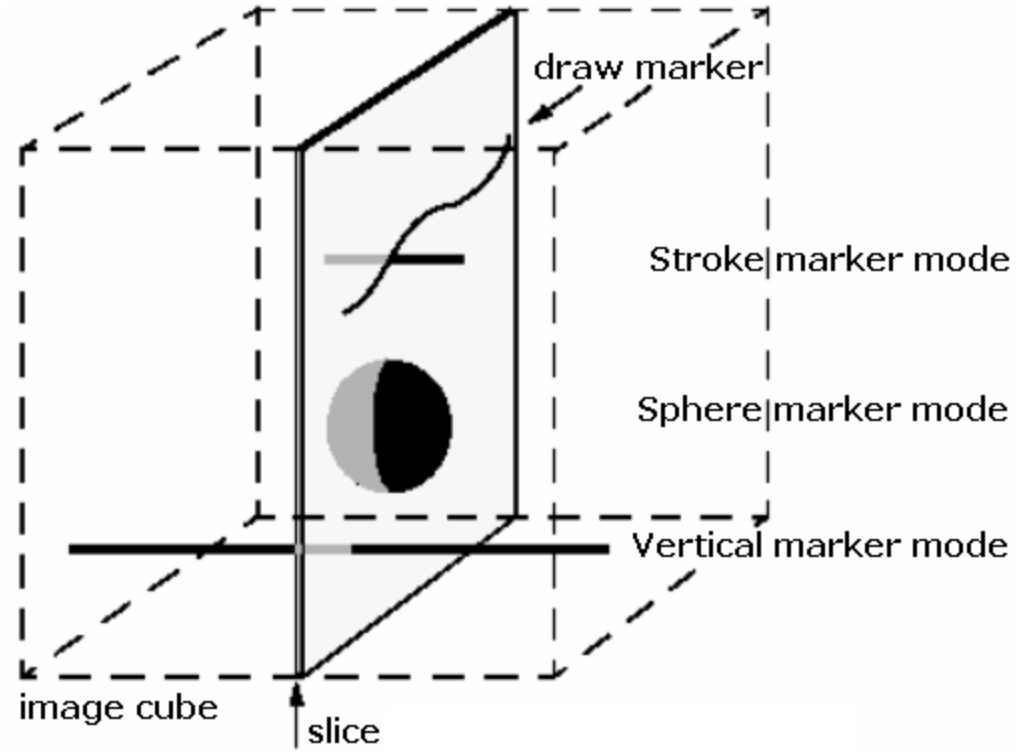
Using Markers

Markers exist in two fashions, **Stop Markers** and **Pass Markers**. They are the means to constrain segmentation by user input or by previous results.

– Stop Markers stop segmentation as a threshold violation would do. They are visualized as a red mask overlaid onto every other image pixel. (Colors for Stop and Pass markers can be changed in the **Colors** panel).
– Pass Markers make segmentation ignore the thresholds and continue growing. They are shown as a green mask overlaid onto every other image pixel.

Stop Markers and Pass Markers cannot coexist on an image voxel. Whenever Stop Markers are defined where Pass Markers already exist, or vice versa, the previous markers are removed. Both types of markers can be defined in a variety of ways:
– A segmented volume can be added to the markers.
– The exterior of a segmented volume can be added to the markers.
– Markers can be deleted.
– Markers can be inverted.
– Markers can be drawn manually.

When drawn, the marker shape is either a sphere or a vertical bar perpendicular to the plane of the Zoom window. Depending on the extension of the markers, they also appear in adjacent slices. A schematic representation of the different marker types available is shown below. See further examples in the **Marker Shape** section just below.

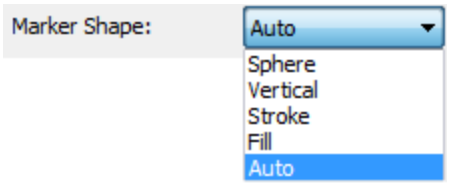


Parameter Dialogs

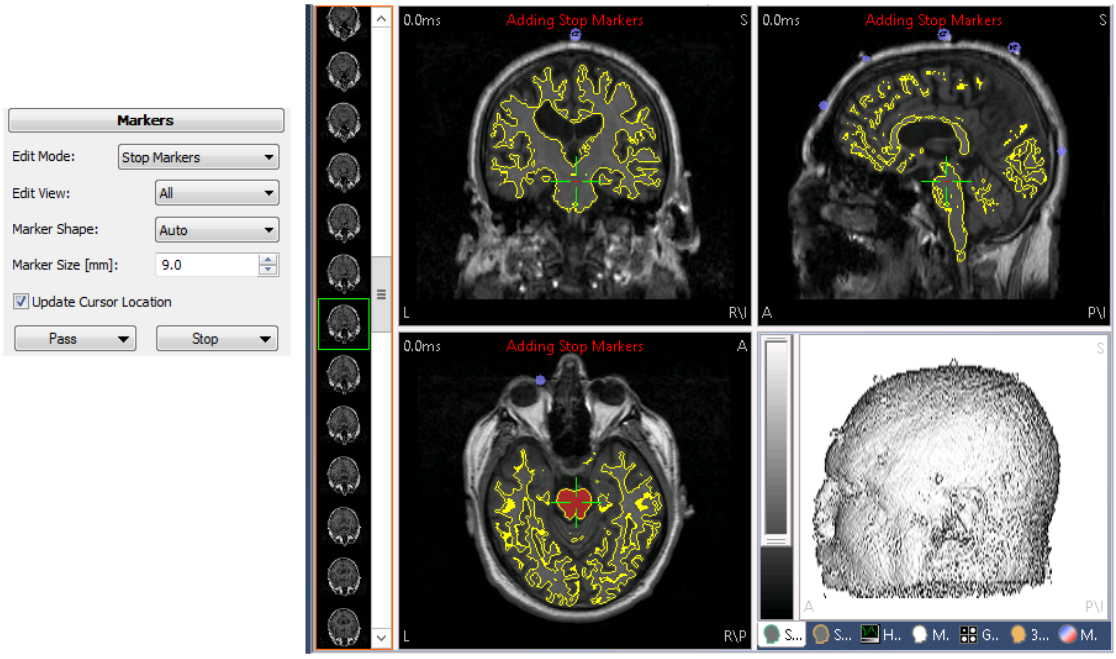
Edit Mode. These options determine which type of markers (Stop Markers or Pass Markers) are set or deleted. Marker editing can be switched Off as well.

Edit View. Select the Sagittal, Coronal, Axial, or All views for editing. In views where editing is enabled, the cursor turns into a small cross-hair. Clicking in the selected view adds Markers, while clicking in non-selected views does not.

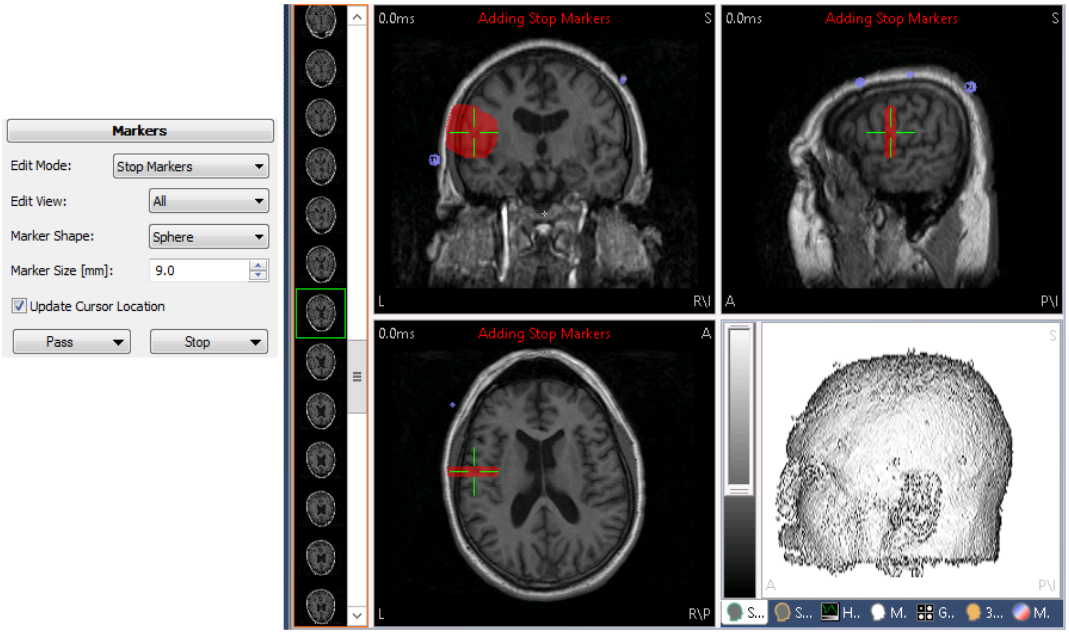
Marker Shape. These options determine the shape of markers.



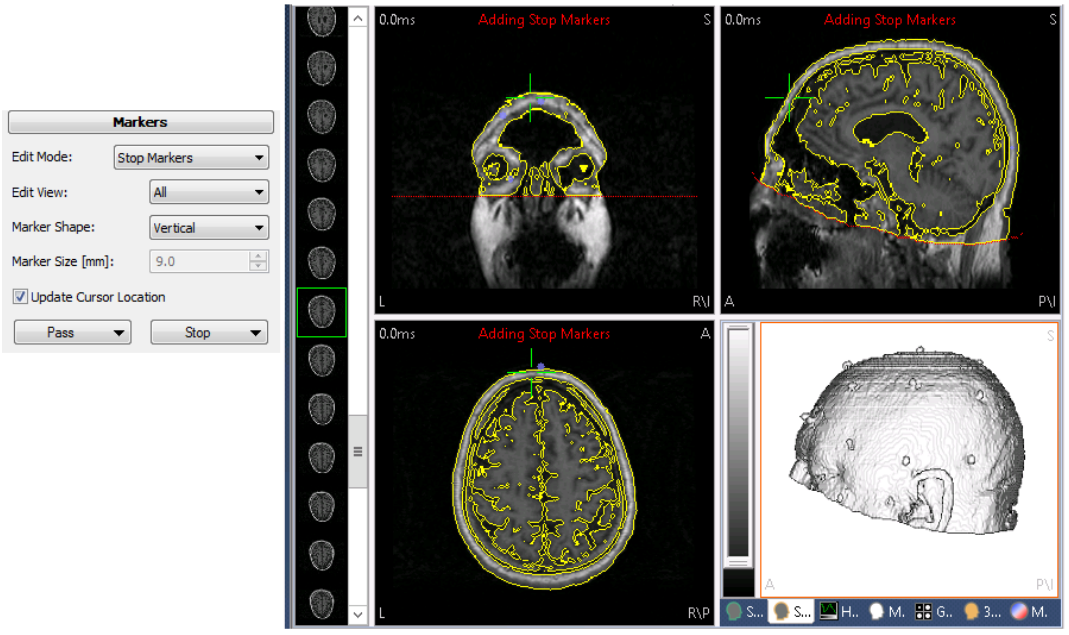
Auto is the default setting, and it functions either as the **Sphere** or the **Fill** options. If there are no yellow segmented areas, it is the same as **Sphere** (described next). If you have yellow segmented areas, **Auto** will fill in the area in which you click, in the particular slice, which is the same as the **Fill** option. Below, we clicked in the brain stem area in the axial slice, and it was filled with stop markers (**Fill**). This is a quick way to remove the brain stem, or cerebellum, or in some cases unwanted structures and nerves about the eyes. If you are in Auto and you click outside of the segmented areas, Auto will operate like Sphere.



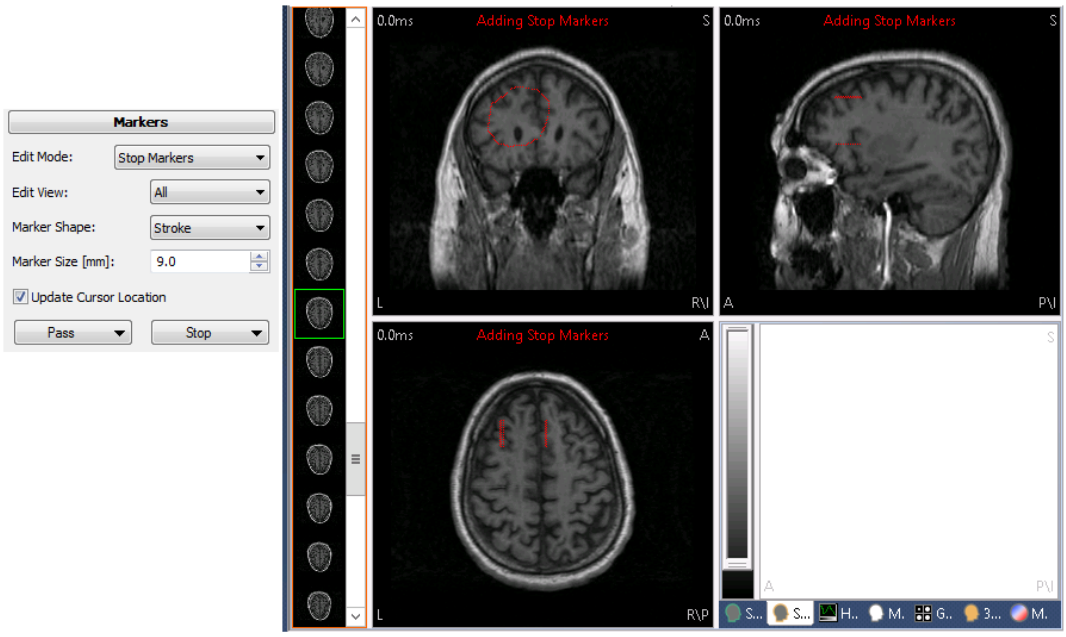
Sphere is a 3-dimensional sphere. You can change the size of the sphere and drag it in the image data to form regions included in segmentation (pass markers) or excluded from segmentation (stop markers). Here, stop markers have been added in the coronal view. The width of the line created by the spheres is 9mm (**Marker Size**). You can extend it further also by going to the adjacent slice and redrawing the markers.



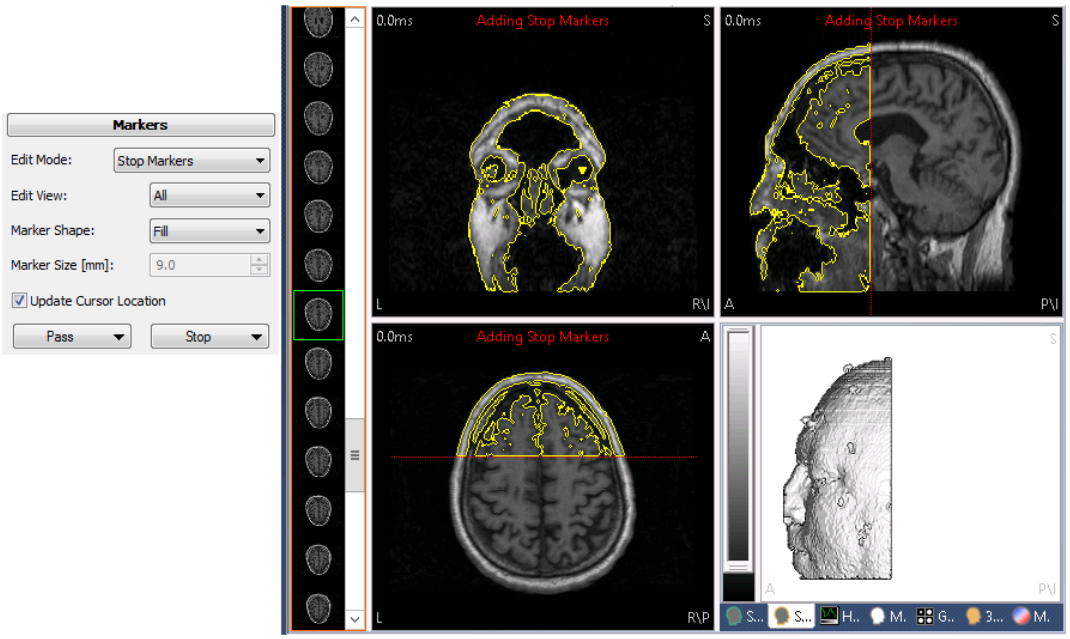
Vertical. Vertical is a fine line extending through the whole image volume. In the example below, we drew the line of stop markers in the sagittal view, and then segmented the Skin. Everything below the line was excluded from the result (the cursor was placed above the line). Vertical is also used, for example, to draw an outline of stop markers around the brain.



Stroke. Stroke is a less frequently used option. The lines it creates do not extend throughout the images. In the example below, we created a ring, 20mm in width. If we had traced the same circular shape with **Vertical**, we would have created a cylinder that extended through all images, rather than just a ring.

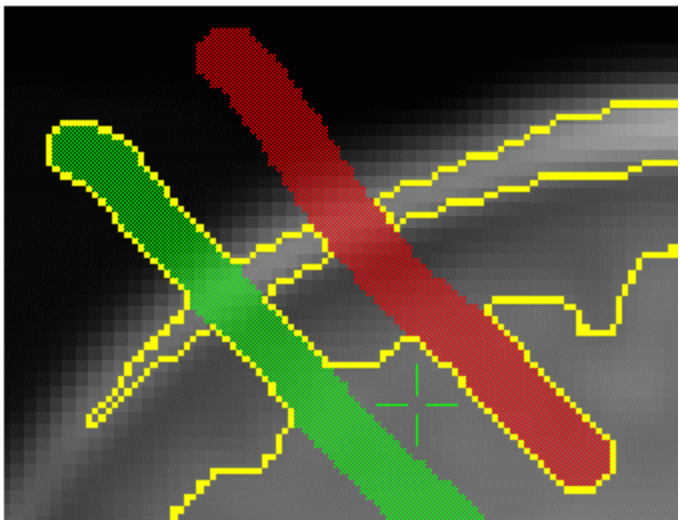


Fill. **Fill** is typically used when you already have segmented structures. It works like **Auto** above, where you may fill in segmented structures with stop or pass markers. If there are no already segmented structures, you can use Fill to insert a vertical or horizontal plane. In the extreme example below, we clicked in the coronal view to create a plane of stop markers. We then segmented the skin to exclude everything behind the plane.



Marker Size [mm]. This field is used to determine the size of spheres and strokes (diameter or extension).

In the figure, the Stop Markers are in red, the Pass Markers are in green, and the shape was a Sphere. The figure displays how the Stop Markers are excluded and the Pass Markers are included within the compartments.

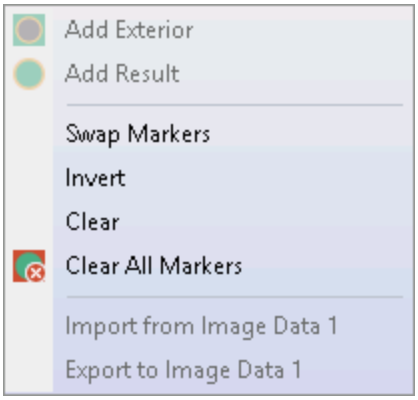


Note
The Markers that you set are applied when you perform segmentation manually, and not when you use the automated segmentation routine, unless you enable **Use Existing Markers**.

Note
Use **Undo** from the Image Data context menu to revoke the last editing action (*Ctrl+z*).

Update Cursor Location. When enabled, the cursor will follow the placement of the Stop and Pass Markers, as will the position in the other iso-image views (facilitates placement of markers).

Pass and Stop buttons. A similar list of options is displayed when you click either the Pass or Stop button.



Add Exterior. Adds the complement of the segmented volume to the markers of the selected **Marker Type**.

Add Result. Adds the complement of the segmented volume to the markers of the selected **Marker Type**.

Swap Markers. Swaps Stop and Pass Markers.

Invert. Inverts **Pass (Stop) Markers**.

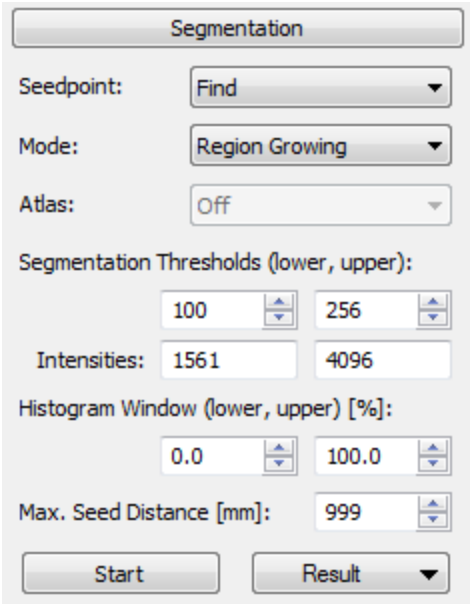
Clear. Clears all **Pass (Stop) Markers**.

Clear All Markers. Clears all Markers.

Import from / Export to Image Data 1. You must have two (or more) image data sets loaded to use these options, and the second (or third) must have the "focus". The second data set can import markers from the first, or export markers to the first.

18.2.2 Segmentation

Using segmentation, 3-dimensional volumes and their surfaces can be generated. The shape of these volumes is controlled by the segmentation algorithm selected, the seedpoint, stop and pass markers, and the segmentation thresholds. Volumes marked with stop markers are never included in the segmentation, regardless of their thresholds, while volumes containing pass markers are included.



General Information

Segmentation is a means of defining regions in an image. In CURRY, segmentation always works in 3D. This means that the segmentation result is a volume. In addition, CURRY's segmentation tools also find the surface of the segmented volume.

In most cases, the automated segmentation routine in CURRY will segment the regions quite successfully. This is accessed from the **BEM/FEM Geometry** panel, with no need for any other operations. In some cases it may be necessary to perform segmentation manually, and this requires interactive steps that involve the **Segmentation**, **Morphology**, and **Create** panels, as well as other steps.

Segmentation Parameters

CURRY has several segmentation algorithms built in, most of which are of the region-growing type. This means that starting from a seedpoint, a volume begins to grow until, locally, certain criteria are violated. These criteria, along with the seedpoint and the chosen algorithm, control the outcome of the segmentation. They are:

- A threshold criterion. Image intensity must lie between given **upper** and **lower Thresholds**. The image intensity range is 0...255. The largest allowed **upper Threshold** is **256**, and the smallest **lower Threshold** is **0**. When thresholds are set or changed, regions in the image that meet the criterion are colored green, and regions violating the criterion are colored red.

$$Lower\ Threshold \leq Intensity < Upper\ Threshold$$

- A **Maximum Distance**. A maximum distance from the seedpoint, measured in iterations of the region-growing process, can be specified. If the parameter is small, segmentation stops prematurely.
- Included regions. Regions marked with Pass Markers or with a selected atlas structure (see **Using Markers**) are included in segmentation, even if they violate the threshold criterion.
- Excluded regions. Regions marked with Stop Markers (see **Using Markers**) stop segmentation, even if they meet the threshold criterion.
- A built-in connectivity criterion assures that the segmented surface is always neighbored to an element of the interior. This criterion makes the segmentation robust and insensitive to noise in the images. It is especially important for the generation of surface triangle nets.

Seedpoint vs Threshold Segmentation. If the area to be segmented is connected (no isolated sections), there will be no difference between Seedpoint and Threshold segmentation. If you use a high threshold, there will be differences because the threshold will result in non-connected results. Seedpoint is based on a start point that is set when selecting the Mode (e.g., Skin sets a seedpoint somewhat frontally, while Cortex sets a seed in the image center, all determined by the respective settings from **Step 5** of the **Image Data Parameters** windows.). In interactive mode, the existing cursor location is used, and in Find mode, a small vicinity search for a seedpoint around the cursor is used. In most general instances, you would use Seedpoint segmentation. For fMRI hotspots, you would use Threshold segmentation.

Predefined Segmentation Thresholds

The segmentation thresholds for different tissue types have been defined during image data import, and can be accessed from the **Segmentation** panel. The estimated thresholds are probably correct for T1-weighted MR images, but they should be checked since the automatic segmentation tools in BEM/FEM Geometry

depend on them. If segmentation should later fail, please remember to review the segmentation thresholds in the **Image Data Parameters** windows.

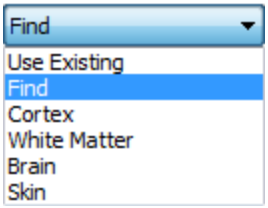
Threshold Determination

The main parameters that control the outcome of segmentation are the thresholds, although they alone are often not sufficient. Thresholds can be set:

- using the **Threshold** textfields in the **Segmentation** panel,
- by setting the threshold in the **Histogram** view, or
- by choosing one of the **Segmentation Mode** and **Seedpoint** options.

Parameter Dialogs

Seedpoint. These options determine how the segmentation seedpoint is found and whether segmentation thresholds are pre-set.

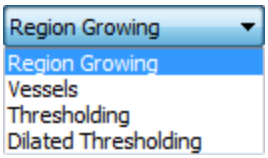


Use Existing. Uses the existing seedpoint and thresholds.

Find. Finds a suitable seedpoint in an axial slice using a spiraling search path.

Cortex, **White Matter**, **Brain**, **Skin**. These all use the appropriate thresholds and search for a seedpoint in the seed slice. Thresholds and slices are set in the **Image Data Parameters** windows.

Mode. There are four segmentation modes. The ordering in which the algorithms are listed is with increasing segmented volume for otherwise equal parameters.



Region Growing. This is a 3-dimensional region-growing algorithm that does not traverse through thin or tube-like structures. Segmentation results depend on the seedpoint used (cursor position) and are connected. This algorithm is typically used.

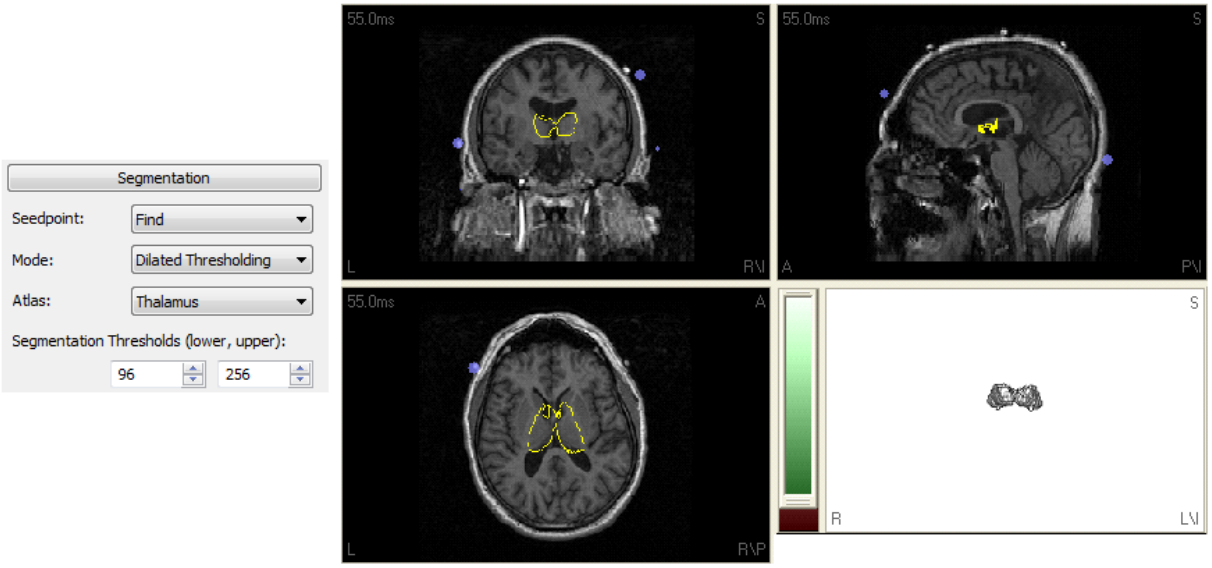
Vessels. This is a 3-dimensional region-growing algorithm that does traverse through thin and tube-like structures. Segmentation results depend on the seedpoint used and are connected. The results are typically similar to the Region Growing method, with some additional structures included.

Thresholding. Finds all volumes satisfying the threshold criteria, omitting small, thin, and tube-like structures. Segmentation results do not depend on the seedpoint used and are not necessarily connected. For example, with Region Growing, where the cursor position is in the brain, typically only the brain will be

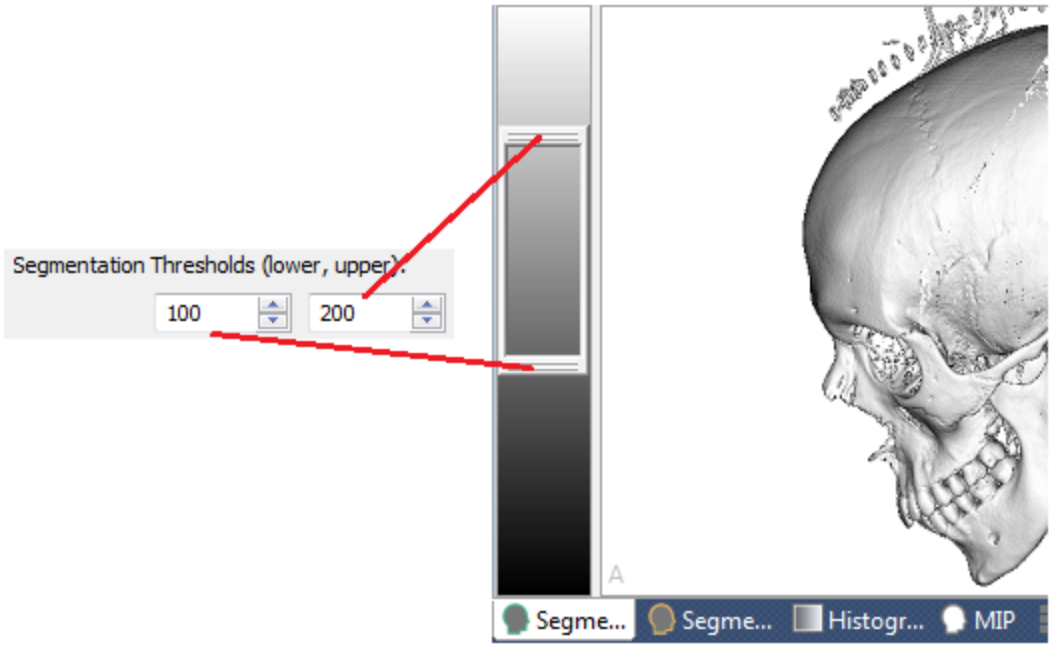
segmented, unless it is connected to the skull\skin. With Thresholding, the cursor position is not used, and there may be more than one segmented result (the cortex and the skin).

Dilated Thresholding. An algorithm like the one before, which segments very small structures as well, because it ignores the connectivity criterion by implicitly inflating the segmented volume by one voxel. It finds all volumes satisfying the threshold criteria, including small, thin, and tube-like structures. Segmentation results do not depend on the seedpoint used and are not necessarily connected.

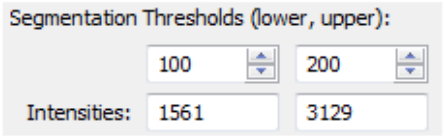
Atlas. The Atlas function lets you segment automatically any of the structures listed in the Talairach atlas. The atlas is available if Talairach parameters have been set. You must use either the Thresholding or Dilated Thresholding modes (Dilated Thresholding may be preferable for smaller structures).

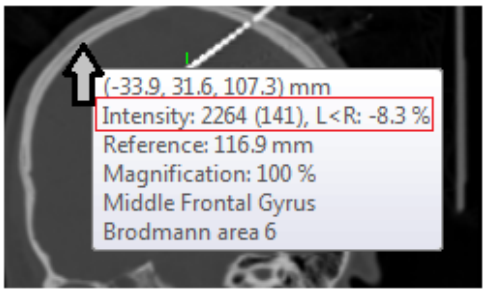


Segmentation Thresholds (lower, upper). Image regions with intensities below the lower segmentation threshold are not segmented. Image regions with intensities above the upper segmentation threshold are not segmented. They control the sliding bar next to the lower right view. The lower segmentation level can be adjusted with the *mouse wheel* (position the cursor in the lower right pane); the upper one uses *Alt+mouse wheel*.

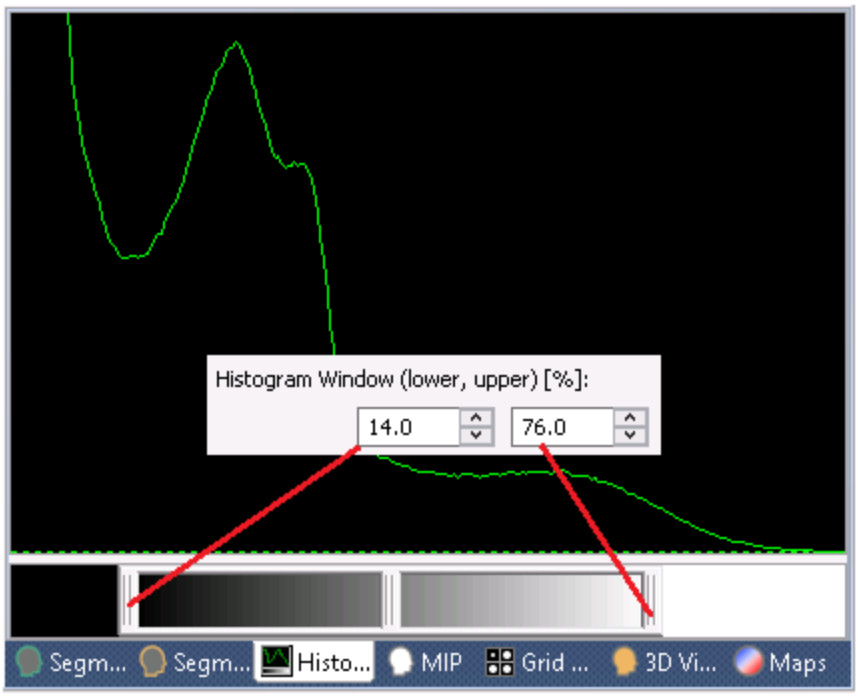


Note also that there are two sets of intensity fields. The first are the CURRY segmentation threshold values, from 0-256. The lower fields use intensity values from other sources, and these may have varying ranges. For example, people sometimes wish to perform segmentation using Hounsfield values. Enter these in the Intensity fields and CURRY will convert them to the CURRY values in the upper fields (after selecting the nearest real world value, if needed). Position the mouse cursor at a point in the Image data (such as the CT bone), and see the Tooltip that appears. The first number is the Housfield value, and the corresponding CURRY value is in parentheses. Other image data files will have statistical or other values.





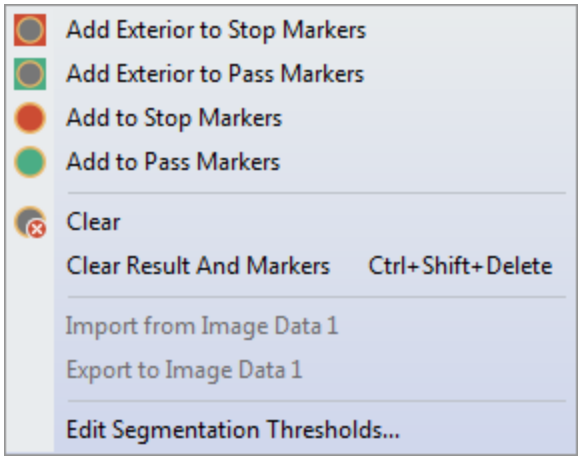
Histogram Window (lower, upper) [%]. These fields control the Histogram thresholds, seen in the sliding bar below the Histogram display.



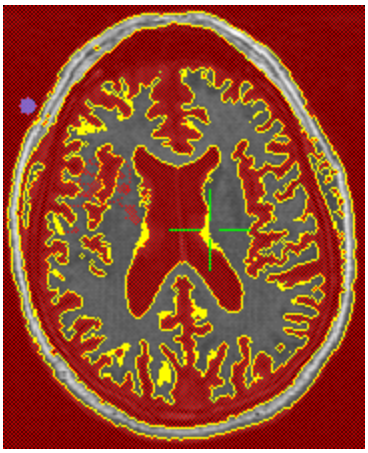
Maximum Seed Distance [mm]. Distance (in mm) controls how far a segmentation can iterate away from the seedpoint. It is typically set to a large value, but can be lowered in order to find the reason for oversegmentation.

Start. Click the Start button to begin the process.

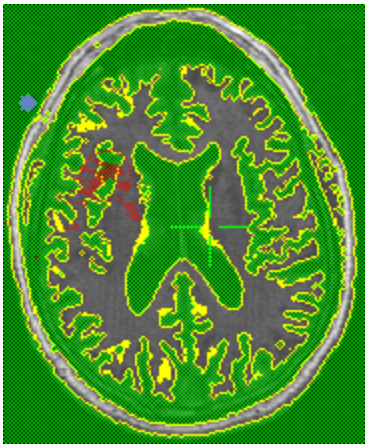
Result. The following options appear when you click the Result button. The indicated options are also accessed from the **Image Data** Toolbar.



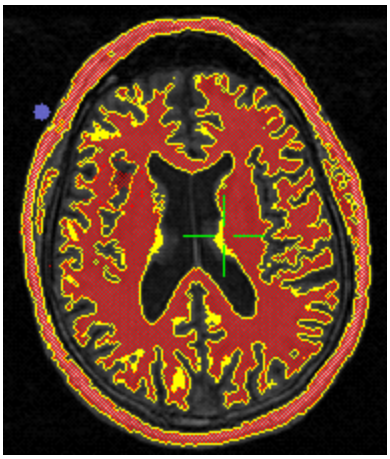
Add Exterior to Stop Markers . Exterior regions will be included with Stop Markers (regions will turn red).



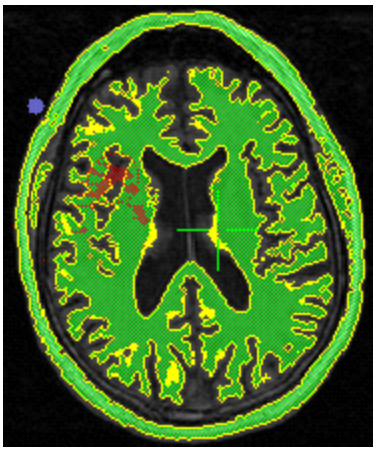
Add Exterior to Pass Markers  . Exterior regions will be included with Pass Markers (regions will turn green).



Add to Stop Markers  . Click this option to include the segmented region with the Stop Markers (regions will turn red).



Add to Pass Markers  . Click this option to include the segmented region with the Pass Markers (regions will turn green).



Clear  . This clears the segmentation results.

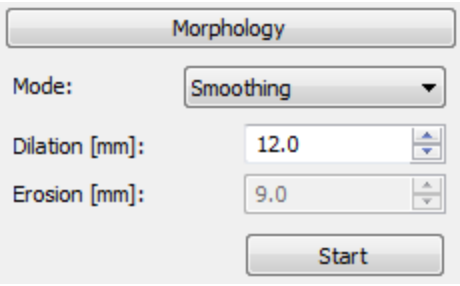
Clear Results and Markers. This clears the segmentation results and markers (*Ctrl+Shift+Delete*).

Import from / Export to Image Data 1. You must have two (or more) image data sets loaded to use these options, and the second (or third) must have the "focus". The second data set can import results from the first, or export results to the first.

Edit Segmentation Thresholds. Selecting this option will take you to **Step 5** of the **Image Data Parameters** windows, where you may edit the segmentation thresholds.

18.2.3 Morphology

Using morphological operations, the shape of segmented volumes can be modified. The basic morphological operations are **Erosion** (deflation) and **Dilation** (inflation).



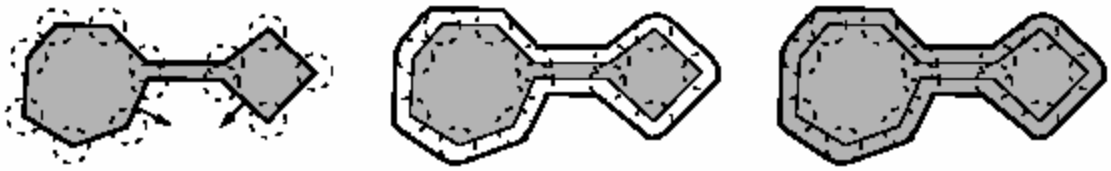
In CURRY, morphological operations use spherical kernels in order to achieve axis-independent results. The segmentation results may need modification for these reasons:

– A cortex segmentation may be enlarged to get the shape of the brain’s envelope.

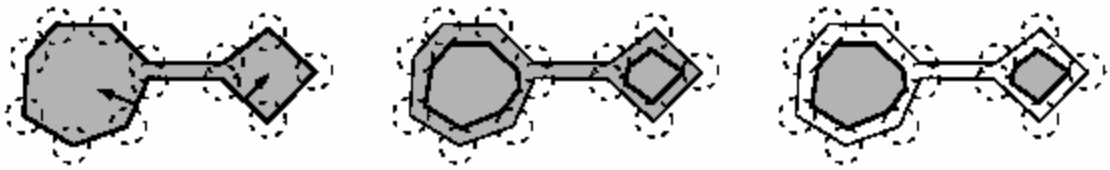
– A segmentation result must be smoothed according to the triangle size because it will be transformed into a triangle mesh (see **Create** below).
– Limiting or minimal volumes for subsequent segmentations may be derived from previous results (see **Using Markers** above). CURRY offers a variety of morphological operations, i.e., shape operations, to perform these tasks.

Dilation and Erosion

The basic morphological operations are dilation and erosion. A dilation operation enlarges the original shape. Thin structures become thicker and more robust by this operation. Compare it to inflating a balloon. In an erosion operation, the original shape is deflated. Large structures connected by thin ones are cut loose. Compare it to letting air out of a balloon. Both operations are illustrated in the figures below.



A schematic presentation of dilation showing inflation of the original shape (left) in three steps.



A schematic presentation of erosion showing deflation of the original shape (left) in three steps.

Dilation is invoked by selecting the **Dilation** for the **Mode**, and entering a radius in the **Dilation [mm]** field. Erosion is invoked by selecting **Erosion**, and entering a radius in the **Erosion [mm] field**.

Dilation [mm]. Dilation Distance. This parameter applies to **Dilation**, **Opening**, **Closing**, and **Smoothing**.

Erosion [mm]. Erosion Distance. This parameter applies to **Erosion**, **Opening**, and **Closing**.

Care
Dilation stops at the borders of the image cube (which equals the borders of the images seen in the **Image Data Parameters** windows). For certain segmentation processes involving dilation, as they are contained in the automated segmentation routine, a certain amount of empty space (5-10mm) around the image in the image cube is important (the amount depends on the dilation distance you use).

Closing and Opening

Closing is a dilation followed by an erosion. It fills concavities, i.e., holes. If the **Dilation** radius is larger than the **Erosion** radius, the segmented object is enlarged as well. Closing is invoked by selecting **Closing** for the **Mode**, and entering a **Dilation** radius and an **Erosion** radius.

Opening is an erosion followed by a dilation. It deletes convexities, i.e., small emerging structures, and opens connections. If the **Dilation** radius is larger than the **Erosion** radius, the segmented object is enlarged as well. Opening is invoked by selecting **Opening** for the **Mode**, and entering an **Erosion** radius and a **Dilation** radius.

Smoothing

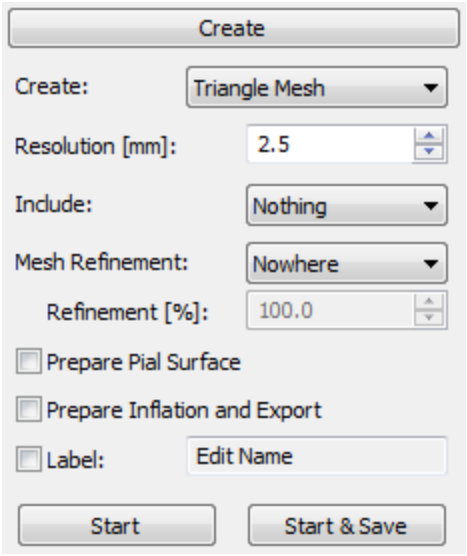
Smoothing is a closing operation followed by an opening operation, where only the **Dilation** radius is used. It preserves object size while removing convexities and filling concavities of smaller radii than the **Dilation** radius. Smoothing is started by selecting **Smoothing** for the **Mode**, and entering a **Dilation** radius.

Note
Use **Undo** from the Image Data context menu to revoke the last morphological operation.

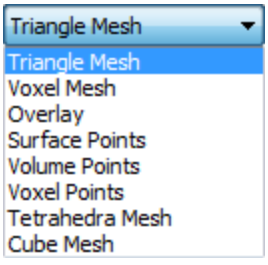
Start. Click the Start button to begin the selected process.

18.2.4 Create

Based on segmentation results, geometrical objects such as triangle meshes or lists of points can be created and used in other parts of the software.



Create. The Create field drop-down list contains the following options.



Triangle Mesh. The triangulated segmented surface, such as the Skin surface.

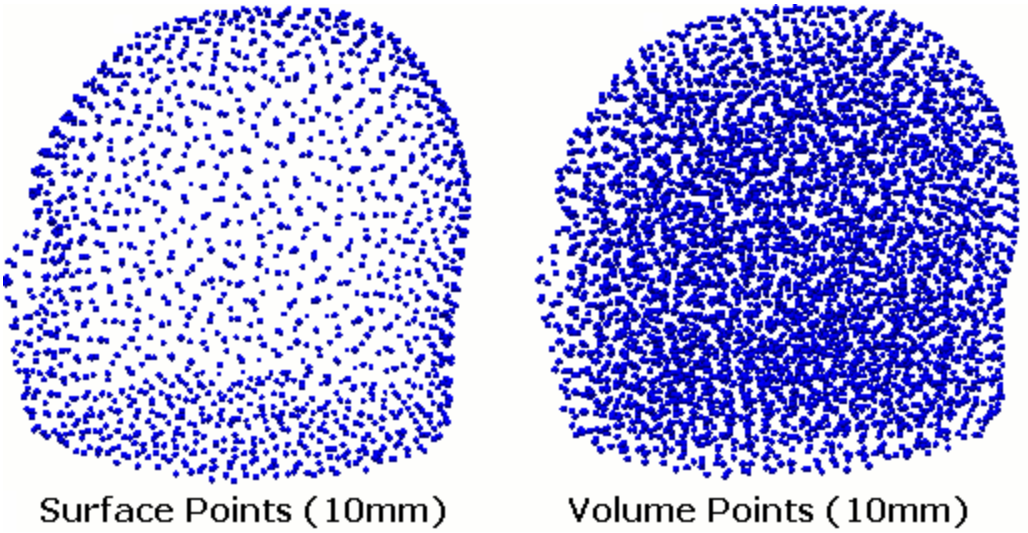
The  icon on the **Image Data** Toolbar performs the same function (or *Ctrl+Shift+I*), but with a fixed **Resolution** of **3mm** (only Default settings are used).

Voxel Mesh. The outside of the triangulated segmented surface, voxel by voxel.

Overlay. A backup of the segmentation result including markers. The  icon on the **Image Data** Toolbar performs the same function (or *Ctrl+Shift+O*), although the **Label** will not be used.

Surface Points. Points distributed on the segmented surface.

Volume Points. Points distributed throughout the segmented volume. Points are typically (albeit rarely) used for source analysis, especially the volume points, which are an alternative to the 3D grids.

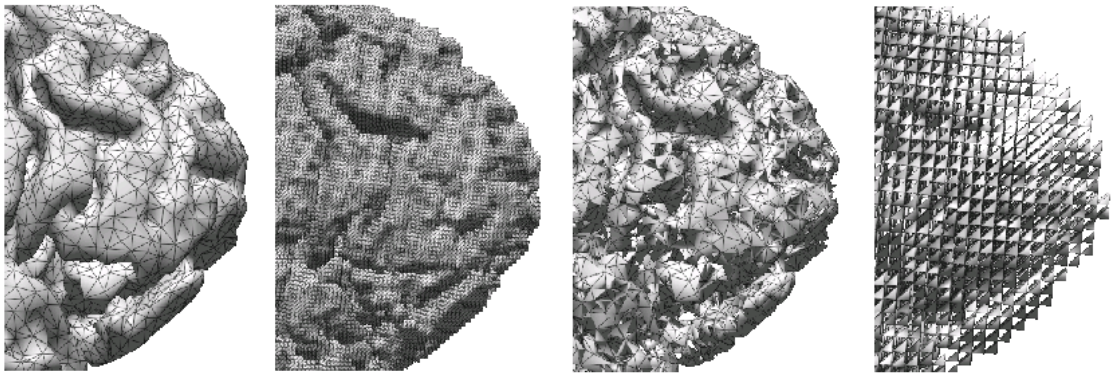


Voxel Points. The points are distributed on a voxel level.

Tetrahedra Mesh. Creates a three dimensional tetrahedral mesh with the segmented surface as the outer hull.

Cube Mesh. Creates a three dimensional cube mesh with the segmented surface as the outer hull.

Examples of the differences in meshes are shown below (with the Wireframe Overlaid).



Resolution [mm]. This field determines the resolution (triangle side length or point distance). A smaller resolution results in more triangles / points. Typically, 2 to 3mm are used for cortical and skin meshes, while 6 to 10 mm are used for BEM meshes.

Resolution is related to Thinning in prior versions of CURRY. Thinning leaves only points on the segmented surfaces with distances larger than the thinning distance (the current **Refinement** distance). Distances are measured along the segmented surface.

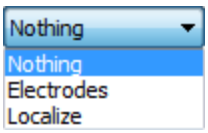
In its generic implementation, thinning selects points on the segmented surface that are distributed as densely and evenly as possible, but do not approach each other more closely than the **Refinement**. Distances are measured along the segmented surface, not in Euclidean (3D) space. The points that remain after thinning are shown instead of the segmented surface in the cross-sections and on the segmented surface in the 3D renderings in the rendered **Image Data** display.

Using Different Resolutions

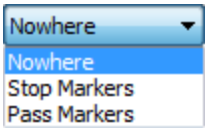
A lower resolution can be used in certain regions. These are specified with the **Mesh Refinement** setting described below (formally referred to as **Wider** and **Wider [%]**).

The **Mesh Refinement** textfield is used to enter the modification factor in percent of the **Refinement** to be used. If **100** is entered, the **Refinement** is the same everywhere, as with the ***Nowhere*** option.

Include. The selection determines whether the **Electrodes** or the **Localize** locations will be part of the generated mesh or points. If **Electrodes** are included, the first found electrodes in any of the result groups are included. If electrodes are not on the segmented surface, they are radially projected using the center-of-mass of the segmented object. This is used to ensure that the electrodes are at the nodes for a BEM Realistic Head Model, skin surface. If **Localize** is selected, the locations in the Localize list will be included (seen under **Results**).



Mesh Refinement. The selection determines whether the resolution will be different at locations with stop or pass markers.



Nowhere. Normal thinning is performed with the given minimum distance.

Stop Markers. A wider thinning distance is used inside Stop Markers.

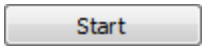
Pass Markers. A wider thinning distance is used inside Pass Markers.

Refinement [%]. This field determines the change of resolution to be used at locations with stop or pass markers, if this is requested.

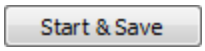
Prepare Pial Surface. This option is only used when you wish to create a cortical triangle mesh. Before pressing **Start**, the segmentation result (yellow outlines) must depict the cortex. Because this is not intuitive, there is a warning that appears once per CURRY session and can silenced. If the option is checked and the prerequisites are met, **Show Pial Surface** will be activated later in the 3D View.

Prepare Inflation and Export. Surfaces in the 3D View (such as the skin and cortex) may be inflated, which has the effect of smoothing rough places on the surface (with low numbers for Inflation), up to removing all features but the general shape. This option is suggested for the skin and for cortical triangle meshes. Initial calculations are required to remove handles, holes, and connecting nodes from the triangle geometry. If these initial calculations are done as part of meshing and before saving the mesh, any subsequent operations will be very fast. If not, these calculations are started when inflation is requested in the 3D View. The cortex that is created with the BEM Geometry procedure is "prepared" by default.

Label. Enable the Label field and enter a label of your choice. Otherwise, "Surface ##" or "Overlay ##" are used as the label, where ## is a consecutive number.

Start. Click the 

button to begin the selected process.

Start and Save. Click the 

button to start the process and save the results.

18.2.5 BEM/FEM Geometry

CURRY can automatically create the typically used triangle meshes (skin, cortex) and define a BEM or FEM Realistic Head Model geometry. The segmentation thresholds and the seed slice defined in the **Image Data Parameters** are used and need to be correct. The different ways to use and define BEM Realistic Head Models are explained first.

Please see the tutorials in the *Image Data Processing* section for instruction in usage.

BEM Realistic Head Model Size

When the surfaces for a BEM Realistic Head Model are created using the automated routine, a realistic three compartment head model can be defined in part by the Resolution. The choice between Low discretization with approximately 3000 nodes, Medium with 4000 nodes, and High with approximately 5000 nodes is offered. Whenever possible, the finer model should be used. However, it is possible to modify the routine to one's own needs by editing the definitions of the variables.

 **Accuracy**

The accuracy of the BEM drops significantly when the distance between a source and a boundary surface is less than about half of the side length of the triangles that are used to describe this surface. Use the BEM source overlay to constrain sources to the inner-most compartment whenever possible in order to ensure that they are at least 3 mm from the boundary between the brain and the inner skull.

The Skin and Cortex, as well as BEM thicknesses for Low, Medium, High, and Very High Resolutions are summarized below, with the approximate number of BEM Realistic Head Model nodes in brackets. ~4000 nodes equal ~8000 triangles. You may instead select **Specify**, and enter the desired values.

Resolution	Skin [mm]	Cortex [mm]	BEM Skin [mm]	Outer Skull [mm]	Inner Skull [mm]	MEG/ECoG Brain [mm]
Low (3000)	3.0	3.0	12.0	10.0	8.0	6.0
Medium (4000)	3.0	3.0	10.0	9.0	7.0	5.0
High (5000)	2.5	2.5	9.0	8.0	6.0	4.0
Very High (6000)	2.0	2.0	8.0	7.0	5.0	3.0

In the amount of memory needed for setup, the IPA matrix and the memory that CURRY and the operating system need are considered. When the amount of memory needed exceeds the amount that your computer has, performance will decrease.

 **Care**

The containment of the compartments can only be verified when the BEM matrix is setup. This takes place when the model is used for source reconstruction for the first time. When one compartment is inside another, none of its nodes must protrude through the boundary surface of the other compartment, or should even come very close to it.

 **MEG**

A single compartment model that consists only of the brain surface could be used for an MEG evaluation. This is created in the MEG/ECoG mode. The accuracy of such a model remains to be compared to that of a three compartment model.

The BEM algorithms are described here and here.

[Fuchs M, Drenckhahn R, Wischmann H, and Wagner M. An improved boundary element method for realistic volume-conductor modeling. Biomedical Engineering, IEEE Transactions, Aug. 1998,
Vol 45:8, p980–997.]

[Fuchs M, Wagner M, and Kastner J. Boundary element method volume conductor models for EEG source reconstruction. Clinical Neurophysiology, August 2001, Vol 112:8 , p1400-1407.]

For a description of the segmentation algorithm, see here.

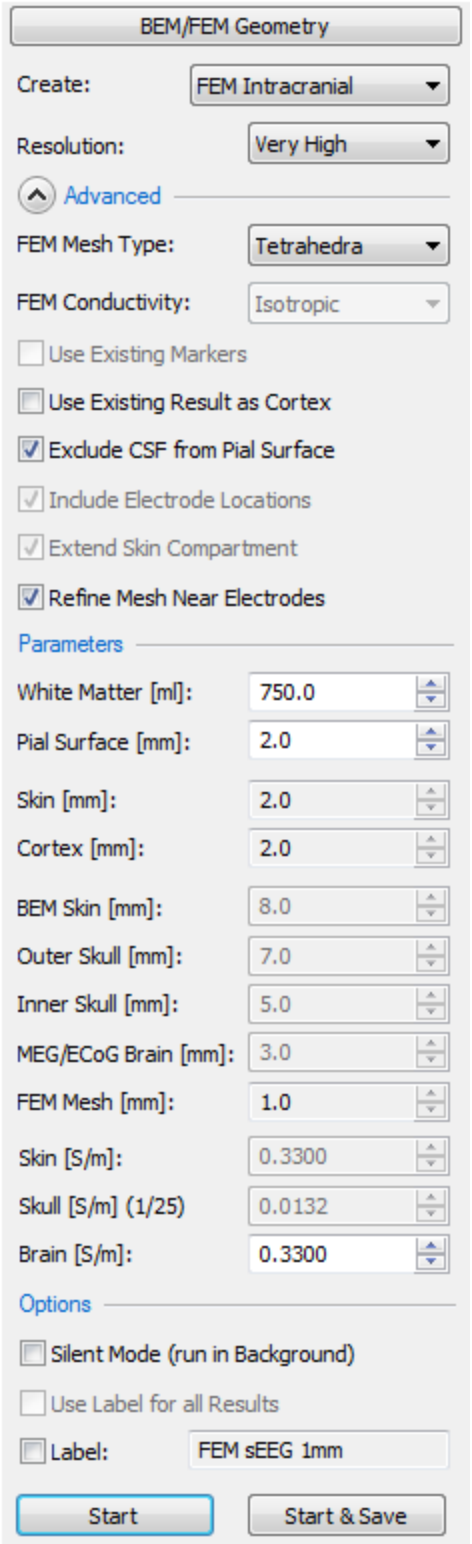
[[Wagner M, Fuchs M, Wischmann H, Ottenberg K, and Dössel O. Cortex segmentation from 3D MR images for MEG reconstructions. Biomagnetism: Fundamental Research and Clinical Applications p433-438, IOS press, Amsterdam 1995.]

For a description of automatic BEM geometry creation, see here.

[Wagner M, Fuchs M, Drenckhahn R, Wischmann H, Köhler Th, and Theißen A. Automatic Generation of BEM and FEM Meshes from 3D MR Data. Neuroimage, 1997, Vol. 5, S389.]

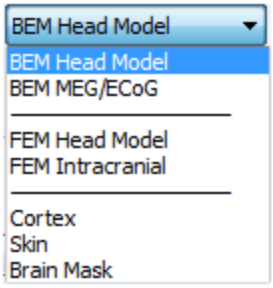
BEM/FEM Options

CURRY can automatically create the typically used triangle meshes (skin, cortex) and define a BEM Realistic Head Model geometry. The segmentation thresholds and the seed slice defined in the **Image Data** → **Segmentation Thresholds** are used and need to be correct.

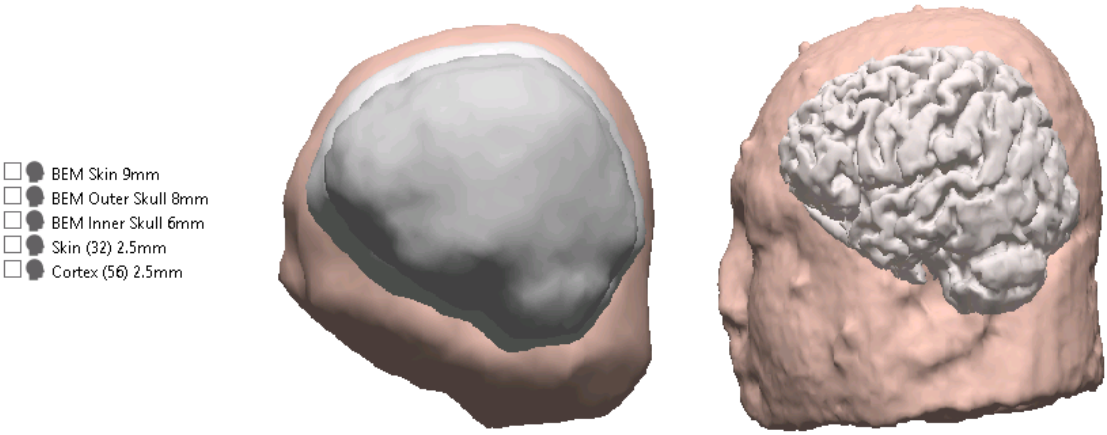


Create. These options are used to create realistic head models and segmented surfaces. The one you select depends on several factors, including whether you have EEG or MEG recordings, scalp, grid or depth electrode recordings, and how much time you have (some models are faster than others when used with source

reconstruction). Briefly, the BEM model uses electrodes that are projected to the outermost surface in the BEM model. It is used with scalp, MEG, and ECoG recordings. The FEM model has nodes throughout the inner compartment, and is used with Intracranial-EEG recordings.



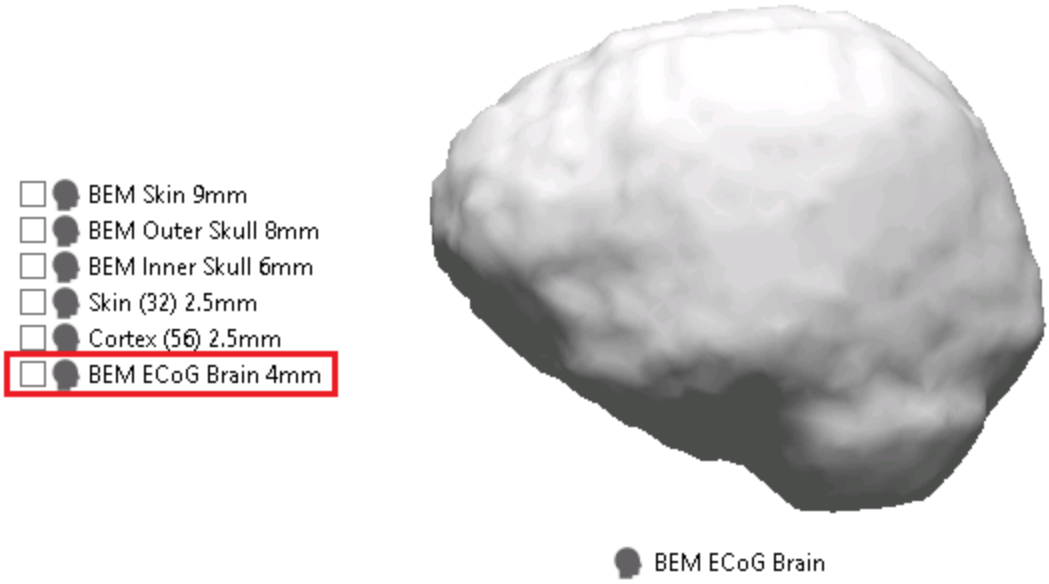
The **BEM Head Model** creates a realistic head model as well as the segmented cortex and skin surfaces.



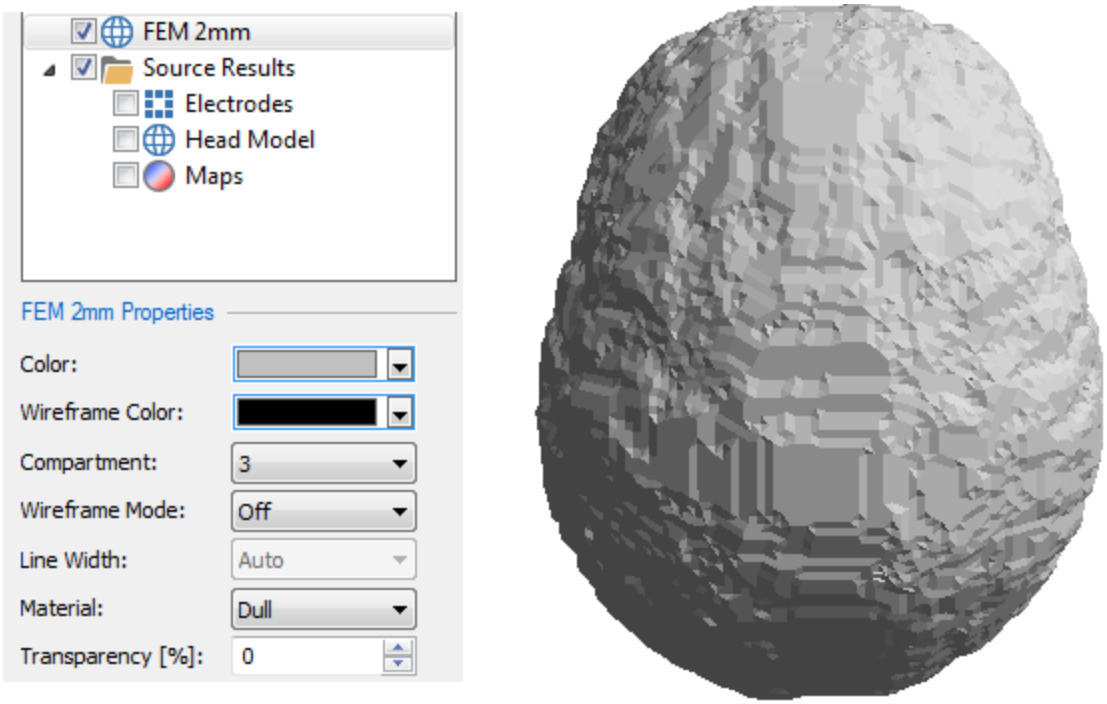
BEM Head Model

Segmented Skin and Cortex

The **BEM MEG/ECoG** model creates the same head model and segmented skin and cortex as the BEM model. Additionally, it creates an inner skull compartment using a higher resolution, and a BEM Realistic Head Model containing the single compartment. This is used with ECoG recordings, where a single component model is appropriate. It has been argued that a single compartment BEM Realistic Head Model is sufficient for MEG recordings, because of the insulating effects of the skull.



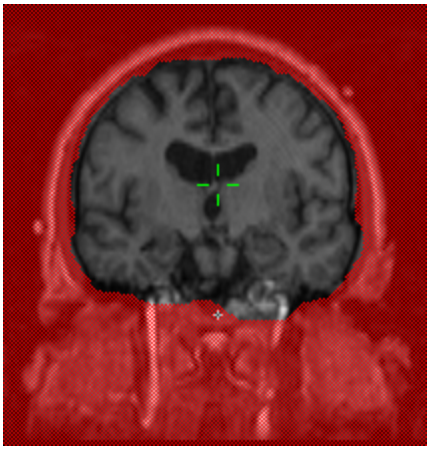
The **FEM Head Model** creates the same segmented cortex as the **BEM Head Model** and **BEM MEG/ECoG** models (for display purposes), plus the FEM Head Model. This is a 3 compartment model, with nodes throughout. When used for source reconstruction, the analysis may become quite time consuming. The BEM model is generally preferred. With the FEM Model, however, the anisotropic properties of the skull (bone) and can be taken into account, and thus the FEM head model will be more precise than the BEM model (although the differences we have seen are generally very slight).



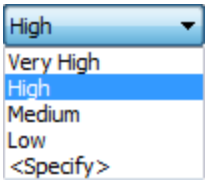
The **FEM Intracranial-EEG** head model creates the same segmented cortex as the **BEM Head Model** and **BEM MEG/ECoG** models, plus it contains the inner skull compartment only. This is used with depth electrodes.

Cortex or **Skin**. Select Cortex or Skin to segment those surfaces only.

Brain Mask. Creates a compartment around the brain with Stop Markers everywhere outside the compartment. (See also **Create Intracranial Electrode Mesh**).



Resolution. The selection determines the resolution of the meshes and BEM Realistic Head Models generated. Select High, Medium, Low or Specify. Typically, **Low** generates models with ~3000 nodes (6000 triangles), while **Medium** leads to ~4000 nodes (8000 triangles), and **High** creates ~5000 nodes (10000 triangles), depending also on the size of the subject's head. As you select High, Medium or Low, you will see some of the mm values change automatically in the Skin, Cortex, Skull and Brain fields. If you select **Specify**, with the BEM Realistic Head Model, all of the fields will become active and you can enter the mm values as desired. With FEM models, the Resolution changes the length of the sides of the tetrahedra. **Medium** will create 4mm sides, **High** will create 2mm sides which is standard, although it will take longer.



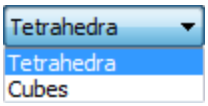
Very High, **High**, **Medium**, **Low, <Specify>**. Select the desired Resolution, or Specify. See the summary table above for the mm values used with each. Selecting **Specify** will activate the **Skin [mm]**, **Cortex [mm]**, etc. fields depending on what you are creating, allowing you to specify your own mm values.

Advanced

FEM Mesh Type. FEM mesh generation in CURRY employs segmentation overlays as input in order to produce volume meshes. Each mesh element is assigned an

isotropic conductivity value according to the tissue type it represents (e.g. skin, bone, brain).

The FEM Mesh Type can be either tetrahedra or cubes (hexahedra). Both available mesh types yield similar results in comparable computation times; however, tetrahedral meshes can better capture smooth compartment boundaries without showing the staircase effect of cube meshes.



M. Wagner, Rekonstruktion neuronaler Ströme aus bioelektrischen und biomagnetischen Messungen auf der aus MR-Bildern segmentierten Hirnrinde, Shaker-Verlag Aachen, ISBN 3-8265-4293-2, 1998.

FEM Conductivity. Here you may select either an **Isotropic** (as in previous versions of CURRY) or an **Anisotropic Skull** (available when you select to Create a FEM Head Model). If you select the latter, it is integrated with the **Skull Anisotropic** section at the bottom of the **FEM Model** panel. To date, the difference between the two methods has been shown to be very small; however, the option has been included for those wishing to use it. The difference between using a realistic head model versus a spherical shell model is far greater than whether you use isotropic or anisotropic models (anisotropic may add a slight improvement).

When applying the anisotropic skull, the automated FEM Model uses the default **Tangential / Radial Conductivity Ratio** of **2.8**, which is the same as assuming a skull conductivity that is ten times lower than the conductivity of the bone marrow.

Fuchs M, Wagner M, Kastner J (2007): Development of volume conductor and source models to localize epileptic foci. Journal of Clinical Neurophysiology 24:101–119.

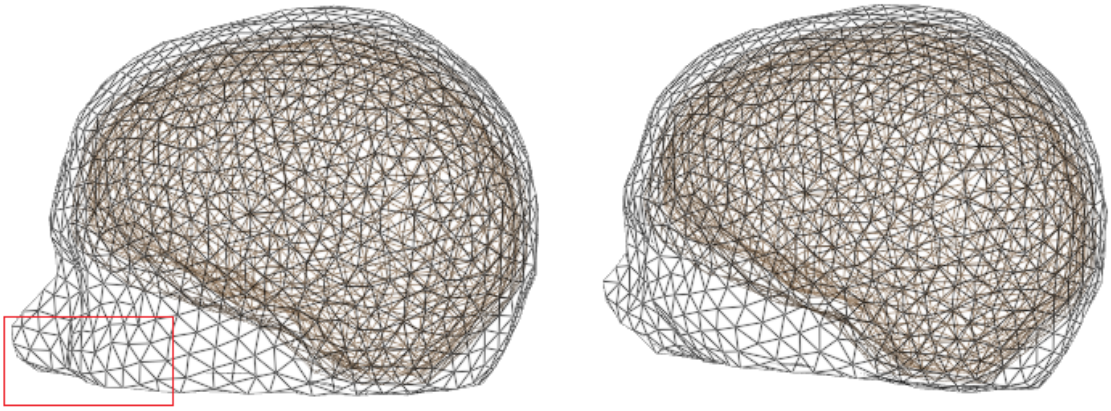
Use Existing Markers. This field will be active if you have placed Pass or Stop Markers. The markers will then be used to constrain the segmentation.

Use Existing Result as Cortex. If enabled, the BEM Realistic Head Model is created based on the momentary segmentation result, which must be a segmentation of the cortex including the cerebellum, instead of segmenting the cortex as part of the procedure. In other words, if you have already segmented the cortex (including the cerebellum), and wish to use that as the basis of a BEM Realistic Head Model, you should enable this option (it will be grayed out if no segmentation result is available). The head model will include the already segmented cortex.

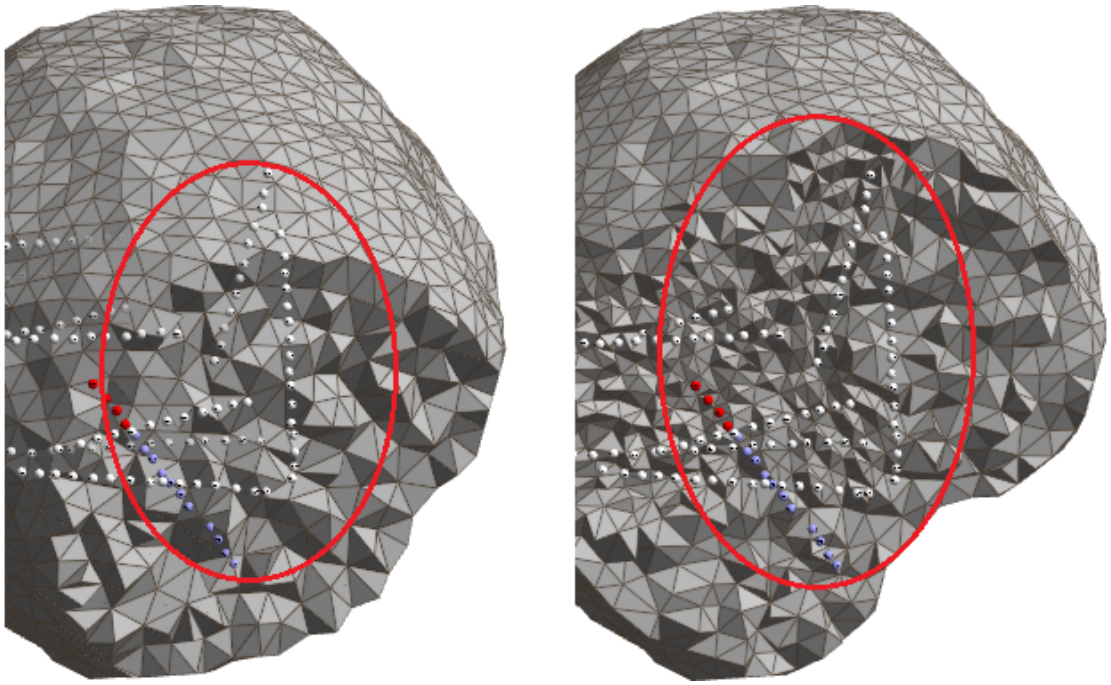
Exclude CSF from Pial Surface. Generally, the cerebrospinal fluid is not included (default). Including it will slightly enlarge the segmented cortex, and may improve its appearance in some cases.

Include Electrode Locations. If enabled, the active electrodes become nodes of the BEM skin mesh.

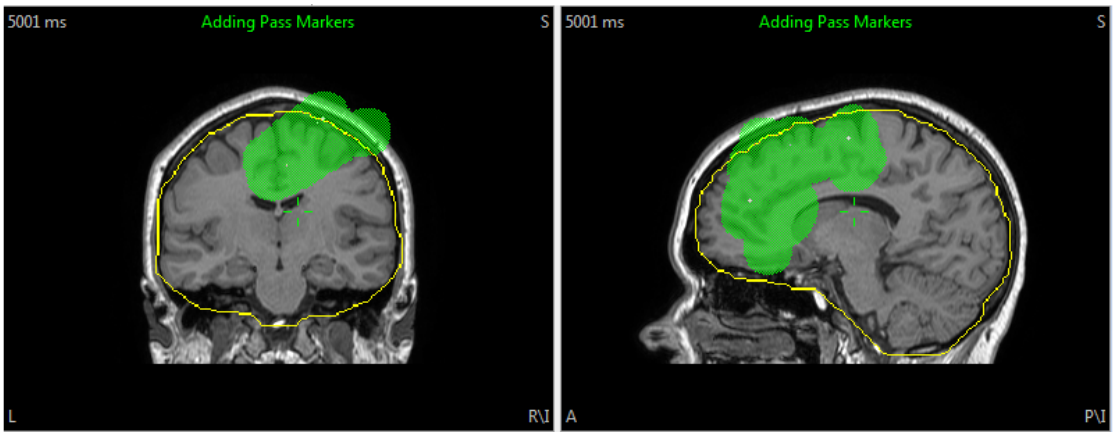
Extend Skin Compartment. This option is sensitive when you have electrodes that extend down to include cheek area, etc., such as when using EGI caps. It is on by default, unless you are using the CURRY 7 Scope. The difference is, with the option enabled, you will see more of the skin compartment in the area from the tip of the nose down and back behind the chin. The model is affected somewhat by conductivities, as these are not known for areas of the cheek that include sinuses, teeth, etc. The skin conductivities are used. This is an illustration of the trade-offs that may occur among models. If you use the standard BEM model with a cap whose electrodes extend further down, the electrode positions will wrap around underneath the base of the model. With the Extended Skin, the electrode positions will me correct, but the BEM model will be affected by the different conductivities.



Refine Mesh Near Electrodes. This option is accessible only when **FEM Intracranial-EEG** has been selected for **Create**, and then it is enabled by default. When selected, the resolution of the mesh near the electrode tracks will increase, thereby providing more accurate source locations. Note the triangle sizes on the left, where the Refine option was not enabled. They are all the same size. On the right, where the Refine option was enabled, the triangles are smaller in the vicinity of the electrodes (70% of the selected mesh side length). In essence, this is like creating a much higher resolution model, without it taking as much time and space. Only the interesting areas have the high resolution. If you are creating a FEM model under FEM Model, you can add Pass Markers and create higher resolution in those areas (see **FEM Model** for more information).



In fact, as the model is being created, you will see pass markers being added automatically along the electrode tracks. The Pass Markers are 30 mm in diameter.



Parameters

White Matter [ml]. This is the assumed volume of the white matter (1ml = 1cc), and should be changed only if the subject's brain is unusually large or small. A segmentation of this amount of tissue must not include any regions outside the brain, as cortex segmentation is later limited to a smoothed and enlarged version of the white matter found using this volume criterion.

Pial Surface [mm]. The pial surface is created by inflating each location on the cortical surface until a) opposing sulcal walls start touching each other, b) the surface extends into the CSF, c) a maximum inflation distance has been reached, which is controlled by this field. The pial surface is a display option available in 3D View for cortical triangle meshes (and derived CDR etc. results) created by "BEM/FEM geometry". When activated, the outer (pial) layer of cortex rather than a middle layer is displayed. Results such as CDR can be displayed on the pial

surface rather than the cortical (middle cortical layer) surface, although they will still have been calculated for the middle cortex layer, as this is where the pyramidal cells are.

Skin [mm], **Cortex [mm]**, **BEM/FEM Skin [mm]**, **Outer Skull [mm]**, **Inner Skull [mm], MEG/ECoG Brain [mm], FEM Mesh [mm]**. These fields are active depending on 1) what you are Creating (BEM, FEM, Cortex, Skin, etc), and 2) the Resolution you have selected. For example, if you are creating a BEM Head Model where you select **Specify**, all fields are active (except MEG/ECoG Brain), allowing you to enter the values. If you create Cortex, and Specify the Resolution, then only the White Matter, Pial Surface, and Cortex fields will be active. If you select Very High, High, Medium or Low Resolution, the fields other than White Matter and Pial Surface will be grayed out, although you will see the values that are used. The **BEM/FEM Skin [mm]**, **Outer Skull [mm]**, **Inner Skull [mm]** fields determine the resolution of the BEM meshes and, as a consequence, the number of nodes of the BEM Head Model.

Skin [S/m], **Skull [S/m]**, **Brain [S/m]**. These fields determine the conductivities of the Head Models, and will vary in accessibility based on the model you select.

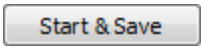
Options
Silent Mode (run in Background). If enabled, the BEM geometry setup will run in the background, allowing you to do other things in the meantime. BEM geometry setup can be stopped using the ESC key.

Use Label for all Results. When enabled, the Surfaces, BEM Realistic Head Model, and Overlays will prepend the **Label** you define. For example, if you define **Label** as *SUB001*, the segmented cortex will be labeled *SUB001 Cortex (97) 3mm* (the number in parentheses is the segmentation threshold that was used).

Label. The autocreated labels will correspond to the type of model you are creating (BEM, Skin, Cortex, etc.), or you can enter your own label.

Start. Click the 

button to begin the selected process.

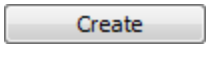
Start and Save. Click the 

button to start the process and save the results. The surfaces, models, etc., will be saved to the HD, using the same file name as the MR data file, and in the same folder. If the files already exist, you will have the option to overwrite them.

See the tutorials under *Image Data Processing* for examples illustrating manual and automated segmentation.

Using Binary Overlays

Segmentation results along with markers can be exported to and imported from binary overlays; CURRY can manage 100 per image dataset. Binary overlays are a convenient way of storing segmentation results, and can be used for:

– Backup of segmentation results and markers. This is performed using **Image Data** section , 

panel, and 

.

An alternate route is to select **Image Data** from the **Main Menu** bar, then **Overlay** → **Create**, or click the icon on the **Image Data** Toolbar.

– Re-import of segmentation results and markers. By selecting Results, Results, choosing an Overlay, and clicking **Import**, segmentation results and markers are overwritten by the new overlay.

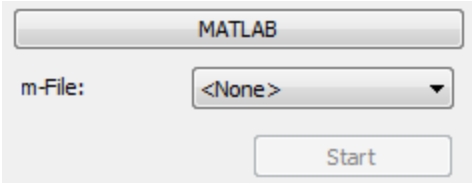
- Transfer of segmentation results and markers. By selecting Results, Results, choosing an Overlay, and clicking **Import**, backed up segmentation results and markers are transferred to the whichever Image Data set you are working with.

- Creation of custom FEM models through the **Results** → **FEM Model** interface.

In addition, the **Properties** panel allows you to save overlays to disk, load overlays from disk, and delete overlays from memory or from disk.

18.2.6 MATLAB

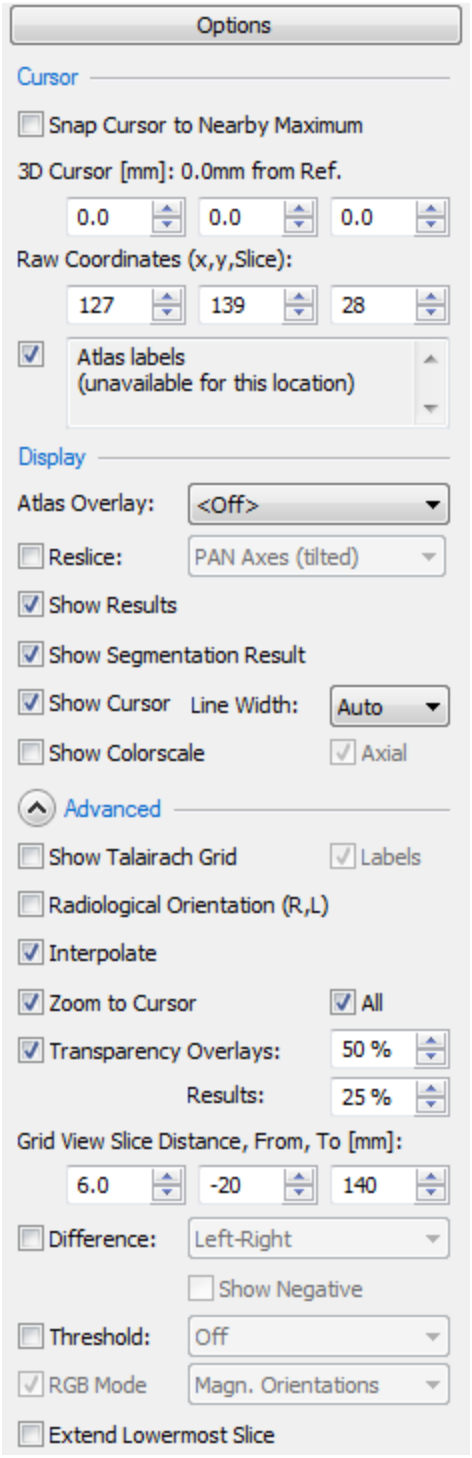
There are several places in CURRY where you may interface with MATLAB. Image data slices are passed to MATLAB, and as a result of MATLAB processing, the current cursor position, reference position, and Nasion, PAL, PAR, AC, and PC landmark locations can be returned.



m-File. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

18.2.7 Options

Various display features have been grouped in the **Options** panel.



Cursor

Snap Cursor to Nearby Maximum. This feature, when enabled, will move the image data cursor to a nearby intensity maximum after clicking in the image data. It is, in a way, a sibling feature to the "magnetic cursor" that can be enabled for manual event marking. It is typically used for defining electrode locations in CT data that are usually rendered as small bright dots.

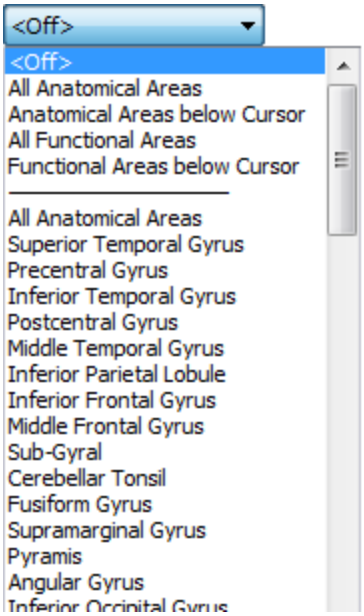
3D Cursor (mm): 0.0mm from Ref. This displays the location of the 3D cursor in the selected coordinate system and its distance from the reference point. In the example shown, the 3D cursor is 58.2mm from the Reference (midline brainstem). The x,y,z coordinates of the current cursor location are displayed. Moving the cursor will update the coordinate positions; entering coordinates will reposition the cursor.

Raw Coordinates (x,y,Slice). The x and y raw coordinates for the cursor position are displayed in raw image coordinates, starting with 0.

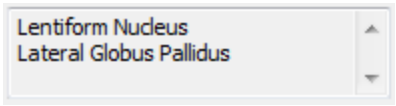
Atlas labels. The structure corresponding to the cursor position is displayed in the text field (as well as informational messages).

Display

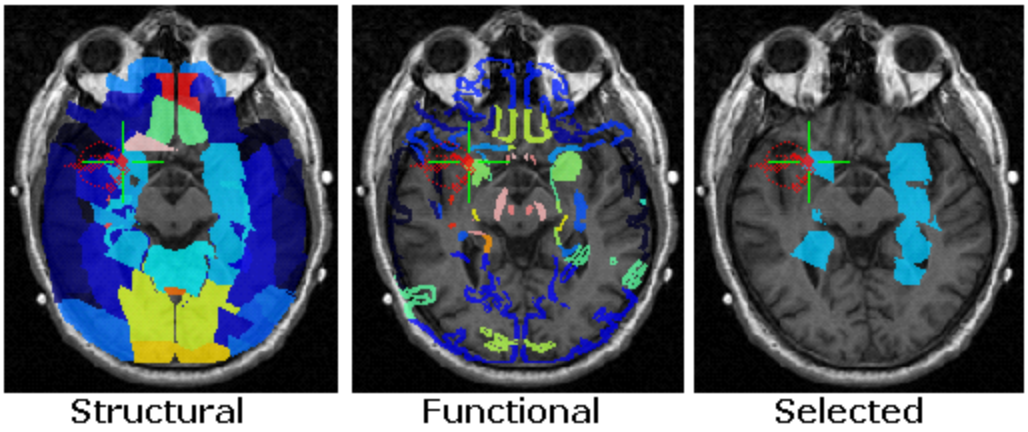
Atlas Overlay. When you enable the Talairach atlas, you have the option to display All Anatomical, All Functional (including Brodmann areas), or any selected anatomical/functional brain structure. This presupposes that you have entered the AC, PC and MS coordinates and boundaries correctly in the Image Data Import steps, described above. If the option is grayed out, this means you need to define the Talairach coordinates. Go to the Workflow display and click **Define Talairach Coordinates**. This will take you to **Steps 6** and **7** of the **Image Data Parameters** windows where you should then define the landmarks and boundaries. (If you are importing an older MR data set - pre Version 6 - and wish to use the Talairach coordinates, you will need to define the landmarks and boundaries).



When you click on a structure in the image display, the corresponding structure is displayed in the text field.

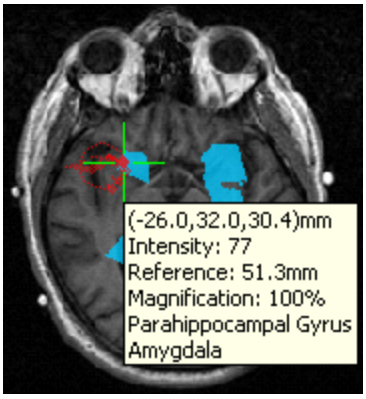


If you select an area from the drop-down list, you will need to position the 3D cursor near that area in order to see the colored section. The Anatomical, Structural, and a selected area are seen as follows.

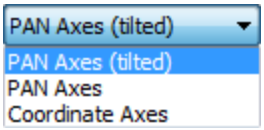


Different areas will be displayed in different colors, as selected in the **Atlas Maps** option in the **Colors** fields, described below.

If you position the mouse cursor at any point in the image data, you will see a Tooltip that shows the cursor position, the intensity, the distance from the Reference, Magnification, and *structure/area* that for that location. If you do not see the Tooltips, go to **View** → **Show Tooltips**, and enable the option.



Reslice. The images are reoriented according to the **PAN Axes (tilted)**, **PAN Axes**, or **Coordinate Axes**.

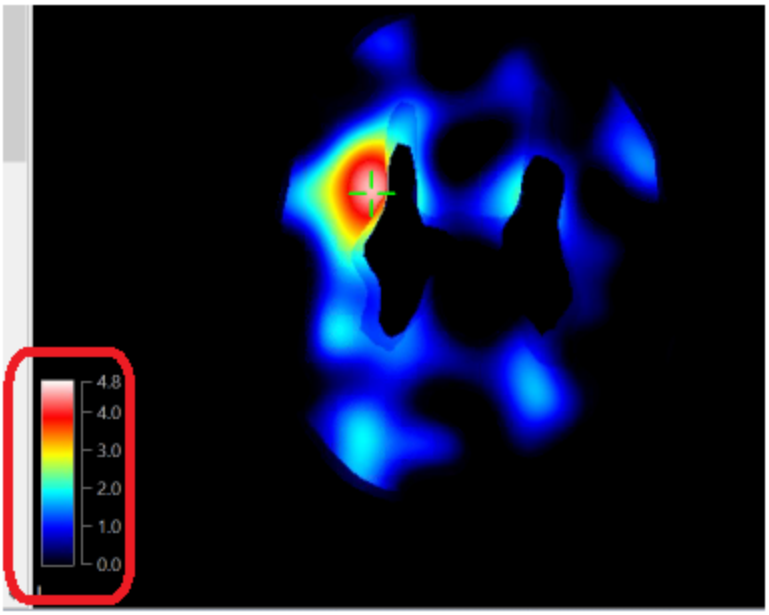


Show Results. This is the same as the  button on the **Image Data** Toolbar (or *Alt+D*), used to toggle the display of the source solutions.

Show Segmentation Result. Toggle the display of the segmentation result. This has the same function as the  icon on the Image Data Toolbar.

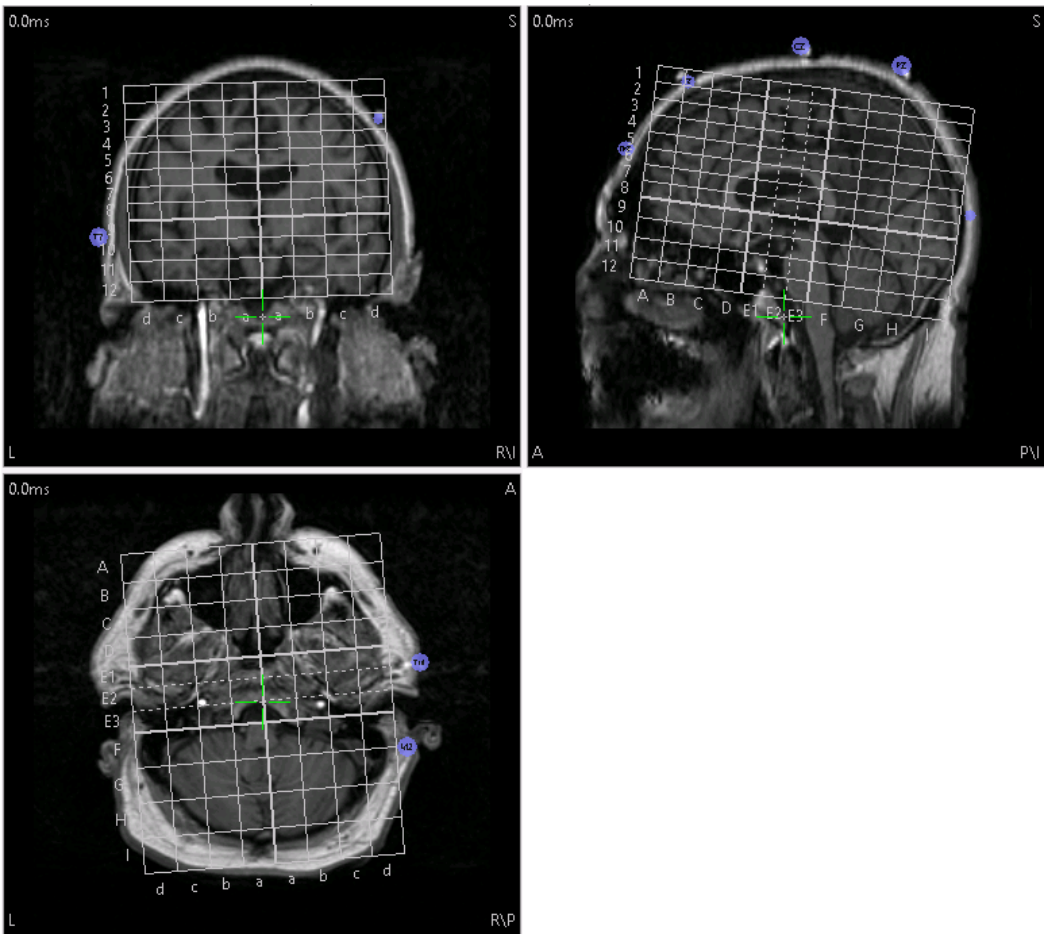
Show Cursor. This is the same as the  button on the **Image Data** Toolbar (or *Alt+C*), used to toggle the display of the cursor cross-hair. Increase the width of the lines with the **Line Width** field (or use **Auto**).

Show Colorscale, Axial. Activates the display of the scale for the iso-images when enabled. You may display it for just the Axial (enable **Axial**) or all of the images (disable **Axial**).



Advanced

Show Talairach Grid. The Talairach grid is superimposed on the iso-images, with or without **Labels**.

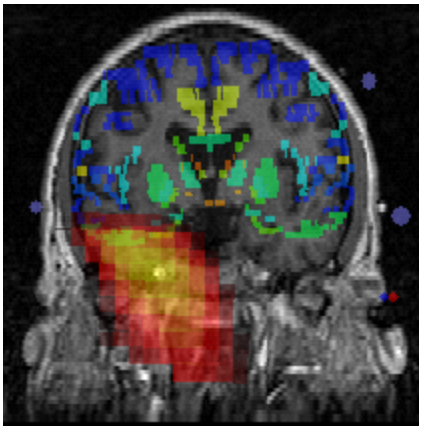


Radiological Orientation (R,L). Reverses right and left in the display as a convenience for radiology versus neurology viewers.

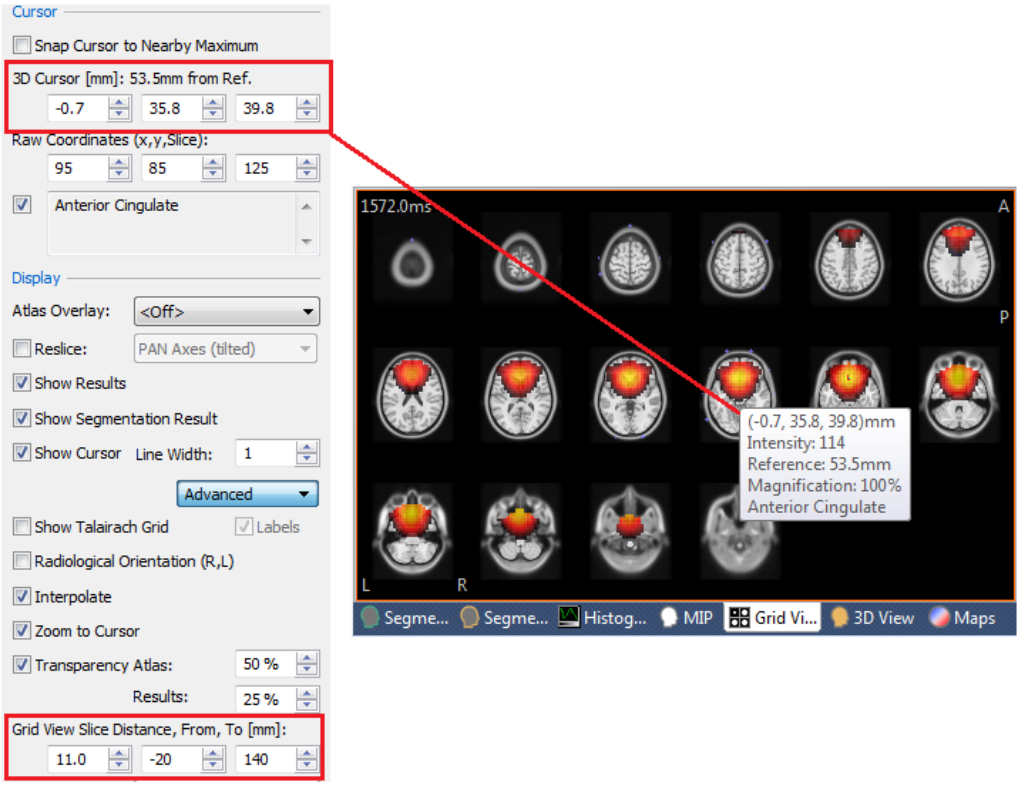
Interpolate. If selected, interpolation is used for rendering pixel values, for saving image data, and for segmentation. Interpolation results in smoother MR images.

Zoom to Cursor / All. If you zoom in to one of the MR image views, you can zoom either to the position of the cursor (enable Zoom to Cursor), or to the center of the image (option disabled). If you have **All** enabled, Zooming In will be seen in all iso-images. If disabled, only the selected one will be zoomed into.

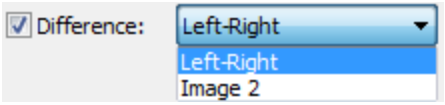
Transparency Atlas (%). When using the Atlas or displaying source reconstruction results with the image data, this field determines how transparent the overlays are. The larger the number, the more transparent the overlay. Transparency can be set independently for the **Atlas** and the **Results**.



Grid View Slice Distance, From, To [mm]. Grid View is a display option in the fourth view of the image data display. It renders the MRI using equidistant horizontal slices, which provides an intuitive way to visualize 3D activations (e.g., CDRs) in a single display. "Distance" is the slice distance (the smaller the values, the more slices are displayed). "To" is the z-axis coordinate (in CURRY's PAN system) of the center of the top-most displayed slice. "From" is the z-axis coordinate of the center of the lowermost slice that is guaranteed to be displayed. Depending on the available size and axis ratio of the display area, the resulting grid layout is automatically and optimally determined, which typically results in a few more inferior slices to be shown than "From" would suggest, just to fill the available space with meaningful data. Clicking in any part of the grid will allow read-out of the respective coordinate in **Options**, while hovering the mouse displays the coordinate in the Tooltip information window.

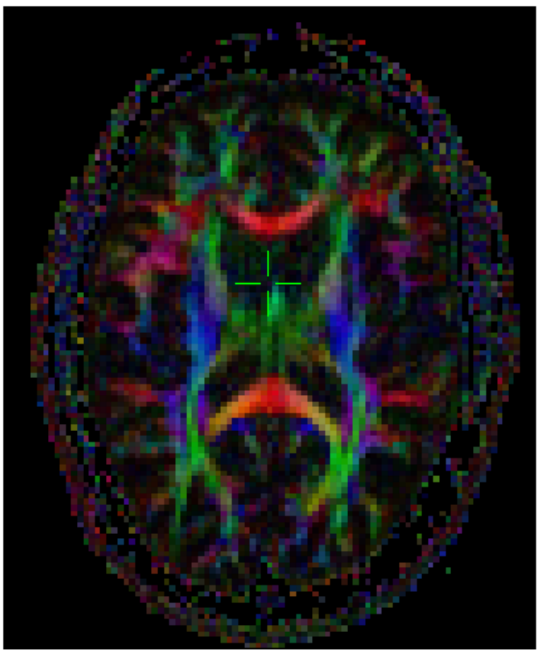


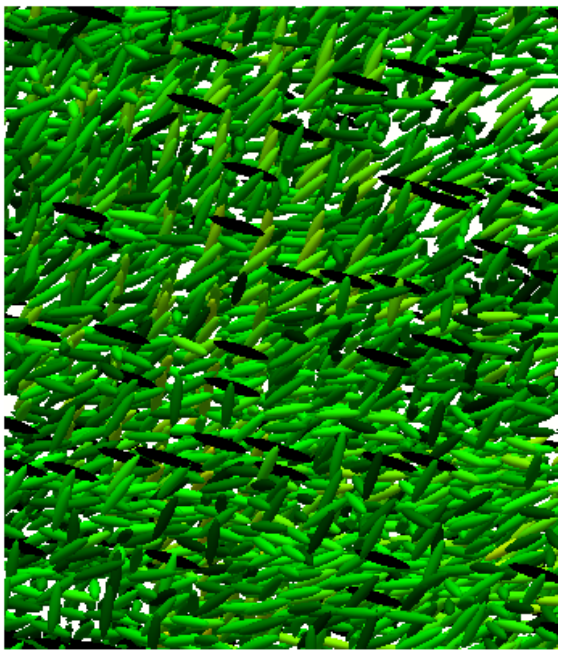
Difference. The option is used to subtract the right side from the left side (with a single data set), or one image data set from another (with two data sets loaded). For properly intensity-adjusted SPECT images, this option can be used to create a SISCOM display. **Show Negative** inverts the BW scale.



Threshold. The option is used to superimpose the image data from one set upon another. It will be active after you load at least two image data sets. If you select it from one data set, you will have the option to select either of the other data sets for superimposition. Note that only the portions above the threshold set in the modality to be added are shown.

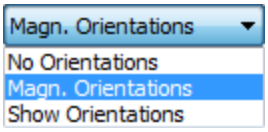
RGB Mode. RGB Mode will be active only when you have loaded image data that contains RGB images. An example would be images for DTI Fiber Track analysis (showing the orientation of the fiber tracks). For an example, please see the *DTI Fiber Track Imaging* tutorial.



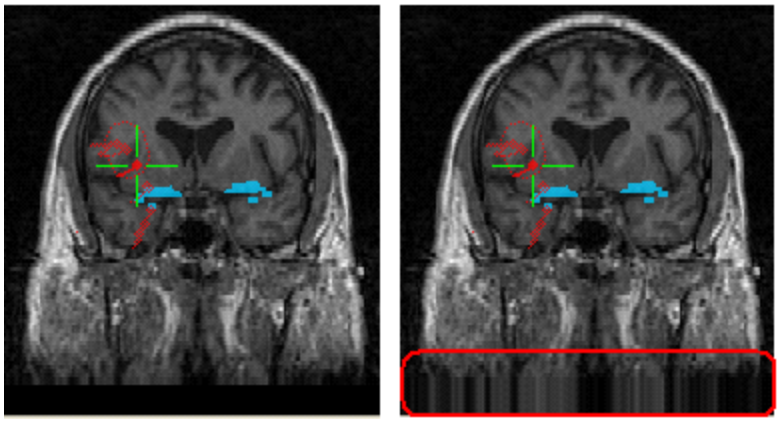


For DTI FA (Diffusion Tensor Imaging Fractional Anisotropy images), the dominating orientation of the conductivity tensor measured by DTI is encoded as an RGB value, where red is transversal, green is longitudinal, blue is vertical. This orientation depicts, for example, the dominating white matter fiber orientation of the respective voxel. "Show Orientations" overlays small orientation symbols (short lines) onto the data display that visualize these (fiber) orientations. "Magnified Orientations" does the same, but only if image data are magnified (eg by pressing

the plus key over the image data display). "No Orientations" just depicts the RGB values.

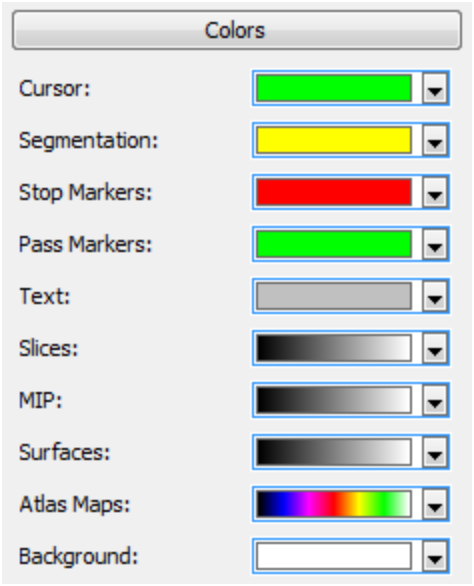


Extend Lowermost Slice. If selected, the bottom slice is extended for image data display, for saving image data, and for segmentation.



18.2.8 Colors

The Colors display provides you with controls to assign colors to different objects. An item color changes when a different color is assigned. The available colors and color scales are shown in the panel. You will see a color palette when you click the drop-down arrow. Some palettes have solid colors, while others offer various color spectra that may be used.



Cursor. The color of the cross-hair cursor and MR slice indicator (rectangle).

Segmentation. The color of the segmented boundaries.

Stop Markers. The color of the Stop Markers.

Pass Markers. The color of the Pass Markers.

Text. The color of the informational text in the views, and the Reference indicator.

Slices. The color of the MR images.

MIP. The color of the Maximum Intensity Projection (MIP).

Surfaces. The color of the Segmentation Preview and Segmentation Results surfaces.

Atlas Map. The color sequence used in the Atlas.

Background. The color of the background.

18.2.9 Additional Segmentation Options

Additional options pertaining to segmentation are found under **Image Data** on the **Main Menu** bar, as well as some options accessed from *right clicking* in the 

display.

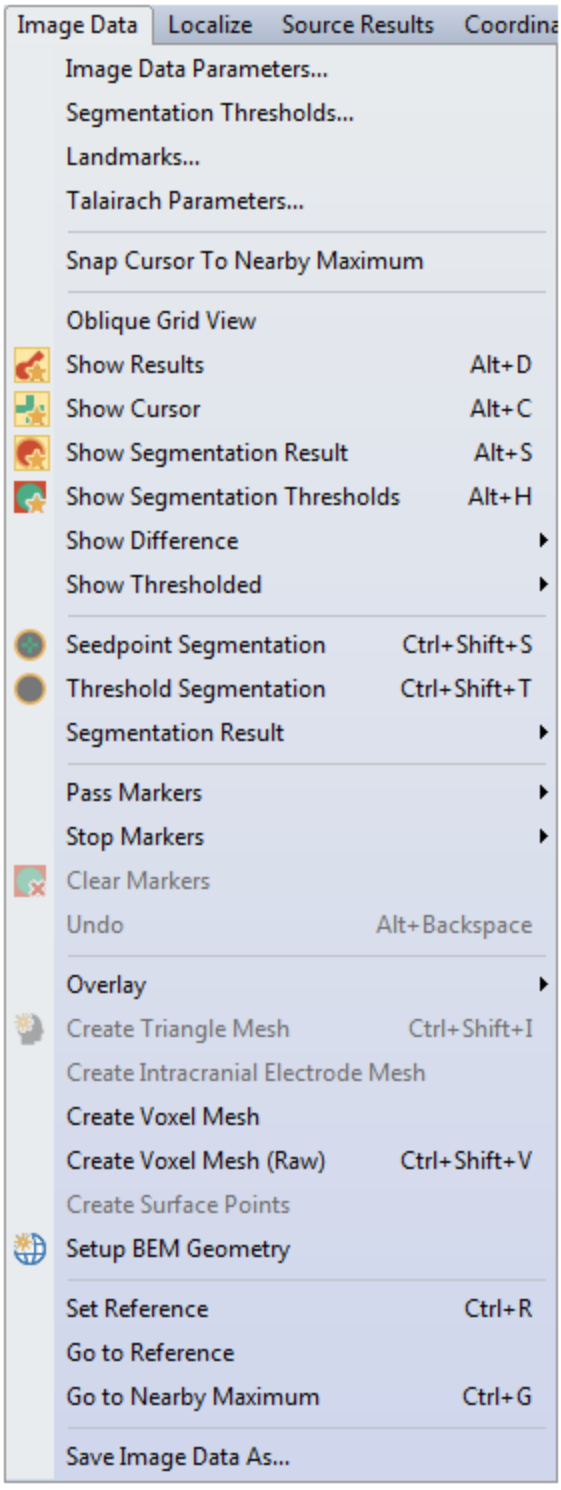


Image Data Parameters. This option opens the **Image Data Parameters** windows **Segmentation Thresholds**. **Step 5** from the **Image Data Parameters** windows is accessed, allowing you to review or modify the segmentation thresholds.

Landmarks. **Step 6** from the **Image Data Parameters** windows is accessed, allowing you to review or modify the anatomical landmarks.

Talairach Parameters. Click this option to review or modify the anatomical landmarks (AC, PC, and MS) and the brain region boundaries as related to defining the Talairach parameters (**Steps 6** and **7** of the **Image Data Parameters** windows will appear).

Snap Cursor to Nearby Maximum. This feature, when enabled, will move the image data cursor to a nearby intensity maximum after clicking in the image data. It is, in a way, a sibling feature to the "magnetic cursor" that can be enabled for manual event marking. It is typically used for defining electrode locations in CT data that are usually rendered as small bright dots.

Show Results. This option toggles the display of the source localizations on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+D*).

Show Cursor. This option toggles the display of the cross-hair cursor on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+C*).

Show Segmentation Result. This option toggles the display of the segmentation results on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+S*).

Show Segmentation Thresholds. Toggles on and off the display of the segmentation thresholds. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+H*).

Show Difference. If you have more than one set if image data opened, you may subtract, for example, Image Data 2 from Image Data 1.

Show Thresholded. The option is used to superimpose the image data from one set upon another. It will be active after you load at least two image data sets. If you select it from one data set, you will have the option to select either of the other data sets for superimposition. Note that only the portions above the threshold set in the modality to be added are shown.

This option may also be used to superimpose DTI data on the MR data (from the same subject). Load the MR data first in the Database. Make sure the MR data has the focus, then select **Image Data 2** to display the DTI data on the MR data. The same result may be obtained by selecting the **Threshold** option from the **Options** panel. Use the **Transparency Atlas** option to adjust the transparency.

Seedpoint Segmentation. This option performs **Region Growing** segmentation. Clicking it has the same function as clicking the 

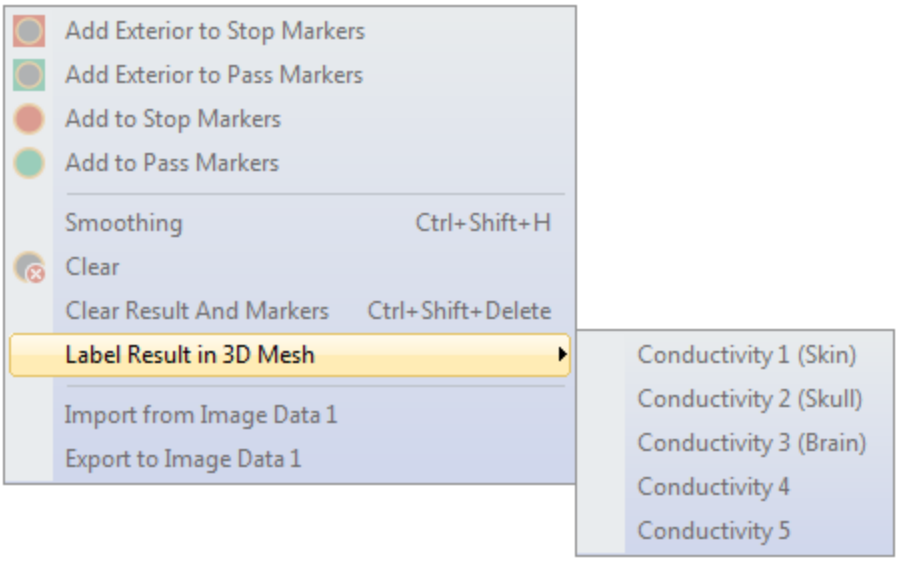
button in the **Segmentation** panel. It is also accessed by the  icon on the **Image Data** Toolbar (or *Ctrl+Shift+S*).

Threshold Segmentation. This option performs **Threshold** segmentation. Clicking it has the same function as clicking the 

button in the **Segmentation**

panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+T*).

Segmentation Result. This accesses a secondary menu with the following options. Pass Markers are generally seen in green, and Stop Markers are in red (you can change the colors in the **Colors** panel under **Image Data**). Most of the same options are seen in the **Segmentation** panel after clicking the Result button.



Add Exterior to Stop Markers. Exterior regions will be filled with Stop Markers (regions will turn red). It is also accessed by the icon on the **Image Data** Toolbar.

Add Exterior to Pass Markers. Exterior regions will be filled with Pass Markers (regions will turn green). It is also accessed by the icon on the **Image Data** Toolbar.

Add [Segmentation Result] to Stop Markers. Click this option to include the segmented region with the Stop Markers (regions will turn red). It is also accessed by the icon on the **Image Data** Toolbar.

Add [Segmentation Result] to Pass Markers. Click this option to include the segmented region with the Pass Markers (regions will turn green). It is also accessed by the icon on the **Image Data** Toolbar.

Smoothing (*Ctrl+Shift+H*). This option is meant to be used to obtain a quick Smoothing result, and so always uses a **12mm Dilation**. Use the **Morphology** panel options for any other parameters, and its **Start** button to apply them.

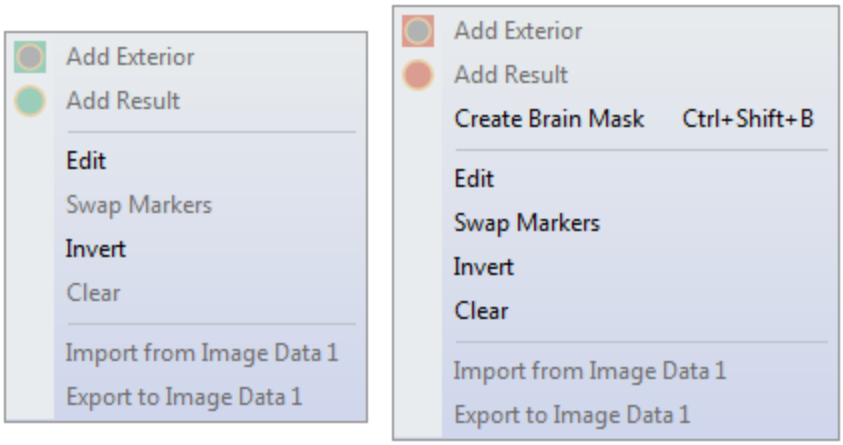
Clear. This clears the segmentation result. It is also accessed by the icon on the **Image Data** Toolbar

Clear Result and Markers. This clears the segmentation result and markers.

Label Result in 3D Mesh. This feature is related to the creation of FEM models. Between creating a tetrahedra/cube mesh and exporting it in CAUCHY format (which can be done from the context menu in Results), one might wish to "label" tetrahedra with respect to which tissue type they represent. This is based on the segmentation result currently in **Image Data**. Because compartments enclose each other, the program starts with the skin, then the outer skull, then the inner skull, overwriting in each step the labeling for the enclosed tetrahedra.

Import from Image Data 1/Export to Image Data 1. You must have two (or more) image data sets loaded to use these options. The second or third data set can import results from the first, or export results to the first.

Pass Markers/Stop Markers. Pass and Stop Markers determine the boundaries or regions used in segmentation.



Add Exterior. Adds the complement of the segmented volume to the markers of the selected **Marker Type**. It is also accessed by the icon on the **Image Data** Toolbar.

Add Result. Adds the segmented volume to the markers of the selected **Marker Type**. It is also accessed by the icon on the **Image Data** Toolbar.

Edit. Selecting this option expands the Markers panel, and sets the **Edit Mode** to **Pass/Stop Markers**.

Swap Markers. Swaps Stop and Pass Markers.

Invert. Inverts **Pass/Stop Markers**.

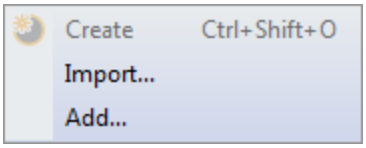
Clear. Clears all **Pass/Stop Markers**.

Import from Image Data 1/**Export to Image Data 1**. You must have two (or more) image data sets loaded to use these options. The second or third data set can import markers from the first, or export markers to the first.

Clear Markers. Select this option to clear the Markers (same as the button on the **Image Data** Toolbar).

Undo. The most recent step is undone.

Overlay. The options are used to Create, Import, or Add overlays. Overlays store segmentation results and markers for later use.



Create. This creates an overlay of the most recently segmented surface(s). It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+O*).

Import. This selects the Doubleclick: Import Overlay mode in the **Properties** panel under Results. Import Overlay shows all Overlays (segmentation results) that can be imported to **Image Data**. Creating a new overlay will *replace* an existing one. Double-click an overlay to import it.

Add. This selects the Doubleclick: Add Overlay mode in the **Properties** panel under Results. New overlays will be *added* to the list. Double-click an overlay to import it.

Create Triangle Mesh. After segmentation, click this option to create a quick triangulated mesh surface, using a fixed **Dilation** of **12mm**. The results will appear in the **Properties** panel as Surface**#** (where # is the number of the next available Surface). The results are displayed in the 3D View. The option is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+I*). Use the parameter fields in the Create panel for other settings, and then click its **Start** button to apply them.

Create Voxel Mesh. A voxel mesh is created (see also Create).

Create Voxel Mesh (Raw). This feature is similar to the Create Voxel Mesh command, which transforms the yellow segmentation result into a voxel mesh and therefore has an inherent resolution of 256x256x256 (the resolution of markers and segmentation result). However, especially for CT, the raw image resolution may be higher, usually 512x512x512, and the "raw" voxel mesh will have the resolution of the raw image data, not using the segmentation result at all, but simply including all voxels that satisfy the threshold (and marker) criteria into the voxel mesh. This results in higher-quality 3D View renderings of e.g., intracranial electrodes.

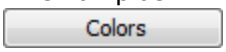
Create Surface Points. After segmentation, click this option to create a surface consisting of points (see also Create). The results will appear in the

Properties panel as Points**#** (where # is the number of the next available set of points). The results are displayed in the 

.

Setup BEM Geometry. This is a shortcut to the 

panel for using the automated BEM Realistic Head Model algorithm. It is also accessed by the  icon on the **Image Data** Toolbar.

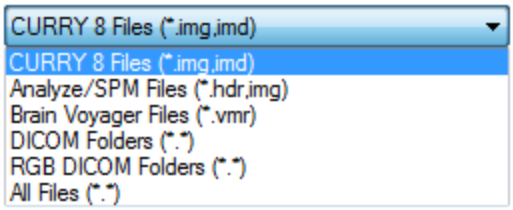
Set Reference. Click this option (or *Ctrl+R*) to set the reference point at the current cross-hair cursor position. A small plus will appear, with the color determined by the **Infos** color setting under 

. The distance from the cursor to the Reference is displayed in the Tooltip and in the **Options** panel.

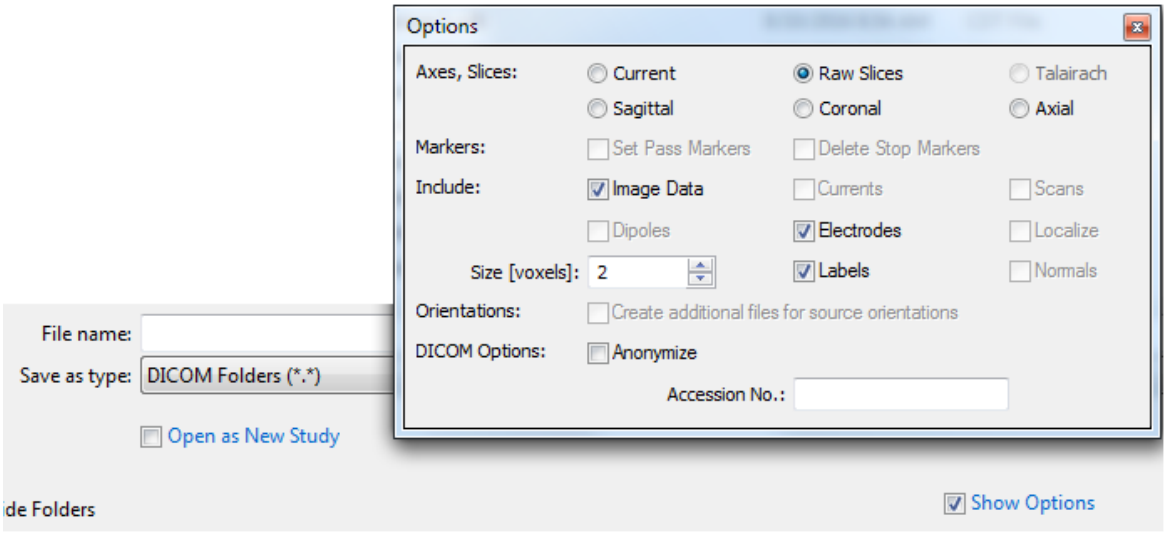
Go To Reference. Select this option to return the cross-hair cursor to the reference point in all three iso-images.

Go To Nearby Maximum (*Ctrl+G*). This is used for finding the exact center of bright dots in an MRI or CT, such as vitamin E markers or ECoG electrodes. "Nearby" translates to a 5mm radius, wherein the center-of-mass is computed. A similar routine in Localize performs the operation for all Localize locations. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, the **3D View**, click the border of the bright area, and this functionality brings the cursor to its center (this can be applied repeatedly).

Save Image Data As. This option allows you to save the MR images in one of several forms:



In the lower part of the Save As dialog are additional options that you may use. Enable **Show Options** to see them.



Axes, Slices. If you have changed the axes or resliced the image data, you have the option to save the **Current** axes and slices, or the **Raw Slices**. The **Talairach** option will be active if you have selected the Talairach coordinate (**Coordinates → Talairach (R,A,S)**). If **Raw Slices** is not selected, a 256x256x256 image cube will be exported.

Markers. If you have included Pass Markers and/or Stop Markers, you can save these. Pass Markers will be seen in white if you select **Set Pass**. Stop markers will be seen in black, unless you enable **Delete Stop Markers**.

Include. Dipole results (etc.) can be exported to surgical navigation system with or without **Image Data** (enabled by default). You can include the **Currents** (thresholded current densities exported as high-intensity markers in 3D images), **Scans**, and **Dipoles** results, the **Electrodes**, and any **Localize** points you have created. You can vary the Symbol **Size** (in voxels). If the **Size** is **3** or larger, you can include the **Normals**. Normals are imprinted in orthogonal slices, which means that a 3D rendering may show more than one tail per dipole.

For whatever components (Dipoles, Localize, Electrodes) are visible in Image Data (controlled by the respective checkbox in **3D View**), the respective checkbox in the Save Image Data dialog becomes active.

Orientations. This option is used when saving CDR results in SPM (image) format. Three additional images for the normal components are created. If not checked, only the strengths are saved.

DICOM Options. Generally speaking, CURRY 8 includes the following meta-information (read from the original image data file) when writing DICOM: modality, field strength, patient name, gender, birthday, age, series description, and study description. The exported information may be modified as follows.

Anonymize. The Anonymize option results in patient name and birthday not being written to the DICOM files.

Accession No. The accession number is a way to store an additional, manually entered 16-character string (usually a number) with the written DICOM files.

Open as New Study. If you enable **Open as New study**, the .imd file will be added to the Database as an unfiled Study, and this image data-only study will be opened.

Exporting results to surgical navigation systems (e.g., Stryker). Please follow the steps below to export the image data and other results to surgical navigation software.

1. Make sure **Show Results** has been enabled  (Toolbar or Image Data context menu).

2. The **Save Image Data As** dialog shows checkboxes for including Dipoles, Electrodes, and Localize (or any) locations in the saved MRI. Formats can be DICOM, etc. (select under **Save as type**).

3. The items that are checked are included with the saved structural MRI as high-intensity markers (their size can also be selected).

4. No overlays are necessary, and coregistration is not an issue.

5. If a second version of the image without markers is desired, resave the image data without the items being checked. The navigation system needs to be able to deal with two 3D images (one with structural data only, one with additional bright spots where the CURRY results are).

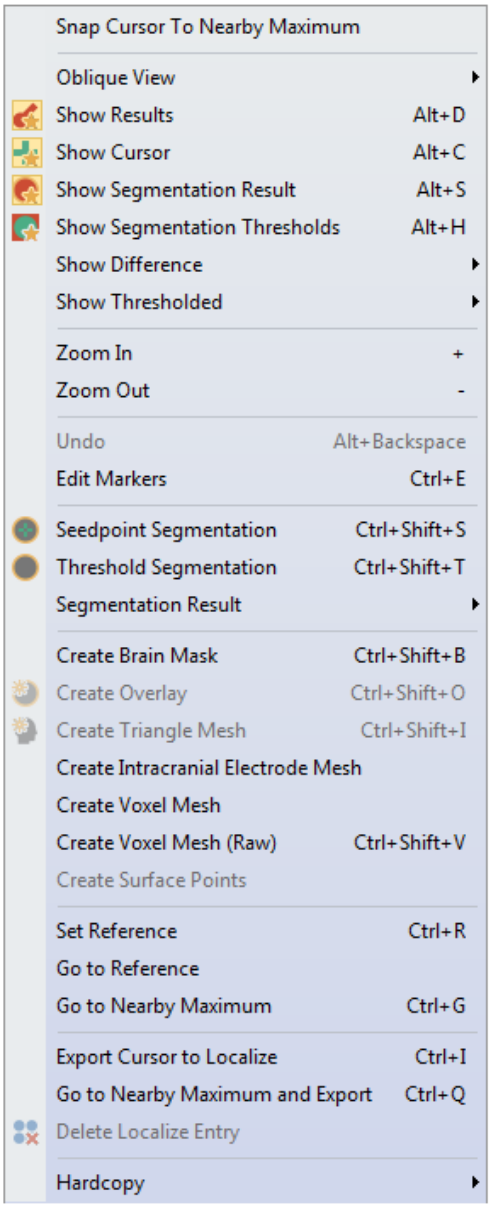
18.2.10 Image Data, Context Menu

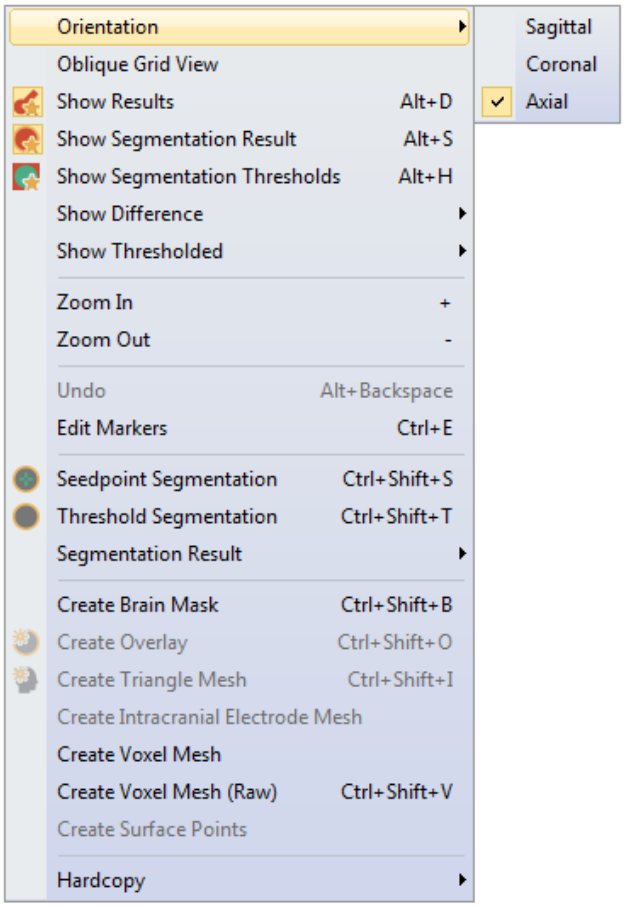
If you click the *right mouse* button inside the 

display, there are additional options pertaining to segmentation (left side in figure below). The option lists vary depending on whether you click one of the 3 iso-images, or in the fourth user selected display. In the latter case, the list varies depending upon what is displayed (MIP, Histogram, etc.). The availability of options in the lists also depends upon whether you have performed a segmentation already (you cannot, for example, create an overlay until segmentation has been performed). Some of the options are used with the 

display, and are therefore grayed out in the list(s) accessed from 

. Fewer items will be seen if you do not have the advanced analysis license. If you *right click* in the Grid View in the lower right display, you will see some additional options (right side in figure below). The options that are unique to the Grid View are listed at the bottom of the list below.



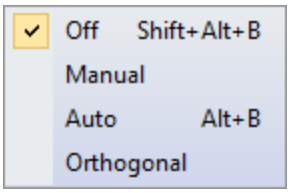


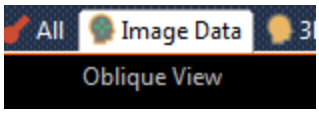
Grid View context menu

The first set of options are accessed from *right clicking* in one of the iso-image displays.

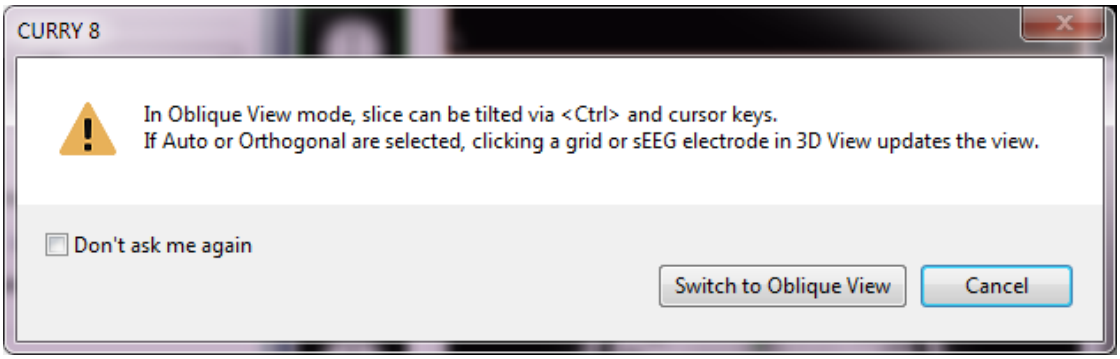
Snap Cursor to Nearby Maximum. This feature, when enabled, will move the image data cursor to a nearby intensity maximum after clicking in the image data. It is, in a way, a sibling feature to the "magnetic cursor" that can be enabled for manual event marking. It is typically used for defining electrode locations in CT data that are usually rendered as small bright dots.

Oblique View. The Oblique View options allow you to alter the perspective of the image data slices. These are useful when you wish to orient the view according to depth electrode tracks.

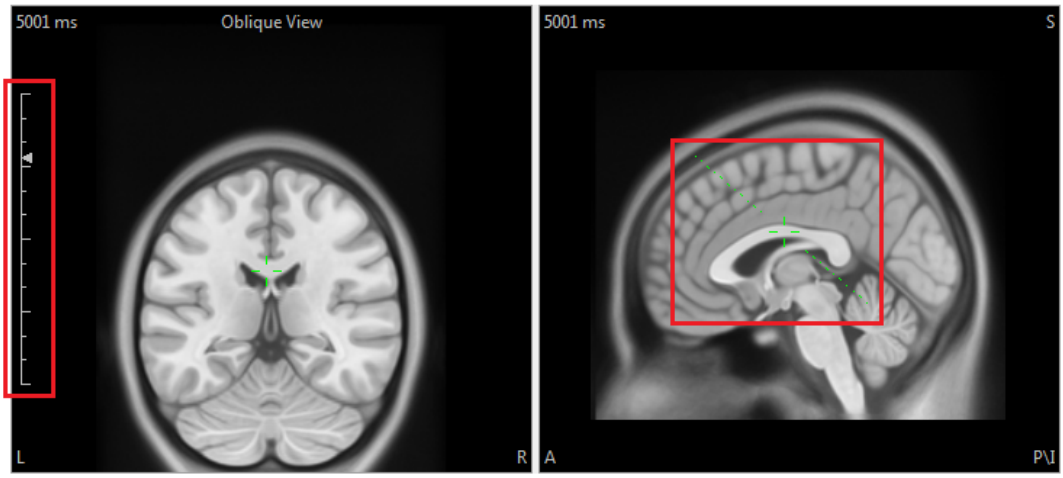


Manual. When you select the option, you will see the following message. This reminds you to use the *Ctrl* and *cursor* keys to control the angle. Click Switch to Oblique View to continue. You will see Oblique View at the top of the image data 

.

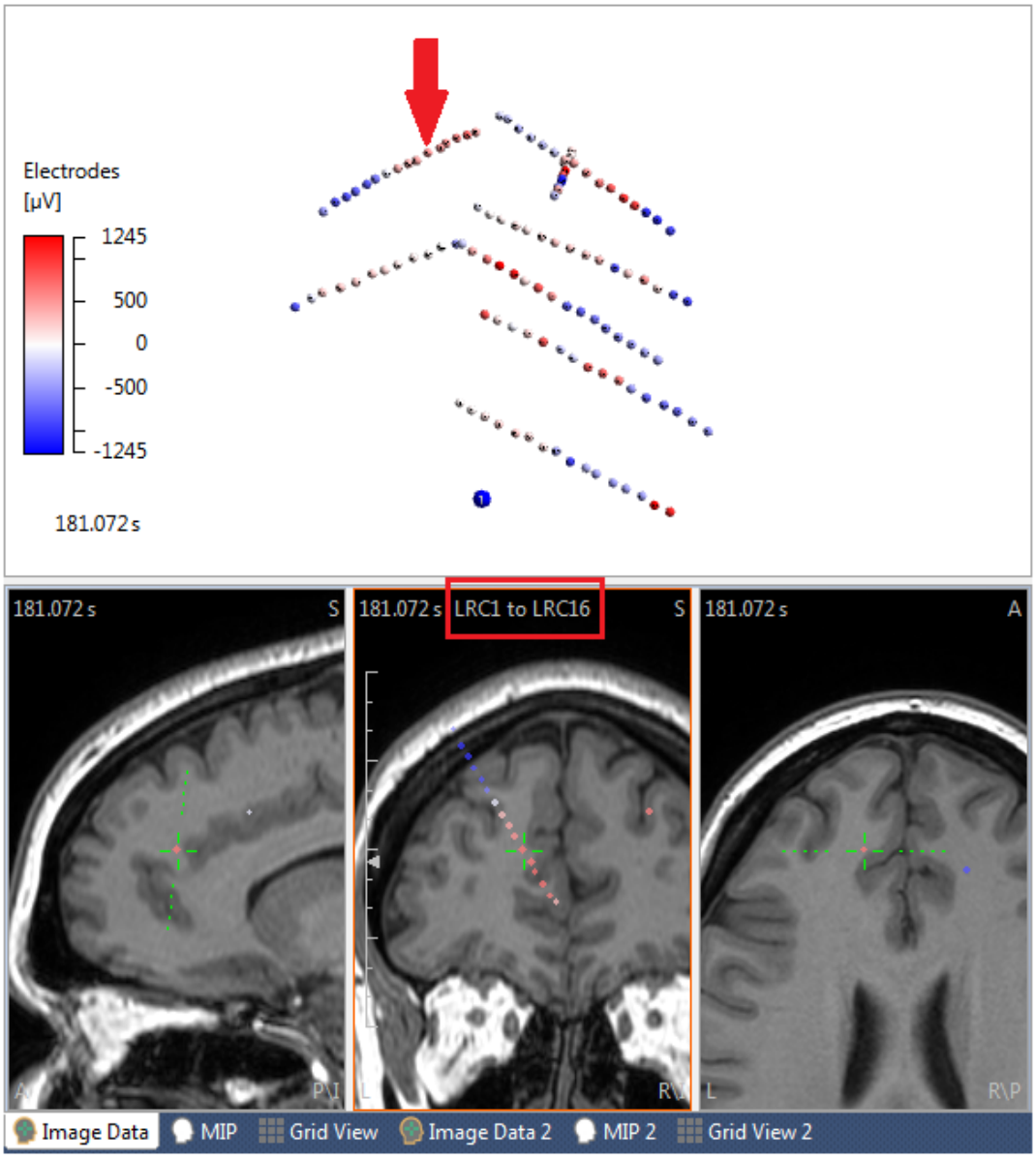


In this case, the mouse was in the axial display, and *Ctrl+up* and *down* arrows were clicked. Note that a tilt angle scale appears on the left. A dotted green line appears in the other images to show the orientation of the changes. You can alter the views in any of the three displays (each is activated individually). You can also use the *left* and *right* arrow keys, as well as *Shift + arrow* keys to alter the display.

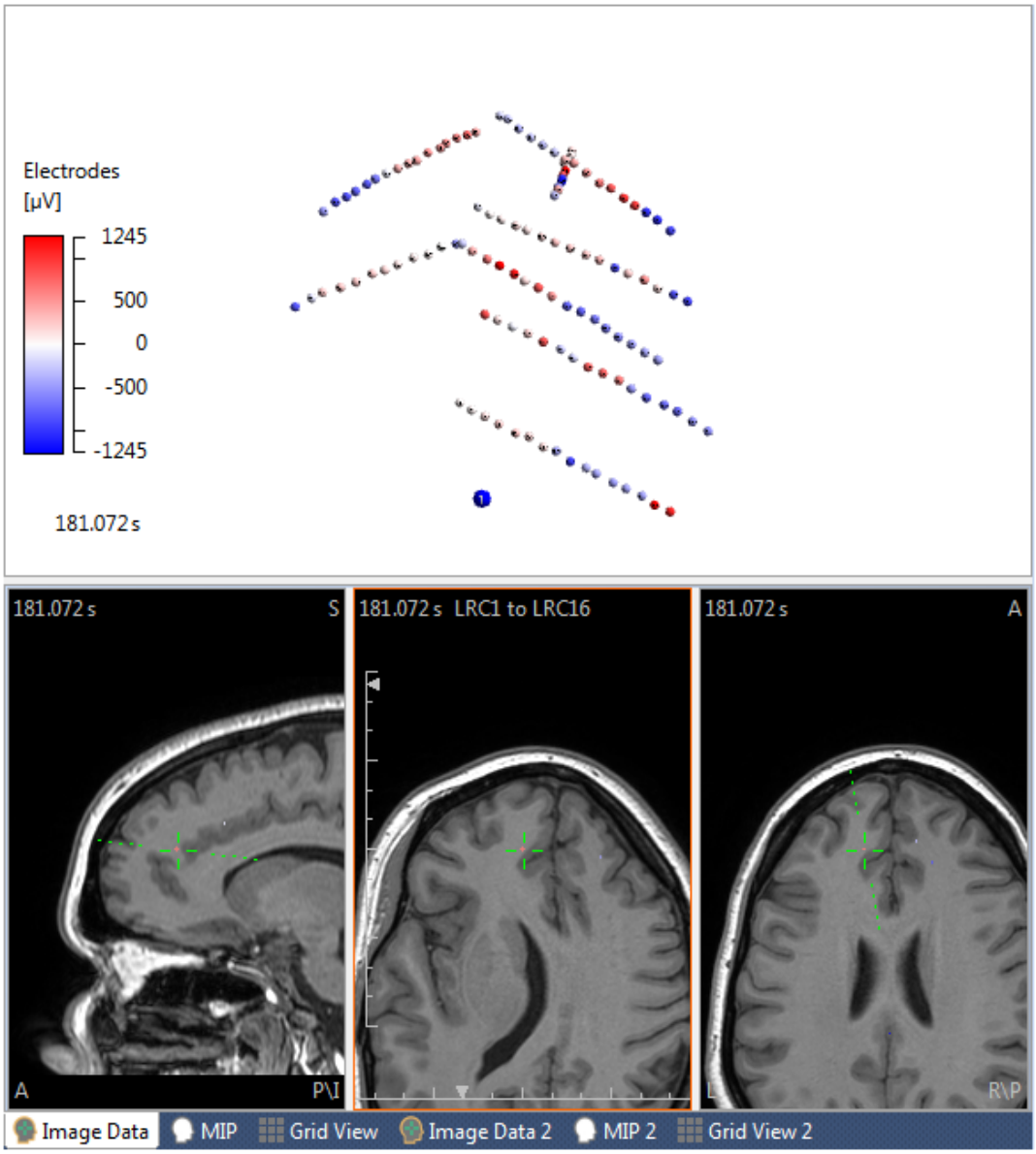


The remaining two options were designed for use with stereo or depth electrodes.

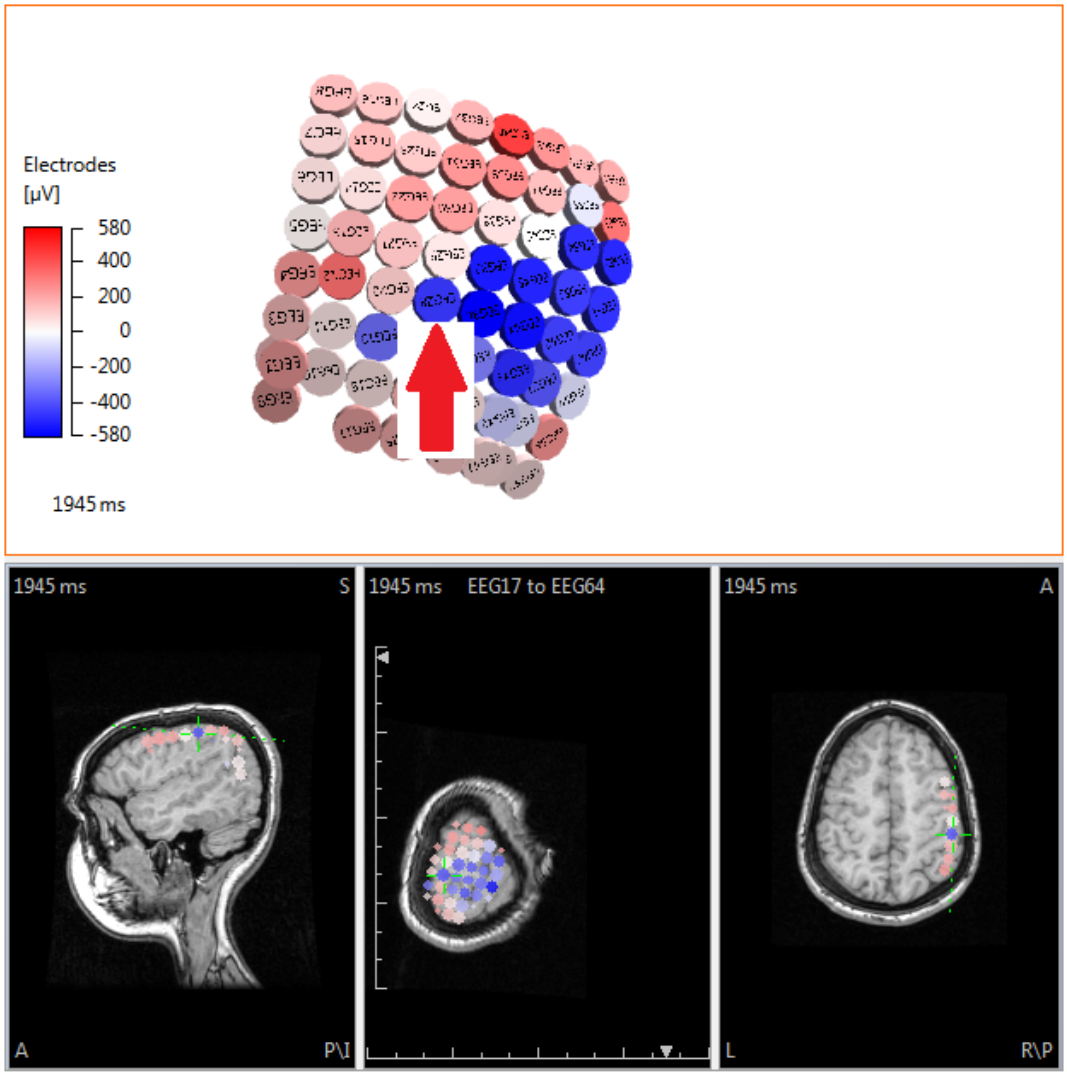
Auto. The purpose is to align the image data view with the depth electrode. In this case, **Auto** was activated in the coronal slice (middle). The indicated electrode was clicked on, in the 3D View. Note at the top of the coronal image data view, you see the labels of the electrodes (LRC1 to LRC16). The image data was shifted automatically to coincide with the angle of the electrode. *Ctrl + mouse wheel* was used to zoom in to the images.



Orthogonal. This is similar to the Auto option, except that the view is orthogonal to the line of electrodes. This is the same electrode as selected above with the Orthogonal view. Use the arrows keys and accelerators to move up and down the axis defined by these electrodes.



Another application with the **Oblique** feature is with grid data. Click on an electrode in the **3D View**, select **Auto** mode, and the oblique view will align itself with the layer of the grid. You can zoom in and out and you will always have a perspective that is parallel to the main grid axis. If you select **Orthogonal** mode and move along one of the axes, the perspective will be perpendicular to the orientation if the grid.



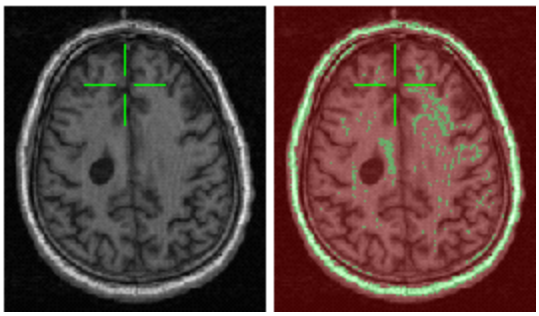
You will find that if you use the + key to zoom in and out, all three displays will zoom together. This is controlled by an option under Image Data 1, in the Options panel - Zoom to Cursor All. When enabled (default), the **Zoom to Cursor** / **All** option will result in zooming to all channels. When All is disabled, you can zoom in to the displays individually.

Show Results. If selected, Results (e.g., segmentation and dipole solutions) are displayed. The various results and how they appear are controlled from the **3D View** options. This is the same as the icon on the **Image Data** Toolbar (*Alt+D*).

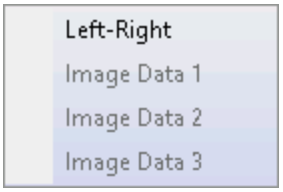
Show Cursor. This option is used to toggle the crosshair cursor on and off. This is the same as the icon on the **Image Data** Toolbar (*Alt+I*).

Show Segmentation Result. Toggles the display of the segmentation result. This is the same as the  icon on the **Image Data** Toolbar (*Alt+H*).

Show Segmentation Thresholds. Enabling the option displays the segmentation threshold on the iso-image views. This is the same as the  icon on the **Image Data**.

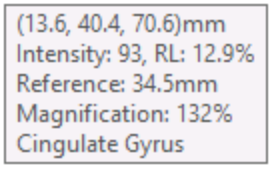


Show Difference. The option is used to subtract the image data from one set from another. It will be active after you load at least two image data sets. If you select it from one data set, you will have the option to select either of the other data sets for subtraction. If you are using Left-Right, be sure to measure the anatomical landmarks accurately, or the subtracted results can be distorted.



Show Thresholded. The option is used to superimpose the image data from one set upon another. It will be active after you load at least two image data sets. If you select it from one data set, you will have the option to select either of the other data sets for superimposition. RGB and Interpolation may be selected for Image Data 2.

Zoom In (+). Use this option to enlarge an image data pane (or click the + key). The Magnification value in the Tooltip displays the percentage of magnification.



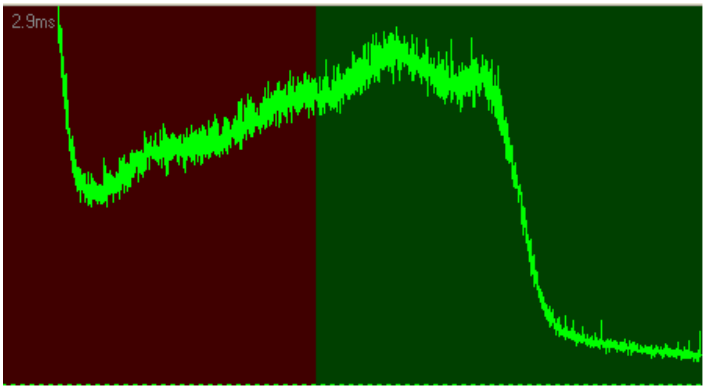
Zoom Out (-). Use this option to Zoom out (or use the - key).

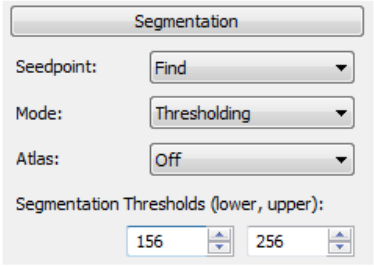
Undo (*Ctrl+Z*). Undoes the previous operation (where applicable).

Edit Markers (*Ctrl+E*). This option expands the Markers panel in anticipation that you wish to edit the Pass and/or Stop Markers (see **Markers** above). You can select the view in which you wish to add markers by *right clicking* in that view to select Edit Markers. This enables marker editing for the selected view only.

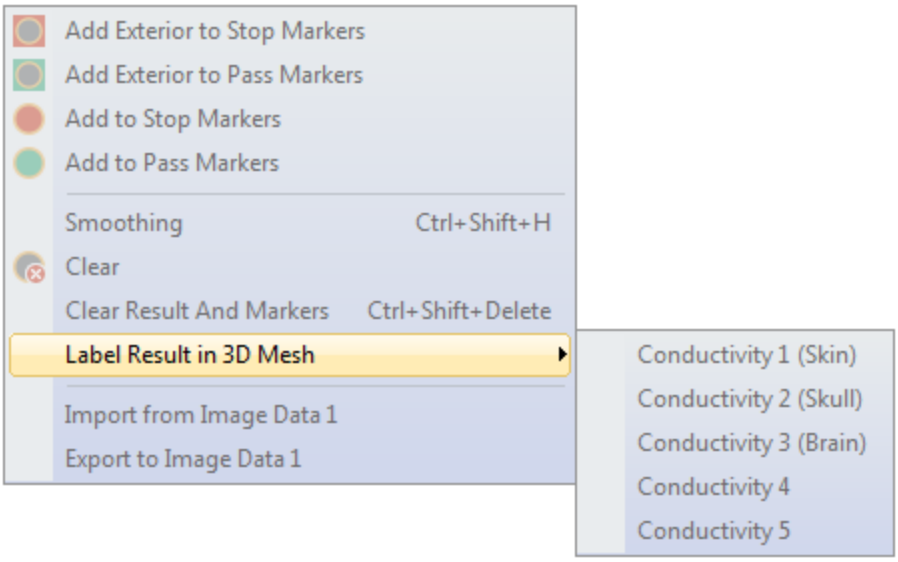
Seedpoint Segmentation. Select this option to search for a suitable seedpoint and start a seedpoint segmentation. This is the same as the icon on the **Image Data** Toolbar *(Ctrl+Shift+S)*.

Threshold Segmentation. Segmentation is performed using the Threshold as seen in the *Histogram* display as well as in the **Segmentation** panel. It is independent of the cursor position. This is the same as the icon on the **Image Data** Toolbar (*Ctrl+Shift+T*).





Segmentation Result. This displays the following list of options. Pass Markers are generally seen in green, and Stop Markers are in red (you can change the colors in the **Colors** panel under **Image Data**). Most of the same options are seen in the **Segmentation** panel after clicking the Result button.



Add Exterior to Stop Markers. Exterior regions will be filled with Stop Markers (regions will turn red). It is also accessed by the  icon on the **Image Data** Toolbar.

Add Exterior to Pass Markers. Exterior regions will be filled with Pass Markers (regions will turn green). It is also accessed by the  icon on the **Image Data** Toolbar.

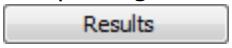
Add [Segmentation Result] to Stop Markers. Click this option to include the segmented region with the Stop Markers (regions will turn red). It is also accessed by the  icon on the **Image Data** Toolbar.

Add [Segmentation Result] to Pass Markers. Click this option to include the segmented region with the Pass Markers (regions will turn green). It is also accessed by the  icon on the **Image Data** Toolbar.

Smoothing (*Ctrl+Shift+H*). This option is meant to be used to obtain a quick Smoothing result, and so always uses a **12mm Dilation**. Use the **Morphology** panel options for any other parameters, and its **Start** button to apply them.

Clear. This clears the segmentation result. It is also accessed by the  icon on the **Image Data** Toolbar

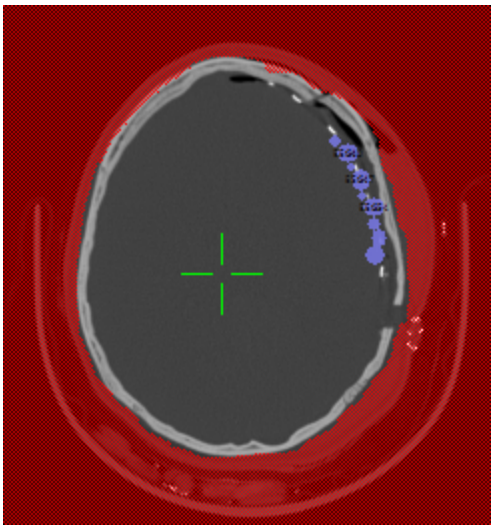
Clear Result and Markers. This clears the segmentation result and markers.

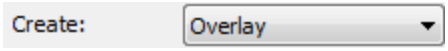
Label Result in 3D Mesh. This feature is related to the creation of FEM models. Between creating a tetrahedra/cube mesh and exporting it in CAUCHY format (which can be done from the context menu in 

), one might wish to "label" tetrahedra with respect to which tissue type they represent. This is based on the segmentation result currently in **Image Data**. Because compartments enclose each other, the program starts with the skin, then the outer skull, then the inner skull, overwriting in each step the labeling for the enclosed tetrahedra.

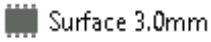
Import from Image Data 1/Export to Image Data 1. You must have two (or more) image data sets loaded to use these options. The second or third data set can import results from the first, or export results to the first.

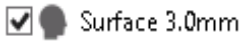
Create Brain Mask. After segmentation, this option will convert all areas outside of the BEM cortex to stop markers (mainly for use with CT data). This is useful for eliminating extraneous structures.



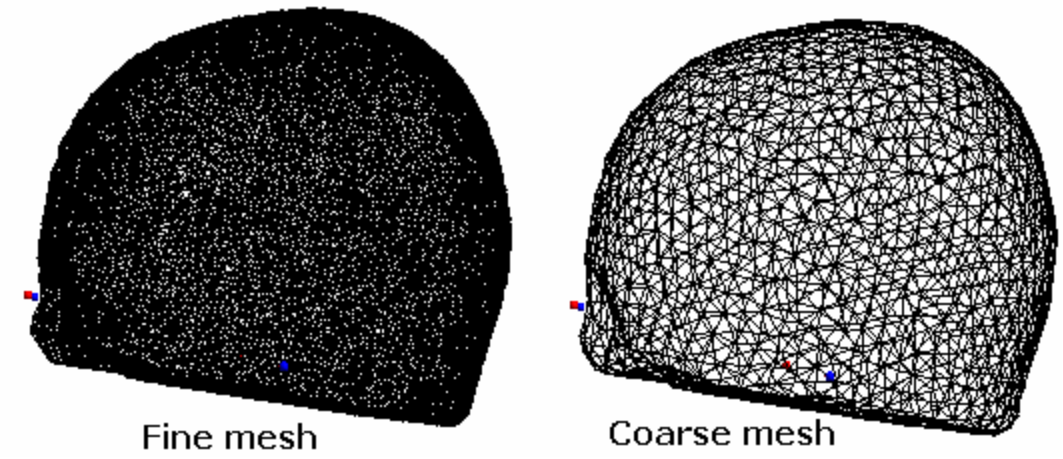
Create Overlay. Use this option to export the segmentation results and markers to an overlay. This has the same function as clicking **Image Data** → **Overlay** → **Create**, or by selecting 

in the **Create** panel. This is the same as the  icon on the **Image Data** Toolbar (*Ctrl+Shift+O*).

Create Triangle Mesh. This option will create a quick triangulated mesh, using a fixed **Resolution** of **3mm**. It will appear in the Surface list under **Results**, **Properties**, as, for example, 

, and may be displayed in the **3D View**  using 

and the *Surface properties*. Use **Wireframe** to select **Off**, **On** or **Overlaid** display options (**On** selected below). This is the same as the  icon on the **Image Data** Toolbar (*Ctrl+Shift+I*). Use the fields in the **Create** panel for different parameter settings, and then use it **Start** button to apply them.



Create Intracranial Electrode Mesh. This is a convenience option that is only available for CT data with depth electrodes, saving you from performing the steps manually. It consists of the following operations.

1. Create brain mask.
2. Find thresholds suitable for intracranial electrodes.
3. Creates a voxel mesh (raw).

The result in the **3D View** Objects list is called Electrode Mesh, and displays the segmented depth electrodes.

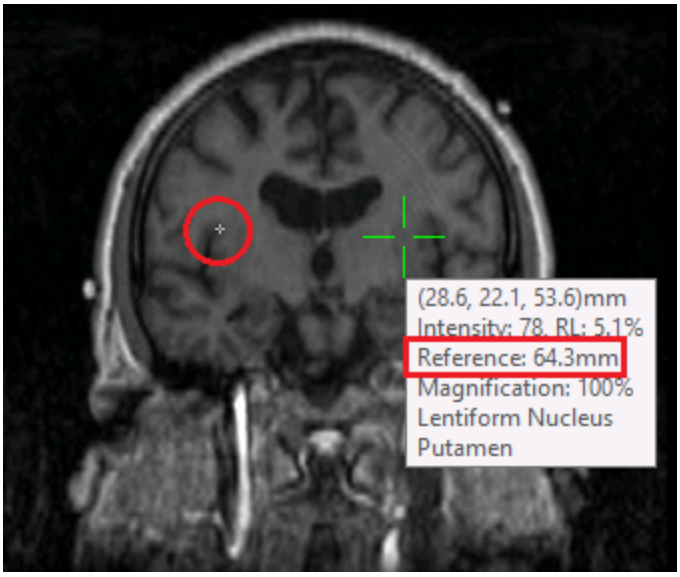
Create Voxel Mesh. Same as Create Triangle Mesh except the mesh is created with voxels. A voxel mesh can be used to visualize disconnected segmentation results.

Create Voxel Mesh (Raw). This feature is similar to the Create Voxel Mesh command, which transforms the yellow segmentation result into a voxel mesh and therefore has an inherent resolution of 256x256x256 (the resolution of markers and segmentation result). However, especially for CT, the raw image resolution may be higher, usually 512x512x512, and the "raw" voxel mesh will have the resolution of the raw image data, not using the segmentation result at all, but simply including all voxels that satisfy the threshold (and marker) criteria into the voxel mesh. This results in higher-quality 3D View renderings of e.g., intracranial electrodes.

Create Surface Points. This option will create a Points display. It will appear in the **Points** list under **Results**, **Properties** and may be displayed in the **3D View** using Surface Points 3.0mm .

Set Reference (*Ctrl+R*) **/ Go to Reference**. Position the mouse at a desired point in the 3D images, then *right click* and select **Set Reference**. A small, white plus will appear at that point, where the color is determined by the selection under Colors, **Text**. The Reference is set in three dimensions. As you move the mouse away from the Reference, you will see the distance (in mms) in the *Tooltip*. If you click the mouse to display different slices or positions, the Reference remains

where you set it. To return to the Reference position automatically, select **Go to Reference**. See also the **Set Reference** option in the 3D View context menu and the **Distance** object description in the 3D View section below.



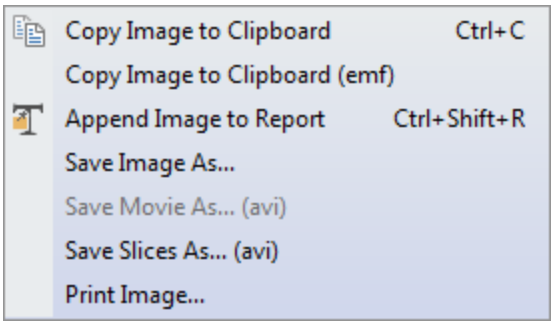
Go To Nearby Maximum (*Ctrl+G*). This is used for finding the center of bright dots in an MRI or CT, such as vitamin E markers or ECoG electrodes. "Nearby" translates to a 5mm radius, wherein the center-of-mass is computed. A similar routine in Localize performs the operation for all Localize locations. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, 3D View, click the border of the bright area, and this functionality brings the cursor to its center (can be applied repeatedly).

Export Cursor to Localize (*Ctrl+I*). Selecting this option (using the cursor position in the Image Data view, or in the MR images in the Localize view) will export the current cursor position to the **Localize** panel list. From Localize, the same functionality is called **Import Cursor**.

Go to Nearby Maximum and Export (*Ctrl+Q*). Set the cursor position in either the Image Data display or in the MR images in the Localize display. Selecting this option moves the cursor to the nearby maximum intensity and adds the coordinates to the Localize list.

Delete Localize Entry (*Ctrl+D*)  . Deletes the most recent point from the Localize list.

Hardcopy. The following options are seen.



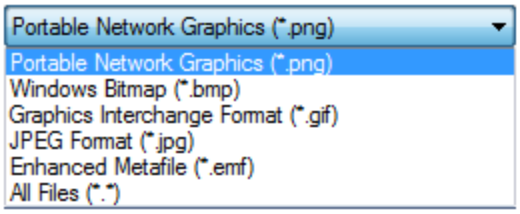
Copy Image to Clipboard. This copies the data channel display (.bmp format) to the Windows clipboard, from which you may Paste it into other Windows applications. This is the same as the  icon on the **Standard** and **Report** Toolbars (*Ctrl+C*).

Copy Image to Clipboard (emf). When pasted into other Windows applications (such as Word), individual components of Metafiles can be edited; whereas, BMP files cannot. (In Word, *right click* on the pasted metafile, and select **Edit Picture**).

Append Image to Report. Copies the section of the data display having the focus to the 

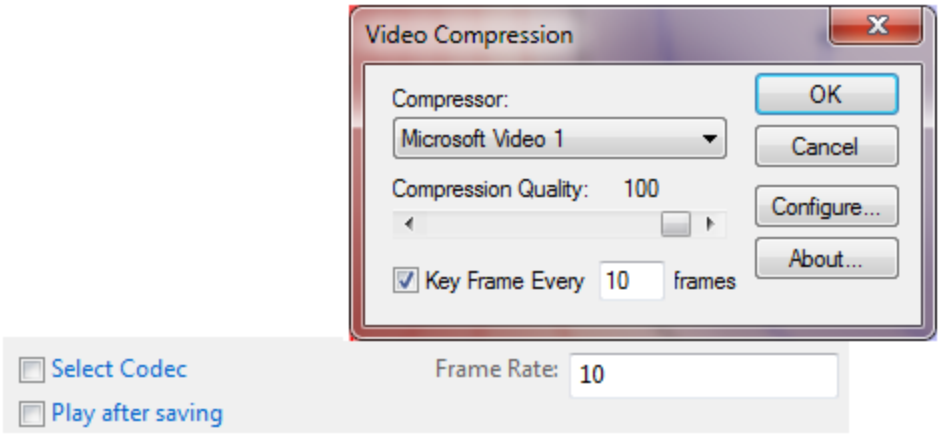
. This is the same as the  icon on the **Report** Toolbar (*Ctrl+Shift+R*).

Save Image As. This option lets you save the graphic display in any of the formats shown.

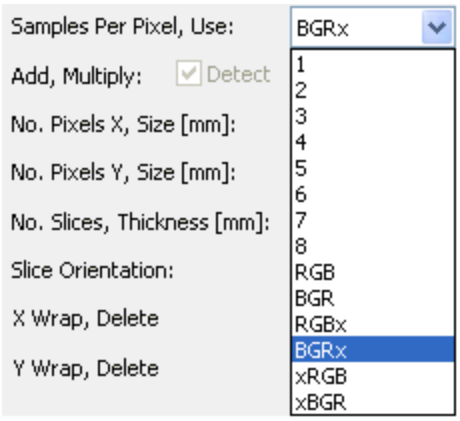


Save Movie As. This option lets you save the Movie in .avi format. (The Movie is across the selected Timerange, and the slices will be adjusted to those that show the dipole solutions). The Save As window for all of these options contains an option to set the speed of the replay of the movie:


. Higher Frame Rates will replay the movie faster. You may also video compression, and you have the option to automatically play the video after the movie is saved.

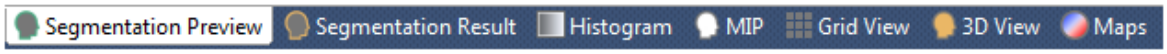


Save Slices As. A movie of the progression of slices for whichever view has been selected will be saved as an .avi file, or the raw slices, including source results, can be saved as an .img file. When you open the .img file in CURRY 8, you will be taken to the **Image Data Parameters** windows. In the second step, select the appropriate selection for **Samples Per Pixel, Use**.

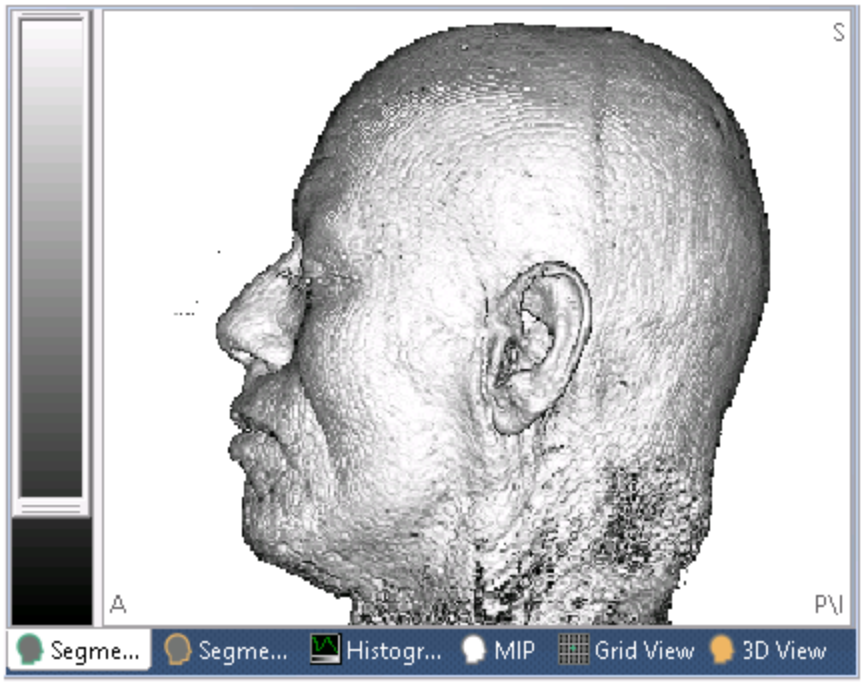


Print Image. The selected pane (that part of the data display that has the focus) will be displayed in the Windows Picture and Fax Viewer, where it can be viewed and printed.

Additional View Options. The view in the lower right quadrant can be varied in several ways, controlled by the tabs at the bottom of the display. Some of these have unique *right mouse* options, as described below. Only the non-redundant options are listed.



Segmentation Preview. This is the depth-buffered segmentation preview display. Depending on the selected view, the surface matching the segmentation thresholds is rendered. Using depth-buffering, the surface locations can still be retrieved. The *right mouse* context menu options are similar to those described above.

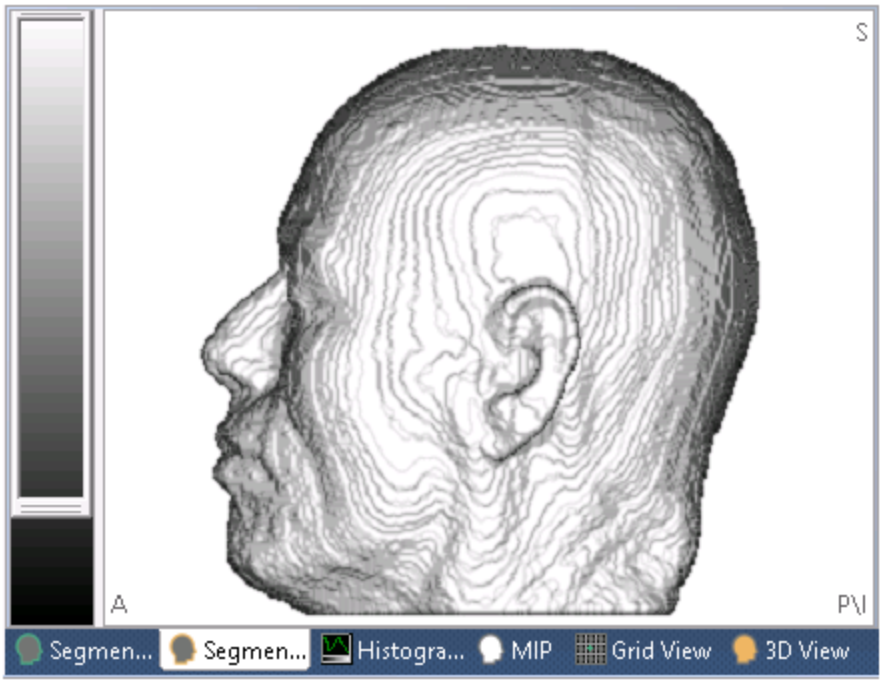


Omit Stop Markers. If there are Stop markers, this option will show their impact on segmentation by "not showing" them. A companion option is **Omit Fore Half**, which shows only the hind half of the image (useful for looking "into" a CT skull).

Left, Right, Top, Bottom, Front and Rear Views. These options are available from several of the displays, and let you change the perspective as indicated.

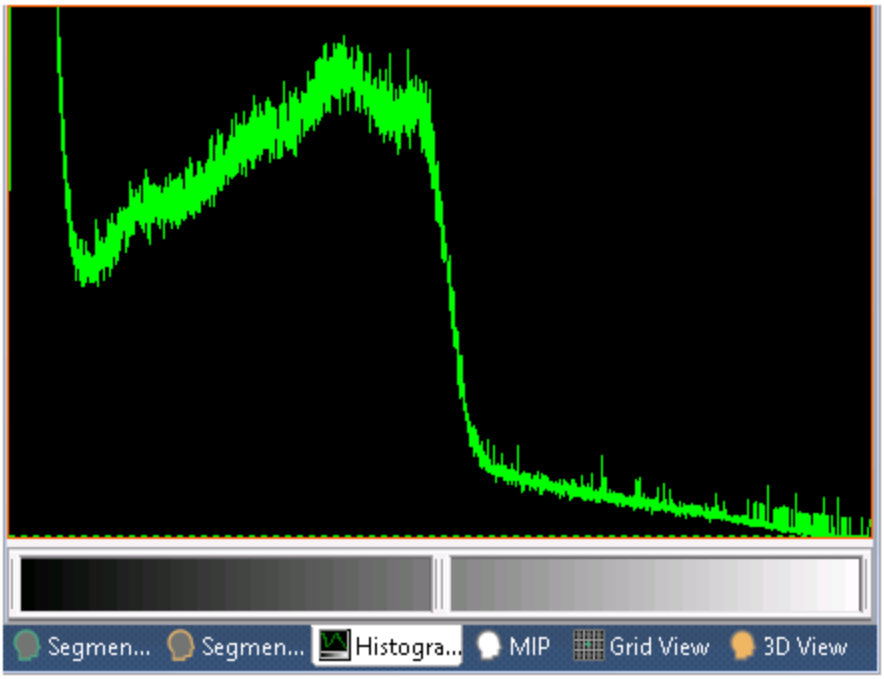
Sliding bar. This allows you to adjust the segmentation thresholds based on image intensity (color).

Segmentation Result. When Segmentation Results are shown in the rendered view area, only the surface of the segmented volume is displayed and superimposed onto the image itself. The *right mouse* options are the same as described above.



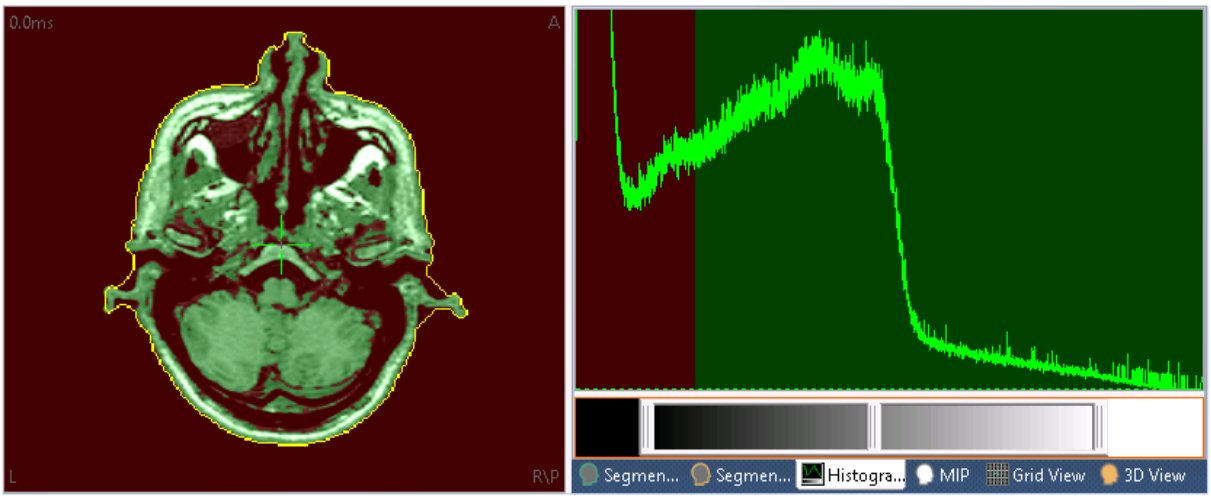
This rendering is depth-buffered, meaning that it retrieves the correct depth along with the x and y coordinates. The slider on the left is the same as for the Segmentation Preview.

Histogram. This is the image data intensity histogram display, together with the segmentation thresholds. In the color scale below it, the color lookup table for the image data can be changed (Hounsfield scaling, level-and-window). Clicking in the histogram window enters the corresponding intensity as the **Lower Threshold** in the **Segmentation** panel. With the cursor over one of the other three views, you can use *Alt+drag* vertically or horizontally to change the Thresholds.



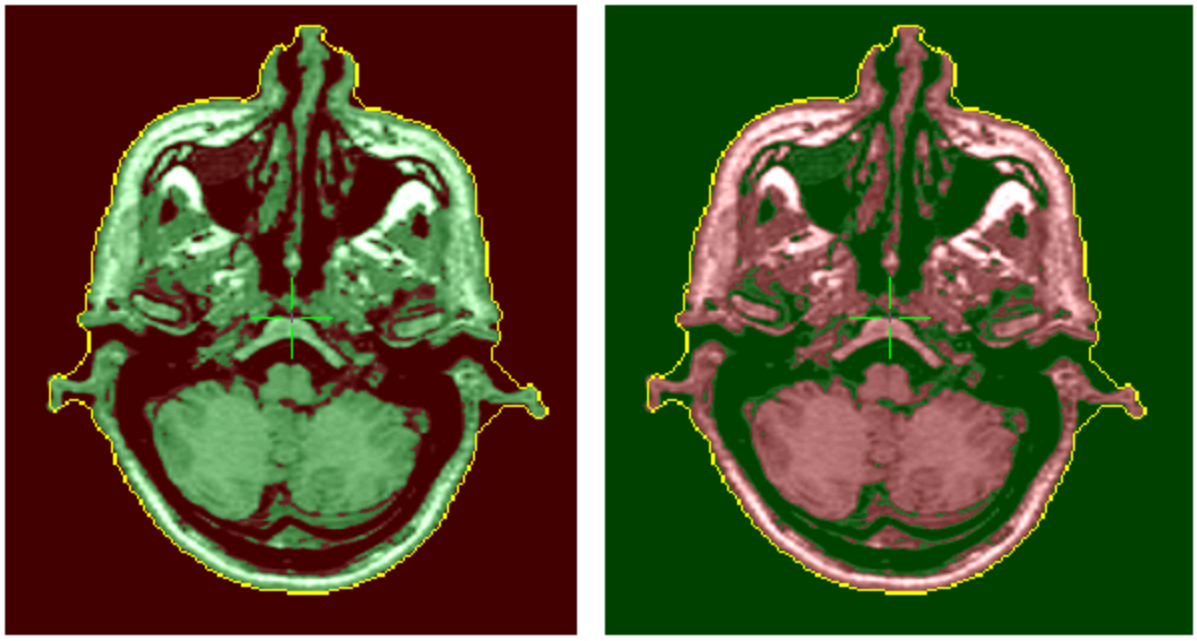
The *right mouse* options accessed from the Histogram display are as follows. The remaining options are as described above.

Show Segmentation Thresholds. Enabling this option displays the segmentation threshold in the *Histogram* and iso-image displays. The green intensities are between the lower and upper segmentation thresholds. You can grab-and-drag the threshold to a new position (the new value will be seen in the **Lower Threshold** field in the **Segmentation** panel).

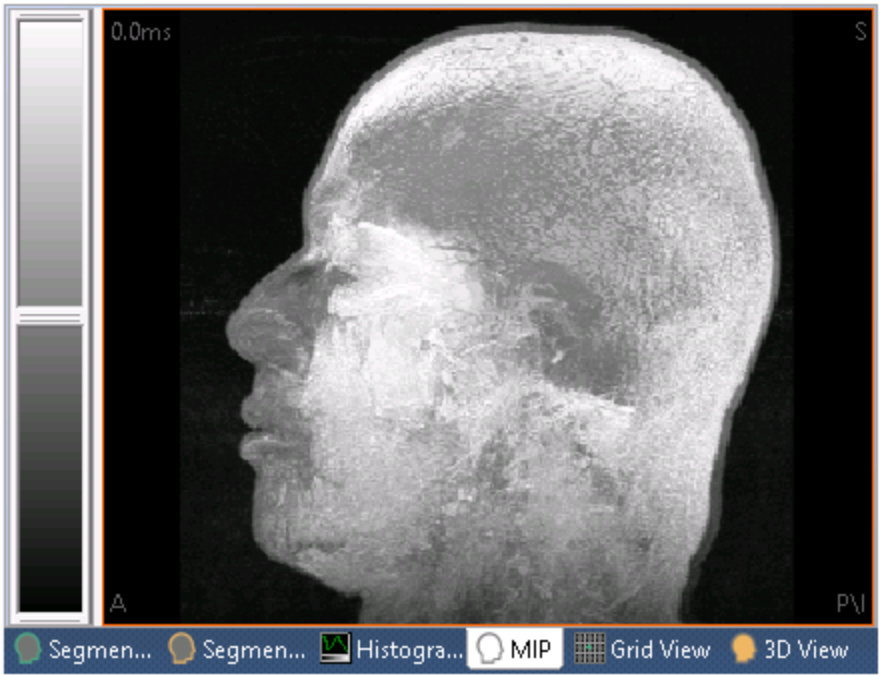


Reset Segmentation Thresholds. Click this option to reset the segmentation thresholds to meaningful values.

Swap Segmentation Thresholds. Click this option to swap the red and green areas and their associated segmentation thresholds.

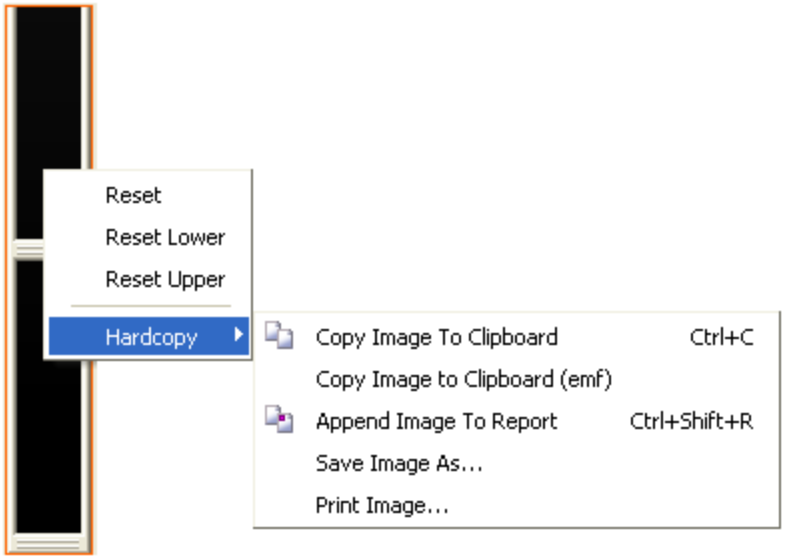


MIP View. This is the depth-buffered Maximum Intensity Projection display. Depending on the selected view, the voxels with the largest intensity are projected onto the view plane. Using depth-buffering, the locations of the maximum intensity voxels can still be retrieved. If you click the *right mouse* button within the Maximum Intensity Projection (MIP) view itself, you will see the same menu list very as seen when accessed from the iso-images.



MIP Scale. In the scale on the left, the lookup table for the MIP can be changed (Hounsfield scaling, level-and-window).

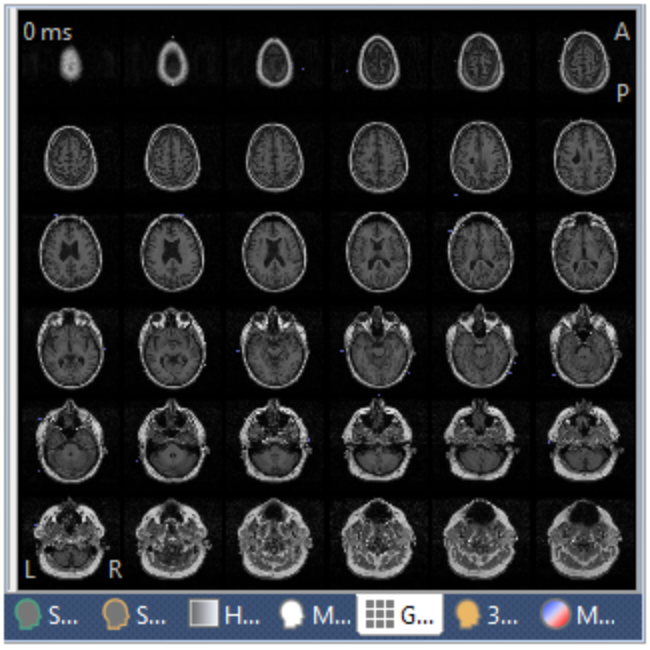
Clicking the *right mouse* button on the scale displays a menu list including the following unique options.



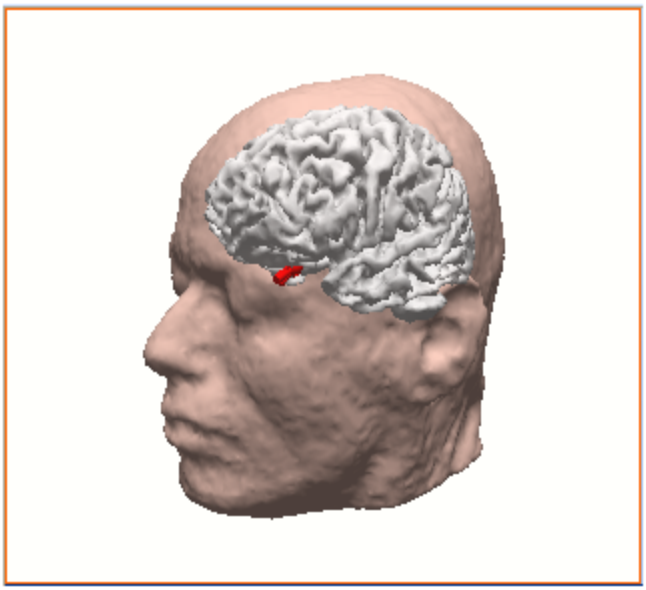
Reset / Reset Lower / Reset Upper. These options are used to reset the intensity scale. Use the upper, middle and lower bars to reposition the scale to best reflect the intensity of the MR images. Click the **Reset** option(s) to return to the default positions.

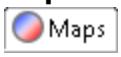
Hardcopy. Displays the standard options for copying, saving, or printing the image.

Grid View. The results may be seen across slices.

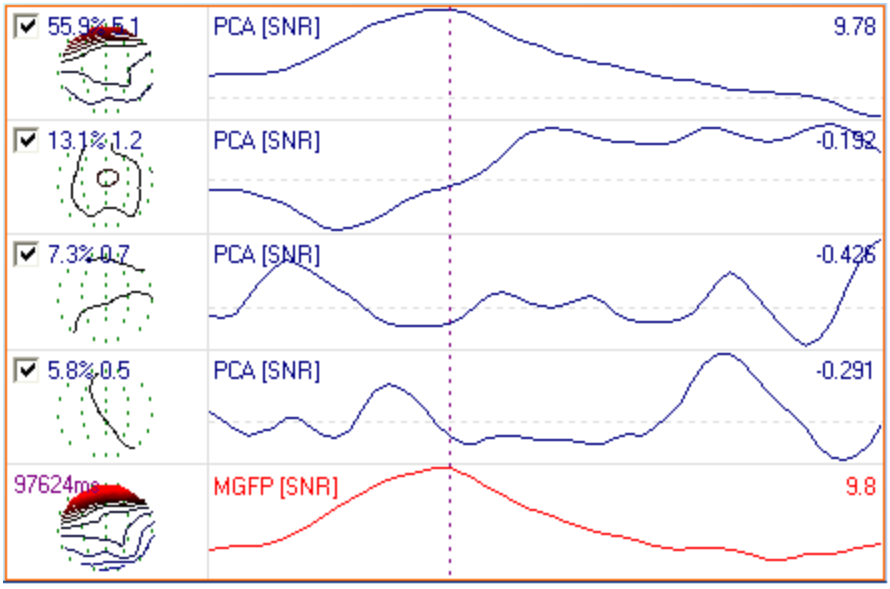


3D View. This option displays the 3D View scenario, allowing for an integrated display of 3D-rendered triangle meshes and source reconstruction results, as well as a possibility to change the display timepoint.



Maps. Selecting this option displays the same Maps display that is seen in the 

tab. *Right click* in the display to access all of the options listed above, under Maps. The Maps display is useful for integrating dipole timecourses and maps with image data and for changing the display timepoint.



Grid View Context Menu Options
These options are unique to the Grid View context menu.

Orientation. Select the Sagittal, Coronal, or Axial view for the slices.

Oblique Grid View. This option allows you to apply the oblique view you set in the iso-images to the Grid View as well. The Oblique Views are described in the **Image Data Context Menu** section.

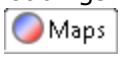
19 Source Reconstruction

The Source Reconstruction chapter describes one of the most important aspects of CURRY. The purpose of source reconstruction is to provide information about the nature and anatomical location of electrical sources that explain the measured EEG and/or MEG data. Due to the nature of the problem, these sources cannot be computed directly from the data. The technique that is used to find a solution is called inverse modeling.

The head model is specified as either concentric spheres (usually fitted to the sensors) or a realistic model derived from anatomical data. The availability of several source and head models allows for an easy comparison of the reconstructed data.

Reconstruction results are shown in the 

and 

displays; the dipole loadings and the dipoles' forward calculated or difference maps can also be displayed in 

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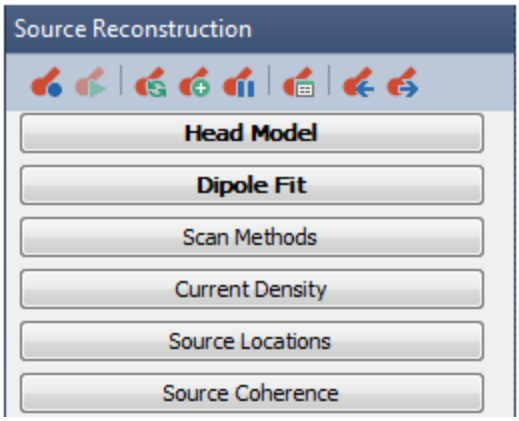
New to Source Reconstruction?
Users new to source reconstruction techniques typically ask questions like: Which dipole model do I use with my data? How do I know what options to use, and what settings to select? How do I interpret the results from the Dipole Strengths, Deviations, and MGFP? Which head model should I use? At this point in time, there are no absolute answers to many of these kinds of questions. Source reconstruction is a hypothesis driven analysis. Therefore, the approach adopted for source reconstruction must be driven by *a priori* assumptions and by known physiological constraints. Even then, it may not be possible to decide which reconstruction model to apply. If you are not sure which dipole or head model to use, try several different ones. Look for converging results across models. Look for results that are reasonable. Use common sense, and rely on established neuroanatomy and neurophysiology as much as possible. For example, if you are looking at dipole source solutions for the major components of an SEP recording, it may not make sense to look for multiple dipoles with *mirrored* results. With auditory stimuli, it is reasonable to expect bilateral, homologous dipoles. In other instances, the expectations and predictions may be more ambiguous.

19.1 Source Reconstruction

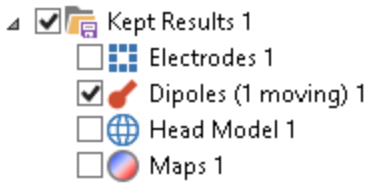
The parameters and settings on the **Source Reconstruction** panels are described first, followed by steps to create a source reconstruction, ad then details regarding the methods used by CURRY.



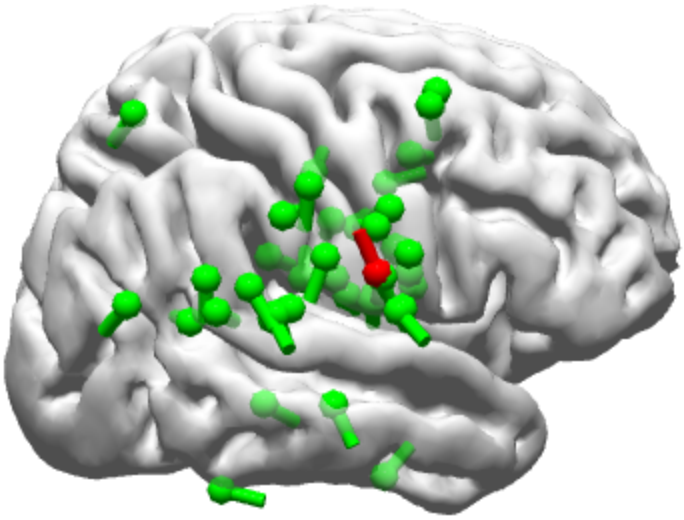
These panels are used to specify the type of head model and type of dipole source reconstruction that you wish to use. Press *F11* at any time to display the panels.

There are Toolbar icons at the top of the **Source Reconstruction** panel.

Keep Results  . The current results will be seen as a new set of display items (labeled Kept Results x).



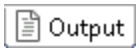
Dipole Cluster  . This option lets you calculate and superimpose source reconstruction results from multiple epochs. It is the same functionality that was previously accessed from **Keep Source Reconstruction Results** and the Scan Epochs button, under Epochs. To use it you will need an epoched file with spikes at the same latency (usually 0 ms). Set the Timerange on the first epoch. Select a **Head Model** and **Dipole Type**. Then click the icon.

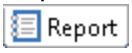


Replace Kept Results  . When active, the most recent results will *replace* the existing Kept Results.

Append Kept Results  . When active, the most recent results will be *appended to* the existing Kept Results.

Pause Fit  . This is used to pause or resume source reconstruction computations.

Append Dipole Description to Report  . Append the dipole description that is seen in the 

section to the information in the 

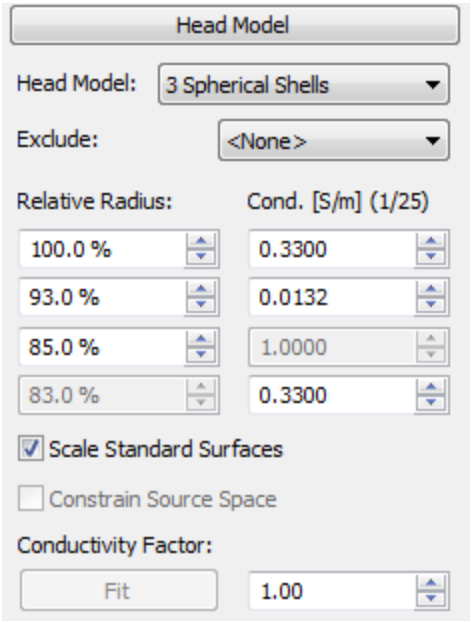
section.

Move to Previous Dipole  . Move cursor to previous dipole.

Move to Next Dipole  **.** Move cursor to next dipole.

19.1.1 Head Model

The head model used for all source reconstruction methods can be chosen here. Classical spherical models (1 to 4 shells) are available and can be compared against more advanced, realistic models.



Spherical head models are still used in the majority of the source reconstruction community, and are good for somatosensory evoked activity, for example, or more generally speaking for sources in spherical parts of the head, where spherical models match the head shape. They are fast and numerically stable.

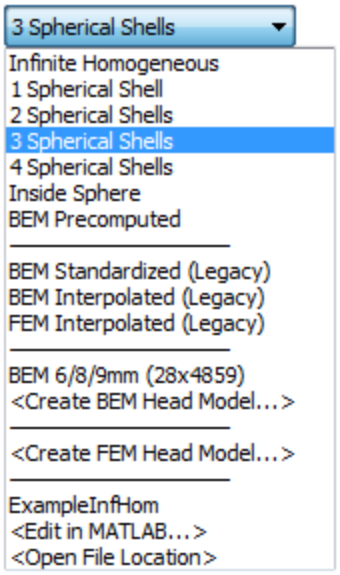
Boundary Element Method (**BEM**) models are superior in non-spherical parts of the head like temporal and frontal lobe or basal parts of the head, where spherical models exhibit systematic mislocalizations of up to 30mm. **BEM** models are slower and less stable if the sources approach the innermost boundary (inside of the skull).

The precomputed models with leadfield interpolation (**BEM Interpolated**, **FEM Interpolated**) overcome the speed problem, but are relatively new, so for comparison the normal slower version of the standardized averaged **MNI** head is also implemented (**BEM Standardized**). The **FEM** model (**FEM Interpolated**) can only be used in the precomputed version, since otherwise days of computation time would be needed. In the **FEM** model an anisotropic bone layer is realized for the first time in a commercially available package.

The precomputed (standardized) BEM Realistic Head Model is described here.

[Fuchs M, Kastner J, Wagner M, Hawes S, and Ebersole J. A standardized boundary element method volume conductor model. Clinical Neurophysiology, May 2002, Vol 113:5, p702-712.]

Head Model. Select a head model from the drop-down menu of options, or select an m-file from MATLAB.



Infinite Homogeneous. This is a homogeneous head model (that may or may not have a single resistance). For MEG, it is essentially air.

1, 2, 3 and 4 Spherical Shells. These are concentric spherical shells models having 1-4 shells and given relative radii and conductivities. For example, with a three spherical shells head model, the first sphere represents the outermost compartment boundary (skin surface). It is fitted to the electrodes, then relative radii as well as conductivity values may be entered. The defaults are standard values from the literature, although you have the option to modify them.

Inside Sphere. This option is used with Intracranial-EEG as it computes potentials inside the brain.

BEM Precomputed. This is a precomputed (BEM) head model where the skin/skull conductivity ratio is 1/25. CURRY 7 used a ratio of 1/80, which seems not to be supported by the more recent literature.

Conductivities used:

Ratio 1/25
Skin 0.33 S/m
Skull 0.0132 S/m
Brain 0.33 S/m

The next three models are from CURRY 7, and they will be available if you have CURRY 7 installed.

BEM Standardized (Legacy). The standardized Boundary Element Method (BEM) model was derived from averaged MRI data set from the Montreal Neurological Institute (MNI). It consists of 9300 triangles overall or 4656 nodes, which describe the smoothed inner skull (2286 nodes), the outer skull (1305 nodes), and the outside of the skin (1065 nodes). The mean triangle edge

lengths (node distances) are 9mm (skin), 6.8mm (skull), and 5.1mm (brain compartment).

BEM Interpolated (Legacy). The interpolated BEM Realistic Head Model, also derived from the averaged MRI data sets, uses a precomputed leadfield matrix (on a regular 3D-grid with 5mm node distance) and a 3D-interpolation scheme. It consists of 8043 nodes and 16,074 triangles overall (inner skull: 3858, outer skull: 2681, and skin: 1504 nodes). The mean triangle edge lengths (node distances) are 7.5mm (skin), 5.1mm (skull), and 3.3mm (brain compartment).

FEM Interpolated (Legacy). Also derived from the MNI averaged MR data set, the Finite Element Model (FEM) uses an anisotropic bone layer, a precomputed leadfield matrix (on a regular 3D-grid with 6mm node distance), and a 3D-interpolation scheme. It depicts the surface using 286k tetrahedra, with an edge length of 4mm.

BEM.... Use this option to select the BEM Realistic Head Model you have created from BEM/FEM Geometry (and saved with a .bd**#** extension). The number in parentheses is the number of nodes in the model. The Standardized and Interpolated BEM/FEM model were created using the averaged MR data set, and reside in CURRY's memory.

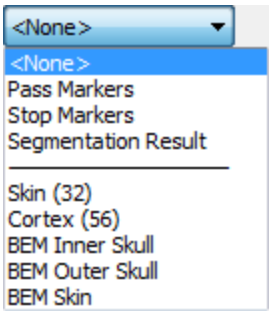
<Create BEM Head Model>. Selecting this option displays the BEM/FEM Geometry panel, where you may create the BEM head model.

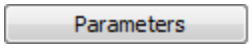
<Create FEM Head Model>. Selecting this option displays the BEM/FEM Geometry panel, where you may create the FEM head model.

Note
The standardized and interpolated BEM and FEM models are based on the built-in MRI dataset. When working without individual image data, these are the models of choice.

MATLAB Interface. The options below the line allow you to interface with MATLAB. An example file is included. You can also edit the file(s) in MATLAB.

Exclude. You may elect to exclude any of the following markers, results or overlays (your list will vary from that shown below).



Relative Radius [%] / Conductivities [S/m]. These are the default relative radii and conductivities for spherical head models, based on the literature, although you have the option to modify them. The center position and outermost radius are determined by a sphere fit to the selected sensors of the selected device, but can be changed in the **Maps** 

. The Conductivities are the absolute conductivity values of the spherical head model shells corresponding to the radii displayed in the left columns.

Note
If you are using an individual's MRI with label-matched sensor positions, you should not scale the head model radii percent values for children or for smaller heads since then the head model would no longer match the electrode positions and the anatomical context. You should see the estimated source positions as rough guesses only and not overinterpret the numerical results. You could scale all numbers off-line by the ratio of the measured head circumference to the used value. Especially for small head sizes, however, exactly measured electrode positions are essential. If landmarks are given, the model head surfaces (skin, skull, and brain envelope) are matched to these landmarks.
Scale Standard Surfaces. Standard surfaces (MNI-brain-derived surfaces for skin, skull, brain, cortex, displayable in 3D View even without individual image data and/or without image data processing) may or may not be scaled to the best possible match (in overall size) that the locations of the EEG electrodes used. This scaling is a simple inflation or deflation around the origin of the built-in PAN coordinate system. The scaling can be switched off, and it is automatically switched off for ECoG and sEEG data, whose presence is detected by analyzing the type of head model that is selected.

Constrain Source Space. This option is active when using the **BEM Precomputed** head model, and, if activated, it effectively removes the cerebellum from the source space.

You may create your own BEM head models in "BEM Setup" that also allow you to constrain the source space. You then need to add an additional, innermost layer (triangle mesh) that describes the valid source space (eg. brain w/o cerebellum) and you must furthermore assign the same conductivity to this layer as you used for the inner skull (brain) compartment.

Conductivity Factor. These fields are active when there are EEG and MEG channels in the data and a single dipole model is selected.

The **Conductivity Factor** between EEG and MEG forward models is of importance if EEG and MEG data are used for combined source reconstructions. Basically, EEG depends on absolute conductivities and MEG on relative ones, so MEG can be used to calibrate the EEG conductivities. The standard conductivities normally used are not exact enough and errors due to this ambiguity dominate the source reconstruction. As a consequence, CURRY allows you to *fit* the **Conductivity Factor** along with a single dipole model which is to be applied at a latency where a well-defined tangential source dominates, as is the case in the SEP/SEF N20 peak.

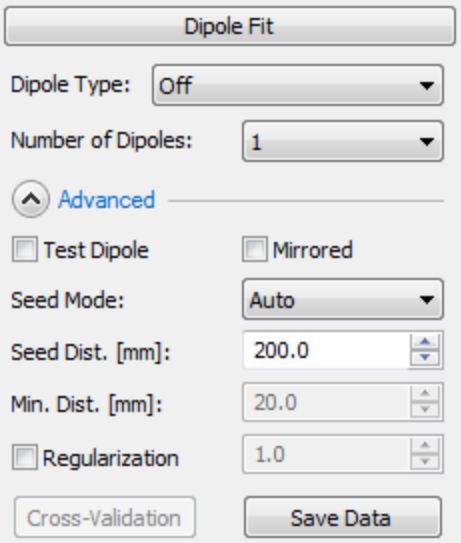
After this **Fit**, the **Conductivity Factor** should be fixed, and all other source models can then be used as well. When not fitted, this factor will be used to set up the leadfields, so if there are EEG+MEG, it is important to have a good estimate of this value.

For a description of combined EEG and MEG analysis and the conductivity factor, see here.

[Fuchs M, Wagner M, Wischmann H-A, Köhler T, Theißen A, Drenckhahn R, and Buchner H. Improving source reconstructions by combining bioelectric and biomagnetic data. Electroencephalography and Clinical Neurophysiology, April 1998, Vol 107:2, p93-111.]

19.1.2 Dipole Fit

The dipole source model is selected in this panel. The simplest dipole model is the single equivalent current dipole. Its three location parameters are fitted, and its three components are determined for a given time point so as to minimize the deviation between measured and forward calculated data. An extension of the single equivalent current dipole is the **Moving** dipole. Its three location parameters per time point are fitted, and its three components are determined for each in a series of time points.



If the location of a moving dipole is held fixed over time, we get the **Rotating** dipole. Its location is jointly fitted for all time points, while its three components are determined for each time point independently. When the three orthogonal main dipole orientations and their associated loadings are extracted from a rotating dipole (using a PCA), we get a **Regional** dipole.

If the location and orientation are kept fixed, we have a **Fixed** dipole: Location and orientation are jointly fitted for all time points, while for each time point the dipole strength is determined only. For **Fixed Coherent** dipoles, common positions and orientations for all time points are fitted, and the dipole strengths for every time point are calculated. If more than one dipole is fitted, all dipoles have coherent loadings (same temporal behavior).

Dipole Constraints

In addition to the requirement that the dipoles to be fitted shall explain the measured data, further requirements can be imposed. These are called *constraints*, and their purpose is to make the dipole fit more stable and its result more reasonable in certain situations.

There are several types of dipole constraints:

- The dipole location does not change over time (rotating dipole).
- The dipole location and orientation do not change over time (fixed dipole).
- The locations of two dipoles are mirrored with respect to the midsagittal plane (mirrored dipoles).

Multiple Signal Classification (**MUSIC**) is a method that does not compute the misfit of a given dipole model per location, but a specific MUSIC metric: The signal subspace is associated with the leading singular values of the measured data matrix standing for the subspace orthogonal to the noise subspace. The number of singular values that make up the signal subspace is a parameter of the method. This metric peaks at the locations of multiple, non-coherent, i.e., temporally independent, sources for a given time range. It gives the best results for temporally independent sources with fixed orientations (e.g., SEPs).

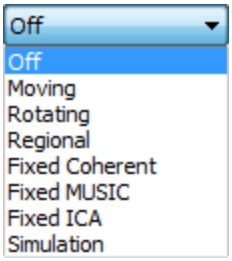
Moving dipoles are the right choice to get a first overview of the activity to be reconstructed and are well suited to model propagating sources like often found in epileptic discharges. **Fixed dipoles (MUSIC)** are good to model well localized and temporally independent sources like the generators of somatosensory evoked potentials. **Coherent fixed dipoles** with the optional mirror constraint can be used to reconstruct simultaneous bilateral auditory evoked activity, for example. Fixed dipoles are spatio-temporal source models that integrate activity over the selected time range and thus lead to a better signal-to-noise-ratio and accordingly to more stable reconstruction results as compared to moving dipoles.

Dipole fits are referenced here and here.

[Fuchs M, Wagner M, Wischmann H-A, Köhler T, Theißen A, Drenckhahn R, and Buchner H. Improving source reconstructions by combining bioelectric and biomagnetic data. Electroencephalography and Clinical Neurophysiology, April 1998, Vol 107:2, p93-111.]

[Mosher J, Lewis P, and Leahy R. Multiple dipole modeling and localization from spatio-temporal MEG data. Biomedical Engineering, IEEE Transactions, June 1992, Vol 39:6, p541-557.]

Dipole Type. There are several dipole models, plus a Simulation.

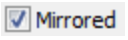


Off. No dipole is computed.

Moving. For each latency in the selected Timerange, an independent fit of the **Dipoles** will be performed. This results in free dipole positions and free dipole orientations. Moving dipoles are the correct choice to get a first overview of the activity to be reconstructed. They are well suited to model propagating sources like those often found in epileptic discharges.

Rotating. For the selected time range the positions of Number of Dipoles selected will be fitted globally. At each latency, independent dipole components will be determined. This results in fixed dipole positions, but free dipole orientations.

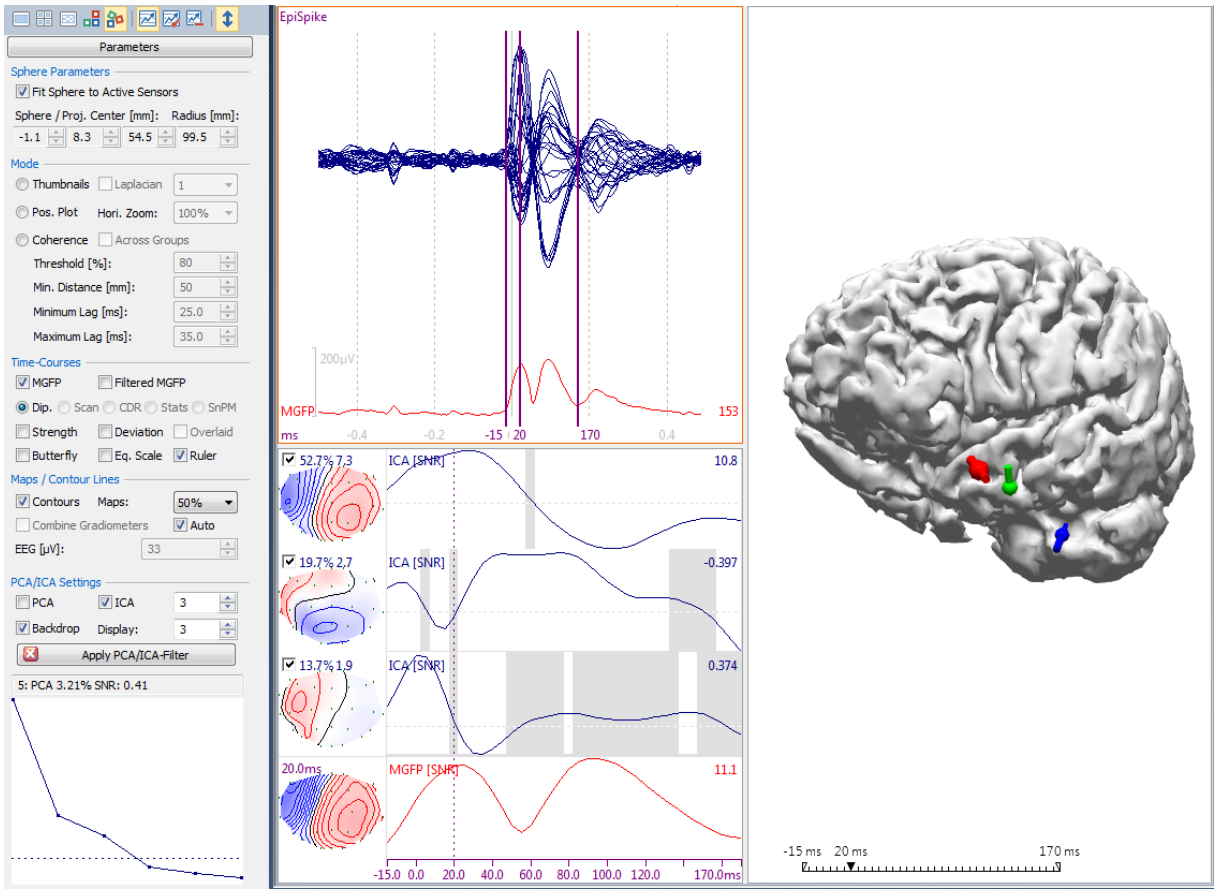
Regional. A Regional dipole is a rotating dipole with an additional postprocessing step. A Singular Value Decomposition is applied to each rotating dipole in order to determine its preferred orientation over time and the two other orthogonal components. Thus, three fixed orthogonal components are obtained per rotating dipole, and their strengths are computed as a function of time. (The Regional model provides comparability to BESA results).

Fixed Coherent. For the selected time range and **Number of Dipoles**, the position of coherent dipoles will be fitted globally and at each latency orientationally fixed dipole components will be determined. This results in temporally dependent dipoles with fixed positions and fixed orientations with coherent strengths, i.e., the orientations and the relative strengths of all dipoles are fixed. The optional 

constraint can be used to reconstruct, for example, simultaneous bilateral auditory evoked activity.

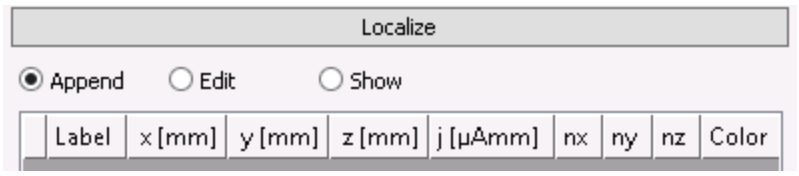
Fixed MUSIC. The specified number (**Number of Dipoles**) of field patterns will be used to fit the same number of dipoles iteratively using the MUSIC algorithm. The data of the selected reconstruction time range recursively fit into the ICA-filtered, measured data. At each latency the independent dipole strengths will be determined. This results in temporally independent fixed dipole positions and orientations. Due to the MUSIC algorithm, regularization of the dipole components is not possible. Fixed MUSIC dipoles provide a good model for well localized and temporally independent source like the generators of somatosensory evoked potentials. See the **Multiple Signal Classification** section below for more details.

Fixed ICA. If you perform an ICA decomposition and then select Fixed ICA, you will see a dipole solution for each independent component. Deselecting one or more components will remove the associated dipole.

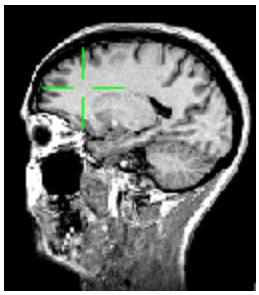


Simulation. The Simulation option allows you to create 1-5 simulated dipoles in a location and orientation you select. It is also used with grids and strips. Perform the following operations to create a simulated dipole(s). See also the *Dipole Simulation* tutorial.

1. Go to the Localize panel and delete any list that might be present.



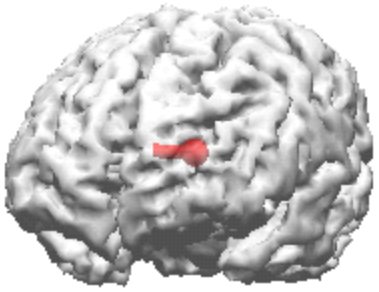
2. In the iso-images in the Localize display, or in the Image Data display, position the crosshair cursor at the point where you want the dipole to appear (click to set it). Make sure that the selected location is inside the head model to be used.

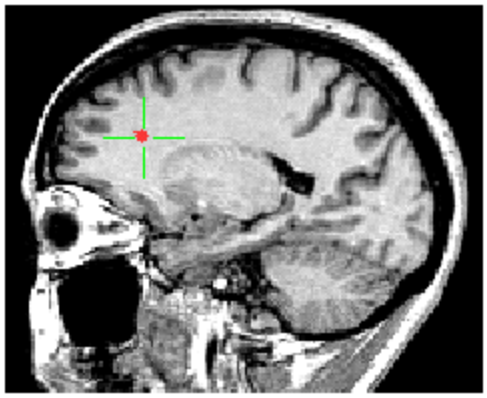


3. *Right click* in the display and select **Export Cursor to Localize**. The XYZ positions will appear in the Localize list, along with the Strength (j [μAmm]). The normals (nx, ny, and nz) determine the orientation. The color is set by Default, which can be changed using the drop down list. Group may be <Undefined> or you may select an EEG grouping (from 1-20).

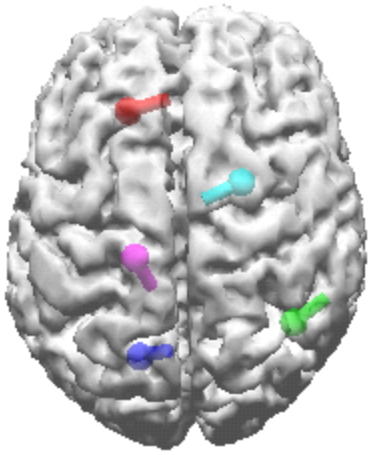
	x [mm]	y [mm]	z [mm]	j [μAmm]	nx	ny	nz	Color	Group
1	-15.1	64.3	57.1	100	0.685	0.727	0.042	<Default>	<Undefined>

4. Go to the 3D View display and then select Source Reconstruction . Under **Dipole Type**, select **Simulation**, with **1** dipole. You will then see the simulated dipole.





5. In the same way, you may increase the **Number of Dipoles** to see them in the 3D View and Image Data displays.



Note
If you enter more locations than **Number of Dipoles**, and are performing a simulation for a Timerange, the locations are distributed among the simulated latencies. For example, for 2 dipoles and 10 samples, up to 20 locations will be used.

If you want to change the position, delete the current location(s) in the Localize list. Move the cursor in the iso-images, and again click **Export Cursor to Localize**. Set the **Dipole Type** to **Off**, then reselect the Simulation option. The new position(s) will be displayed.

Number of Dipoles. Number of dipoles sources used to fit the measured data. The maximum number of dipoles is 10. More than 5 nearly always result in unstable results and large confidence ellipsoids. If there are really more than 5 sources active you should split the Timerange into intervals where fewer sources are active simultaneously.

Advanced
Test Dipole. The test dipole can be used after a successful fit (e.g., two rotating dipoles) in order to determine if there is some portion of the data left unexplained. The test dipole options increases the number of fitted dipoles by one. The original results are fixed, and a dipole of the same kind is fitted using the adjusted parameters (seed distance, etc.) to see how much of the data can be explained by this additional source. The test dipole should not alter the locations, orientations, strengths, and goodness-of-fit of the original solutions, else these may not be stable.

Mirrored. Two of the dipoles to be fitted will obey a mirrored locations constraint. Their locations are interdependent and mirrored along the mid-sagittal plane of the internal coordinate system.

Seed Mode. Dipole fitting as implemented in CURRY works by iteratively optimizing dipole locations until the dipoles explain the data best. The initial locations are called seeds. There are three methods for controlling which seeds are used:

Auto. This performs a coarse deviation scan on a set of predefined locations and uses the best ones as seeds. Use this for dipole fitting unless you have reason to do otherwise.

Localize. Instead of precomputed seeds for the simplex optimizer, **Localize** locations are used. If enough locations are specified, different seeds are used for each latency. This is used, for example, if the seeds are actually fMRI hotspots and you want to have a dipole close to each hotspot. Mark each fMRI hotspot in Localize and fit the corresponding number of dipoles in the **Localize** seed mode.

Cursor. Cursor (analogous to the CDR dipole Cursor mode) is a quick way to explore how the dipole solution reacts to an updated seed point (there can be only one seedpoint available in this mode).

Seed Dist. [mm]. The seed distance is the maximum distance of the best fit positions (seed points) from the start position of the multi-dimensional non-linear Nelder-Meade fit algorithm. The default distance is large - 200 mms - to include the entire head. Along with the Seed Mode options, a maximum distance that the dipole may be apart from the seed points can be specified. Use 0 to find out where the seeds actually were. Use a small value, such as 5-20mm, to keep the dipole in the vicinity of its seedpoint. This is used, for example, if the seeds are actually fMRI hotspots and we want to have a dipole close to each hotspot (which is what the **Localize** mode is for).

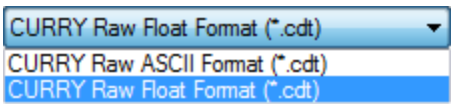
Minimum Distance [mm]. For more than one dipole, a minimum distance between the dipole positions can be chosen to avoid strong opposing (canceling) source configurations.

Regularization. Regularization can be applied in order to suppress meaningless dipole components (e.g., quasi-radial components in BEM Realistic Head Models used for MEG reconstructions). It adds a second term to the misfit term in a weighted fashion, assuring that only dipole components are reconstructed that explain a significant portion of the data. The parameter is in relation to the estimated SNR; due to the uncertainty of the noise estimation, a range of 0.5 to 2 is suggested. See the **Dipole Component Regularization** section below for more details.

Cross-Validation. Clicking the 

button computes the dipole solution in an iterative fashion, where one sensor is omitted in each pass. It provides another means for assessing the validity of a dipole solution. Note that if there is one "bad" channel, all solutions but the one without this channel may be bad, which indicates that an outlier could in fact be the best solution.

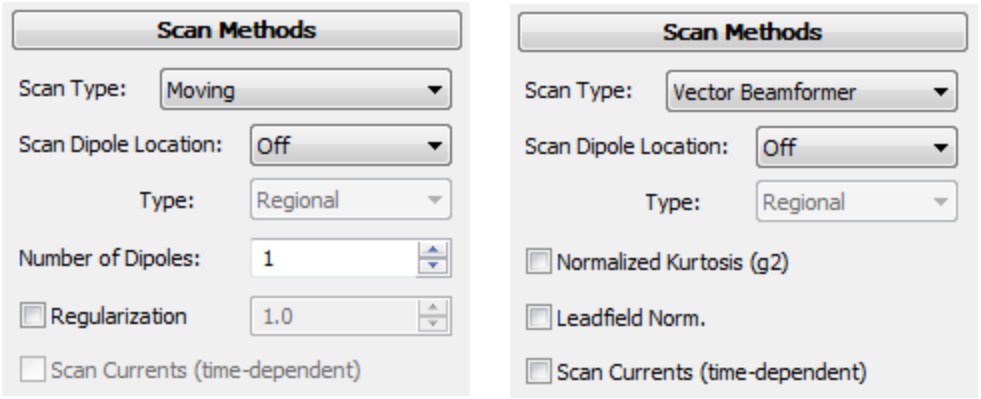
Save Data. The waveform data used in the dipole reconstruction Timerange will be saved in either Float Format or ASCII Format.



19.1.3 Scan Methods

It is possible to explicitly scan the parameter space. This approach is called *Dipole Scan* or *Deviation Scan*. For a one dipole model, this would mean to compute for each possible source location the best fitting dipole components and the misfit value. The result is the dipole fit's error hypersurface. It allows you to estimate regions of confidence, i.e., the regions where a dipole would explain the data well enough. For models with more than one dipole, each location is assigned the lowest misfit value that a dipole pair/triple/... involving this location can achieve.

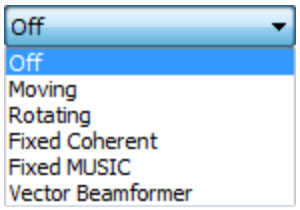
The options change if you select **Vector Beamformer**.



Scan methods work on fixed source positions specified by the Source Locations panel, thus scanning can be constrained to certain regions, e.g., the cortical surface. They can additionally be restricted to predefined orientations. If **Scan Type** is **Fixed**, the dipole orientations are also fixed and given. With a one dipole scan, i.e., the best fit single dipole, orientations and strengths are determined for all source locations successively. The results are given as the inverse of the residual variance as symbol size (color coded and/or clipped and/or with border lines, if activated). By this way confidence regions for one dipole source models and the shape of the fit deviation hypersurface can be visualized. If the **Number of Dipoles** is larger than one, all possible configurations are tested and the smallest deviation possible for the location under consideration together with the best other dipole locations is stored. This can lead to excessive computation times.

Performance
With the exception of the MUSIC variant, for more than one dipole the computational complexity explodes. It is roughly proportional to the number of scanned locations raised to the number of dipoles; a 2-dipole scan for 10000 locations takes 10000 times longer than a one dipole scan.

Scan Type. The types of Scans are: Moving, Rotating, Fixed Coherent, Fixed MUSIC, and Vector Beamformer.



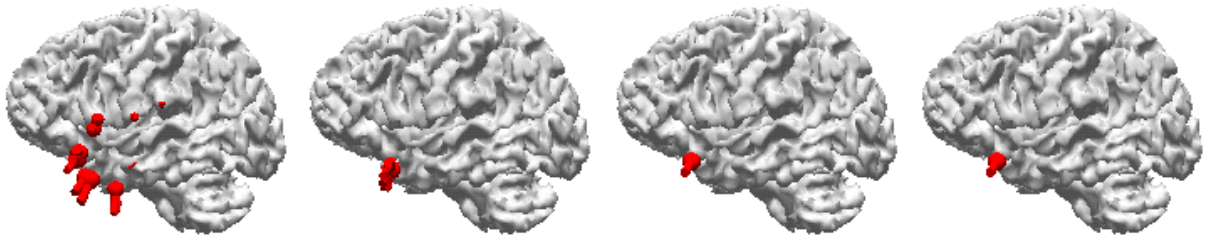
Moving. For every latency in the selected timerange an independent scan is performed (in analogy to Moving Dipole Type reconstructions). This may be very time consuming, especially if the timerange is wide and more than one dipole is selected.

Rotating. For the whole selected latency range, the global best fit for all locations is determined with free dipoles in all their components. This results in rotating dipoles.

Fixed Coherent. For the whole selected latency range the global best fit is determined with dipoles having a fixed, best fit orientation. If more than one dipole is selected, coherent dipoles will be assumed as source model.

Fixed MUSIC. Single dipole scans are performed by the MUSIC algorithm. These are for the chosen number of PCA components (or Eigenvalues) within the selected latency range. They are chosen so the locations of non-coherent dipoles can be found. Afterward this number of fixed dipoles is set to the minima of the deviation hypersurface and their best fit orientations and strengths are determined.

The dipole results for the types of Scans are similar to those seen for the types of single equivalent dipoles.



Vector Beamformer. Beamforming is a method from general signal processing that is often used with MEG data. It is used to compute overall activity and extract source waveforms for brain locations. Beamformer computes a solution where *not* all sources to be seen are active simultaneously. All brain locations are treated independently ,which means that the result for a location will not change if you compute a result for a different location. Basically, beamformers are deviation scans that take data covariances into account. Beamformers are similar to MUSIC in that they are good in localizing anything but multiple coherent sources (AEPs). The method CURRY uses is basically the method described in Sekihara's vector beamformer paper. Note that there are also LCMV beamformer and SAM beamformer methods, as well. Typically, Beamformers are used with continuous data - primarily MEG data - since you

need literally a few thousand data points to obtain an accurate result. Beamforming gives an idea of what is going on in a large segment of data, as opposed to just a few samples.

When Vector Beamformer is selected, you will see additional options appear.

Normalized Kurtosis (g2). Kurtosis (excess kurtosis g2) is a method that emphasizes the spikiness of the waveforms in Beamformer scans (used with MEG measurements).

Leadfield Normalization. When normalizing the leadfield, the gain will be the same for superficial dipoles and deeper dipoles.

Scan Currents (time-dependent). When selected, the currents will be computed for each time point, instead of the probabilities. The computations can require large amounts of memory. If you see a memory related message, deselect this option.

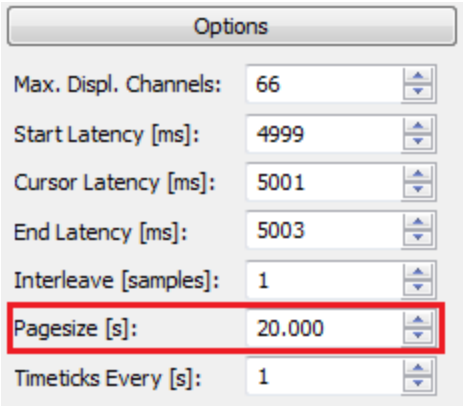
For a description of depth weighting techniques (also called lead field normalization), see here.

[Kohler Th, Wagner M, Fuchs M, Wischmann H.-A, Drenckhahn R, and Theissen A. Depth normalization in MEG/EEG current density imaging Engineering in Medicine and Biology Society, 1996. Bridging Disciplines for Biomedicine. Proceedings of the 18th Annual International Conference of the IEEE, p812 - 813.]

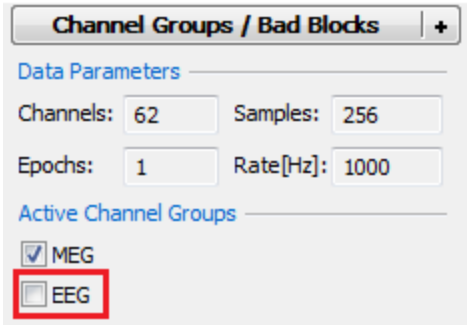
See also: Reconstructing spatio-temporal activities of neural sources using an MEG vector beamformer technique**.** Sekihara, K.; Nagarajan, S.S.; Poeppel, D.; Marantz, A.; Miyashita, Y.; Biomedical Engineering, IEEE Transactions on , Volume: 48 Issue: 7 , Jul 2001 p760 -771.

When using Vector Beamformer, it has been our experience that best results are obtained when using MEG data alone, rather than MEG+EEG, or EEG data alone. We recommend the follow parameters to get the best results.

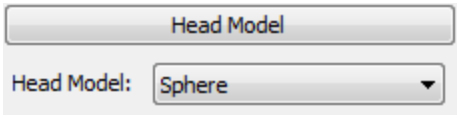
Select a Timerange that encompasses the entire data display, such as **10 seconds** or longer (display more seconds as desired; use *Ctrl+double click* to spread the cursors).



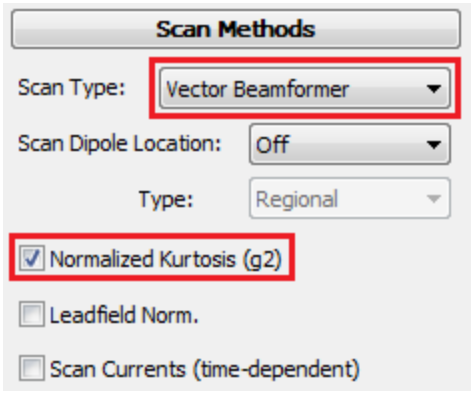
Select **MEG** data only, if you have MEG and EEG in the same file.



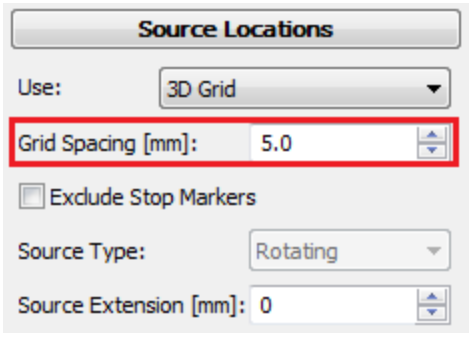
Use a **Sphere** Head Model.



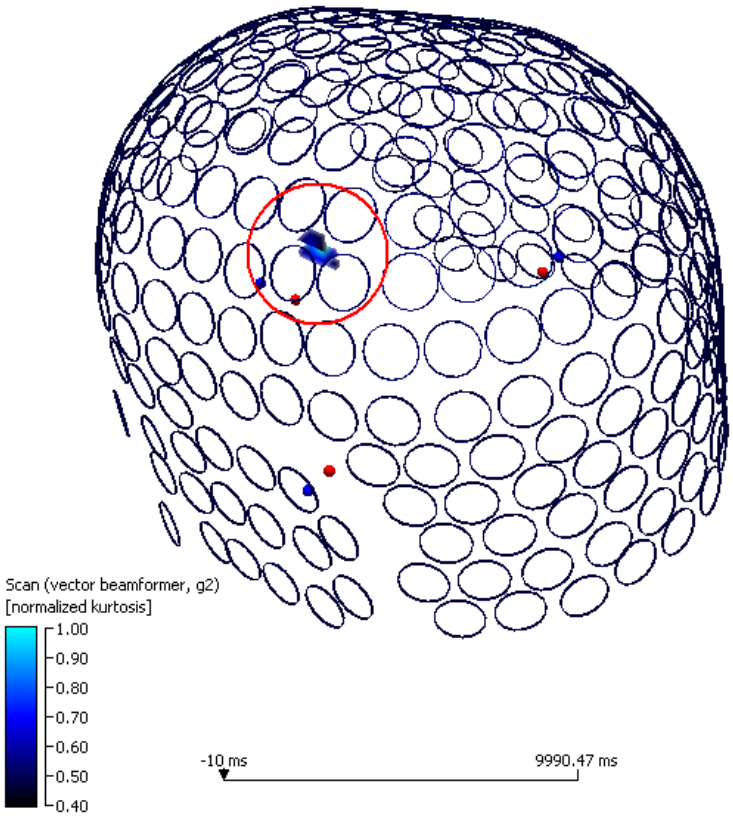
In **Scan Methods**, select **Vector Beamformer** and enable **Normalized Kurtosis (g2)** to accentuate the spikiness.



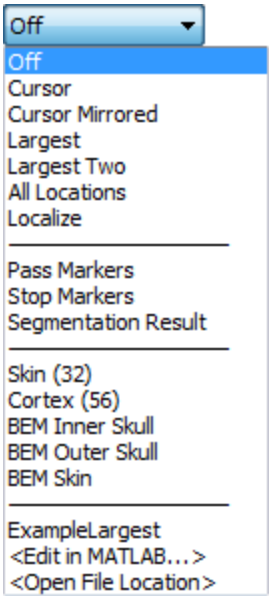
In **Source Locations**, reduce the **Grid Spacing** to, for example, **5**mm.



Start with those parameters and adjust as needed to obtain very focal results.



Scan Dipole Location. You may constrain the Scan dipoles to various locations and surfaces. The Scan Dipole Location options deal with the locations for the Scan dipoles (for which locations do you want to know the source activity time course?).



Cursor. The dipole position is moved to the location of the cursor in the iso-images and/or the 3D View. The cursor places the Scan dipole, and the Scan dipole provides the time course of Scan activity at that location.

Cursor Mirrored. Similar to **Cursor** except there is a "mirrored" dipole at the homologous site on the other side of the brain as well (mirrored across the midsagittal plane, which is defined by the PAL/PAR/NAS landmarks).

Largest. The location with the largest current, either per timepoint (if Moving is selected below), or overall.

Largest Two. The two locations with the largest currents, either per timepoint (if Moving is selected below), or overall. The second location is identified as the second independent peak of activity, which only works for 3D grid source locations.

All Locations. Each and every location is used for the Scan (creates many Scan dipoles).

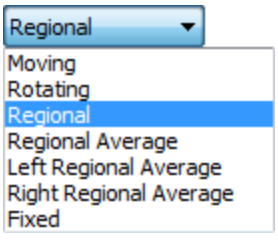
Localize. Similar to **Cursor**, except the **Localize** locations are the probes.

Pass Markers/Stop Markers/Segmentation Result. Choice of binary overlays: all locations within the selected markers/structure are used. In this context, it is good to know that the **Segmentation** panel allows to segment Atlas structures as well.

Skin, Cortex, BEM Inner Skull, BEM Outer Skull, BEM Skin. You may also select the segment Skin or Cortex surfaces, or any of the BEM compartment surfaces.

ExampleLargest, **<Edit in MATLAB...>**, **<Open File Location...>**. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

Type. Scan dipoles are a means to extract source waveforms for certain locations and be able to display them in **Maps**. The different Scan dipole types differ in how these locations are specified, and if a dominating orientation is computed or not (fixed modes).



Moving dipoles have a new location and orientation for each time point. This is only possible if the **Scan Dipole Location** selection allows locations to change with time, which is the case for **Largest** and **Largest Two**. In all other cases, this reverts to **Rotating**. The dipole waveform is always positive and scales with the CDR source strength.

Rotating is the same as Moving, except the location does not vary with time.

Regional dipole location also does not vary with time. Three dipole waveforms per location are extracted (using an SVD, just like for the **Regional** dipole model in **Dipole Fit**). This is the default option.

Regional Average is similar to Regional, but for more than one location. First the average Scan over all locations is calculated, and then the three regional dipole waveforms are calculated. This is especially useful with the **Pass/Stop/Segmentation Result** choice of binary overlays options.

Left Regional Average and **Right Regional Averages** may be computed separately. These are typically used when segmentation of bilateral structures using the atlas has been done, and where the interest is on one side or the other.

Fixed. The Fixed option is similar to the others, except only the strongest waveform is shown. This option is only for backward compatibility. It used to be the suggested option in Curry 7, because (unlike Moving/Rotating) it shows a positive/negative waveform.

Number of Dipoles. Enter the number of dipoles, or use the up and down arrows.

Regularization. Regularization can be applied in order to suppress meaningless dipole components (e.g., quasi-radial components in BEM Realistic Head Models used for MEG reconstructions). It adds a second term to the misfit term in a weighted fashion, assuring that only dipole components are reconstructed that explain a significant portion of the data. The parameter is in relation to the estimated SNR; due to the uncertainty of the noise estimation, a range of 0.5 to 2 is suggested. See the **Dipole Component Regularization** section below for more details.

19.1.4 Current Density

Current density is defined as dipole moment per volume (unit: μAmm/mm3, which is uA/mm²). A current density distribution is discretized into a large number of elementary dipoles. Each dipole represents the current density in a given volume *V*. The dipole moment is proportional to the current density that it stands for.

Distributed source models or current density models are characterized by two properties:

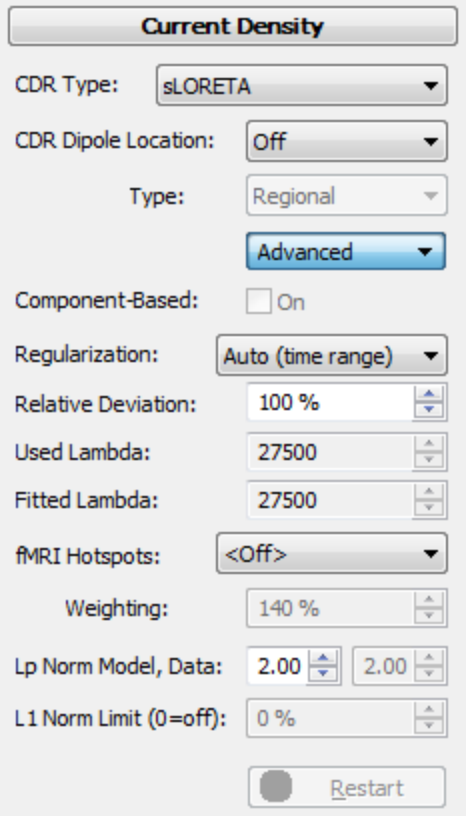
- The source locations are given in advance, either as a 3D grid or as a surface. This has the effect that also the leadfield matrix *L* remains the same throughout the fit.
- There is always a model term *M(j)* and a regularization parameter λ by which it is linked to the data term *D(j)*.

$$\Delta^2 = D(j) + \lambda M(j)$$

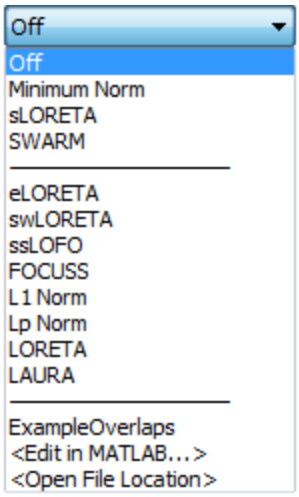
The model term is necessary because there are so many source locations that the problem would otherwise have no unique solution due to the large number of free parameters. If source orientations are free, there are three unknown dipole moments

per location. If source orientations are fixed, e.g. to be perpendicular to the source surface, there is one unknown dipole component or strength per location.

Current Density Reconstructions (CDRs) assume simultaneous activity at a large number of possible source locations. There is a trade-off between the goodness-of-fit (deviation) and the conformance of the reconstructed distribution to a given source model. Different source models make different assumptions about the nature of the sources, typically sources are assumed to be small (**Minimum Norm, sLORETA, SWARM, eLORETA, L1 Norm, Lp Norm,**), or of similar strength as their neighbors (**LORETA**). Normally, a goodness-of-fit on the order of 1/SNR is seen as a good trade-off between data and model. Controlling this trade-off is called regularization, and the respective parameter is called Lambda (λ). The solution space is defined in Source Locations below.



CDR Type. The drop-down list contains the types of CDRs that are contained in CURRY. The list is divided into two groups, plus the MATLAB interface. The upper group - Minimum Norm, sLORETA, and SWARM - are the ones that are generally used, and the ones we recommend you use unless you have a need and the experience to use the other methods. They also tend to be run faster. The lower methods - some are relatively old and some are relatively new - are just some of the other CDR methods that are possible. These have been included because of their historical relevance, or because users have requested them. Again, you should not really use these lower ones unless you have a reasonable familiarity with them.



Upper Group

Minimum Norm. The best-known Minimum Norm method is Minimum Norm Least Squares (MNLS, L2 Norm). It computes rapidly, but has a tendency to reconstruct sources that are too superficial and artificially "smears" focal sources. Other norms, called Lp norms, where 1 <= p <= 2, deliver results that are more focal. When Minimum Norm is activated, Lp norms can be selected by changing the Lp Norm parameter. It is included in CURRY because of its long history, although we do not recommend using it for the reasons stated above.

For a comparison of Minimum Norm methods, see here.

[Fuchs M, Wagner M, Köhler T, and Wischmann H-A. Linear and Nonlinear Current Density Reconstructions, Journal of Clinical Neurophysiology: May 1999, Vol 16:3, p267-295.]

sLORETA. **sLORETA** (standardized Low Resolution Electromagnetic Tomography) is a modification of **MNLS**, where not the current distribution but rather a statistical measure, namely (for each location) the current strength divided by its error bar is computed. **sLORETA** is nearly as fast as **MNLS**, and localizes better. When used with values of p < 2, the sLORETA metric is computed based on the respective Lp norm. The name of this method is sARETA (standardized Adjustable Resolution Electromagnetic Tomography). The F-scale is more of a unitless pseudo-F scale, meaning that it is not possible to compare one set of sLORETA results with another (higher values do not necessarily mean increased activation).

sLORETA is generally the method of choice, except in rare situations. Some have reported that it may fail when analyzing auditory evoked potentials. In that case, try Minimum Norm.

sLORETA is described here and here.

[Pascual-Marqui, RD. Standardized low resolution brain electromagnetic tomography (sLORETA). Groupal & Clinical Pharmacology, 2002, Vol. 24D, p5-12.]

[Wagner M, Fuchs M, and Kastner J. Evaluation of sLORETA in the Presence of Noise and Multiple Sources, Brain Topography, Vol 16:4, 277-280.]

SWARM. SWARM (sLORETA-Weighted Accurate Minimum Norm; Australian patent no. 2006332443) is sLORETA-weighted Minimum Norm, i.e., sLORETA is used (instead of, for example, fMRI) to indicate source locations. The goal is to have a CDR method that localizes exactly and delivers current densities (dipoles) and not, as sLORETA does, statistical values. SWARM is based upon sLORETA in that it is an sLORETA-weighted MNLS. SWARM thus "inherits" the zero-error property from sLORETA. You can think of SWARM as being like sLORETA except you are seeing brain current flow (dipole activity per volume) rather than statistical measures.

SWARM can be used with ICA (or PCA) based source reconstruction (with **Component-Based** enabled). Computations will be much faster, especially with large Timeranges.

SWARM is described here.

[Wagner M, Fuchs M, and Kastner J. SWARM: sLORETA-weighted accurate minimum norm inverse solutions, International Congress Series, Vol 1300, June 2007, p185-188.]

Lower Group

eLORETA. eLORETA is an inverse method that computes neuronal current flow with zero localization error for point sources. What is the difference between sLORETA and eLORETA? It differs from sLORETA in that sLORETA does NOT compute neuronal current flow; it computes a statistical map. The differences between SWARM and eLORETA are that SWARM is faster, and tends to produce more focal localizations where eLORETA gives broader, more widespread results.

eLORETA is described here.

See also Wagner M, Fuchs M, and Kastner J. sLORETA, eLORETA, and SWARM in the Presence of Noise and Multiple Sources. In: Biomagnetism – Interdisciplinary Research and Exploration Eds.: R. Kakigi, K. Yokosawa, S. Kuriki., Hokkaido University Press, 2008, 74-76.

swLORETA. Standardized weighted low-resolution electromagnetic tomography (swLORETA) is an improved version of sLORETA, obtained by incorporating a singular value decomposition-based lead field weighting. The precision of the source localization can further be improved by a tomographic phase synchronization analysis based on swLORETA. For more information, see:

Palmero-Soler E, Dolan K, Hadamschek V and Tass PA. swLORETA: A Novel Approach to Robust Source Localization and Synchronization Tomography. Phys. Med. Biol. 52 (2007) 1783-1800.

ssLOFO. Standardized Shrinking LORETA-FOCUSS (ssLOFO) uses a recursive process which takes the smooth estimate of sLORETA as initialization and then employs the re-weighted minimum norm introduced by FOCUSS. Standardization

is involved in the recursive process to enhance the localization ability. For more information, see:

Liu H, Schimpf PH, Dong G, Gao X, Yang F and Gao S. Standardized Shrinking LORETA-FOCUSS (SSLOFO): A New Algorithm for Spatio-Temporal EEG Source Reconstruction. IEEE Transactions on Biomedical Engineering, Vol 52, No 10, October 2005.

FOCUSS. Focal Underdetermined System Solution combines the desired features of the two major approaches to electromagnetic inverse procedures. Like multiple current dipole modeling methods, FOCUSS produces high resolution solutions appropriate for the highly localized sources often encountered in electromagnetic imaging. For more information, see:

Gorodnitsky I and Bashkar D. Sparse Signal Reconstruction from Limited Data Using FOCUSS: A Re-weighted Minimum Norm Algorithm. IEEE Transactions on Signal Processing, Vol 45, No 3, March 1997.

L1 Norm. The **L1 Norm** is a method where not the sum of squares of currents is demanded to be small, but rather the sum of absolute values (included for historical reasons). This method produces only a few active sources per latency and is very sensitive, but also very artifact-prone. It works best with fixed source orientations and extended sources. The difference between this implementation of the L1 norm and Minimum Norm or Lp norm with p = 1 is that the algorithm used here delivers the sparsest result possible (most sources are exactly zero), and that a maximum current density constraint can be used. While the L1 norm algorithm is still available in CURRY, Minimum Norm with a model term of p will normally be used.

The Minimum L1 Norm is described here.

[Wagner M, Fuchs M, Wischmann H-A, Drenckhahn R, and Köhler T. Current Density Reconstructions Using the L1 Norm. Advances in Biomagnetism Research: Biomag96, 1998, Springer-Verlag, New York.]

Lp Norm. **Lp Norm** is somewhere between **MNLS** and **L1 Norm**, with p between 1 and 2 (included for historical reasons). The difference between this implementation of the Lp norm and Minimum Norm is that here, the value of p for the data term (which measures the ability of the sources to explain the data) and the model term (which measures the p-Norm of the source distribution) can independently be adjusted, allowing, for example, for a Minimum L2 Norm model term (as in MNLS), but with a robust L1 norm data term that accounts for outliers in the data. However, in this implementation, lambda is not adjusted automatically and the **Restart** button typically needs to be pressed to ensure correct regularization. While the Lp norm algorithm is still available in CURRY, Minimum Norm with a model term of p will normally be used.

LORETA. **LORETA** (Low Resolution Electromagnetic Tomography) is the slowest method, assuming neighboring sources to be of similar strength. In this implementation, lambda is not adjusted automatically and the **Restart** button typically needs to be pressed to ensure correct regularization.

For LORETA, see here and (for cortical LORETA) here.

[Pascual-Marqui R. LORETA in 3D Solution Space. ISBET Newsletter, 1995, Vol. 6, 22-28.]

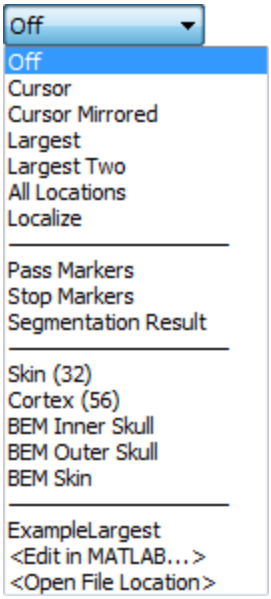
[Wagner M, Fuchs M, Wischmann H-A, Drenckhahn R, and Köhler T. Smooth reconstruction of cortical sources from EEG or MEG recordings, NeuroImage 1996, Vol. 3, p S168.]

LAURA. Local Autoregressive Average is a regularization strategy based on autoregressive models for spatial data combined with the concept of averages (included for historical reasons). For more information, see:

Menendez RG and Andino SG. Comparison of Algorithms for the Localization of Focal Sources: Evaluation with Simulated Data and Analysis of Experimental Data. International Journal of Bioelectromagnetism, 2002, Vol 4, No 1.

ExampleOverlaps. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

CDR Dipole Location. Generally speaking, CDR dipoles are a way to extract time course information from CDR images for a set of given locations and display them in the Maps window. The CDR Dipole Location options deal with the locations for the CDR dipoles (for which locations do you want to know the source activity time course?).



Cursor. The dipole position is moved to the location of the cursor in the iso-images and/or the 3D View. The cursor places the CDR dipole, and the CDR dipole provides the time course of CDR activity at that location.

Cursor Mirrored. Similar to **Cursor** except there is a "mirrored" dipole at the homologous site on the other side of the brain as well (mirrored across the midasgittal plane, which is defined by the PAL/PAR/NAS landmarks).

Largest. The location with the largest current, either per timepoint (if Moving is selected below), or overall.

Largest Two. The two locations with the largest currents, either per timepoint (if Moving is selected below), or overall. The second location is identified as the second independent peak of activity, which only works for 3D grid source locations.

All Locations. Each and every location is used for the CDR (creates many CDR dipoles).

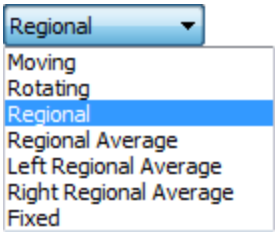
Localize. Similar to **Cursor**, except the **Localize** locations are the probes.

Pass Markers/Stop Markers/Segmentation Result. Choice of binary overlays: all locations within the selected markers/structure are used. In this context, it is good to know that the **Segmentation** panel allows to segment Atlas structures as well.

Skin, Cortex, BEM Inner Skull, BEM Outer Skull, BEM Skin. You may also select the segment Skin or Cortex surfaces, or any of the BEM compartment overlays.

ExampleLargest, **<Edit in MATLAB...>**, **<Open File Location...>**. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

Type. CDR dipoles are a means to extract source waveforms for certain locations and be able to display them in **Maps**. The different CDR dipole types differ in how these locations are specified, and if a dominating orientation is computed or not (fixed modes).



Moving dipoles have a new location and orientation for each time point. This is only possible if the **CDR Dipole Location** selection allows locations to change with time, which is the case for **Largest** and **Largest Two**. In all other cases, this reverts to **Rotating**. The dipole waveform is always positive and scales with the CDR source strength.

Rotating is the same as Moving, except the location does not vary with time.

Regional dipole location also does not vary with time. Three dipole waveforms per location are extracted (using an SVD, just like for the **Regional** dipole model in **Dipole Fit**). This is the default option.

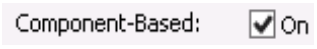
Regional Average is similar to Regional, but for more than one location. First the average CDR over all locations is calculated, and then the three regional

dipole waveforms are calculated. This is especially useful with the **Pass/Stop/Segmentation Result** choice of binary overlays options.

Left Regional Average and **Right Regional Averages** may be computed separately. These are typically used when segmentation of bilateral structures using the atlas has been done, and where the interest is on one side or the other.

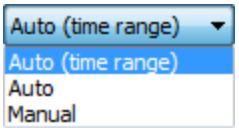
Fixed. The Fixed option is similar to the others, except only the strongest waveform is shown. This option is only for backward compatibility. It used to be the suggested option in Curry 7, because (unlike Moving/Rotating) it shows a positive/negative waveform.

Advanced
The Advanced section can generally be ignored, especially if you are using the upper group of CDR methods. When it is needed (e.g., LORETA and Lp Norm), the Advanced section will open automatically. Generally, these options are used only by very advanced users or those with especially difficult to analyze recordings (like high noise).

Component-Based. This option is used when performing PCA or ICA based source reconstruction; it is the CDR counterpart to PCA/ICA dipoles. When enabled 

, the analyses are restricted to the selected components in **Maps**, which significantly speeds up CDR calculations for large timeranges.

Regularization. **Auto (time range**) is the default (in previous versions of CURRY). A best value of lambda for the whole Timerange is found and used.



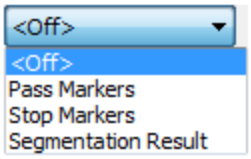
This option is faster than **Auto**, where one value of lambda per latency is used. **Auto** regularization means that the CDR algorithm used tries to achieve a given goodness-of-fit. Auto is the same as performing an independent CDR for each sample consecutively. For MNLS, sLORETA, SWARM, and L1 Norm, this is achieved in one iteration. For LORETA and Lp Norm, a converging approach is pursued and the **Restart** button may need to be pressed, depending on the discrepancy between achieved and computed goodness-of-fit. In order to achieve fast regularization convergence for Lp norm and LORETA, perform a Minimum Norm CDR with p = 2 for the Timerange of interest first. This will initialize lambda to a meaningful value. **Manual** regularization means that the used value of Lambda is specified.

Relative Deviation. [%]. The **Relative Deviation** is the desired goodness-of-fit, measured in percent of the optimal value, which is 1/SNR. This parameter should normally be set to 100. In the result log, the achieved relative deviation can be seen. In some instances, it may be useful to increase the value to, for example, 200% or greater. The effect this has is, in essence, to "spatially filter" out lesser features and focus more on more major features (as can be seen in the 2D Maps topography).

Used Lambda. In **Manual Regularization** mode, this is the regularization parameter. In **Automatic Regularization** mode, this is the recently used regularization parameter.

Fitted Lambda. This is the value of lambda that is necessary to achieve the desired **Relative Deviation**. After each source reconstruction, this parameter is estimated based on the achieved and the desired goodness-of-fit. In **Automatic Regularization** mode, this is the regularization parameter.

fMRI Hotspots. In CURRY 8, there is a dropdown with many choices, including Pass Markers, Stop Markers, and Segmentation Results. At these locations, an increased source probability is assumed. In other words, it is possible to constrain, or to give different weights, or hints to the current density calculations regarding the expected location of the activity in the brain. For example, if you place Stop Markers in the Image Data, and then select Stop Markers from the list, the analyses will, to the extent possible, place the source of the activity where the hot spots (Stop Markers) are (see the **Weighting** section next). In addition to Stop Markers, you may use any of the markers or results listed. See the *fMRI Weighting* tutorial for an illustration of the use.



Weighting. **fMRI Weighting** can be used to emphasize or suppress locations that are to be used for current density reconstruction based on **Image Data** information. The **Image Data** image itself (containing, e.g., an fMRI activation map), as well as information derived from an image (surface, volume, stop or pass markers) can be used to deduct weights.

This weighting of locations is implemented in addition to depth weighting. Weights are normalized and multiplied with the depth weights determined as a part of leadfield setup. A setting of 100% means to ignore the hot spots. If this value is different from 100%, the source locations specified as hotspots will obtain a higher (>100%) or lower (<100%) weight than unmarked locations, which effectively modifies the probability of source activity at that location. Very high percentages (up to infinity) mean do not place any results outside of the hot spots. Low percentages mean to place everything outside of the hot spots.

Large weights will increase the probability of a location carrying source activity by producing a smaller model term compared to unweighted or downweighted locations. A reasonable value for fMRI Weighting is 140% (default) for locations near hot spots (and 100% for all other locations).

For fMRI-weighting, perform a threshold segmentation of the hotspots, and dilate (inflate) the segmentation result. Then, select Segmentation Result 2 as the hotspots (assuming fMRI is Image Data 2) and set the weighting to 140%.

fMRI-constrained CDR is described here and here.

[Wagner M, Fuchs M, Wischmann H-A, Köhler T, Theißen A, and Willemsen S. fMRI-constrained source reconstructions, Recent Advances in Biomagnetism, Tohoku University Press, Sendai 1999, 137-140.]

[Wagner M and Fuchs M. Integration of functional MRI, structural MRI, EEG and MEG, Int. J. of Bioelectromag, 2001, Vol 3 (1).]

Lp Norm Model, Data. These are the parameters for the Lp Norm model and (for several of the models) data terms. Lp Norm with both of these values set to **2** is the same as Minimum Norm Least Squares (MNLS). Smaller values of p give more focal results.

L1 Norm Limit (0=off). For the **L1 Norm**, an upper limit for the reconstruction current densities can be imposed. This upper limit is measured based on a typical cortical current density of 0.25μAmm/mm3 (100%). If set to zero, no limit is used.

Restart. The 

button restarts the CDR analysis if **Used Lambda** and **Fitted Lambda** are different. This may be necessary for **LORETA** and **Lp Norm** (or **Manual Regularization** Mode). In order to achieve fast regularization convergence for Lp norm and LORETA, perform a Minimum Norm CDR with p = 2 for the Timerange of interest first. This will initialize lambda to a meaningful value (see **Regularization** above).

For more information regarding CDRs, see the **Distributed Source Models** section below.

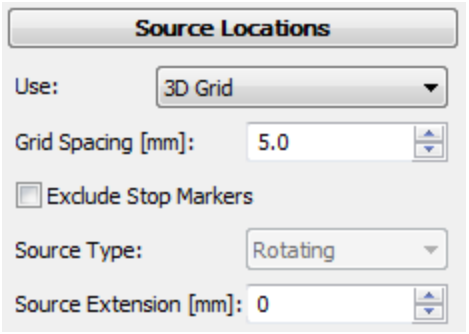
Please see also the *Current Density Reconstruction* tutorial for an example using CDRs.

19.1.5 Source Locations

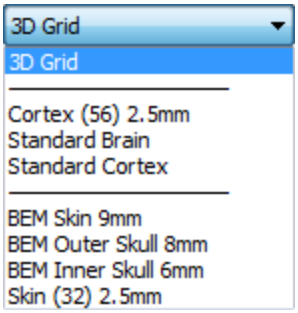
Distributed source models are characterized by the source locations given in advance, either as a 3D grid, as points, or as a mesh created in Image data. (This also has the effect that the leadfield matrix remains the same throughout the fit).

Source Locations let you select which surface and source type (fixed or rotating) to use. If you have not created points or other surfaces, you may use the 3D Grid or Standard Cortex. If you have created the standard BEM/FEM Realistic Head Model (as with 

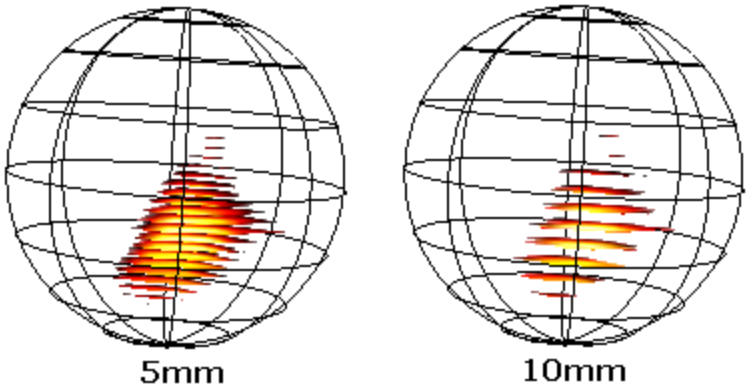
), the cortical surface will be available.



Use. The 3D Grid and Standard options are always available; the other options depend on what you have created (all triangle meshes and points files stored in the MR data file folder will be displayed). The items below the second section are only included for completeness, they usually should not be used.



Grid Spacing [mm]. This parameter defines the 3D Grid source locations. A typical value is 5 to 10mm.



Exclude Stop Markers. If Stop Markers are present in Image Data 1, they can be excluded by enabling this option.

Source Type. Select either a **Rotating** or **Fixed** source. If you select **Rotating**, no orientation information is taken from the given source locations. Rotating allows source orientations to adapt so that the data are best explained. **Fixed** forces source orientations to align with the triangle mesh or point normals (not available for 3D grids). For planes, this is the orientation perpendicular to the plane.

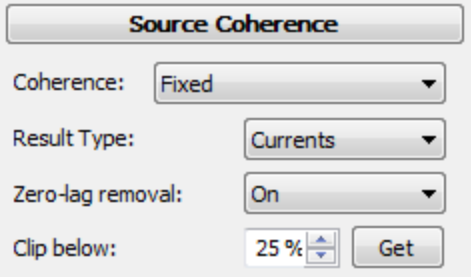
Source Extension [mm]. If the source extension is larger than zero, extended source patches are reconstructed instead of dipoles. This makes sense since cortical activations as measured with the EEG or MEG are always extended. The option should be used with the **Fixed** Source Type and cortical triangle meshes only.

For a description of extended sources, see here.

[Wagner M, Köhler T, Fuchs M, and Kastner J. An Extended Source Model for Current Density Reconstructions, in: BIOMAG 2000, Helsinki University of Technology, Espoo 2001, p749-752.]

19.1.6 Source Coherence

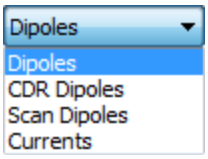
Coherence, or sensor coherence as it is sometimes referred to in CURRY, is a correlational measure between pairs of electrodes, based on the EEG data. Source coherence, as implemented in CURRY, is a postprocessing tool for source analysis results that tells you if a *source waveform* is similar in shape to another *source waveform*, but shifted in time. As with Coherence, the direction of the lag is shown by the arrows (points to the later site). Source coherence can be used for any type of source analysis results. It is intended mainly for use with fixed dipoles and CDRs computed on low-res 3D Grids (15mm or above). See the *Source Coherence* tutorial for an example.



Coherence. Select either **Fixed** or **Rotating** dipoles. If you compute coherence for **Rotating** sources (with all-positive waveforms), the quality of the results is reduced and the coherence values are generally higher. The **Fixed** mode computes (per location) the dominating orientation using an SVD, and feeds a projection of dipole moments onto that orientation into the coherence calculations. These strengths are positive/negative, which can easily be verified because the same algorithm is also available in several CDR dipole options, such as **Cursor fixed** and **Localize fixed**.

MATLAB options. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

Result Type. Select the type of result you wish to use (which have been computed).



Dipoles. These are the Fixed or Rotating dipoles created under Dipole Fit.

CDR Dipoles. These are the CDR Dipoles that are created in the CDR Dipole Type under Current Density.

Scan Dipoles. These are the Fixed or Rotating dipoles created under Scan Methods.

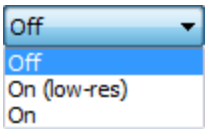
Currents. These are the CDR currents created under Current Density. If Current density has calculated too many currents (for example, because you performed a cortical CDR), you can either:

1) use a 3D grid with 15mm or more instead as the source locations, or

2) compute CDR dipoles in Localize mode, with a 15mm (or more) 3D grid defined in Localize's Grid setup options using the 3D Grid type.

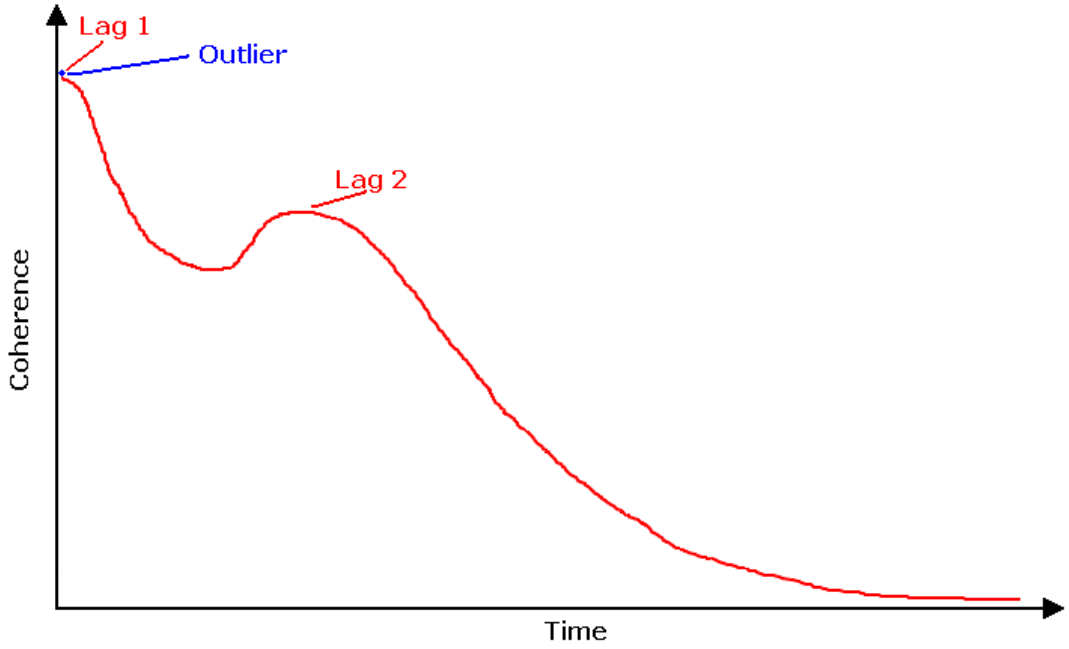
Either way, the number of locations used for the coherence calculations will be reduced.

Zero-lag removal. There is one step in the coherence analysis where the curve is coherence as a function of the lag, and this curve is analyzed per coherence arrow in order to find the coherence/lag pair that this arrow shall represent.



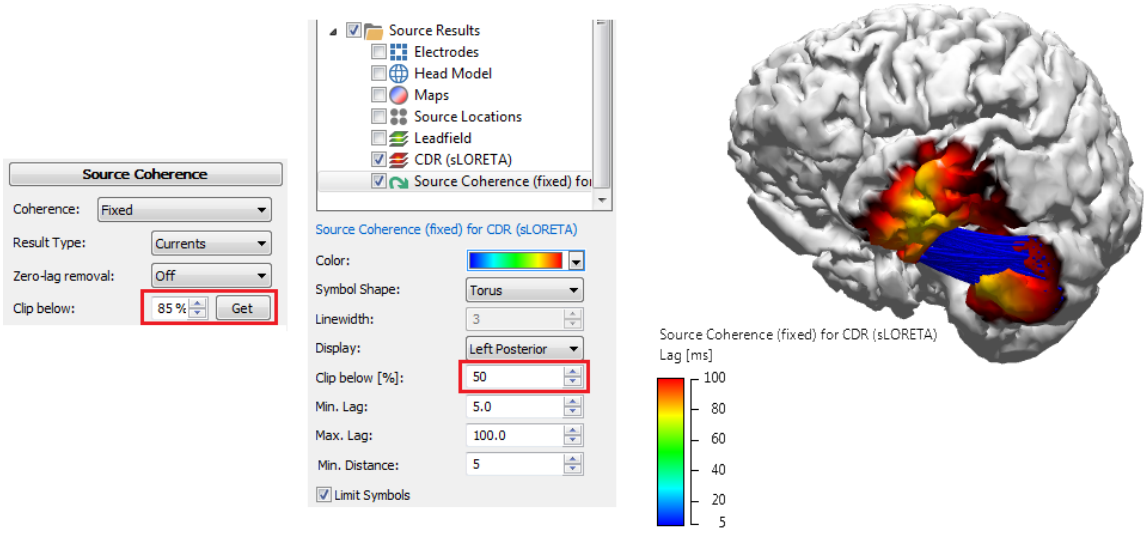
With Zero-lag removal switched off, the coherence value and lag determined for a given pair of source locations and used for display are the largest coherence (as a function of the lag) and the corresponding lag. Often, a lag of zero yields the largest coherences. This is the case if the same source waveform occurs at both locations. With zero-lag removal activated in low-res mode, CURRY ignores a coherence maximum for a lag of zero and searches for a secondary maximum instead. With zero-lag removal activated, this search for a secondary maximum uses a smoothed coherence(lag)-function.

Imagine the curve has a maximum at sample #2 (where the curve includes or goes through the Outlier blue dot). Without Zero-lag removal, the lag of the blue dot is used (the maximum). With Zero-lag removal (low-res), the lag of the blue dot is used (Zero-lag is ignored; largest maximum besides zero-lag is found - which is the blue dot). With Zero-lag removal (**On**), lag 2 is used (the Zero-lag and the blue outlier are ignored). if the curve has no second maximum (monotonically decreasing), Zero-lag will be found in all modes.



Clip below. Sources with strengths below the Source Coherence clipping threshold are not considered for coherence analysis. The **Clip below** threshold determines the absolute value of the source waveforms relative to the maximum value (percentage of the maximum source strength) of the source waveforms that is accessed by the coherence analysis, thus, small sources can be ignored. Click the **Get** button to initialize the threshold with the one that is currently used for the result. For example, if you are using CDRs, and have the Clip Below value for the CDR set to 50%, pressing Get will transfer the 50% to the Clip below value for Source Coherence. Links will not be displayed if the CDR strength is below 50%, in this example.

Below, the **Clip below** value for CDR (sLORETA) was set for **85%** (not shown). Only currents larger than this threshold are used in the coherence calculations. The **Get** button under **Source Coherence** was clicked to apply that threshold for the links that are displayed. The **Clip below** threshold for **Source Coherence** clips the display of the links based on their correlation values.



Please see the *Source Coherence* tutorial for more information.

19.1.7 Source Reconstruction in Detail

It is important to realize which kinds of information affect source reconstruction. These are:

- The measured data and their SNRs.
- Sensor locations. Sensor locations are part of the forward model. They can also be used to fit a spherical head model.
- Anatomical information. Anatomical information can be used to define the head model as well as the initial, the allowed, and the preferred source locations.
- The expertise of the user. It is reflected in the choice of data preprocessing and time ranges, the forward model, the source model, and its initial parameter estimates.

In the following, the steps mentioned above are described in more detail.

The Forward Model

The classic model for currents in the human body is the so-called *equivalent current dipole*. It comprises a short, thin current path (impressed current) and the return currents in the surrounding material (volume currents).

The volume currents depend on the conductivity of the surrounding head model and can be described by the formula $jV = \sigma E$, where jV is the current generated, σ is the electrical conductivity of the tissue, and E is the underlying electrical field.

Any biological current distribution can be seen as an overlay of current dipoles. If the conductivity and geometry of the head model are known, it is possible to calculate the potentials at all locations, thus also at the sensor positions. Once the potentials are known, the corresponding magnetic fields can be derived as well.

Spherical Head Models

If concentric spheres of isotropic, homogeneous conductivities are used as the head model, comparatively simple formulae can be found.

Performance
This head model allows fast forward calculations.

Accuracy
Spherical models are not accurate for sources in large parts of the head due to their oversimplifying assumptions.

Spherical models are adequate, if
- Quick, qualitative results are desired, or
- Sources are located in spherically shaped regions of the head, as is the case for superficial parietal sources, for example.

They are inadequate, if
- Exact results shall be obtained, and
- Sources are not located in spherically shaped regions of the head. Near lesions and deep, frontal, basal, lateral, or occipital sources are examples where the spherical models would be inadequate.

CURRY supports spherical models with up to four concentric shells for EEG evaluations, and a sphere model that is optimized for MEG data alone.

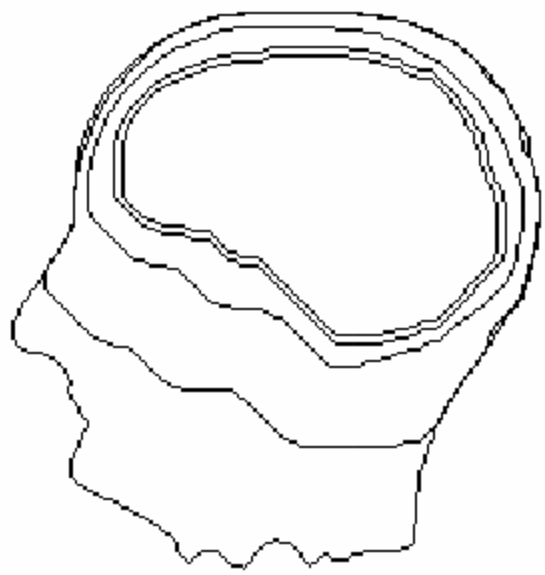
Eccentricity Correction
CURRY supports eccentricity-corrected spherical models: Here, the eccentricity of a source relative to an overlay is used for determining the source's location in the sphere.

Realistic BEM Head Models

If non-intersecting, closed surfaces separating compartments of isotropic, homogeneous conductivities are used as a head model, the Boundary Element Method (BEM) can be used for forward modeling. Surfaces are described in terms of triangle meshes. In most cases, three triangle meshes suffice, modeling the surface of the skin, the outer skull surface, and the inner skull surface. CURRY can store up to ten BEM Realistic Head Models per subject.

Accuracy
Realistic head models are more accurate in the case of realistic anatomies. Accuracy and computational demands for a BEM Realistic Head Model rise with the number of nodes. The number of nodes (triangle vertices) in a model is about half the number of triangles. The Isolated Problem Approach (IPA), virtual triangle refinement, and a spherical ansatz are methods to increase accuracy for a given number of nodes.

The figure presents a schematic representation of a realistic head model. A sagittal view of the three compartments of the BEM Realistic Head Model is shown. The outermost line shows the segmented skin surface for comparison, while the innermost line delimits the source compartment, where the sources should be confined when the BEM Realistic Head Model is used.



EEG

All relevant compartment borders have to be included in the BEM Realistic Head Model, as only the effects of secondary currents are measured.

MEG

In most cases, it is sufficient to set up one-compartment models describing the inside of the skull only, as the corrections due to the comparably small secondary currents outside this surface can be neglected.

Isolated Problem Approach

The Isolated Problem Approach (IPA) is applicable if a layer of relatively low conductivity exists. This is the case for the skull. The subproblem for the currents inside this surface is solved separately and then overlaid to the solution of the full problem, resulting in a numerically more stable formulation of the problem.

Virtual Triangle Refinement

Virtual triangle refinement splits each original triangle into four subtriangles. It adds accuracy in two important steps of the BEM computations without changing model size:

- The computation of the solid angles, i.e., the angles under which triangles 'see' one another.
- The computation of the discretized potential distribution over each triangle.

Performance

Forward calculations using BEM Realistic Head Models are slower than spherical models by a factor of about 100. The setup time for BEM Realistic Head Models is in the order of several minutes, if the BEM matrix fits into main memory. For larger models, performance decreases due to paging.

- Accuracy increases with the number of nodes.
- Forward calculation time rises linearly with the number of nodes.

- Setup time rises with the second (full matrix setup, see below) and third (full matrix decomposition) powers of the number of nodes.
- Memory requirements during setup rise quadratically with the number of nodes.
- Setup time rises if the model size exceeds the amount of RAM available.

Geometry Description and Transfer Matrix

A BEM Realistic Head Model can be defined and stored in one of two ways:

- The geometry description alone.
- The geometry description plus the transfer matrix.

The geometry description comprises the surfaces and conductivities which make up the BEM Realistic Head Model, along with some parameters to be used for setup, e.g., whether or not IPA is to be used. The geometry description uniquely defines a BEM Realistic Head Model. The transfer matrix describes the relationship between any source and a given sensor array and is normally stored as 'the' BEM Realistic Head Model. Once sensor locations change, the transfer matrix becomes invalid. CURRY can handle the case of superfluous sensors in the transfer matrix.

To compute the transfer matrix, the full matrix has to be set up and decomposed. The full matrix is much larger than the transfer matrix. It is not possible to store the full matrix on hard disk.

Model Geometry

In order to determine the adequate model geometry, the following criteria have to be kept in mind:

- The compartment borders will match anatomy as closely as possible, at least in the vicinity of the sensors and the sources. Basal regions are in most cases less important.
- Accuracy decreases if sources are closer to a compartment border than about half the triangle size.
- Accuracy decreases if boundary surfaces are separated by less than about one third of the triangle size.
- Accuracy decreases if EEG electrode locations do not coincide with skin compartment nodes.

From these considerations it follows as a rule of thumb that a practical model should fulfill the following demands:

- Triangle size is 7 to 10 mm for the brain compartment, and slightly larger for the skull and skin compartments.
- Compartments are smooth with respect to their triangle sizes.
- Compartments have minimum distances of 3 to 4 mm.
- Compartments follow anatomy as closely as possible with regard to the previous criteria.

Such a model would comprise about 3000 nodes, and have a setup time in the order of minutes.

The following table presents the BEM Realistic Head Model geometry parameters for an ~3000 nodes model.

Compartment	Triangle Size	Thickness	No. Triangles	No. Nodes
Liquor	8 mm	4-5 mm	2400	1200
Skull	10 mm	6-8 mm	2000	1000
Skin	12 mm	6-8 mm	1600	800

The following table presents the BEM Realistic Head Model geometry parameters for an ~4000 nodes model.

Compartment	Triangle Size	Thickness	No. Triangles	No. Nodes
Liquor	7 mm	4-5 mm	3000	1500
Skull	9 mm	6-8 mm	2200	1100
Skin	10 mm	6-8 mm	2400	1200

The total time needed for the preparation of a BEM Realistic Head Model is the sum of setup time and decomposition time. Up to several thousand nodes, setup times dominate. Setup times depend quadratically on the number of nodes, while decomposition time depends cubically on the number of nodes.

Care
3000 nodes (Low Resolution) is the minimum for a three-compartment BEM Realistic Head Model. 4000 (medium) or 5000 (High) nodes are more favorable and should be used whenever possible.

Automated Segmentation Routine
CURRY's automated segmentation routine generates a model that obeys the demands stated above. In its initial section, variables control triangle sizes and compartment distances. These can be changed by the user to match specific needs.

Realistic FEM Head Models

Unlike BEM models, where the electrodes are projected to the outermost surface, FEM models have nodes inside the head. This means 1) that you can localize sources within the brain, using depth electrodes, and 2) that it takes longer to compute the models. Instead of thousands of elements in the BEM model, the FEM model may have millions.

FEM models are created much like BEM models are, using the BEM/FEM Geometry parameters. The Intracranial Head Model (Intracranialtaxic, or depth electrode EEG) can only use the FEM model (only the inner skull compartment is created). A medium resolution (4mm) is recommended for exploratory source analyses to reduce the computation time (2mm is state of the art). Currently, the resolution is the same throughout all compartments, while this may change in future versions. In a 4mm FEM model, the 4mm is the length of the sides of the tetrahedra. The Output display give the relevant information, including the number of compartments, the number of nodes, and the number of tetrahedra.

For advanced users, you may also create a FEM model using the FEM Model parameters. The process is very similar to the BEM Model parameters, with the exception of the Sensor Type and Dipole Model. FEM models are primarily used with Intracranial-EEG; Intracranial-EEG must always use FEM models. Intracranial-EEG has electrodes inside the volume; whereas, EEG uses electrodes that are projected to the surface (as with BEM). Dipoles models are the way dipoles are represented in the FEM model. There are two dipole models, **Venant** and **Subtraction**. Venant (blurred dipole) is chronologically older and represents a dipole by placing monopoles in the neighboring nodes closest to the dipole position. Subtraction takes the analytical infinite homogeneous solution as basis for representing the dipole singularity, and makes use of a correction potential by means of numerical integration to account for the individual conductivity profile in the model. While Subtraction has shown higher accuracy in some scenarios, Venant has proved to be a more practical approach due to its computational performance [1].

CURRY's FEM engine is based on the SimBio software package [2].

[1] Vorwerk J. ”New Finite Element Methods to Solve the EEG/MEG Forward Problem”, PhD thesis, Westfälische Wilhlms-Universität Münster, 2016.

[2] SimBio Development Group. *"SimBio: A generic environment for bio-numerical simulations"*, online, https://www.mrt.uni-jena.de/simbio.

Generally, BEM models are better; they are faster, more stable, and more accurate. In later versions, the anisotrophy of the bone and white matter may be added, which will make the FEM models more advantageous.

The Source Model

A source model is a configuration of generators, which makes sense for the given data. It is the responsibility of the user to choose an adequate source model, and it is the task of CURRY to find the free model parameters that best match the data.

Source models are defined by:
- the number of dipoles,
- the temporal characteristics of the dipoles,
- the dipole locations, and
- the dipole strengths.

For given source locations, a leadfield matrix *L* can be set up, which links the dipole component vector *j* (unit: μAmm) with one row per dipole component, and the forward calculated data vector *mf* with one row per sensor:

$$m_f = Lj$$

It can be seen that the relation between *j* and *m* is of a linear nature for given *L*. When source locations change, a new leadfield matrix has to be set up. Each dipole location can have up to three dipole components and thus correspond to up to three rows of *j* and columns of *L*.

When CURRY tries to find the optimal source model parameters, the variance, i.e., the squared deviation Δ2 between measured data *m,* and forward calculated data is taken

into account (and normally minimized). It is computed as the sum of squares of the misfits per sensor:

$$\Delta^2 = \|m_f - m\|^2 = \|Lj - m\|^2$$

Note
All data vectors *m* and *mf* as well as the leadfield matrix *L* are set up for SNR-transformed data, i.e., their entries are in units of SNR.

Depending upon which source model parameters are given and which are free, a variety of possible models emerge, which can be divided into two classes: dipole models and distributed source models.

Dipole Models

Dipole models are made up of a small number of dipoles, which hardly ever exceeds ten. Each dipole is characterized by six parameters per timepoint, namely its location and its components. In the magnetic case and if a spherical head model is used, the number of parameters is five, as only the two tangential dipole components have an effect upon the magnetic field.

Single Dipole Models

The simplest dipole model is the *single equivalent current dipole*. Its three location parameters are fitted, and its two or three components are determined for a given timepoint so as to minimize the deviation between measured and forward calculated data.

An extension of the single equivalent current dipole is the *moving dipole*: Its three location parameters per timepoint are fitted, and its two or three components are determined for each in a series of timepoints.

If the location of a moving dipole is held fixed over time, we get the *rotating dipole*: Its location is jointly fitted for all timepoints, while its two or three components are determined for each timepoint independently. Rotating dipoles whose location is not fitted but specified by the user are also possible. If the location and orientation are kept fixed, we have a *fixed dipole*: Location and orientation are jointly fitted for all timepoints, while for each timepoint the dipole strength is determined only. Fixed dipoles where location and possibly orientation are provided by the user are also supported.

Dipole Constraints

In addition to the requirement that the dipoles to be fitted shall explain the measured data, further requirements can be imposed. These are called constraints, and their purpose is to make the dipole fit more stable and its result more reasonable in certain situations.

CURRY supports several types of dipole constraints, some of which have already been mentioned:

- The dipole location does not change over time (rotating dipole).
- The dipole location and orientation do not change over time (fixed dipole).
- The locations of two dipoles are mirrored with respect to the midsagittal plane (*mirrored dipoles*).

– The sum of squares of the dipole contributions is maximized. Maximization is performed along with the minimization of the data misfit, and the two are linked using *regularization* (see below).

Dipole Component Regularization
Regularization is a method which adds a second term to the misfit term in a weighted fashion. The positive weighting parameter λ is called the regularization parameter. We get an extended variance $\Delta 2$ which reads

$$\Delta^2 = D(j) + \lambda M(j)$$

with a data term

$$D(j) = \|Lj - m\|^2$$

and a so-called model term *M(j)*. The minimization of the combined expression guarantees closeness to the data *and* a small model term. Depending on the formulation of the model term, various constraints regarding the sources can be realized.

Regularization is used in all distributed source models, where a variety of model terms is offered (see below). For dipole component regularization, the model term is

$$M(j) = \|Rj\|^2$$

with

$$R = WV^T$$

The diagonal matrix *W* and the Rotation *VT* are defined via an SVD of the leadfield matrix *L*:

$$L = U\Sigma V^T, w_i = \sigma_i / \left(\sqrt{\sum_{t=1}^{N_t} m^T(t) U_i U_i^T m(t)} \right)$$

It assures that only dipole components are reconstructed that explain a significant portion of the data. To understand this concept, one must keep in mind that there exist sources or source configurations that hardly generate any data. Prominent examples are close, opposing dipoles or nearly radial sources in the MEG case.

Optimization
An optimizer finds the parameter constellation which minimizes $\Delta 2$ and gives the optimal source configuration as a result. CURRY uses a nonlinear simplex algorithm for fitting source locations, while the best-fit dipole components are computed analytically.

Dipole Scans

On the other hand, it is possible to explicitly scan the parameter space. This approach is called *Dipole Scan* or *Deviation Scan*. For a one dipole model, this would mean to compute for each possible source location the best fitting dipole components and the misfit $\Delta 2$. The result is the dipole fit's error hypersurface. It allows you to estimate regions of confidence, i.e., the regions where a dipole would explain the data well enough. For models with more than one dipole, each location is assigned the lowest misfit $\Delta 2$ that a dipole pair/triple/... involving this location can achieve.

Dipole scans work on a predefined set of locations, thus scanning can be constrained to certain regions, e.g., the cortical surface. It can additionally be restricted to predefined orientations.

Performance

For more than one dipole, the computational complexity explodes. It is proportional to $\binom{N_l}{N_d}$ with *Nl* the number of scanned locations and *Nd* the number of dipoles.

As the candidate locations are known, the leadfield matrix can efficiently be precomputed before scanning starts.

Multiple Signal Classification

Multiple Signal Classification (MUSIC) is a scanning method which does not compute the misfit of a given dipole model per location, but a specific MUSIC metric:

$$\Delta^2 = \frac{1}{\lambda_{min}(U^T \tilde{U}_m \tilde{U}_m^T U)}$$

with $\lambda\min(X)$ the minimum Eigenvalue of the matrix *X* and the SVDs of the one-dipole leadfield matrix *L* and the spatiotemporal measured data matrix *m*, respectively:

$$L = U\Sigma V^T \text{ and } m = U_m \Sigma_m {V_m}^T$$

The signal subspace is associated with the leading singular values of *m*. *Um* stands for the subspace orthogonal to the signal subspace and is associated with the trailing singular values of *m*. The number of singular values that make up the signal subspace is a parameter of the method.

This metric peaks at the locations of multiple, non-coherent i.e., temporally independent, sources for a given time range in just a single scan.

The Fixed (MUSIC) algorithm is very similar to the RAP MUSIC approach (*JC Mosher, RM Leahy: Recursive MUSIC: A Framework for EEG and MEG Source Localization, IEEE Trans Biomed Eng 45, 1998, 1342-1354*), combining an iterative SIMPLEX minimization using the MUSIC metric and the projection of the already found sources from the data and the lead-field matrix (*JA Nelder, RA Mead: A simplex method for function minimization. Comput J 7, 1965, 308-313*). (See also *JC Mosher, PS Lewis, RM Leahy: Multiple Dipole Modeling and Localization from Spatio-Temporal MEG Data, IEEE Trans Biomed Eng 39, 1992, 541-557*).

Distributed Source Models

Distributed source models or current density models are characterized by two properties:

- The source locations are given in advance, either as a 3D grid or as a surface. This has the effect that also the leadfield matrix *L* remains the same throughout the fit.

– There is always a model term *M(j)* and a regularization parameter λ by which it is linked to the data term *D(j)*.

$$\Delta^2 = D(j) + \lambda M(j)$$

The model term is necessary because there are so many source locations that the problem would otherwise have no unique solution due to the large number of free parameters. If source orientations are free, there are three unknown dipole moments per location. If source orientations are fixed, e.g., to be perpendicular to the source surface, there is one unknown dipole component or strength per location. (For a comparison of CDR methods, see *M Fuchs, M Wagner, T Kohler, HA Wischmann: Linear and non-linear current density reconstructions, J Clin Neurophysiol 16, 267-295, 1999*).

Dipoles and Current Density
Current density is defined as dipole moment per volume (unit: μAmm/mm3). A current density distribution is discretized into a large number of elementary dipoles. Each dipole represents the current density in a given volume *V*. The dipole moment is proportional to the current density that it stands for.

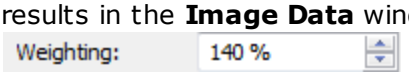
Minimum Norm Least Squares
For Minimum Norm Least Squares (MNLS), the source and model terms are given by

$$D(j) = \|Lj - m\|^2 \text{ and } M(j) = \|Wj\|^2$$

with a diagonal location weighting matrix *W* which can be defined in a variety of ways (see below). MNLS is a fast and straightforward method, which reconstructs source distributions that are artificially smeared (*JZ Wang, SJ Williamson, L Kaufmann: Magnetic source images determined by a lead-field analysis: The unique minimum-norms least-squares estimation, IEEE Trans Biomed Eng, 39, 1992, 665-675*).

Depth Bias Removal
MNLS and all other Distributed Source Models use a diagonal location weighting matrix *W* for depth bias removal. Different source locations have different gains, where the gain is the norm of the data generated by a unit dipole. Sources with low gain need larger currents to generate the same field strength as sources with high gain and are thus suppressed as the model term punishes overall source strength. Location weighting is used to remove the resulting bias towards high-gain locations, which are usually the superficial ones.

Explicit Location Weighting (fMRI Weighting)
In addition to depth bias removal, information about more and less probable source locations can be inferred. This information is derived from images or segmentation results in the **Image Data** windows of CURRY, in conjunction with the



option in the **Current Density** panel.

Explicit location weighting is the way to perform fMRI-, PET-, or SPECT-constrained current density reconstructions (see **fMRI Weighting** above).

Regularization

If the regularization parameter λ is very large in $\Delta^2 = D(j) + \lambda M(j)$, the model term dominates and large reconstruction errors may occur. If λ is very small, the data term wins, and chaotic source distributions are reconstructed which mainly explain the noise in the data. By choosing the correct value for λ, an equilibrium between goodness of fit and closeness to the model is achieved. CURRY offers the following method for determining the optimal value of λ using the χ2 criterion: The χ2 criterion relies on the assumption that a reasonable Δ2 is in the order of the amount of noise in the data. A user-defined multiplicative factor *f*, which is in the order of 1, can be used for fine-tuning. The regularization parameter λ is automatically changed until the χ2 criterion is met.

$$\Delta^2 = f\frac{1}{SNR}$$

sLORETA (standardized Low Resolution Electromagnetic Tomography)
sLORETA is a postprocessing of MNLS results that basically divides each current by the size of its associated error bar, yielding F scores of activation rather than current densities. It can be shown that sLORETA produces blurred but accurate localizations of point sources. See *Pascual-Marqui AD, 2002: Standardized low resolution brain electromagnetic tomography (sLORETA). Groupal & Clinical Pharmacology 24D, 5-12.*

Performance
sLORETA and MNLS compute very fast.

SWARM
SWARM is sLORETA-weighted Minimum Norm, yielding a current distribution instead of a statistical measure.

Minimum Lp Norm
While MNLS minimizes sums of squares, which corresponds to an L2 norm measure, the Lp norm with offers a range of measures. Smaller values of *p* have different effects upon the data and the model terms:

- In the data term, more robustness towards outliers is achieved. Outliers are errors not modeled by the estimated noise covariances, e.g., sensor mislocalizations or errors in the forward model.
- As to the model term, the artificial smearing introduced by the L2 norm is reduced.

CURRY supports Minimum Lp norm reconstructions with different values of p for the data and the model terms:

$$D(j) = \|Lj - m\|_{p_d} \text{ and } M(j) = \|Wj\|_{p_m}$$

Performance
Lp norm reconstructions cannot be implemented as efficiently as L2 norm reconstructional and are slower by a factor of 10 to 100. For smaller values of *p*, the method converges more slowly. The χ2 criterion can only be realized by successively repeating the method.

Minimum Norm
Minimum Norm computes Lp norms with the same value of p for the data and model terms:

$$D(j) = \|Lj - m\|_{p_m} \text{ and } M(j) = \|BWj\|_{p_m}$$

However, the $\chi 2$ criterion can be achieved automatically without repeating the method.

Minimum L1 Norm
Being a special case of the Lp norm family of source reconstructions with $p_d = p_m = 1$, L1 norm methods can be implemented using linear programming. This has several consequences for source reconstruction:

- The $\chi 2$ criterion can be built into the method and thus be achieved within a single step.
- Sparse source configurations are reconstructed where most source locations carry no currents.
- A maximum current density per volume of tissue can be taken into account.
- Rotating sources can only be taken into account in a discretized fashion and are not reconstructed optimally.

Performance
Although L1 norm reconstructions are faster than Lp norm reconstructions, especially for time ranges, they can become very slow if a large number of sensors is used, if a large number of source locations is used, or if rotating sources are allowed.

LORETA (Low Resolution Tomography)
Unlike sLORETA, LORETA (*RD Pascual-Marqui, CM Michel, D Lehmann: Low resolution electromagnetic tomography: A new method for localizing electrical activity in the brain, Int J Psychophysiol 18, 1995, 49-65*) uses a Laplacian model term. The Laplacian measures the second derivative of source strengths. This has the effect that neighbored sources tend to have similar strengths, and that smooth current distributions are reconstructed. LORETA works with

$$D(j) = \|Lj - m\|^2 \text{ and } M(j) = \|BWj\|^2$$

where *B* is the Laplacian coupling matrix. In the original implementation, LORETA uses a regular grid with 13 mm spacing. In CURRY, LORETA can be used

- on arbitrary regular grids. In this case, a spatial Laplacian is minimized, using a boundary condition that prefers smaller source strengths at the grid borders.
- on surface nets including the cortical surface. A surface Laplacian is used in these cases, and the vector average of source strengths is kept small.

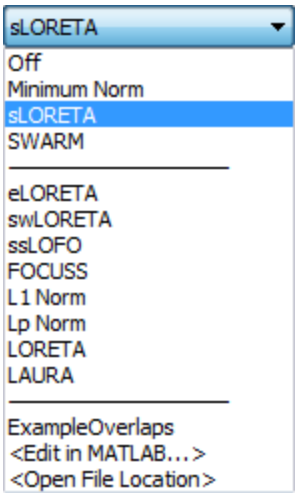
In addition, CURRY supports the Lp norm instead of the L2 norm for the LORETA data and model terms:

$$D(j) = \|Lj - m\|_{p_d} \text{ and } M(j) = \|BWj\|_{p_m}$$

This makes it possible to use LORETA with a robust data term and with a model term that induces less smearing than in the L2 version.

Performance
LORETA reconstructions use the same algorithm as the Lp norm reconstructions. They are slower, as, due to coupling, more constraints are present.

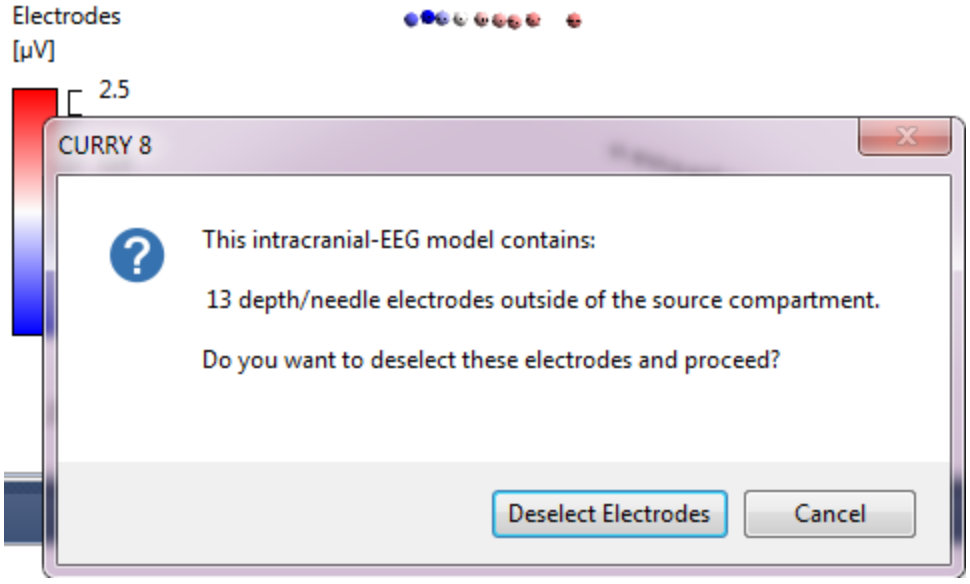
There are many more CDR algorithms in existence. Some, because of popular request, have been included in CURRY, and more may be added upon request. The current list is shown here, and also described, with references, in the **Current Density** section. As stated elsewhere, sLORETA is the algorithm we recommend for most uses. If you do not want a statistical measure and instead want a measure of current activity, use SWARM. Minimum Norm is another option, although its localization capability is not as good. The remaining options are included for historical reasons or, as mentioned, due to demand. You are encouraged not to use them unless you fully understand the algorithms.



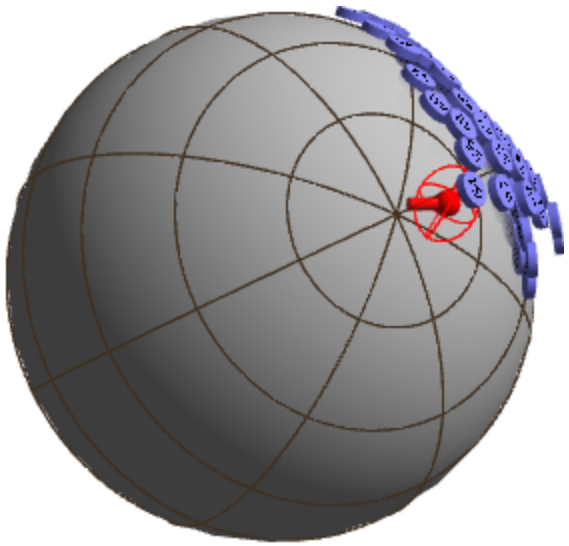
19.1.8 Selection and Projection with Intracranial Electrodes

In different situations, CURRY will deselect or project intracranial electrodes in order to attain valid source results, as described in the following examples.

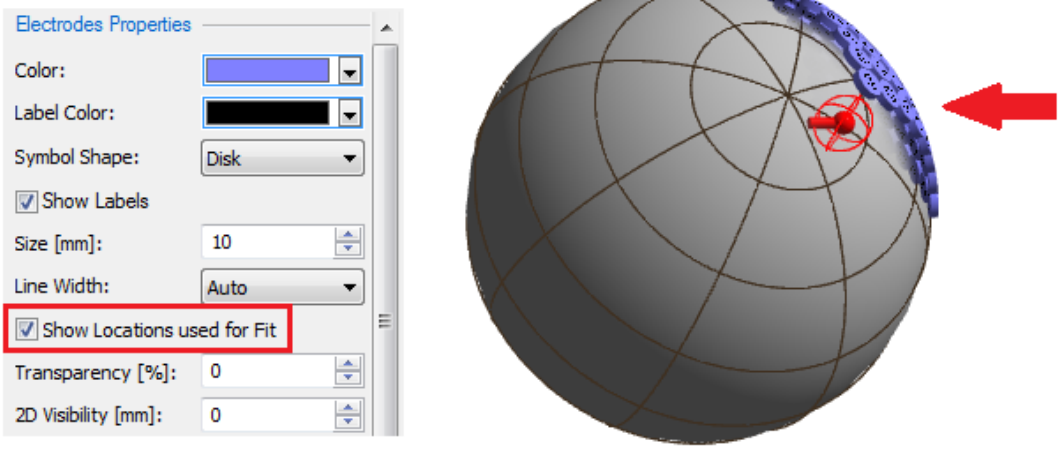
1. In this case we have depth electrodes, and we have selected the **Inside Sphere** head model. When we select a Dipole Type (Moving). CURRY will detect that there are depth electrodes (or grids/strips), and a message will appear. In this case, 13 depth electrodes are outside of the source compartment. Your only options are to deselect them (excluding them from the source analysis), or to **Cancel** and not do source reconstruction. After deselecting them the dipole will appear.



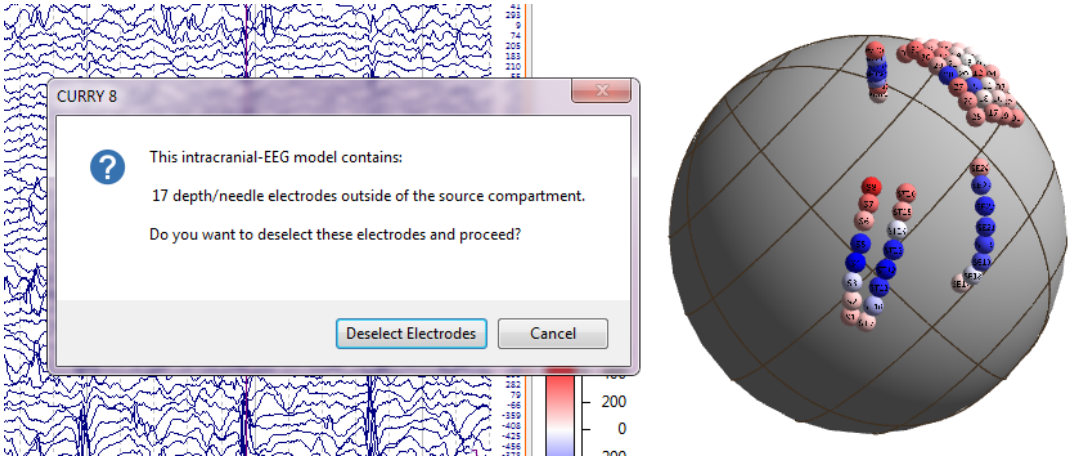
2. In the second example, we have grid electrodes, again with an **Inside Sphere** head model (which is selected automatically when depth electrodes are detected). Note that some of the electrodes are not on the surface of the sphere. When you select a Dipole Type, CURRY will detect that a grid/strip is present and project the electrodes to the surface of the sphere. The dipoles results will be computed.



The electrodes that are inside or outside the sphere are projected to its surface. To see them, enable **Show Locations used for Fit** in the **Electrodes Properties**.



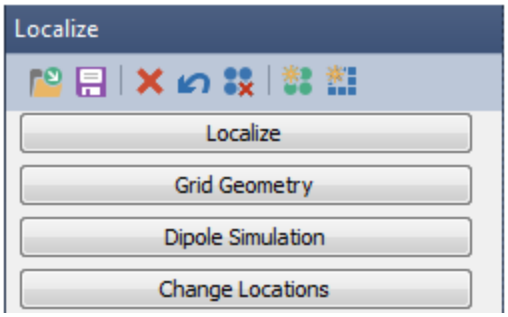
3. The third example combines both depth and grid/strip electrodes. CURRY will detect that this is an intracranial model and select the **Inside Sphere** model. In this case there are depth/needle electrodes that are outside of the source compartment. Select **Deselect Electrodes** to remove these and to continue. The grid electrodes will be projected to the surface, as in the above example. To see them, enable **Show Locations used for Fit** in the **Electrodes Properties**. The deselected electrodes will be seen in gray in the Functional Data display.



Should you need to remove individual electrodes manually, you may do so by using *Ctrl+Shift+click* on the electrode.

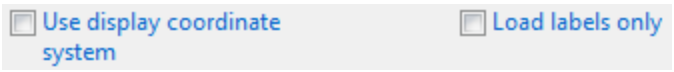
20 Localize

The Localize section of CURRY is a general purpose location editor. It is mainly used to position sensors (on the scalp or for grids and strips, define simulated dipoles, and specify CDR dipole locations). The results are saved sensor position files, which may be imported into the Functional Data Parameter Wizard.



At the top of the Localize display are several shortcut icons  .

Load  **.** Clicking this button loads a .pom file into the **Localize** mode. Select the **All Files** option for **Files of type** to see additional formats. On the Open File dialog, there are options to **Use display coordinate system** and to **Load** [Localize] **labels only**. If **Use display coordinate system** is checked, locations and normals in the file are interpreted to be in the current display coordinate system (as opposed to CURRY's internal coordinate system, or the coordinate system implicit to a CURRY-format file's transformation matrix). A typical application would be if you have an ASCII file with three columns x,y,z that you know to be in Talairach coordinates - in this case one would switch the coordinate system to Talairach, and check the box.



Save  **.** Clicking this button saves the .pom file. For generating anatomical localization files, use **Create and Edit Anatomical Localization** instead.

Delete All Entries  **.** Clicking this button deletes all entries in the Localize list. It has the same function as in the context menu.

Undo Last Edit  . Undo most recent edit (such as, repositioning an electrode).

Delete Localize Location  **.** Clicking this button deletes the most recent localize entry. It has the same function as **Delete Entry** in the context menu.

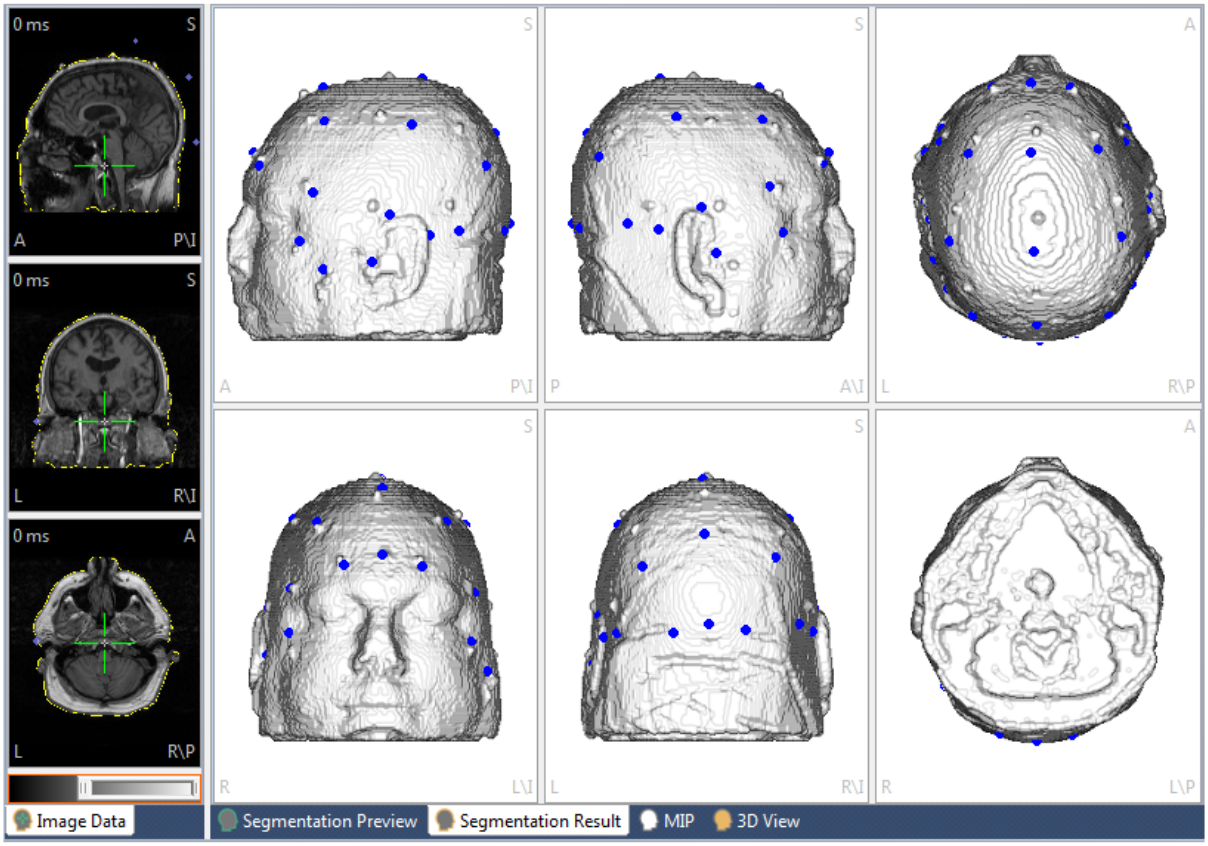
Create Points  **.** Creates an .sp**x** file containing the selected points in the Localize list, and displays the points file.

Save and Use as Digitizer File  . Clicking this button uses the entered locations as sensor (electrode) positions and modifies the current study. A Save As utility will appear, allowing you to specify the folder of the Database. After saving, the Functional Data Parameter Wizard opens. Click **Finish** in the wizard in order to use the new sensor locations.

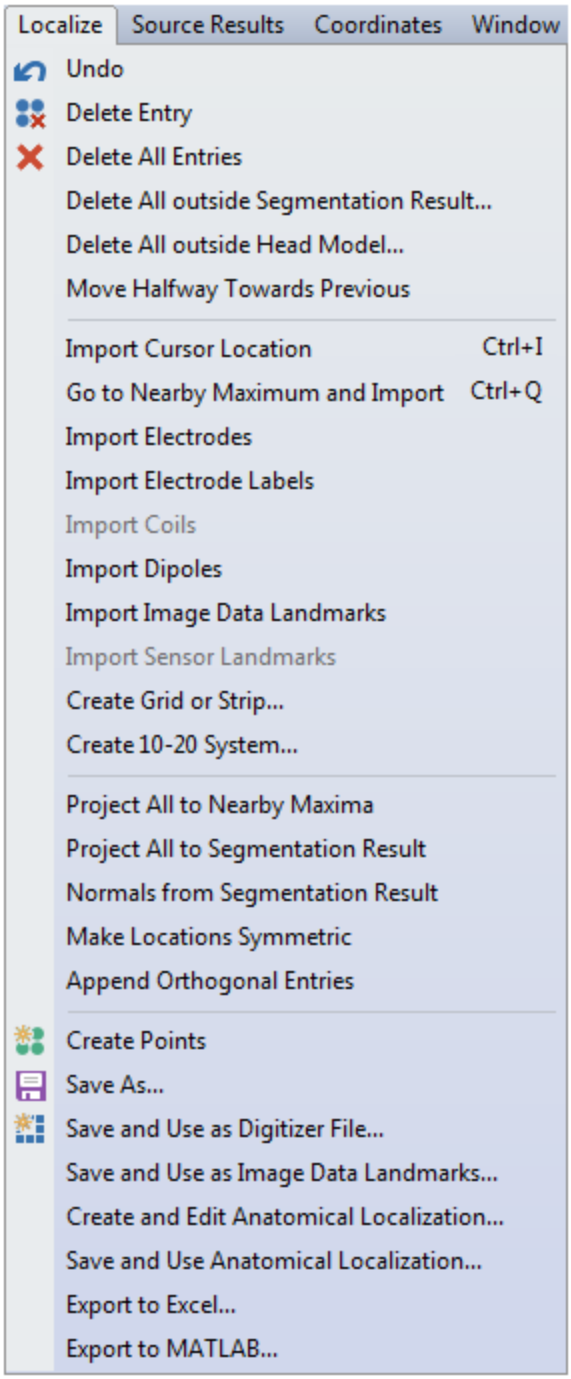
The Localize display is shown below, with the segmented Skin results.

The three orthogonal views from Image Data are shown on the left.

Six views of either the Segmentation Preview images or Segmentation Result image can be selected, using the tabs below the display.



These options are used in conjunction with the Localize display. See also the **Localize, Context Menu** for more information.

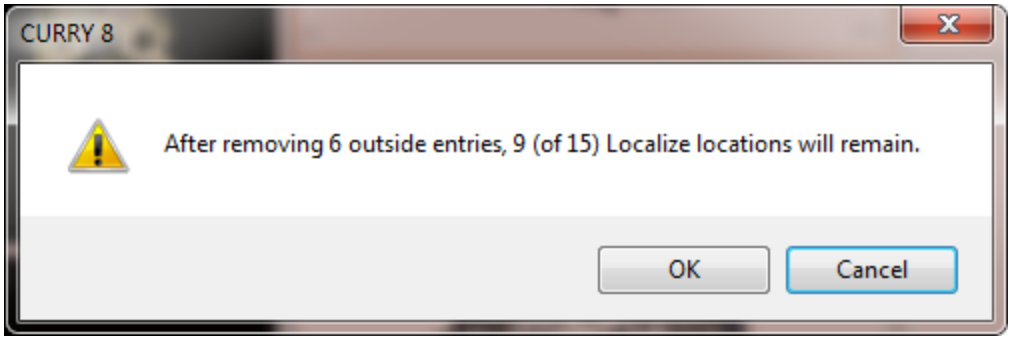


Undo . Undo last step or entry.

Delete Entry . Click this to delete the most recent entry in the list. Delete Entry is grayed out in Append Mode; deselect Append Mode to access Delete Entry.

Delete All Entries . All entries in the list will be deleted.

Delete All Outside Segmentation Result. If localize positions exist outside of the segmentation result, you may delete these. A message will appear telling you how many such positions were detected.



Delete All Outside Head Model. Locations outside of the head model will be deleted.

Move Halfway Towards Previous. When digitizing grid electrodes in Localize, sometimes an electrode cannot be seen. In this case, click the next electrode instead and select Move Halfway Towards Previous. The value of the estimated position will be entered into the list.

Import Cursor Location. Use this option to set the edited point to the 3D Cursor location. This is used to fill the Localize cells with information you might wish to work on (typically, modify).

Go to Nearby Maximum and Import. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, the **3D View**, click the border of the bright area, and this functionality brings the cursor to its center (this can be applied repeatedly).

Import Electrodes. Selecting this option imports the electrode positions from the digitizer file to the Localize panel, and displays the positions on the iso-images in the Localize display. For example, if we want to modify electrode locations, we can:

1) import them
2) change them (using the Change Locations parameter panel)
3) Save and use as Digitizer File.

Import Electrode Labels. The electrode labels from the open data file will be imported in the same order as they appear in Functional Data. These labels will replace the labels in the Localize matrix.

Import Coils. Selecting this option imports the MEG coil positions from the digitizer file to the Localize panel, and displays the positions on the iso-images in the Localize display.

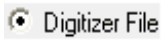
Import Dipoles. Selecting this option imports the dipole positions from the digitizer file to the Localize panel, and displays the positions on the iso-images in

the Localize display. Other source results can be imported by *right clicking* them in the results tree.

Import Image Data Landmarks. The anatomical landmarks that were determined when the image data were loaded are imported to the Localize list, and displayed on the Localize images.

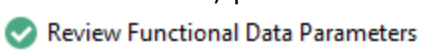
Import Sensor Landmarks. The anatomical landmarks that were digitized along with the sensor positions are imported to the Localize list, and displayed on the Localize images.

Create Grid or Strip. Opens the **Create Grid** panel. To define a grid, enter its four corner points (either clockwise or counterclockwise). To define a strip, enter its first, any intermediate, and its last point. Then, call the appropriate item of this submenu. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  .

Create 10-20 System. This option is used to create the positions of the extended 10-20 system. If electrodes with recognized labels are found in the study, you may choose to create their positions only. Otherwise, the ordering and selection of the positions is based on the **NUMBER_POM_xxx** entries in the Study Parameters file, if present, or the *GlobalParameters.cfg* file. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  . Then select the new .pom file for the 

. This option uses the **Image Data** segmentation result for measuring distances along a curved surface, so a skin surface (e.g., the **Skin overlay**) should typically have been imported first.

Project All to Nearby Maxima. Projects the locations onto the nearby maxima. Maxima are the centers-of-gravity of the spherical volumes around the **Localize** locations. A radius of 5mm is used.

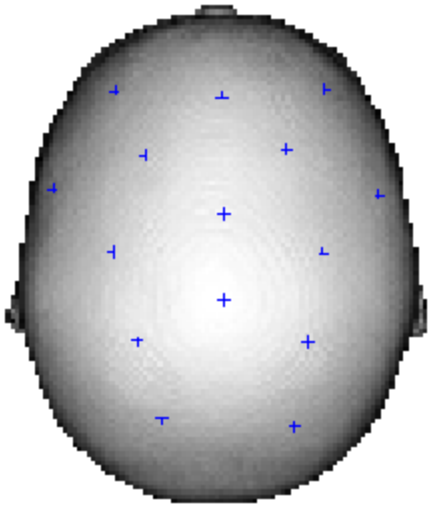
Project All to Segmentation Result. This option projects the locations onto the **Image Data** segmentation result, radially towards its center-of-mass. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  and select the 

option from the 

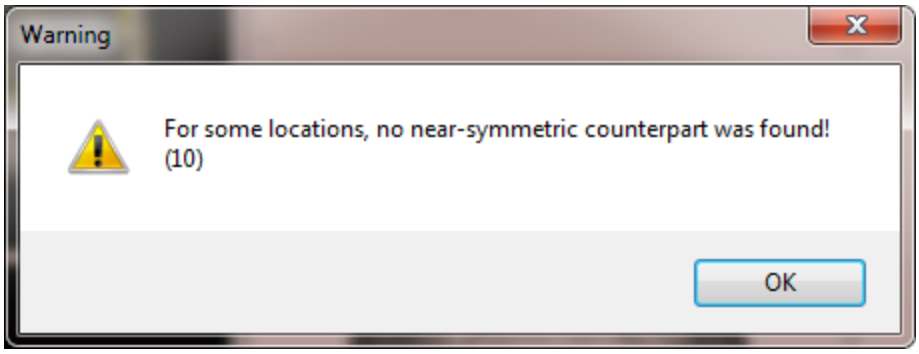
window. This option uses the **Image Data** segmentation result for projection, so a skin surface (e.g. the **Skin overlay**) should typically have been imported first.

Normals from Segmentation Result. The normals (nx, ny, nz) are replaced with those from the segmentation results (assuming locations were projected onto the segmentation result, but not actually changing the locations).

Make Locations Symmetric. This option is used when creating a standardized location file that will be used with multiple subjects. In that case, you will likely want the positions to be symmetrically located. In **Localize**, click to create the positions as closely as possible.



Then click **Make Locations Symmetric**. This will make the homologous positions symmetric, and move the midline electrodes to the exact midline. Normals are not adjusted. A given electrode and its counterpart position must be within 10mm to be recognized as homologous. The new positions given to both will be the average of the two. Midline electrodes must be with 5mm of the midline to be recognized as midline electrodes. You may see a message such as the following that will tell you how many locations did not fall within the location criteria, and therefore not made symmetric (the lowermost pair above is an example). Move one of the positions manually by selecting the Edit option under **Localize**, and click **Make Locations Symmetric** again.



Append Orthogonal Entries. In some cases, you have a location/orientation, and you wish to have (actually, or in addition) representations of the other two orthogonal orientations. This is typically used for dipole simulations, for example, when (for MEG simulations) tangential sources are of interest.

Create Points . Points can be used to backup or individually display several sets of Localize locations. Clicking this option will create a new entry in the Points list in the **Properties** panel (under Results), containing the point locations in the list. It will also create an entry under **Objects** in the 3D View options. Enabling it will display the locations as small 3D stars in the 3D Display. In the **Points x properties**, you can change the Color, Size, Shape and Transparency.

Save As. Saves the locations to a .pom file. This has the same function as the icon above the **Localize** panel.

Save and Use as Digitizer File. This uses the entered locations as sensor (electrode) positions and modifies the current study. This has the same function as the icon above the **Localize** panel.

Save and Use as Image Data Landmarks. It allows you to change image data's NAS, PAL, PAR landmarks based on what you have in Localize. Three locations with these labels must exist for the button to work. Other locations are ignored. This is used in cases where, for example, a digitized skin (including landmarks) is moved around in Localize, and these landmarks shall finally be used. (Note that the Load button, when Files of type is set to All Files, will let you select the 3dd and 4D (BTI) hs_file formats).

Create and Edit Anatomical Localization. Selecting this option prepares an anatomical localization file for editing or opens an existing one for review. Labels from the digitizer file are used. If the landmarks cannot be created automatically, you will need to identify them individually. After selecting the option, a Save As utility will appear, allowing you to specify the folder and file name (.pom extension).

Save and Use Anatomical Localization. This uses the entered locations as anatomical landmarks (.pom file is saved) and modifies the current study.

Export to Excel. Localize points may be exported to Excel (.csv files).

Export to MATLAB. Localize points may be exported to MATLAB (.mat files).

Toolbar Icons

Position the mouse near the top left corner of any of the **Localize** panes and you will see the following Toolbar icons. These all exist elsewhere also, and are presented in the Localize panes for your convenience.

Seedpoint Segmentation . This option performs **Region Growing** segmentation. Clicking it has the same function as clicking the Start button in the **Segmentation** panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+S*).

Threshold Segmentation . This option performs **Threshold** segmentation. Clicking it has the same function as clicking the Start button in the **Segmentation** panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+T*).

Clear Segmentation Result . Clears the segmentation result.

Create Overlay  . This creates an overlay of the most recently segmented surface(s). It is also accessed by the  icon on the **Image Data** Toolbar (or *Ctrl+Shift+O*).

Create Triangle Mesh  . After segmentation, click this option to create a triangulated mesh surface, using a fixed **Dilation** of **12mm**. The results will appear in the **Properties** panel as Surface**#** (where # is the number of the next available Surface). The results are displayed in the  . The option is also accessed by the  icon on the **Image Data** Toolbar (or *Ctrl+Shift+I*). Use the parameter fields in the  panel for other settings, and then click its **Start** button to apply them.

Setup BEM Geometry  . This is a shortcut to the  panel for using the automated BEM Realistic Head Model algorithm. It is also accessed by the  icon on the **Image Data** Toolbar.

Left, Right, Top, Bottom, Front, Rear Views  . Select one of the standard viewing perspectives.

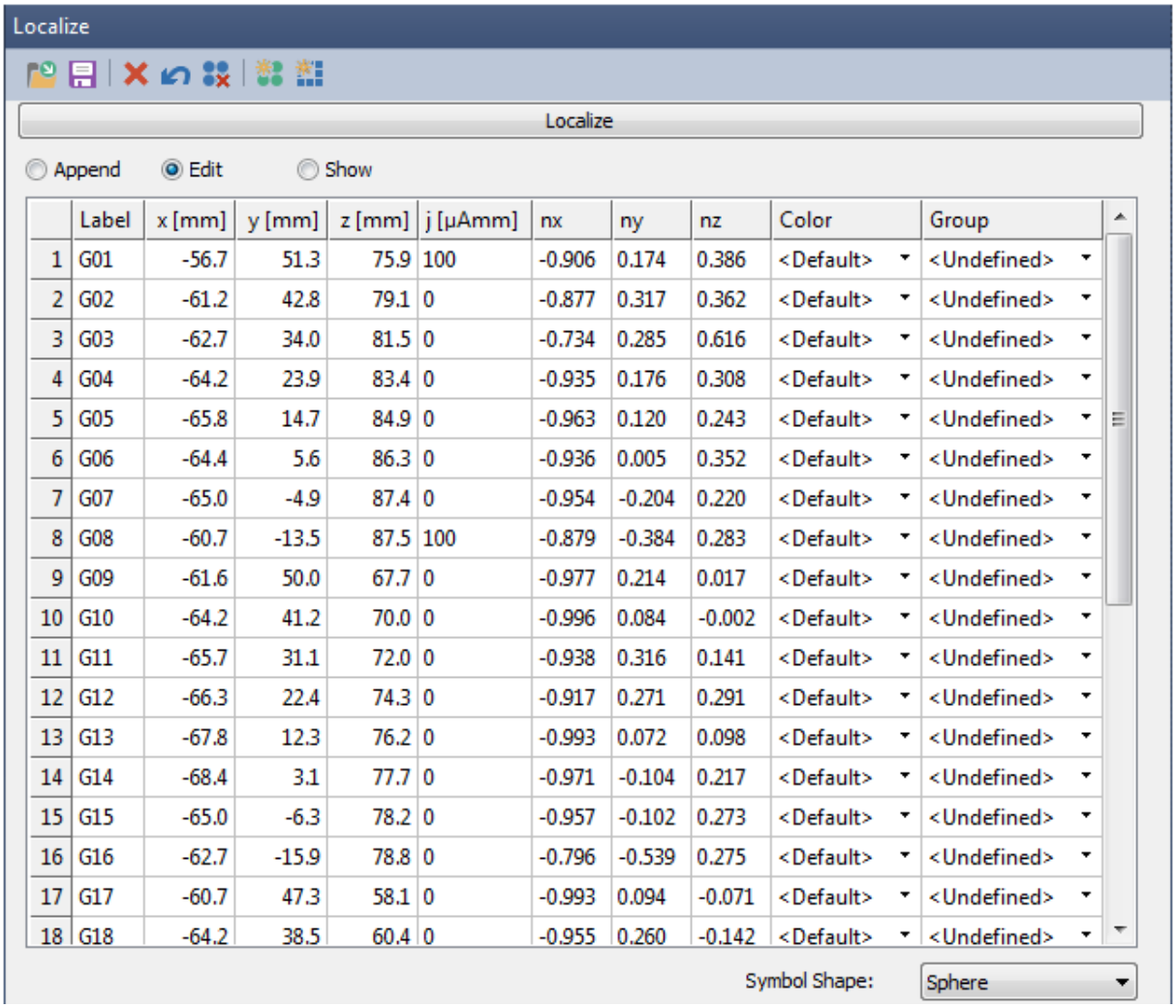
Show Results  . This option toggles the display of the source localizations on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+D*).

Timerange Mode  . This toggles between displaying results for a single time point and for all time points within the Timerange.

Ellipsoid Mode  . This toggles on and off the display of the Confidence Ellipsoids (the 1 SD ellipsoid volume displaying the certainty of the source results).

20.1 Localize

In the **Localize** module, the labels, locations, normals (define the direction), and strengths can be viewed and edited. Color can be assigned as desired, and up to 20 EEG groups may be defined (when using multiple grids, strips, depth electrodes, etc.). The functions of the icons at the top are described **here**.



	Label	x [mm]	y [mm]	z [mm]	j [µAmm]	nx	ny	nz	Color	Group
1	G01	-56.7	51.3	75.9	100	-0.906	0.174	0.386	<Default>	<Undefined>
2	G02	-61.2	42.8	79.1	0	-0.877	0.317	0.362	<Default>	<Undefined>
3	G03	-62.7	34.0	81.5	0	-0.734	0.285	0.616	<Default>	<Undefined>
4	G04	-64.2	23.9	83.4	0	-0.935	0.176	0.308	<Default>	<Undefined>
5	G05	-65.8	14.7	84.9	0	-0.963	0.120	0.243	<Default>	<Undefined>
6	G06	-64.4	5.6	86.3	0	-0.936	0.005	0.352	<Default>	<Undefined>
7	G07	-65.0	-4.9	87.4	0	-0.954	-0.204	0.220	<Default>	<Undefined>
8	G08	-60.7	-13.5	87.5	100	-0.879	-0.384	0.283	<Default>	<Undefined>
9	G09	-61.6	50.0	67.7	0	-0.977	0.214	0.017	<Default>	<Undefined>
10	G10	-64.2	41.2	70.0	0	-0.996	0.084	-0.002	<Default>	<Undefined>
11	G11	-65.7	31.1	72.0	0	-0.938	0.316	0.141	<Default>	<Undefined>
12	G12	-66.3	22.4	74.3	0	-0.917	0.271	0.291	<Default>	<Undefined>
13	G13	-67.8	12.3	76.2	0	-0.993	0.072	0.098	<Default>	<Undefined>
14	G14	-68.4	3.1	77.7	0	-0.971	-0.104	0.217	<Default>	<Undefined>
15	G15	-65.0	-6.3	78.2	0	-0.957	-0.102	0.273	<Default>	<Undefined>
16	G16	-62.7	-15.9	78.8	0	-0.796	-0.539	0.275	<Default>	<Undefined>
17	G17	-60.7	47.3	58.1	0	-0.993	0.094	-0.071	<Default>	<Undefined>
18	G18	-64.2	38.5	60.4	0	-0.955	0.260	-0.142	<Default>	<Undefined>

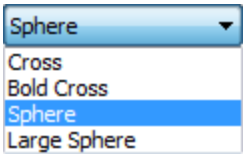
Append/Edit/Show. At the top of the Localize display are the three modes:

Append. In Append Mode, clicking the left mouse button will add the cursor position to the Localize list. In operation, enable Append Mode when you want to add positions to the Localize list.

Edit. In Edit Mode, you can change the positions of the points. The new position is transferred to the corresponding entry in the Localize List.

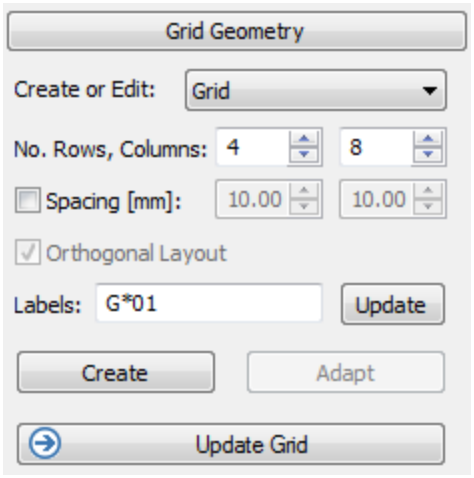
Show. Clicking the images in the Localize panes while in Show mode has no effect on the entries in the Localize list; it will update the MR images.

Symbol Shape. Select a shape for the electrode symbols.

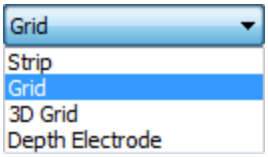


20.2 Grid Geometry

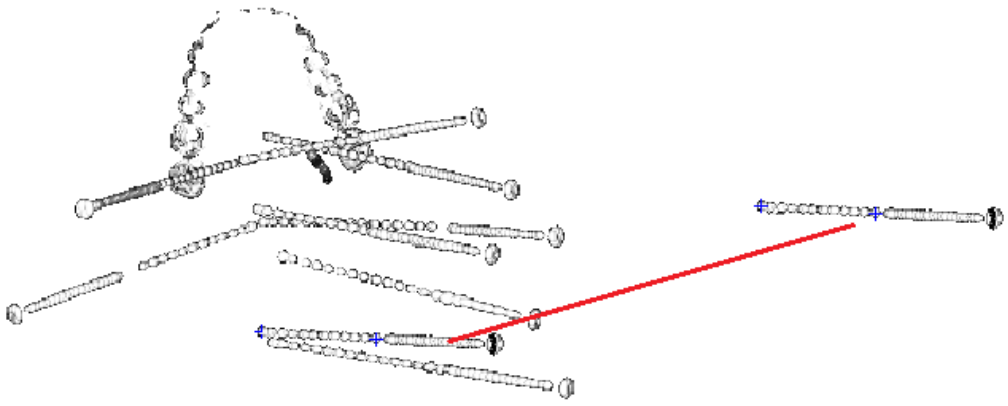
In the **Grid Geometry** module, electrode grid and strip layouts can be defined and modified. See the *ECoG Grid Setup* tutorial for more information.



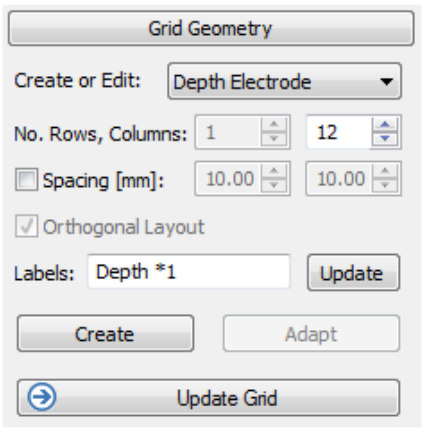
Create or Edit. Select to create an electrode grid or strip. **Grids** are created by inserting the 4 corners, in a clockwise or counter-clockwise order. The remaining positions will be filled in based on the settings below. **Strips** are created by inserting the first, an intermediate, and the last location. The **3D Grid** option creates points in a three dimensional sphere.

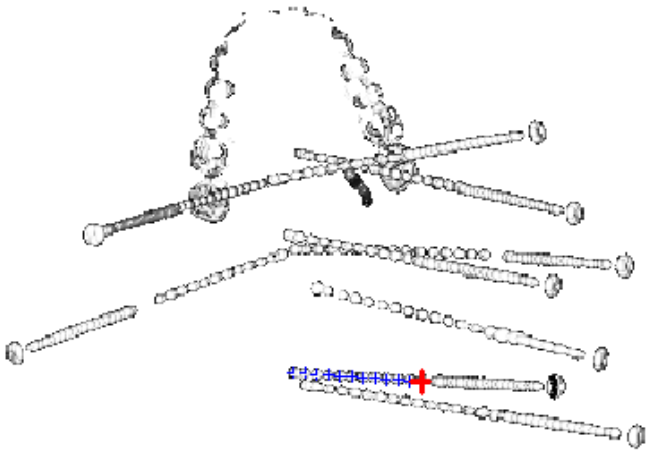


The **Depth Electrode** option is used to define depth (needle) locations. In **Localize**, make sure the first and last contacts are available by selecting them from the high resolution CT data in **Image Data** and clicking *Ctrl-I*, or **Export Cursor to Localize** from the context menu.



In **Grid Geometry**, change the grid type to **Depth Electrode** and enter the number of contacts in the **Columns** field. Then click **Create**.





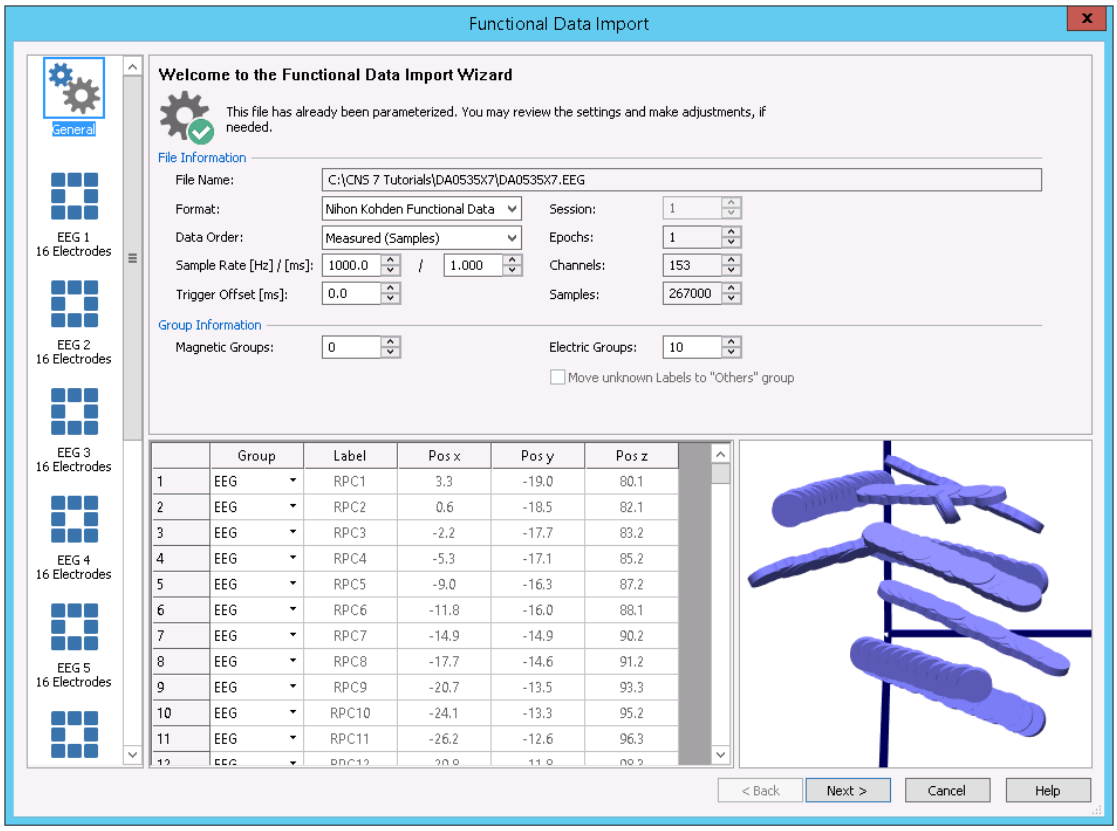
You will see the positions in the **Localize** list. Repeat the process for each electrode, making sure you follow the same order as in the data file. Relabel the contacts as desired (the labels do not have to match those in the data file; the order is what matters). When finished, click the **Save and Use as Digitizer File** button  .

Localize

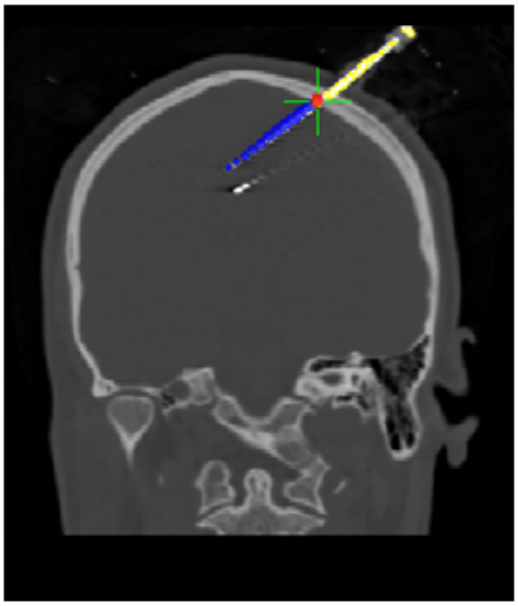
Append Edit Show

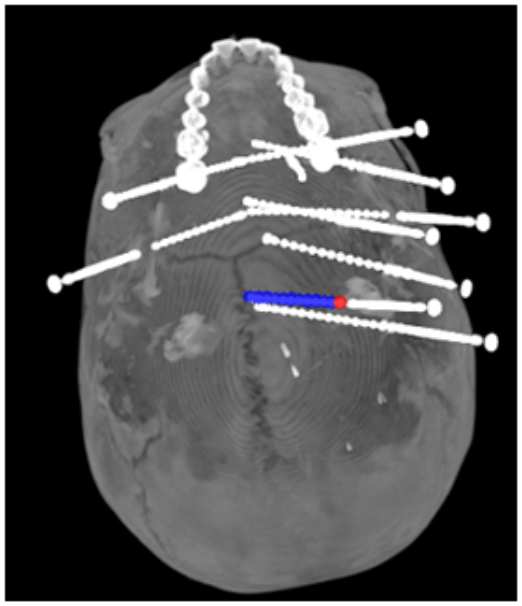
	Label	x [mm]	y [mm]	z [mm]
1	Depth 1	-5.4	24.1	87.4
2	Depth 2	-2.5	23.8	89.5
3	Depth 3	0.4	23.6	91.7
4	Depth 4	3.2	23.4	93.8
5	Depth 5	6.1	23.1	95.9
6	Depth 6	9.0	22.9	98.1
7	Depth 7	11.9	22.7	100.2
8	Depth 8	14.7	22.4	102.3
9	Depth 9	17.6	22.2	104.4
10	Depth 10	20.5	22.0	106.6
11	Depth 11	23.4	21.7	108.7
12	Depth 12	26.2	21.5	110.8

In the Functional Data Import Wizard, verify the number of Electrode Groups is the same as the number of depth electrodes. The groups will be seen in the column on the far left. In the Groups column, the contacts should be seen as EEG 1, EEG 2, EEG 3, etc.

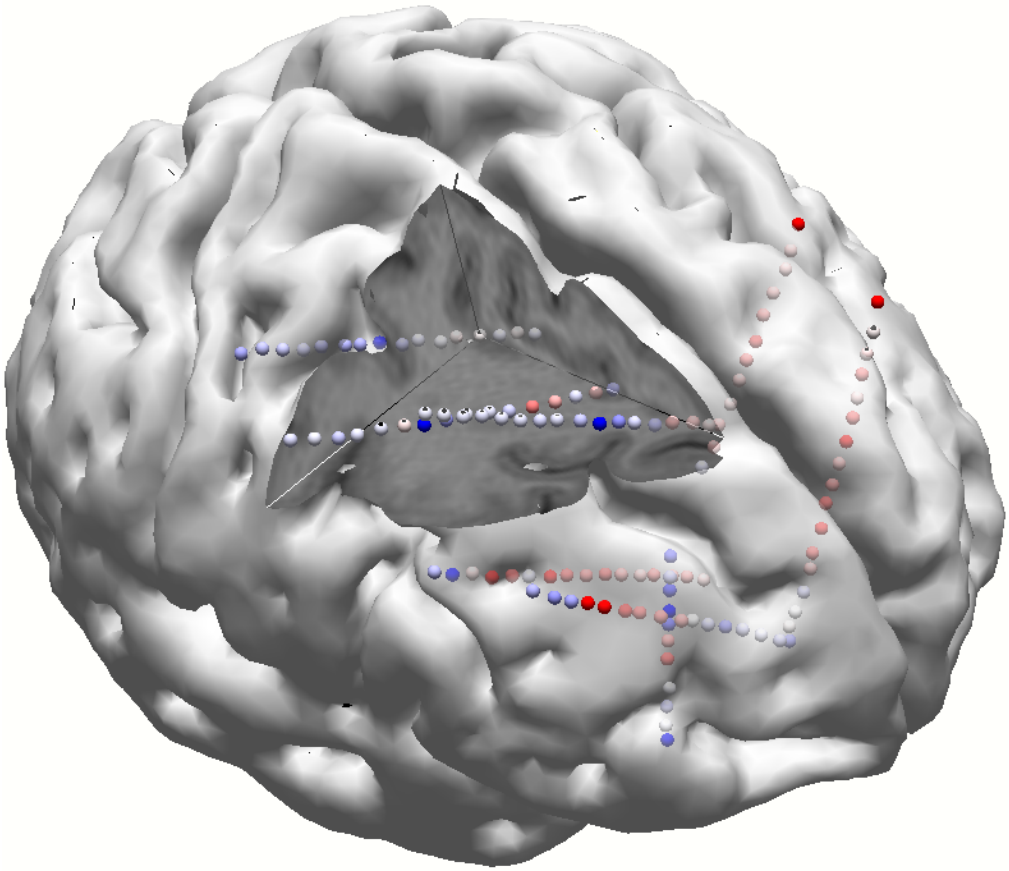


After segmentation, you will see the segmented electrode on the CT (right side is the **MIP** display).

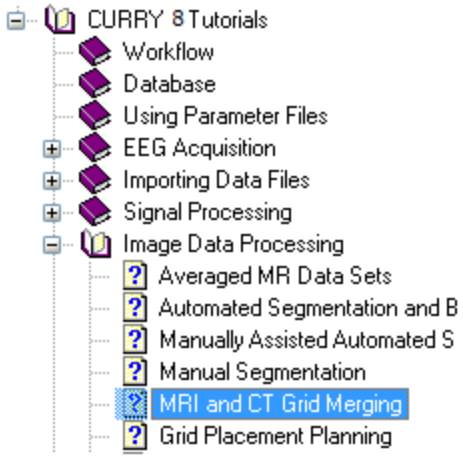




You can select a color scale for the contacts, and superimpose the electrodes on the segmented cortex, with Cut Planes to expose the electrodes.



The steps are very similar to those for displaying ECoG data (see the latter half of the **MRI and CT Grid Merging** tutorial in the *CURRY Tutorials*).



No. Rows. Number of electrodes in the rows of the grid.

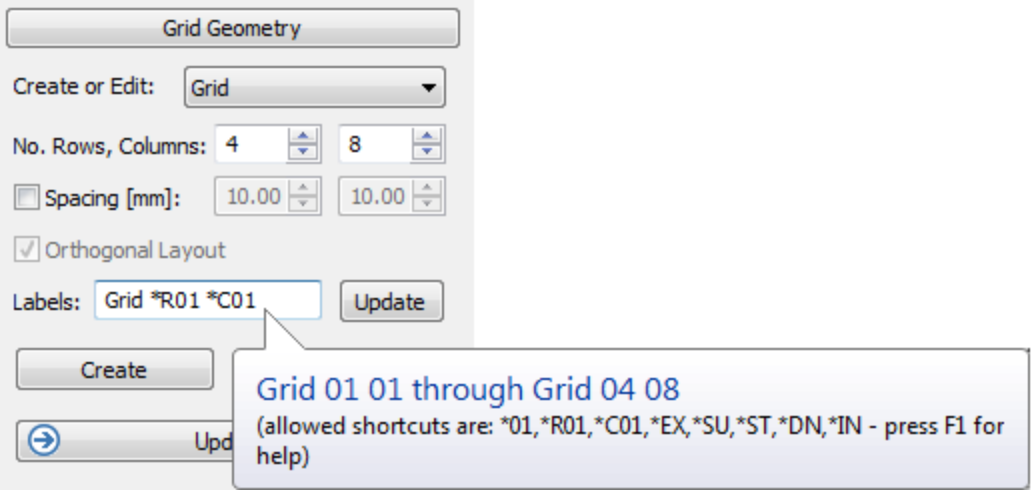
No. Columns. Number of electrodes in the columns of a grid, or electrodes in a strip, or contacts in a depth electrode.

Spacing [mm]. If you are using this section for planning of the grid placement, you may not have the actual electrode grid. You can try out different spacings and numbers of electrodes to determine the optimum size.

When Spacing is deselected, repositioning a corner electrode will stretch or compress the other positions (when you click Adapt). When selected, repositioning a corner electrode will move the entire grid, keeping the distances between electrodes constant.

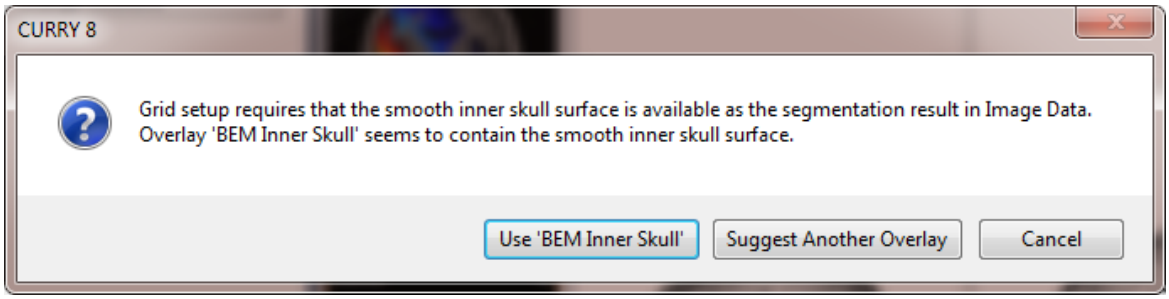
Orthogonal Layout. Forces grid layout to be based on 90 degree corners (as in a rectangle). Disabled allows the grid to be created using non-ninety degree corners (as in a parallelogram).

Labels. These are the labels that will be created automatically for the grid electrodes, where **R**=row and **C**=column. "Grid *R01 *C01" will produce labels: Grid 01 01, Grid 01 02, Grid 01 03, etc.

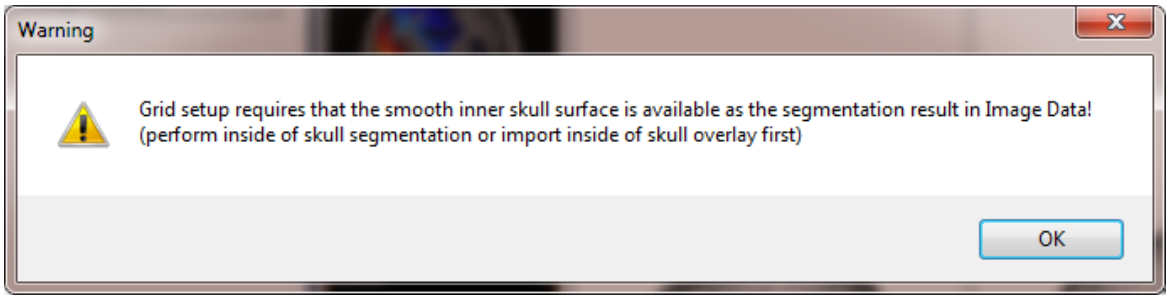


Note that certain shortcuts are allowed. You can substitute the name of the Group - ***EX** (from the Database), the Subject name - ***SU**, the Study name - ***ST**, the functional data file name - ***DN**, or the image data file name - ***IN**.

Create. The grid creation process requires a smooth surface inn the segmentation result. CURRY will assist you in this process with the following message. Typically you should select the **BEM Inner Skull**, although CURRY will locate additional overlays.



CURRY will guide you through the process when possible.



Adapt. Applies changes that have been made (unless **Update Grid** has been enabled).

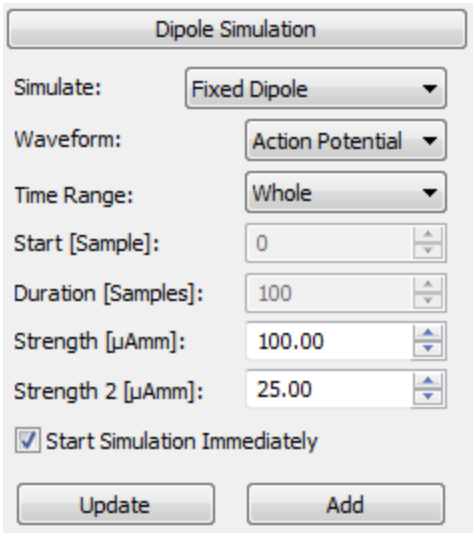
Update Grid. This button is a toggle. When activated, the changes you make will be updated without the need to click the **Adapt** button.

20.3 Dipole Simulation

CURRY can create EEG and MEG data based on simulated dipoles. Simulated dipoles are used in a variety of ways: testing your own algorithms, teaching/demonstration purposes, and seeing the scalp distributions from simulated sources on the surface of or from deeper structures within the brain. The procedures used here are more involved than those available with the **Simulation** option found under **Dipole Fit**. If that option does not provide the dipole simulation functionality you need, use the options below.

You will need first to open a Study containing an averaged data file. The file is used to supply the AD Rate, number of electrodes, the electrode positions, etc., but the waveforms themselves are not used. Or, in the Database, *right click* and select the **Insert New Simulation** option (see the *Dipole Simulation* tutorial for an example).

You will also need to create some starting dipole locations (in Localize). See the *Dipole Simulation* tutorial for examples of the method in operation.



Simulate. You can create **Fixed**, **Moving**, or **Random** dipoles. **Fixed** dipoles create a single dipole with a fixed orientation, with varying strength. **Moving** dipoles are

created between two dipole locations you enter. The **Random** dipoles option creates dipoles for each data point in the Timerange, with randomly selected locations within the selected head model's source compartment.

Waveform. You may select **Constant** (unvarying strength), **Linear** (sloping strength), **Depolarization** (positive and negative with varying strength), **Sine** waveforms (varying strength with a definable offset/phase), or the **Action Potential** (positive/negative waveform resembling an action potential).

Time Range. Select the **Whole** interval or **Specify** a time range. If you select Specify, the **Start** and **Duration** fields become active.

Start (Sample). You may start the waveforms at any defined point, based the number of samples rather than the latency.

Duration. The Duration of the waveforms is selected, in number of samples.

Strength 1. Enter the desired Strength of the simulated dipole.

Strength 2. (Linear Waveform only) The strength will transition from Strength 1 to Strength 2 across the Timerange.

Start Simulation Immediately. Generally, this option should be enabled. Loosely speaking, it creates a linkage between this panel and the settings in the **Dipole Fit** panel (under **Source Reconstruction**). If disabled, the settings are independent and will need to be selected manually.

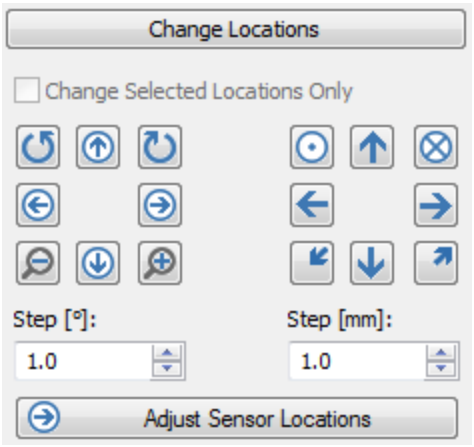
Update. Replaces existing list with new dipole only.

Add. Adds new dipole to existing list.

See the *Dipole Simulation* tutorial for a demonstration.

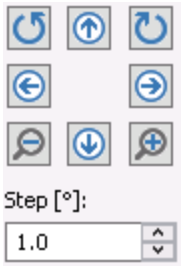
20.4 Change Locations

The Change Locations buttons can either be used to move all (or just the selected) Localize locations, or to reposition the EEG or MEG sensors. You would typically position the sites first by 1) selecting **Import Electrodes**, 2) selecting **Create 10-20 System**, 3) positioning the electrodes manually, or 4) create a grid. All of the electrodes will be moved in the directions indicated by the arrows (a Tooltip will appear to provide more information).



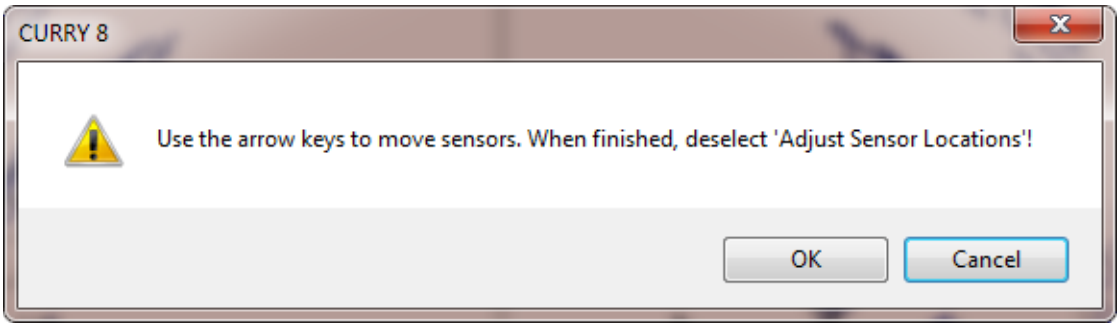
Change Selected Locations Only. If you highlight desired channels in the **Localize** list, you have the option to change their locations only.

The group of buttons on the left side are used to move the positions in the arrows indicated, in a spherical direction. The center button deflates the locations radially with respect to their center-of-mass. The movements are in increments of degrees set in the **Step [°]** field.



The group of buttons on the right side are used to move the sensor positions in the directions indicated. The center button is used to inflate the locations radially with respect to their center-of-mass. The movements are made in mm increments set in the **Step [mm]** field.

Adjust Sensor Locations. When pressed, you can use the arrow buttons to move EEG or MEG sensors, together with the Localize locations (which could for example be a digitized headshape). It is generally a good idea to display a semitransparent skin mesh in 3D View before activating this option. Changed sensor locations are actually used when the  button is released, and can later be saved as part of the functional data parameters.



20.5 Additional Localize Options

Some of the options pertaining to Localize are accessed from the Localize Toolbar; others are found in the context menu, in the next section.

Seedpoint Segmentation . This option performs **Region Growing** segmentation. Clicking it has the same function as clicking the Start button in the **Segmentation** panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+S*).

Threshold Segmentation . This option performs **Threshold** segmentation. Clicking it has the same function as clicking the Start button in the **Segmentation** panel. It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+T*).

Clear Segmentation Result . Clears the segmentation result.

Create Overlay . This creates an overlay of the most recently segmented surface(s). It is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+O*).

Create Triangle Mesh . After segmentation, click this option to create a triangulated mesh surface, using a fixed **Dilation** of **12mm**. The results will appear in the **Properties** panel as Surface**#** (where # is the number of the next available Surface). The results are displayed in the 3D View. The option is also accessed by the icon on the **Image Data** Toolbar (or *Ctrl+Shift+I*). Use the parameter fields in the Create panel for other settings, and then click its **Start** button to apply them.

Setup BEM Geometry  . This is a shortcut to the 

panel for using the automated BEM Realistic Head Model algorithm. It is also accessed by the  icon on the **Image Data** Toolbar.

Show Results  . This option toggles the display of the source localizations on the Image Data display. It is also accessed by the  icon on the **Image Data** Toolbar (or *Alt+D*).

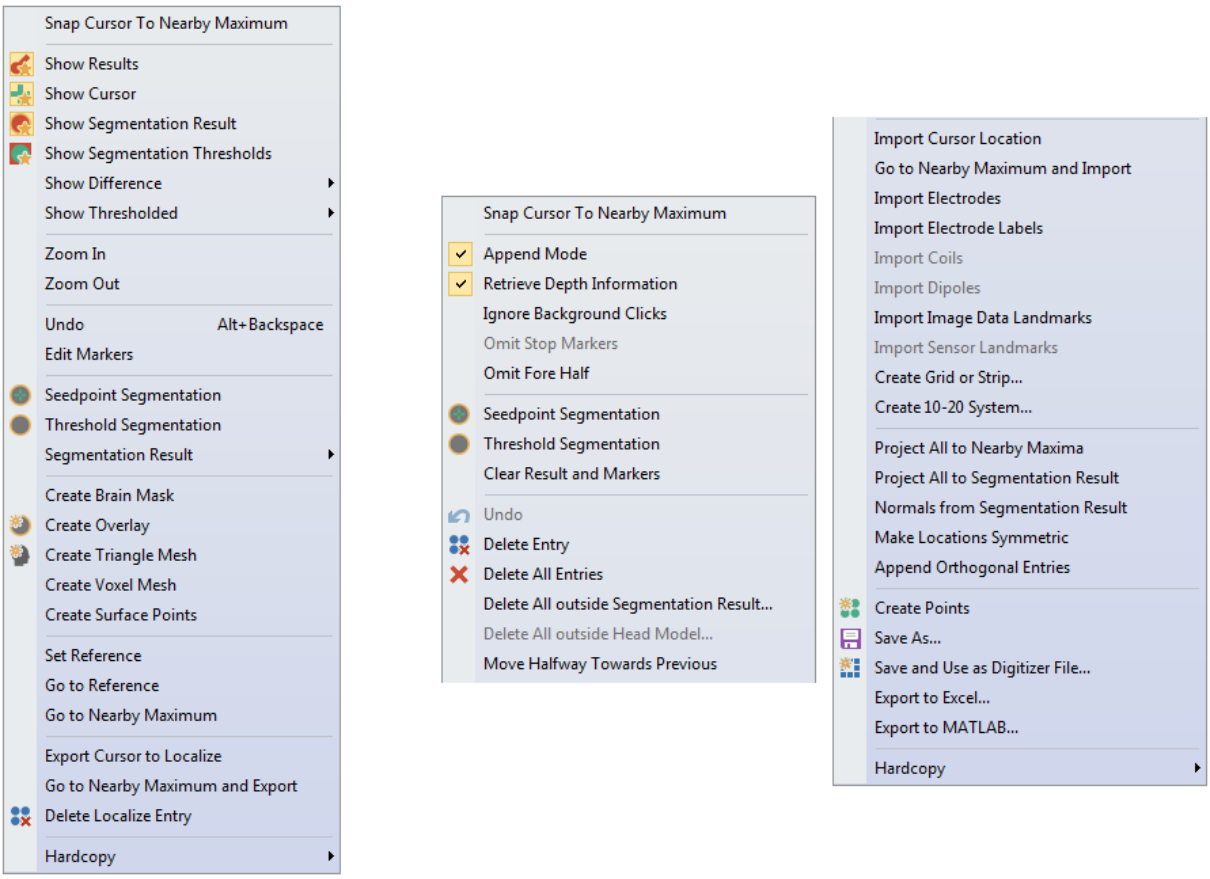
Timerange Mode  . This toggles between displaying results for a single time point and for all time points within the Timerange.

Ellipsoid Mode  . This toggles on and off the display of the Confidence Ellipsoids (the 1 SD ellipsoid volume displaying the certainty of the source results).

20.6 Localize, Context Menu

Click the *right mouse* button within the **Localize** windows to see additional options. Those specific to the 

display are as follows. The menu on the left is accessed by clicking the image film strip on the left side of the display. These pertain primarily to segmentation and are described in the **Segmentation** section above. The one on the right is accessed from within the Localize display.



Snap Cursor to Nearby Maximum. This feature, when enabled, will move the image data cursor to a nearby intensity maximum after clicking in the image data. It is, in a way, a sibling feature to the "magnetic cursor" that can be enabled for manual event marking. It is typically used for defining electrode locations in CT data that are usually rendered as small bright dots.

Append Mode 

. When selected, each mouse click creates a new **Localize** location.

Retrieve Depth Information. If selected (the default setting), depth information is retrieved. If deselected, only the x and y position of the point are changed when clicking with the mouse. Sometimes (rarely), you may not want to "land" on the surface, but rather just adjust a location in the plane-of-view. In that case, you would deselect this option.

Ignore Background Clicks. When enabled, clicks outside of the images in the Localize panes will be ignored (not added to the Localize list).

Omit Stop Markers. If there are Stop markers, this option will show their impact on segmentation by "not showing" them. A companion option is **Omit Fore Half**, which shows only the hind half of the image (useful for looking "into" a CT skull).

Omit Fore Half. This displays only the hind half of the image (useful for looking "into" a CT skull).

Seedpoint Segmentation. Initiates seedpoint segmentation. This has the same function as the icon on the **Image Data** Toolbar (*Ctrl+Shift+S*).

Threshold Segmentation. Initiates threshold segmentation. This has the same function as the icon on the **Image Data** Toolbar (*Ctrl+Shift+T*).

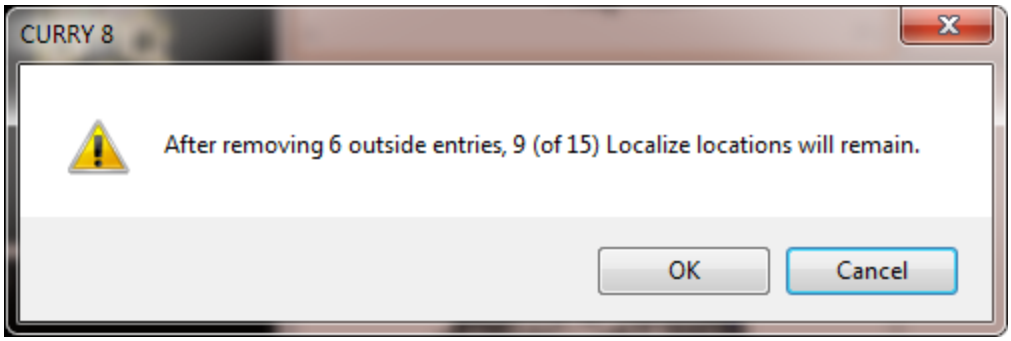
Clear Result and Markers. Clears segmentation results and Pass/Stop markers.

Undo. Undo the most recent operation.

Delete Entry (*Ctrl+D*). Click this to delete the most recent entry in the list. Delete Entry is grayed out in Append Mode; deselect Append Mode to access Delete Entry.

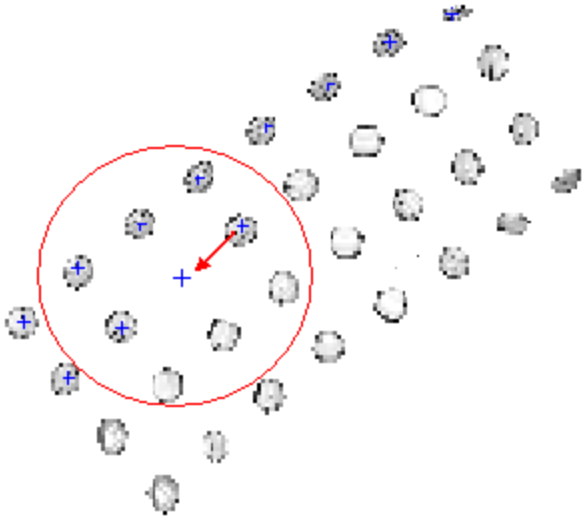
Delete All Entries. Click this to delete the entire Localize list. You may also use the button above the Localize list.

Delete All Outside Segmentation Result. This option will decimate your Localize locations and only retain ones inside the (yellow) segmentation result. A message will appear informing you how many locations will remain. In this example, only the CDR sources inside the segmented cortex remained.



Delete All Outside Head Model. Locations outside of the head model will be deleted.

Move Halfway Towards Previous. When digitizing grid electrodes in Localize, sometimes an electrode cannot be seen. In this case, click the next electrode instead and select Move Halfway Towards Previous. The value of the estimated position will be entered into the list.

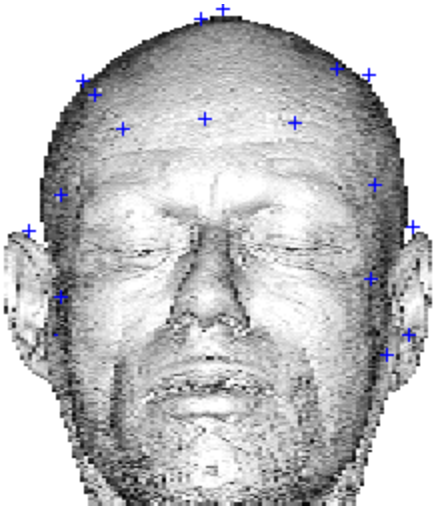


Import Cursor Location (*Ctrl+I*). Use this option to set the edited point to the 3D Cursor location. This is used to fill the Localize cells with information you might wish to work on (typically, modify). For example, if we want to modify electrode locations, we can:

1) import them
2) change them (using the Change Locations parameter panel)
3) Save and use as Digitizer File.

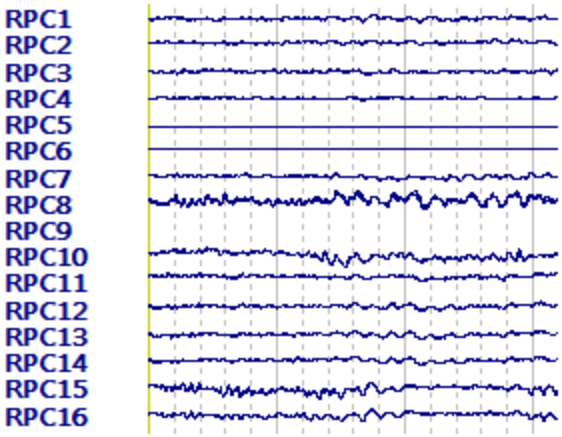
Go to Nearby Maximum and Import. This is typically used in the context of manually clicked ECoG electrodes in CT data - after thresholding and displaying in, for example, the **3D View**, click the border of the bright area, and this functionality brings the cursor to its center (this can be applied repeatedly).

Import Electrodes. Selecting this option imports the electrode positions from the digitizer file to the **Localize** panel, and displays the positions on the iso-images in the Localize display.



Import Electrode Labels. This is a useful option especially with depth electrodes where you have the labels in the Functional Data and you wish to include them in the Localize list of electrodes you measure manually.

For example, you have functional data with electrode labels.

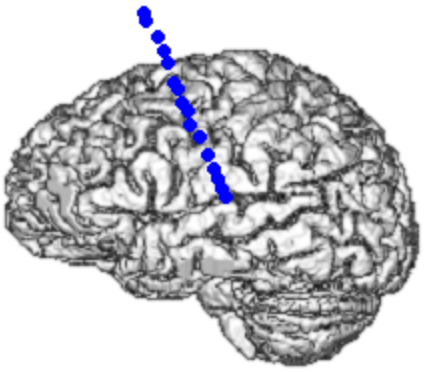


You manually measure where the electrodes are. The labels are numbers at this point.

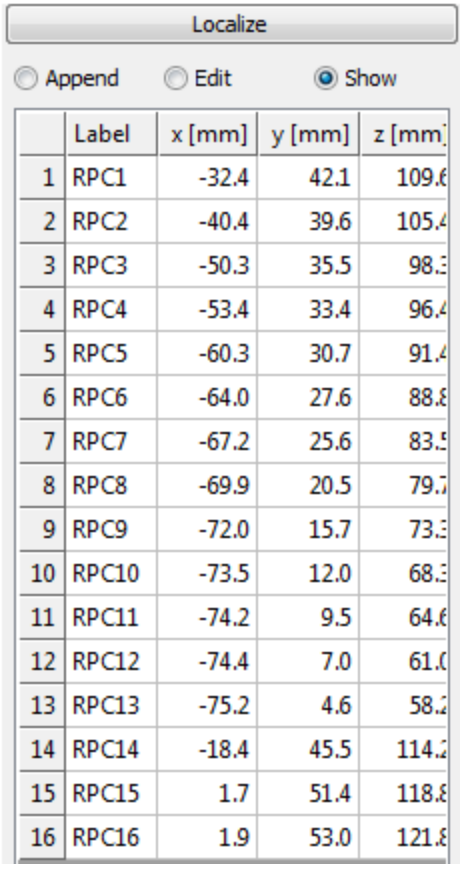
Localize

Append Edit Show

	Label	x [mm]	y [mm]	z [mm]
1	1	-32.4	42.1	109.6
2	2	-40.4	39.6	105.4
3	3	-50.3	35.5	98.3
4	4	-53.4	33.4	96.4
5	5	-60.3	30.7	91.4
6	6	-64.0	27.6	88.8
7	7	-67.2	25.6	83.5
8	8	-69.9	20.5	79.7
9	9	-72.0	15.7	73.3
10	10	-73.5	12.0	68.3
11	11	-74.2	9.5	64.6
12	12	-74.4	7.0	61.0
13	13	-75.2	4.6	58.2
14	14	-18.4	45.5	114.2
15	15	1.7	51.4	118.8
16	16	1.9	53.0	121.8



Right click and select **Import Electrode Labels** to up[date the Localize list with the actual labels (be sure you do this in the order they appear in the Functional Data).



	Label	x [mm]	y [mm]	z [mm]
1	RPC1	-32.4	42.1	109.6
2	RPC2	-40.4	39.6	105.4
3	RPC3	-50.3	35.5	98.3
4	RPC4	-53.4	33.4	96.4
5	RPC5	-60.3	30.7	91.4
6	RPC6	-64.0	27.6	88.8
7	RPC7	-67.2	25.6	83.5
8	RPC8	-69.9	20.5	79.7
9	RPC9	-72.0	15.7	73.3
10	RPC10	-73.5	12.0	68.3
11	RPC11	-74.2	9.5	64.6
12	RPC12	-74.4	7.0	61.0
13	RPC13	-75.2	4.6	58.2
14	RPC14	-18.4	45.5	114.2
15	RPC15	1.7	51.4	118.8
16	RPC16	1.9	53.0	121.8

Import Coils. Selecting this option imports the coil positions from the digitizer file to the **Localize** panel, and displays the positions on the iso-images in the Localize display.

Import Dipoles. Select this option to import the dipole solutions into Localize and display them in the Localize list.

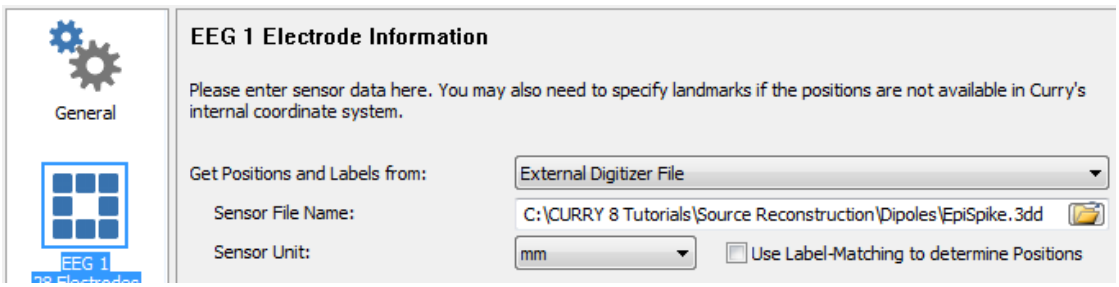
Import Image Data Landmarks. The anatomical landmarks that were determined when the image data were loaded are imported to the Localize list, and displayed on the Localize images.

	Label	x [mm]	y [mm]	z [mm]
1	Nasion	-0.0	100.8	0.0
2	PAL	-81.2	-0.0	-0.0
3	PAR	80.5	0.0	0.0
4	Inion	-2.7	-80.5	47.2
5	Vertex	-1.6	52.9	122.9
6	AC	0.3	37.0	38.0
7	PC	-0.8	5.9	49.8
8	Midsagittal	-2.7	27.6	79.6

Import Sensor Landmarks. The anatomical landmarks that were digitized along with the sensor positions are imported to the Localize list, and displayed on the Localize images.

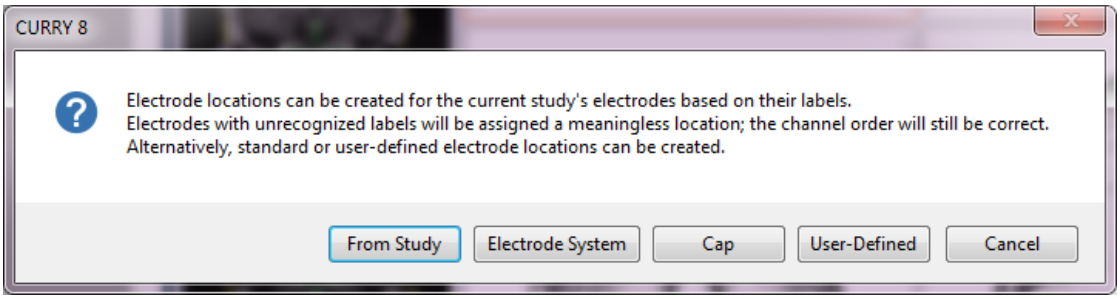
Create Grid or Strip. To define a grid, enter its four corner points (either clockwise or counterclockwise). To define a strip, enter its first, any intermediate, and its last point. Then, call the appropriate item of this submenu. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  .

Create 10-20 System. This option is used to create the positions of the extended 10-20 system (including 10-5; 180 positions recognized and labeled). If electrodes with recognized labels are found in the study, you may choose to create their positions only. Otherwise, the ordering and selection of the positions is based on the **NUMBER_POM_xxx** entries in the study parameters file, if present, or the *GlobalParameters.cfg* file. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  . Then select the new .pom file for the **External Digitizer File**, in the Functional Data Import Wizard.



This option uses the **Image Data** segmentation result for measuring distances along a curved surface, so a skin surface (e.g., the **Skin overlay**) should typically have been imported first.

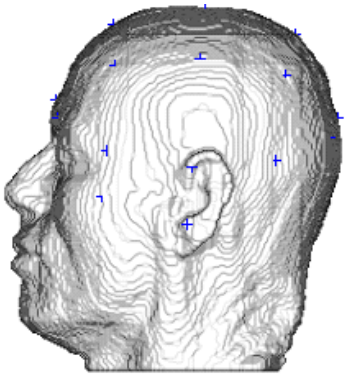
After clicking the **Create 10-20 System** option, you will see the following message.



If you click **From Study**, CURRY will generate 10/20 positions for (and based on) the electrodes in the Study.

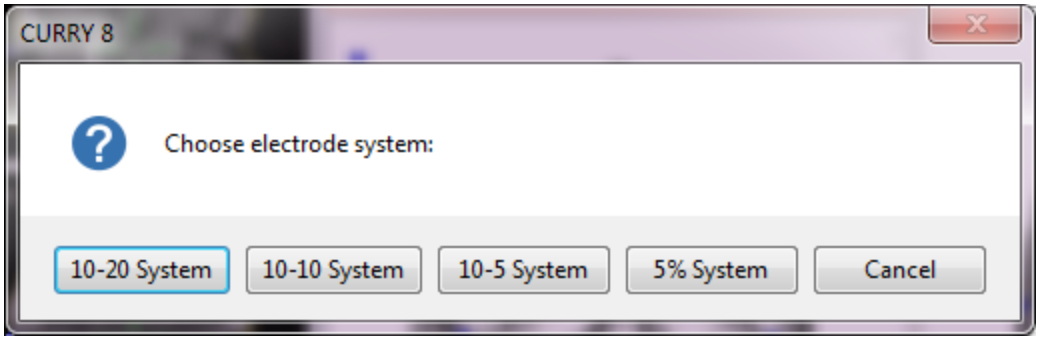
The recognized positions are plotted and displayed in the **Localize** list. These can be repositioned manually or with the Change Locations buttons, if needed.

	Label	x [mm]	y [mm]	z [mm]	j [µAmm]	nx	ny	nz
1	O1	-26.1	-76.9	58.4	100	-0.382	-0.858	0.345
2	OZ	-0.4	-79.9	64.7	100	-0.034	-0.986	0.163
3	P3	-47.0	-45.5	97.8	100	-0.525	-0.695	0.491
4	P7	-66.6	-45.7	46.8	100	-0.901	-0.432	-0.037
5	T7	-77.7	6.7	37.9	100	-0.994	-0.111	-0.007

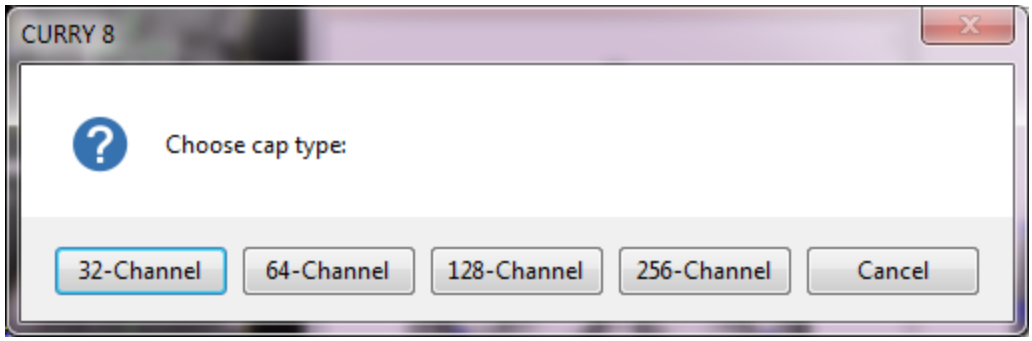


For a description of the automatic 10/20 system setup, see here.

[Wagner M, Fuchs M, and Kohlhoff H. Automatic generation of the 10/20 electrode system. Brain Topogr. 8 (1996), p. 409.]
If you select **Electrode System**, you will see the following options. Selecting one of these will display the locations of the electrodes within the various systems (with or without the sub-temporal electrode option that you will also see). These are primarily for display of the electrode systems.

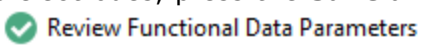


If you select **Cap**, you will see the various cap types. These will display the distributions of electrodes for the caps as shown.



The **User Defined** option displays all positions. You can use the localize list to keep or remove the electrodes you want.

Project All to Nearby Maxima (*Ctrl+G*). Projects the locations onto the nearby maxima. Maxima are the centers-of-gravity of the spherical volumes around the **Localize** locations. A radius of 5mm is used. This does the projection for all locations, yielding a quicker workflow for ECoG grid digitization: click the electrode positions (typically in Localize's 3D View, for all electrodes), and then Project All to Nearby Maxima.

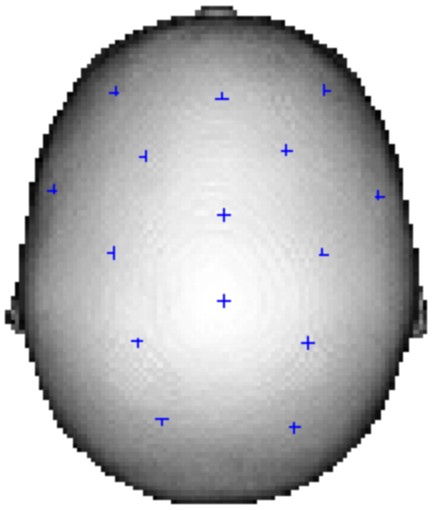
Project All to Segmentation Result. This option projects the locations onto the **Image Data** segmentation result, radially towards its center-of-mass. To use the created positions as electrodes, press the **Save and Use as Digitizer File** button  and select the 

option from the **Workflow** window. This option uses the **Image Data** segmentation result for projection, so a skin surface (e.g. the **Skin overlay**) should typically have been imported first.

Normals from Segmentation Result. This option uses the surface orientation of the brain (the inner skull), which is close enough for the normals, but does NOT change the orientation. This is like the **Project to Segmentation Result** option (which also computes normals), except only the normals are used while the locations remain unchanged.

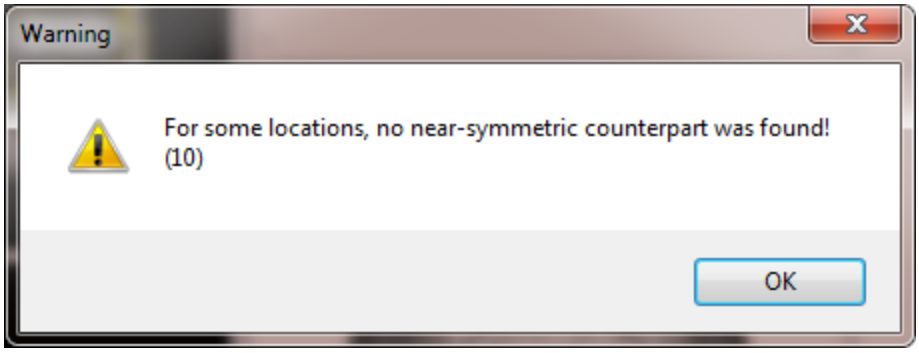
One of the places where this option is useful is where the electrodes are positioned at an angle (perpendicular in this case) to the brain surface. This can happen when you load positions from an external file that does not contain normals (left). In that case, create a segmentation result from your image data (such as, the Brain). Once you have the yellow outlined segmented brain in the **Image Data**, go to **Localize** and select **Normals from Segmentation Result**. The orientation of the electrodes is in line with the segmented surface, while their positions are unchanged (right).

Make Locations Symmetric. This option is used when creating a standardized location file that will be used with multiple subjects. In that case, you will likely want the positions to be symmetrically located. In **Localize**, click to create the positions as closely as possible.

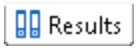


Then click **Make Locations Symmetric**. This will make the homologous positions symmetric, and move the midline electrodes to the exact midline. Normals are not adjusted. A given electrode and its counterpart position must be within 10mm to be recognized as homologous. The new positions given to both will be the average of the two. Midline electrodes must be with 5mm of the midline to be recognized as midline electrodes. You may see a message such as the following that will tell you how many locations did not fall within the location criteria, and therefore not made symmetric (the lowermost pair above is an example). Move one of the positions manually by selecting the 

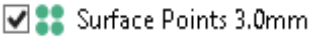
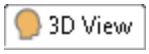
option under **Localize**, and click **Make Locations Symmetric** again.

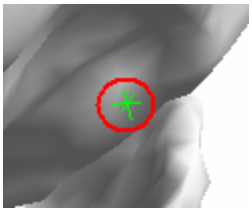


Append Orthogonal Entries. In some cases, you have a location/orientation, and you wish to have (actually, or in addition) representations of the other two orthogonal orientations. This is typically used for dipole simulations, for example, when (for MEG simulations) tangential sources are of interest.

Create Points (*Ctrl+L*). Clicking this option will create a new entry in the Points list in the **Properties** panel (under 

), containing the point locations in

the list. It will also create a  entry under **Objects** in the  options. Enabling it will display the locations as small 3D stars in the 3D Display (shown in the red circle in the figure below). In the **Points x properties**, you can change the Color, Size, Shape and Transparency.



Save As. Saves the locations to a .pom file. This has the same function as the  icon in the **Localize** panel.

Save and Use as Digitizer File. This has the same function as the  icon in the **Localize** panel (described above).

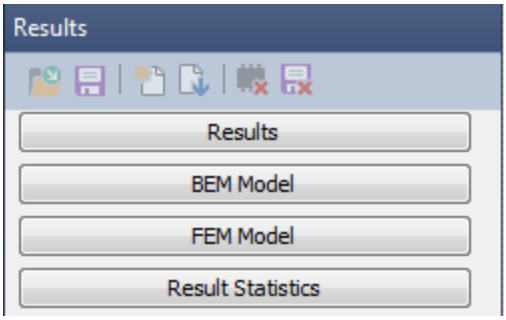
Export to Excel. Localize points may be exported to Excel (.csv files).

Export to MATLAB. Localize points may be exported to MATLAB (.mat files).

Hardcopy. This has the same Copy, Save, and Print options described above.

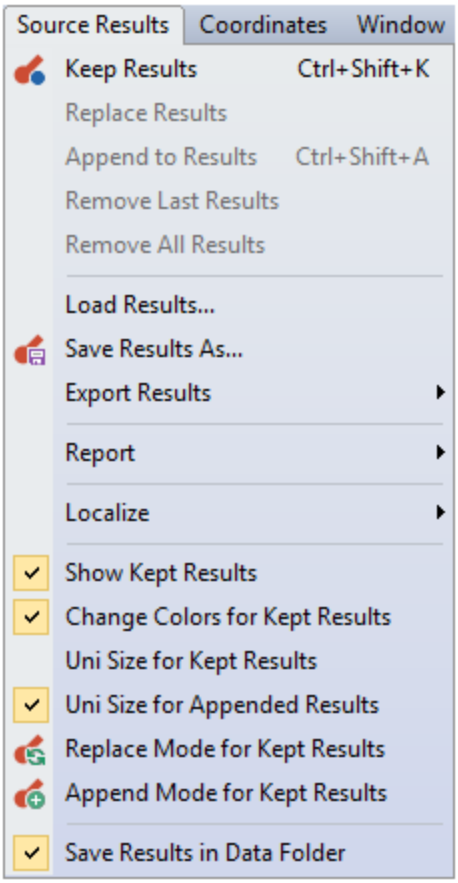
21 Results

The **Results** section of CURRY is used to manage functional data, source, and image processing results - Functional Data, Surfaces, Points, BEM and FEM Realistic Head Models, Overlays, etc. - that may then be displayed, saved, etc. Groups of sensor positions can be shifted, expanded, or deflated. Press *F12* at any time to display the panels.

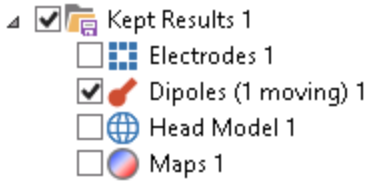


Some of the Results options are accessed from the **Source Results** option in the Main Menu Bar.

The Source Results options are accessible after you have performed source reconstruction, and allow you to keep, save, load, export,etc. the results.



Keep Results. The current results will be seen as a new set of display items (labeled Kept Results x). It is also accessed by the icon on the **Standard** Toolbar (or *Ctrl+Shift+K*) and at the top of the **Source Reconstruction** panel.



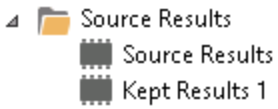
Replace Results. When selected, the last Kept Results will be replaced with the latest results.

Append to Results. When using continuous data files, where there are multiple source results that are Kept, use this option to save the results to a single Kept Result.

Remove Last Results. When selected, the last Kept Results will be removed.

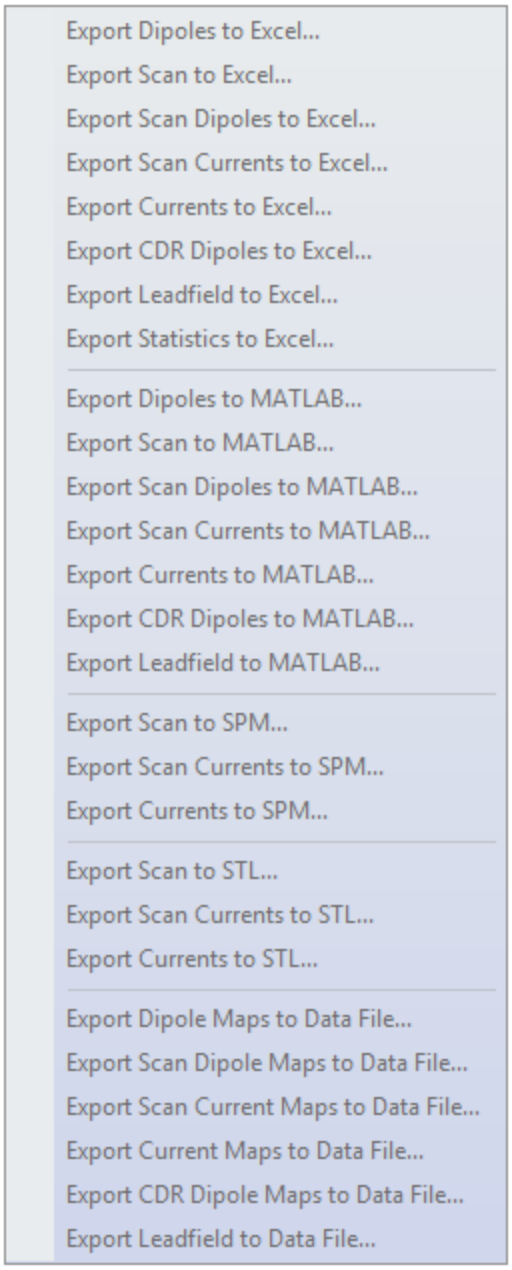
Remove All Results. All Kept Results will be removed.

Load Results. This option allows you to load previously saved results. The results will appear under the Source Results folder in the **Results** panel.



Save Results As. Use this option to save results files. It has the same function as **File** → **Results** → **Save Results As**, or the button when Results are selected in the **Properties** panel under Results. The option is also accessed from the icon on the **Standard** Toolbar.

Export Results. The source reconstruction and statistics results may be exported to Excel, MATLAB, SPM, STL, and to Data Files.



If you export the CDR results, for example, to Excel, you will see a large matrix with the time points for the columns and several variables for the rows, including the following:

Residual Deviation (normalized),
Residual Deviation (original),
Explained Variance (normalized), and
Explained Variance (original).

Residual Deviation is rDev = 1 - [goodness of fit].

The explained variance is eVar = 1 - rDev * rDev, so for 10% rDev (=90% explained field), this gives 99% explained variance. Since 99% is closer to 100% than 10% is to 0%, the latter is sometimes preferred, although both are exported.

The difference between (normalized) and (original) is due to the SNR transformation: If performed channelwise (user-defined time range), each channel is "multiplied" by it's individual SNR, thus downweighting noisy channels. Fit algorithms are applied in SNR (normalized) space, resulting in Residual Deviation (normalized) or Explained Variance (normalized). The best fitting (normalized) result is then backtransformed to "µV" (original) space. Note that in a perfect world (where all channels have the same amount of noise), normalized and original give exactly the same values. The same is true if you specify a global noise level for all channels. Typically, the difference is not that great, since one tends to switch off bad channels before performing noise estimation.

These are followed by the Strengths, Locations (XYZ coordinates), and Normals (direction information, in XYZ coordinates).

Export <Results> to Excel. The Dipoles, Scan Dipoles, Scan Currents, Currents, CDR Dipoles, Leadfield, and Statistics results can be exported to Excel.

Export <Results> to MATLAB. The Dipoles, Scan Dipoles, Scan Currents, Currents, CDR Dipoles, and Leadfield can be exported to MATLAB.

Export <Results> to SPM. The Scan, Scan Currents and Currents can be exported to SPM as 3D images. **Statistical Parametric Mapping** (SPM) is third-party software for the construction and assessment of spatially extended statistical processes used to test hypotheses about functional imaging data.

Export <Results> to STL. STL is the file format used for 3D printing. There are several variations of this file format, which can be selected from the drop-down list.

Export <Results> to Data File. Source results contain forward calculated ("explained") data, which can also be shown in Maps. This option will create a CURRY-format data file that contains, as data, the forward calculated maps.

 **Note**

Export Leadfield to Data File. The term leadfield comes from the observation that when you enforce a voltage difference between two leads (electrodes), i.e. inject a current, you will obtain a distribution of currents throughout the head, which is called the leadfield. Reciprocally, if you place a current dipole inside the brain, you will obtain a distribution of currents throughout the head resulting in voltage differences at the leads. This (linear) relationship between a current dipole moment (for a dipole with fixed location and orientation) and the resulting voltage topography can be written as a vector. For many dipoles, it can be written as a matrix - the leadfield matrix. Typically it has #sensors x (#sourcelocation x 3) entries (three orthogonal dipoles per source location). The leadfield matrix thus describes the linear relationship between dipole moments and voltage maps, but also (reciprocally) between imposed voltage

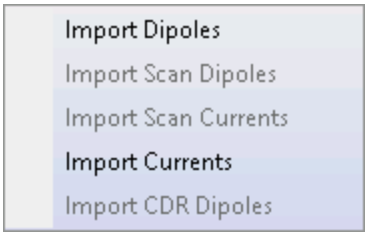
differences and resulting current flow in the head. The latter can be visualized in 3D View when displaying the lead field.

The Scan Leadfield can be exported as a .cdt file. In the process, .dpa and .pom files are created with the same root name, and in the same folder. If you retrieve the .cdt file in the Database, you will see one timepoint per (#sourcelocation x 3). If you are performing a moving dipole fit, for example, you get exactly the unit dipoles that were used to set up the leadfield matrix.

The leadfield may also be exported to Excel and MATLAB.

Report. The source reconstruction results may be appended to the Report.

Localize. The selected source reconstruction results may be imported to the Localize display.



Show Kept Results. If enabled, the Kept Results will be displayed automatically. If disabled, the checkmark for Kept Results will be off.

Change Colors for Kept Results. When enabled, the Kept Results will automatically be assigned a new color to better distinguish them (which can be changed in its Properties).

Uni Size for Kept Results. This option is typically used when doing Dipole Clusters. When enabled, the Kept Results all have the same size dipoles.

Uni Size for Appended Results. This option is typically used when doing Dipole Clusters. When enabled, the Appended Results all have the same size dipoles.

Replace Mode for Kept Results  . Replaces existing Kept Results.

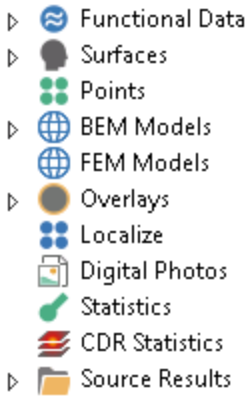
Append Mode for Kept Results  . Appends current results to Kept Results.

Save Results in Data Folder. When enabled, the Results will be saved in the Data Folder (where the data file came from). If the option is disabled, CURRY memorizes the last one that was used (the one you entered in the Save dialog).

21.1 Results

The **Results** panel is used to Load, Create, Unload, Save, Import and Erase the various Surfaces, Points, BEM Realistic Head Models, Overlays, Localize data, and Results that are or may be displayed in the 

or other displays.



Functional Data. Functional Data results can be saved from this location (*right click* and select **Save As**).

Surfaces. Surfaces are the results from segmentation, and include the skin and cortex, as well as the surfaces of the BEM Realistic Head Model compartments.

Points. Points can be distributed on the segmented surfaces, or throughout the segmented volume. They are typically (albeit rarely) used for source analysis, especially the volume points, which are an alternative to the 3D grids. If you have multiple Points files, these may be displayed individually (loaded first, if need be).

BEM Models. BEM Head Models that have been created are listed here.

FEM Models. FEM Head Models that have been created are listed here.

Overlays. Overlays store segmentation results and markers for later use, so that they do not have to be reconstructed at later times. They can be saved, imported, and loaded.

Localize.These are the files that have been created in the Localize part of CURRY, and typically contain sensor positions.

Digital Photos. Digital photos can be imported and used in 3D View.

Statistics. Statistical results can be retrieved and loaded.

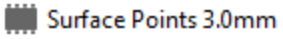
CDR Statistics. The CDR grand mean results can be retrieved and loaded.

Sensor Coherence. These are the coherence results among sensors.

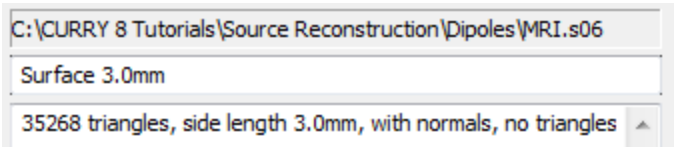
Source Coherence. These are the source coherence results.

Source Results. The results that are saved from **Source Results** → **Save Results As** are listed here.

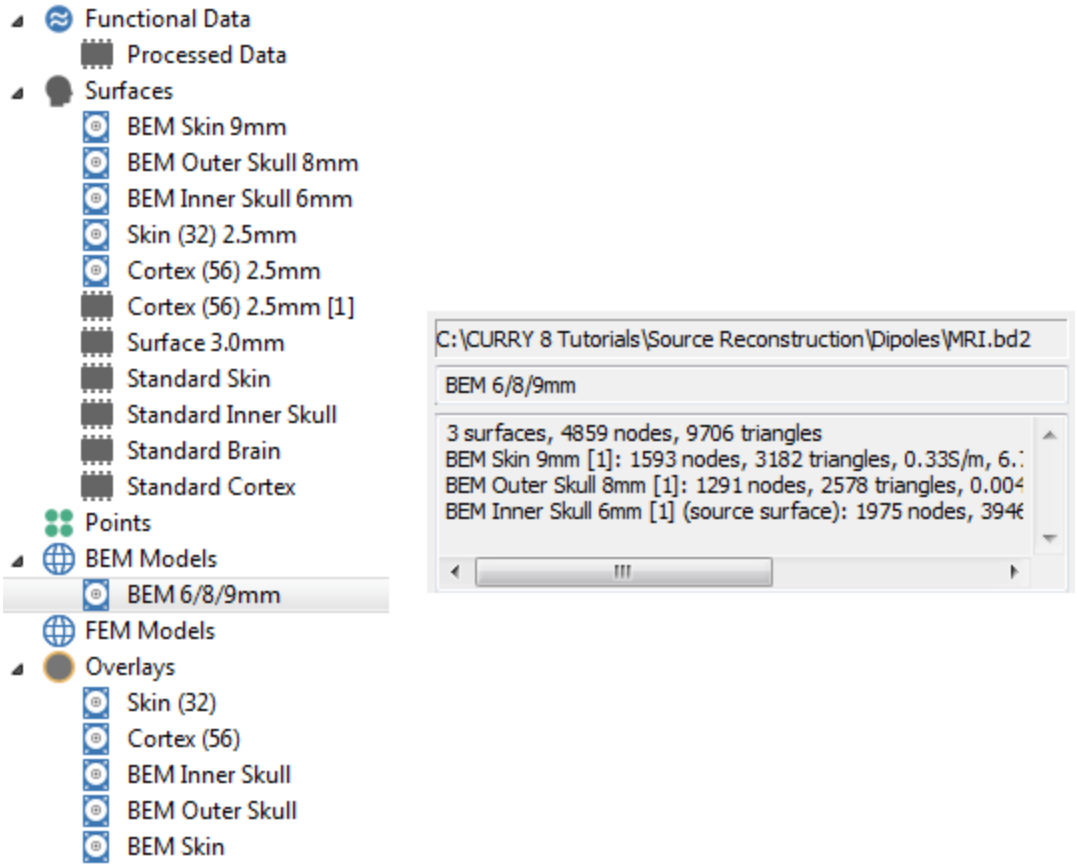
See the activated buttons and the context menu or the **Doubleclick** (mode) selection for each item's options.

The tree starts out empty, and is filled in automatically as Surfaces, Points, etc. are created or retrieved. For example, say you **Create a Triangle Mesh**. You will see a new entry under **Surfaces** in the tree: 

. If you highlight it, you will see the relevant details in the lower parts of the **Results** panel. In this case, the actual file name is MRI.s06, where MRI.img was the name of the image data file. You can rename the item if desired. Information about the file is shown as well.

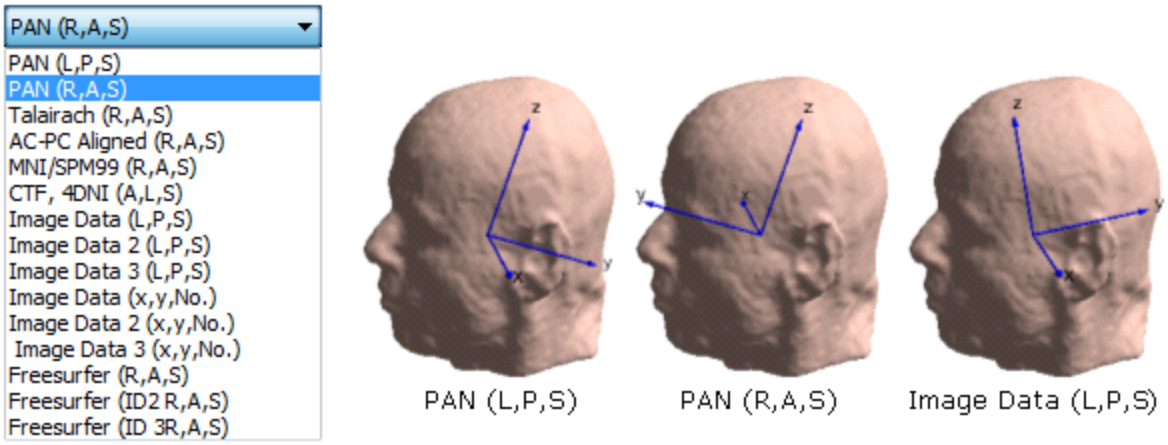


Similarly, if you create a BEM Realistic Head Model you will see the new Surfaces, BEM Realistic Head Model and Overlays that were created. Click on one of these to display the corresponding information in **Result Properties**,



as well as the BEM Realistic Head Model details. For each result in the list, a memory chip symbol ( ) indicates that the file is loaded into memory, but not saved; the hard drive symbol indicates the file has been saved on the hard drive, but not loaded; and the chip with a check mark ( ) indicates that the file is saved and loaded.

Coordinates. Once landmarks have been defined and saved, the coordinate system which CURRY uses for input and output can be freely chosen. "L,P,S, or left, posterior, superior", for example, refers to the direction of the XYZ axes. (L = left; R = right; A = anterior, P = posterior; S = superior). Image Data 2 and 3 refer to additional image data sets that may have been loaded. (The same options are found under the **Coordinates** option on the Main Menu bar).



PAN (L,P,S). This is CURRY's Internal Coordinate system, with the x axis going through PAL and PAR and pointing left, the y axis extending through the back of the head (on a line with the nasion site), and the z axis pointing upward.

PAN (R,A,S). The x axis goes through PAL and PAR and points right, the y axis goes through the nasion, and the z axis points up.

Talairach (R,A,S). Uses the Talairach atlas coordinate system. AC is the origin, the y axis points anterior and goes through AC and PC. The x,y plane is defined by AC, PC, and MS, and the x axis points to the right. All readings are scaled to match the atlas, based on the extensions of the brain as specified in the **Image Data Parameters** windows.

AC-PC Aligned (R,A,S). Used to be called Talairach [mm]. The origin is AC. y axis goes through PC and points anterior. x axis points right. z axis points up. Axes are **not** normalized according to brain dimensions.

MNI/SPM99 (R,A,S). Uses the Montreal Neurological Institute / Statistical Parametric Mapping (99) coordinates. The x axis points right, the y axis points anterior, and the z axis point upward.

CTF, 4DNI (A,L,S). Uses the coordinate definition from the CTF MEG software. The x axis extends through the nasion, the origin is halfway between PAL and PAR, and the x,y plane is defined by PAL, PAR, and Nasion. The z axis points upward.

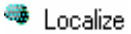
Image Data (L,P,S). The axes are aligned with the raw image data slices. Axes point approximately in the left (X), back (Y), and up (Z) directions.

Image Data 2 (L,P,S), **Image Data 3 (L,P,S)**. These options allow you to select among the Image Data sets you have loaded (up to 3).

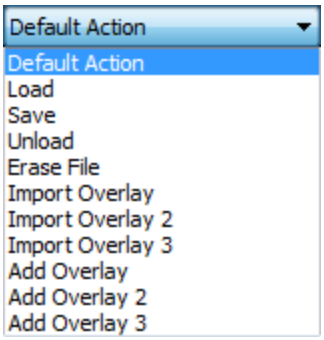
Image Data (x,y,No.), **Image Data 2 (x,y,No.)**, **Image Data 3 (x,y,No.)**. x and y are in-slice coordinates and No. is the slice number. These options are useful if the results need to be placed in relation to the original MRI slices.

Freesurfer (R,A,S), Freesurfer (ID2 R,A,S), Freesurfer (ID3 R,A,S). CURRY 8 (in Results) allows you to load Freesurfer-created segmentation results (triangle

meshes) such as lh.pial or rh.pial (these are their typical file names), and automatically co-register them into CURRY's coordinate system. An external tool plus some manual editing of files need to be used to achieve the same goal in the context of CURRY 7. In order to offer this new functionality, the co-registration between Freesurfer image data, Freesurfer triangle mesh data, and CURRY coordinates needs to be known. This is enabled by automatically detecting all required co-registration parameters when loading a Freesurfer T1.mgh or T1.mgz image data file (these are their typical file names). As a byproduct of and in order to verify the just described capability, CURRY 8 can output results in Freesurfer coordinates, where x points towards the right, y points anteriorly, and z points up.

Doubleclick. The Doubleclick list determines which actions are taken when you double-click on an item in the tree below. For example, select **Load** and double-click on 

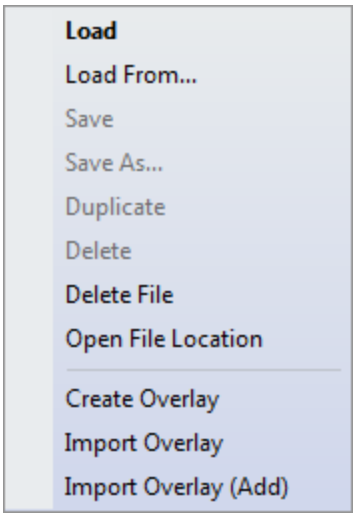
. An Open File utility will appear allowing you to select and Load a saved .pom file. Similarly, select **Save**, and double-click on an item in the last to save it. **Unload** shows all loaded results. **Erase File** shows all loadable results. **Import Overlay** shows all overlays (segmentation results) that can be imported to **Image Data** (or Image Data 2 or 3). **Add Overlay** adds the selected segmented compartment to the Image Data. These options are useful if the same operation shall be executed for several objects in quick succession. Hint: switch back to Default action when finished!



Context Menus

If you *right click* on an item in the list, you will see options similar to the ones shown. The options will vary depending upon which object you select, and the prior steps that have been performed. They will generally include **Load**, **Load From...**, **Save**, **Save As...**, **Duplicate**, **Delete**, **Delete File**, and **Open File Location**. Some of these have the same functions as the buttons below the display:

. The options below will vary from item to item.



If **Doubleclick** mode is set for **Default Action**, *double-clicking* will perform the action printed in bold in this menu. If a specific **Doubleclick** mode (not **Default Action**) is selected, *double-clicking* on a result in the tree will perform the selected action.

Load. Loads the item into the working area of CURRY.

Load From.... Opens an Open File window to select a stored file from the hard drive.

Save. Saves the item. A unique extension is added to the file, varying according to the type of file you are saving. The list below summarizes the basic extension scheme.

Surfaces: *.s00, *.s01, *.s02...
Points: *.sp0, *.sp1, *.sp2...
BEM Realistic Head Models: *.bd0, *.bd1, *.bd2...
Overlays: *.bo0, *.bo1, *.bo2...
Localize: *.pom
Results: varies according to the type of results being saved.

Alternatively, .pom files can be Loaded and Saved from the Localize panel. BEM Realistic Head Models can be Created and Saved from the BEM Model panel.

Save As.... Lets you save the file with a name of your choosing.

Duplicate. Creates a copy of the selected item.

Delete. Highlight an item in the list and click  to unload the item and delete it from the hard drive.

Delete File. Highlight an item and click  to delete the file associated with the item.

Open File Location. Open the Windows Explorer program.

Depending on the item clicked, you will also see one of the following: **Create Mesh**, **Import Mesh**, **Create Points**, **Create BEM (from Surfaces)**, or **Create Overlay**. These are additional places to create surfaces, points, etc.

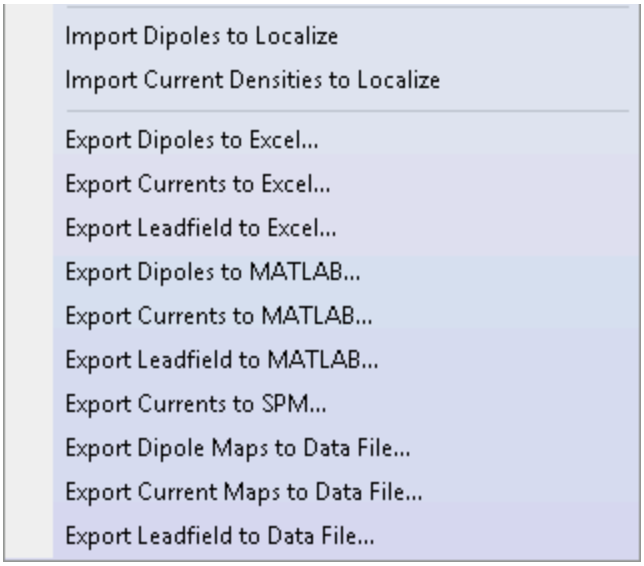
You may also see **Import Mesh**, **Import Points (to Localize)**, **Create BEM**, **Create BEM (from Surfaces)**, **Import BEM (to Surfaces)**, **Save (MATLAB Format)**, **Create Overlay**, **Import Overlay**, and **Import Overlay (Add)**. The item is imported and added to, for example, the **Surfaces** list, and also into the **Objects** list in the **3D View**.

Additional options from certain context menus include:

Prepare Inflation. Surfaces in the 3D View (such as the skin and cortex) may be inflated, which has the effect of smoothing rough places on the surface (with low numbers for Inflation), up to removing all features but the general shape. Initial calculations are required to remove handles, holes, and connecting nodes from the triangle geometry. If these initial calculations are done as part of meshing and before saving the mesh, any subsequent operations will be very fast. If not, these calculations are started when inflation is requested in the 3D View.

Save (CAUCHY Format). CAUCHY is the FEM software used in CURRY 4.6 to optionally compute leadfields. It is provided for those who work with software that evolved out of CAUCHY. The data are saved in the CAUCHY ASCII file format.

Append/Export Results to Report, Excel, MATLAB, and SPM. Source results can be appended to the Report, imported to Localize, or exported for use in third party programs.



Properties Icons

At the bottom of the panel are icons for several common functions.

Load. Clicking the button loads the Result.

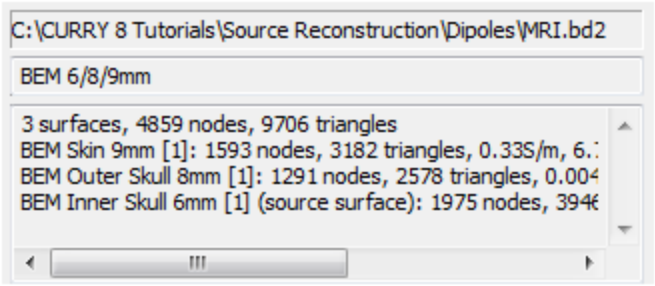
Save. Save any of the items on the list using the button.

Create. The Create button provides a way to create a new Surface, Point cloud, BEM Realistic Head Model, Overlay or Results. The action depends on the type of result. Highlight an existing Surface, BEM Realistic Head Model, etc., and click to create a new Surface, BEM Realistic Head Model, etc. In most cases, the highlighted item will be replaced with the newly created one. In some cases, such as with Results, a new item will be created with an incremented number.

After creating the new items, you may wish to go to the 3D View display, and select the items to be plotted using the **3D View**, Objects list to select the components to be included in the display. The list will correspond to the one you see in the **Results** Results list.

Import. Clicking imports the result. The action depends on the type of result.

Below the tree are three additional fields. The first shows the filename under which this result has been or would be saved. The next is the short name by which this result is referred to in the other parts of CURRY. Below that is a longer description of the result, usually generated by CURRY when the result is created. Both can be changed. Changes will be reflected in saved files after **Save** has again been selected.



Delete. Highlight an item in the list and click to unload the item and delete it from the hard drive.

Delete File. Highlight an item and click to delete the file associated with the item.

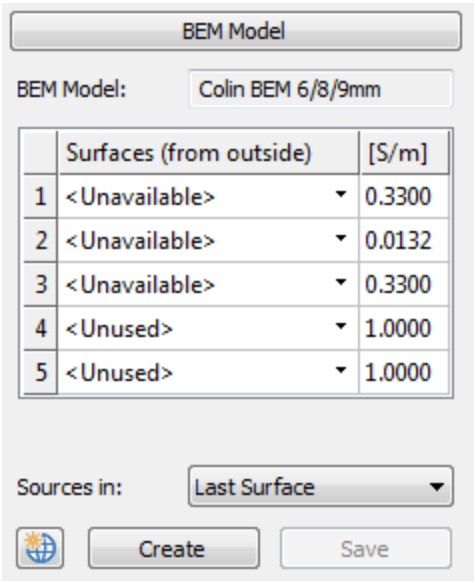
21.2 BEM Model

The functionality of BEM and FEM Model dialogs is twofold:

1. For reviewing/editing the properties of existing models. This can be done by opening both Results and BEM Model or FEM Model simultaneously via *CTRL+click* and choosing the model to review from the BEM Models or FEM Models list under Results.

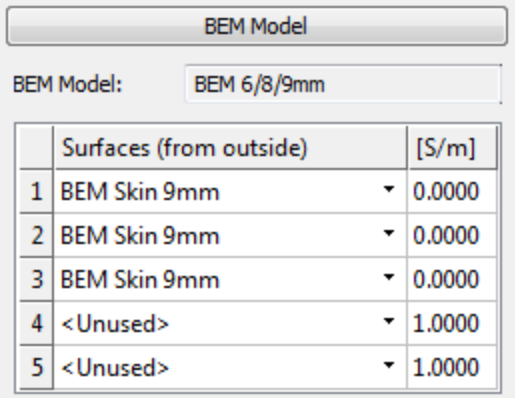
2. For creating custom models from the available (previously generated) surfaces in the case of BEM and overlays in the case of FEM.

The BEM Model panel is used to specify the surfaces and conductivities that comprise a BEM Model from the outside to inside. The top field shows the selected BEM Model (if you have more than one in the list). These fields are used if you are creating a BEM model manually, as opposed to using the automated method under BEM/FEM Geometry (please try the automated method first).

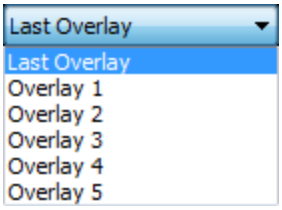


Surfaces. This lists the surfaces defining the borders of differently conducting compartments of the head model. The source surface is usually the last (innermost) surface. There are five potentially usable surfaces and their conductivities, listed from the outer to the innermost surface (skin to cortex, for example). The conductivities may be changed, if desired (*keyboard* input). All surfaces are initially <Unused> if no surfaces have been created. The Create and Save buttons will be grayed out initially. If surfaces exist, the default surfaces may initially by selected (review and change them if necessary). The **Setup New FEM Model** button allows you to switch from reviewing/editing to creating new models. When this button is pressed, the compartment list with the available surfaces or overlays is refreshed, so you can configure the new model and generate it by pressing Create.

After creating initial BEM Model surfaces (manually or from **BEM/FEM Geometry**), the drop-down list will contain the surfaces created.



Sources in. These are the source surfaces containing the sources of EEG and MEG activity. This is usually the last (innermost) surface.



Create. Clicking the Create button will create a new BEM Realistic Head Model using the selected surfaces (and any conductivity changes). The new model will appear in the **Result Properties** list New BEM Model and in the **Objects** list New BEM Model (under 3D View).

Save. Clicking the Save button lets you save the BEM Realistic Head Model (.bd**#**).

21.3 FEM Model

The functionality of BEM and FEM Model dialogs is twofold:

1. For reviewing/editing the properties of existing models. This can be done by opening both Results and BEM Model or FEM Model simultaneously via *CTRL+click* and choosing the model to review from the BEM Models or FEM Models list under Results.

2. For creating custom models from the available (previously generated) surfaces in the case of BEM and overlays in the case of FEM.

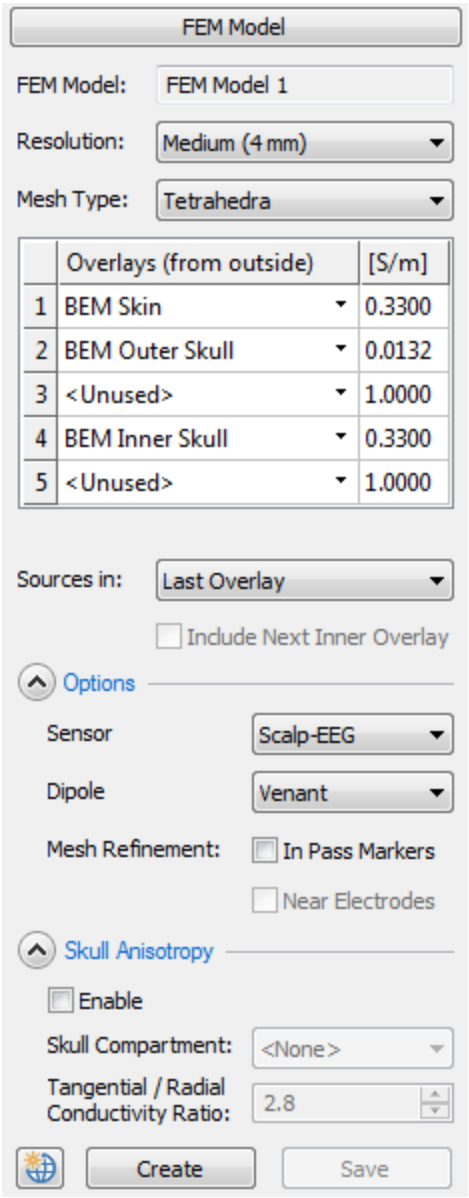
For advanced users, you may create a FEM model using the FEM Model parameters. The process is very similar to the BEM Model parameters, with the exception of the **Sensor Type** and **Dipole Model**. FEM models are primarily used with Intracranial-EEG; Intracranial-EEG must always use FEM models.

Generally, BEM models are faster, more stable and accurate when using source reconstruction methods in scalp EEG. FEM models offer the following advantages:

1. Better representation of depth electrodes (in particular intracranial-EEG, which is otherwise not possible using BEM); and

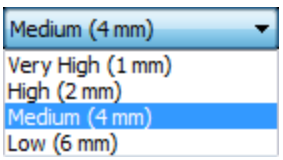
2. Allow the use of a more anatomically faithful anisotropic skull compartment. In later versions, white matter anisotropy may be added, which will make the FEM models more advantageous.

The FEM Model panel is used to specify the surfaces and conductivities that comprise a FEM Model from the outside to inside. The top field shows the selected FEM Model (if you have more than one in the list). These fields are used if you are creating a FEM model manually, as opposed to using the automated method under BEM/FEM Geometry (please try the automated method first).

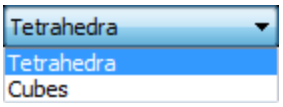


FEM Model. Name of selected model or of model to be created.

Resolution. Resolution refers to the element side length in the FEM volume mesh. Given that FEM is computationally intensive, Medium and Low resolutions allow quick estimates when performing source analysis, making it easier for experimenting with different methods (e.g. dipole type, current reconstruction type) . When producing final results, one should move to higher resolutions, which also reflect higher accuracy.



Mesh Type. Mesh type refers to the FEM mesh element type, which can be either Tetrahedra or Cubes (hexahedra). Both available mesh types yield similar results in comparable computation times. However, tetrahedral meshes can better capture smooth compartment boundaries without showing the staircase effect of cube meshes.

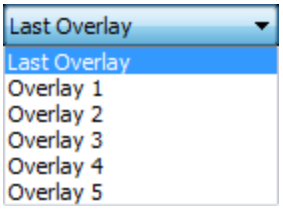


Overlays. This lists the overlays defining the borders of differently conducting compartments of the head model. The source compartment is usually the last (innermost) overlay. There are five potentially usable overlays and their conductivities, listed from the outer to the innermost overlay (skin to cortex, for example). The conductivities may be changed, if desired (*keyboard* input). All overlays are initially <Unused> if no overlays have been created. The Create and Save buttons will be grayed out initially. If overlays exist, the default overlays may initially by selected (review and change them if necessary). Click the  button to set up a new FEM Model.

After creating initial FEM Model overlays (manually or from BEM/FEM Geometry), the drop-down list will contain the overlays created.

	Overlays (from outside)	[S/m]
1	FEM Skin	0.3300
2	FEM Outer Skull	0.0132
3	FEM Inner Skull	0.3300
4	Skin (70)	1.0000
5	Cortex (170)	1.0000

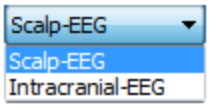
Sources in. These are the source surfaces containing the sources of EEG and MEG activity. This is usually the last (innermost) surface.



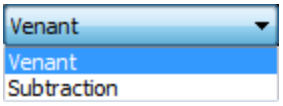
Include Next Inner Overlay. This option is used to expand the source compartment. For example, say you have selected Overlay 1 (FEM Skin) as the source compartment. If you enable **Include Next Inner Overlay**, the next Overlay (FEM Outer Skull) will be included in the source space. (This is the only place this option exists; it is not found in BEM/FEM Geometry).

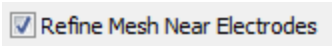
Options

Sensor Type. **Intracranial-EEG** has electrodes inside the volume; whereas, **Scalp-EEG** uses electrodes that are projected to the surface (as with BEM).



Dipole Model. These models are the way dipoles are represented in the FEM model. There are two dipole models, **Venant** and **Subtraction**. Venant is a chronologically older, blurred dipole, which is relatively fast in computation (default selection). The Subtraction model has a better accuracy overall; however, its computation is substantially more expensive.



Mesh Refinement. These options can be used when you want to locally refine the mesh to increase the resolution and thereby improve the accuracy of the source solutions. This is the manual version of what happens automatically when you select 

under 

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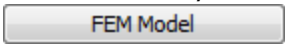
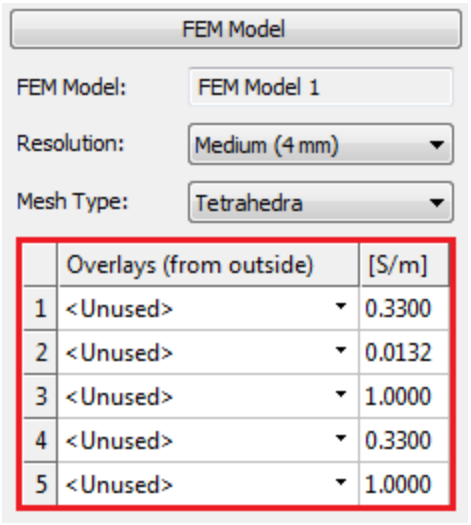
In Pass Markers. When enabled, you can set Pass Markers manually in an area where you want the increased resolution (see example just below).

Near Electrodes. When enabled, CURRY will automatically create areas of increased resolution in the areas along the electrode tracks (having first set the Pass Markers automatically). The sides of the mesh are reduced to 70%, and the Pass Markers are 30 mm in diameter (hard wired settings). This option will only be accessible when you select **Tetrahedra** for the **Mesh Type**.

To illustrate the two options, we will create a custom FEM model with both options enabled.

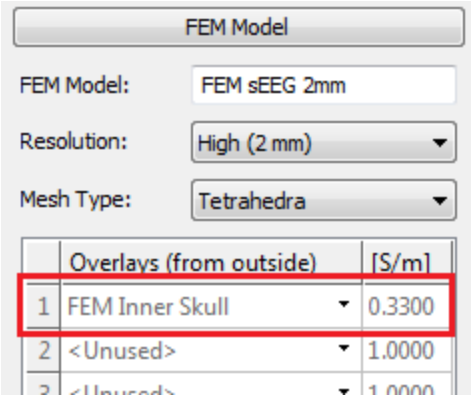
1. First we need to have a layer to work with. Without it, you will see nothing in the 

Overlay section. If we try to create a FEM Model now, we will get a message saying there is no overlay.

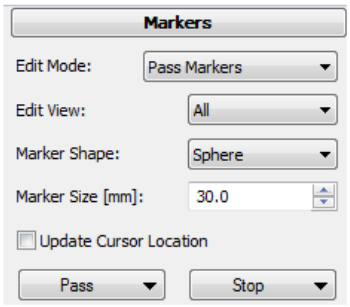


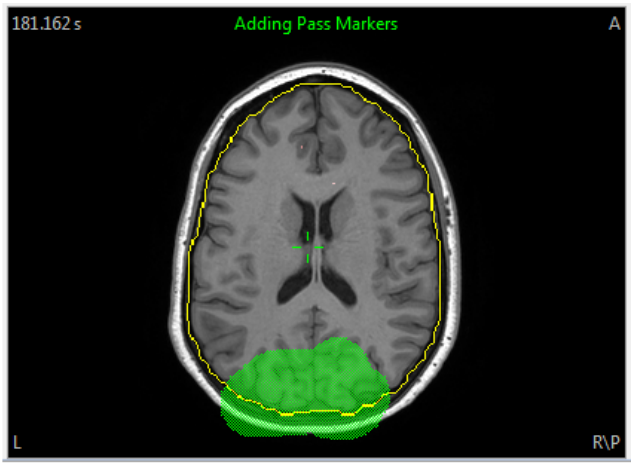
2. Create an overlay from the BEM/FEM Geometry panel. It does not matter what model you use to create the overlay - we will use the **FEM Intracranial-EEG** model Create: FEM Intracranial. Accept the defaults and click **Start**.

3. Back in the FEM Model panel, we now have a layer to work with.

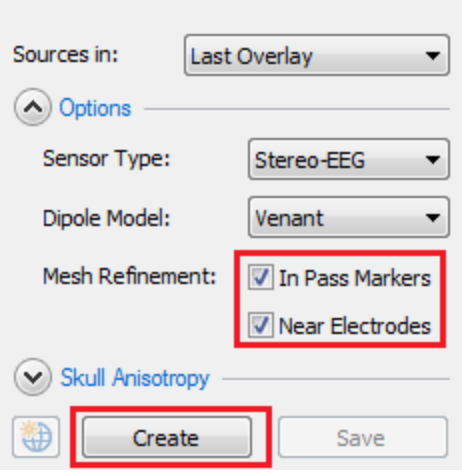


4. To use the **In Pass Markers** option, we need to place Pass Markers in the vicinity where we want the increased resolution. In this case we will just add them to the back of the head to make them easier to see. The **Marker Size** was increased to make it easier to mark a larger section.

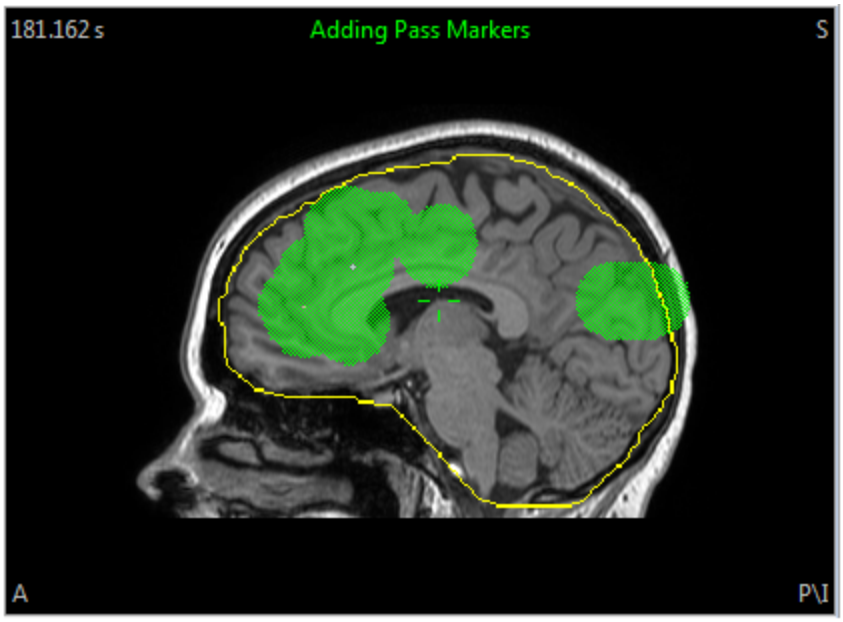




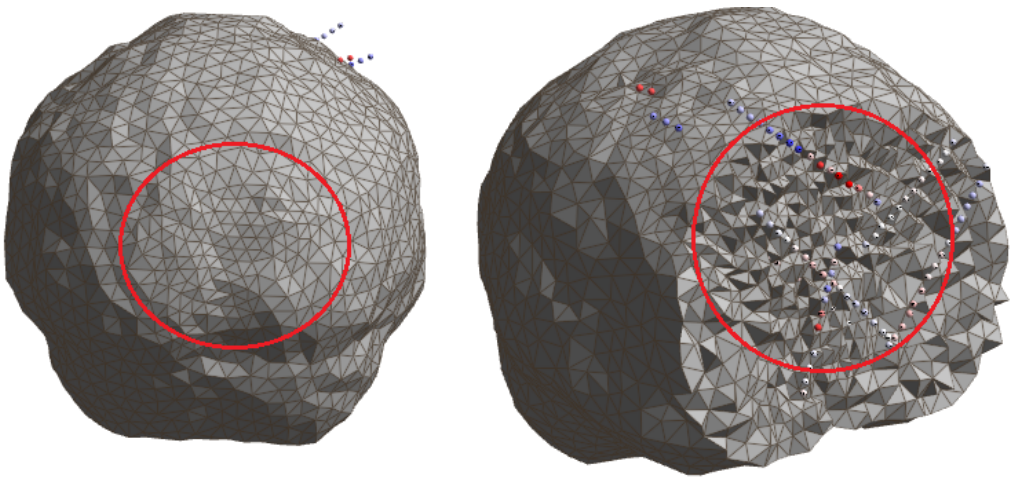
5. Back in the FEM Model panel, click the **Setup new FEM Model** button (lower left corner). Now we can select both the **In Pass Markers** and the **Near Electrodes** options. Select a lower resolution Resolution: Low (6 mm) (to save space and time), and you must select **Tetrahedra** rather than **Cubes** for the **Mesh Type** Mesh Type: Tetrahedra. Then click **Create**.



6. In the process you will see Pass Markers both at the back of the head (the In Pass Markers), and along the electrode tracks (the Near Electrodes).



7. In the 3D View, select the FEM Model FEM sEEG 2mm. You will see the increased resolution (smaller triangles) at the back of the head, as well as in the vicinity of the electrode tracks.



Skull Anisotropy

The skull anisotropy that can be applied to FEM models is based on a three-layer model of the skull, composed of compact-spongy-compact bone [1]. The middle layer (spongy bone and marrow) has been shown to be considerably more conductive than compact bone.

If we model these three layers as resistors in series for the radial conductivity or in parallel for the tangential conductivity, the tangential equivalent conductivity is higher that the radial one by a factor - *ft*. Considering spongy bone is more conductive that compact bone by a factor - *fb*, the ranges of conductivity found in the literature [2] yield for example:

with fb = 10, ft = 2.8 or
with fb = 5, ft = 1.7.

In CURRY, ft is called the **Tangential / Radial Conductivity Ratio**, and can be adjusted in the **Advanced** section of the **FEM Model** panel. By default, it is set to **2.8**. First select the **Skull Compartment** you are using from those in your current model (select the skull compartment overlay in your model).

The anisotropic conductivity of the skull compartment is then assigned by obtaining the normal vector to the skull outer surface for each of the corresponding mesh elements. The normal vector defines radial and tangential orientations, which are used for creating the symmetric conductivity tensor.

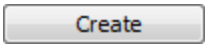
The tangential and radial conductivity values are obtained by following a volume constraint from the isotropic reference. This is done by fitting the volume of the ellipsoid defined by the anisotropic conductivity tensor, to the volume of the ellipsoid in the isotropic case. For this reason, in the UI only the isotropic conductivity value has to be defined.

[1] Fuchs M, Wagner M, Kastner J (2007): Development of volume conductor and source models to localize epileptic foci. Journal of Clinical Neurophysiology 24:101–119.

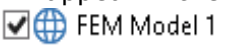
[2] Akhtari M, Bryant HC, Marnelak AN, Flynn ER, Heller L, Shih JJ, Mandelkern M, Matlachov A, Ranken DM, Best ED, DiMauro MA, Lee RR, Sutherling WW (2002): Conductivities of three layer live human skull. Brain Topography 14:151–167.

Setup New FEM Model  . This button allows you to switch from reviewing/editing to creating new models. When this button is pressed, the compartment list with the available surfaces or overlays is refreshed, so you can configure the new model and finally generate it by pressing 

.

Create. Clicking the 

button will create a new FEM Realistic Head Model using the selected surfaces (and any conductivity changes). The new model will appear in the **Result Properties** list

and in the **Objects** list 

(under **3D View** ).

Save. Clicking the 

button lets you save the FEM Realistic Head Model (.fd**#**).

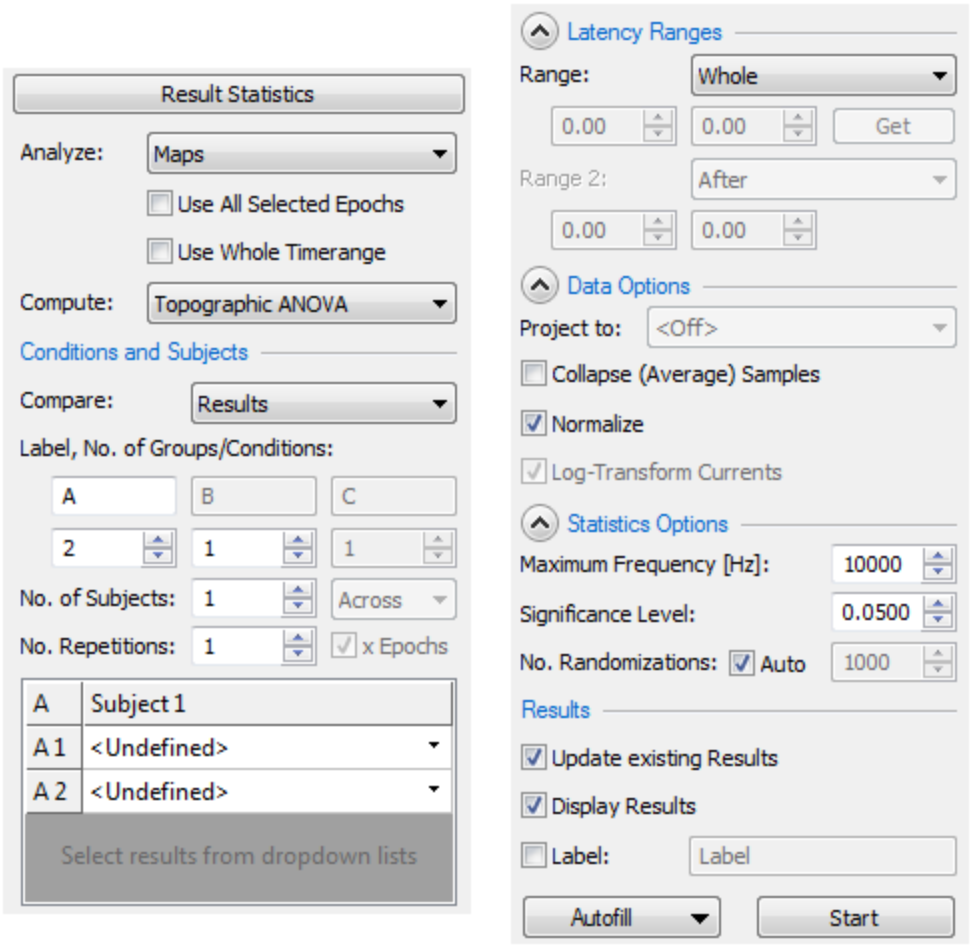
21.4 Result Statistics

CURRY 8 uses two methods of topographical ANOVA (TANOVA) randomization statistical methods. The first - Topographic ANOVA is based on Murray M, Brunet D, Michel C. Topographic ERP Analyses: A Step-by-Step Tutorial Review, Brain Topogr (2008) 20:249–264, and Koenig, T and Melie-Garcia L. A Method to Determine the Presence of Averaged Event-Related Fields Using Randomization Tests, Brain Topogr (2010) 23:233–242). These methods have been used in EEG for more than 10 years, although

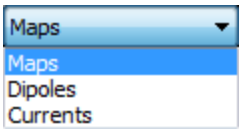
they have received less attention because of the high computational demands. They have become more popular recently as computer capabilities have increased. They do not depend on the same assumptions as parametric tests, and yet the results can be as powerful as parametric tests when the assumptions are met.

The second method - Maps SnPM - was developed in house. It has the advantage of displaying statistical measures for each sensor in the results, as opposed to the degree of contribution for each sensor. This difference will become apparent in the information below as well as in the *Statistical Comparisons - Maps* and *Statistical Comparisons - Dipoles, CDRs* tutorials. It is used with either waveform data or with CDR results.

It is possible to make group to group comparisons, event type to event type comparisons (single subject), or single event type comparisons (single subject signal versus noise). These are all demonstrated in the statistics tutorials (*Statistical Comparisons - Maps* and *Statistical Comparisons - Dipoles, CDRs*).



Analyze. Select the type of data that you wish to analyze. Basically, you are selecting between functional data (Maps) or source reconstruction results (Dipoles or CDR).



Maps. This option is used when you wish to compare the functional data (here called Maps) results across epochs. Typically, the epochs in this case are the Eps from individual subjects. The data matrix is filled based on the order of the epochs, which is based on the order in which they appear in the Study in the Database.

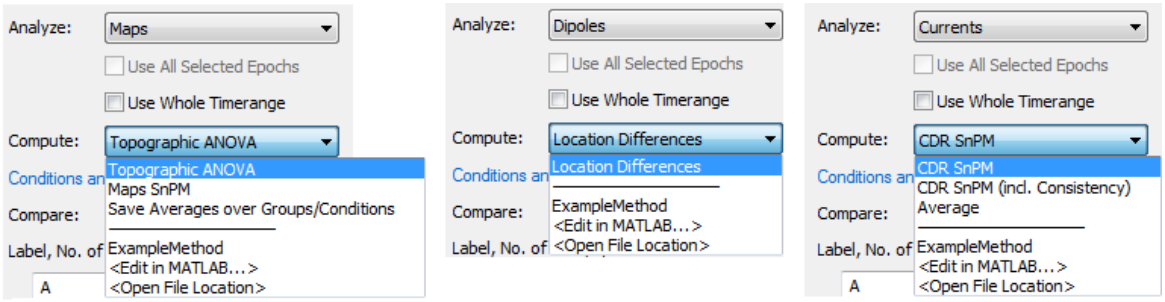
Dipoles. Select this option if you wish to compare Dipole results. The results are taken from the **Kept Results** (from the **3D View** display).

Currents. Select this option if you wish to compare CDR Currents results. The results are taken from the **Kept Results** (from the **3D View** display).

Use All Selected Epochs. To perform the statistical analyses with functional data, the epochs need to be overlain. Enabling this option performs the same operation as the **Use All** option under **Epochs**.

Use Whole Timerange. When enabled, the entire Timerange will be used for the analyses. Otherwise, the Timerange defined by the two outer vertical cursors will be used.

Compute. Select the type of statistics you wish to compute. The options will vary depending on whether you selected Maps, Dipoles, or Currents in the previous step.



Maps

Topographic ANOVA. This performs within-group consistency tests first and then the between-group difference tests. The resulting MGFPs for each group, as well as the p-values for the Timerange, can be displayed in **Maps**. Use the **Display** parameter in the **3D View** properties of the statistics results to select the results you want to see in the **Maps** display. 2D maps show the topographical distributions of the differences.

When looking at the functional data (Maps) or CDRs, the program performs within group consistency tests first in order to show that there are no initial differences across subjects, especially within the latency range that you will be analyzing. The results appear to similar to those shown in the figure below.

The program also performs the between groups differences tests and the interaction. After determining that there is significant consistency within the

Groups/Conditions, you will generally then look for differences across Groups/Conditions.

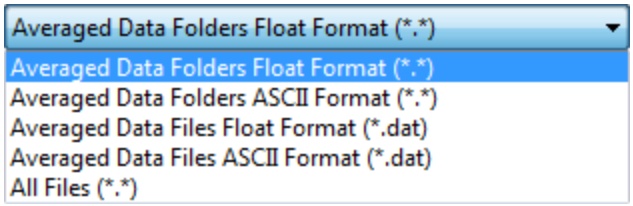
Please see the *Statistical Comparisons - Maps* tutorial for an example demonstrating how to perform the statistical analyses with Maps.

Maps SnPM. Briefly, **Maps SnPM** (Statistical non-Parametric Mapping performed on Functional Data, or Maps) is a method that analyzes waveform results that have been obtained for all files in a given experiment or all epochs of a given file or a combination of both. The results are readily available in the Statistics matrix dropdown lists and can be auto-filled just as in the TANOVA case. The results of Maps SnPM are a) the already known p-value plots that appear in Maps, plus (this is new and special for Maps SnPM) b) 3D distributions that show where in the brain the activity is significant (the p-value plots communicate that for this latency significant activations are found somewhere in the brain, while the 3D distributions show where this is the case).

M. Wagner, C. Ponton, R. Tech, M. Fuchs, & J. Kastner. Non-Parametric Statistical Analysis of EEG/MEG Map Topographies and Source Distributions on the Epoch Level, Kognitive Neurophysiologie des Menschen, 2014, 7 (1), 1-23.

M. Wagner, R. Tech, M. Fuchs, J. Kastner and F. Gasca. Statistical non-parametric mapping in sensor space, Biomed. Eng. Lett., 2017, Feb.

Save Averages over Groups/Conditions. This option is used to create averages for each of the subgroups. These will be saved in floating or ASCII format, either as files or in a folder using the file name you enter.



Dipoles
When comparing Dipoles differences between or among groups, it is necessary to first compute the dipole results and retain them using **Results → Keep Results** (see the *Statistical Comparisons - Dipoles, CDRs* tutorial). You may then select these Kept Results to fill in the analysis matrix.

The results consist of the distances between dipoles, the ratios of the strengths between dipoles, and the differences in orientation (in degrees) between dipoles.

Please see the *Statistical Comparisons - Dipoles, CDRs* tutorial for an example.

Currents
As with Dipoles, you need to compute the CDRs first for each group and retain them as Kept Results. The Kept Results are used to fill in the analysis matrix. Please see the *Statistical Comparisons - Dipoles, CDRs* tutorial for an example. This type of statistical analysis has not been used extensively with CDR data, and so these procedures should be considered exploratory.

CDR SnPM / CDR SnPM (incl. Consistency). Briefly, **CDR SnPM** (Statistical non-Parametric Mapping performed on Current Density Reconstructions) is a method that analyzes CDR results that have been obtained for all files in a given experiment or all epochs of a given file or a combination of both. This is similar to TANOVA, but in TANOVA the (readily available) maps are analyzed, while calculating CDRs for all of those maps is an additional processing step that needs to be performed as a prerequisite of calculating CDR SnPM. To do this, simply activate the desired CDR method (sLORETA is the method of choice because its results have some favorable properties that make it a more suitable candidate for CDR SnPM than e.g., MNLS; see the reference below) and the desired timerange (typically the complete timerange-of-interest or just everything as is usually done for TANOVA), and, in Threshold Criteria, "Keep Source Reconstruction Results" while scanning through the data. The results are readily available in the Statistics matrix dropdown lists and can be auto-filled just as in the TANOVA case. The results of CDR SnPM are a) the already known p-value plots that appear in Maps, plus (this is new and special for CDR SnPM) b) 3D distributions that show where in the brain the activity is significant (the p-value plots communicate that for this latency significant activations are found somewhere in the brain, while the 3D distributions show where this is the case). After calculations and if the "Display" option is checked, the data display is automatically reconfigured to show these 3D Distributions in Image Data's "Grid View" as well as in 3D View. Because CDR SnPM has been shown to calculate mostly meaningless consistency analysis results (see reference), consistency analysis is per default not performed, while still available as the special option **CDR SnPM (incl.Consistency)**. It must be mentioned that storing CDR results for all epochs of a real-world epoched data file, and a timerange that comprises more than just a few samples, requires huge amounts of memory and is therefore practically applicable only with using a 64-bit installation of Curry.

M. Wagner, C. Ponton, R. Tech, M. Fuchs, & J. Kastner. Non-Parametric Statistical Analysis of EEG/MEG Map Topographies and Source Distributions on the Epoch Level, Kognitive Neurophysiologie des Menschen, 2014, 7 (1), 1-23.

Average. This option averages CDR results across the Kept Results that are included in the matrix (grand average).

MatLab Interface. You must have MATLAB installed in order to use these options. Please refer to the **Interfacing with MATLAB** section.

Conditions and Subjects

Compare. Select the **Results**, the **Latencies**, or the **Latencies in Results** option.

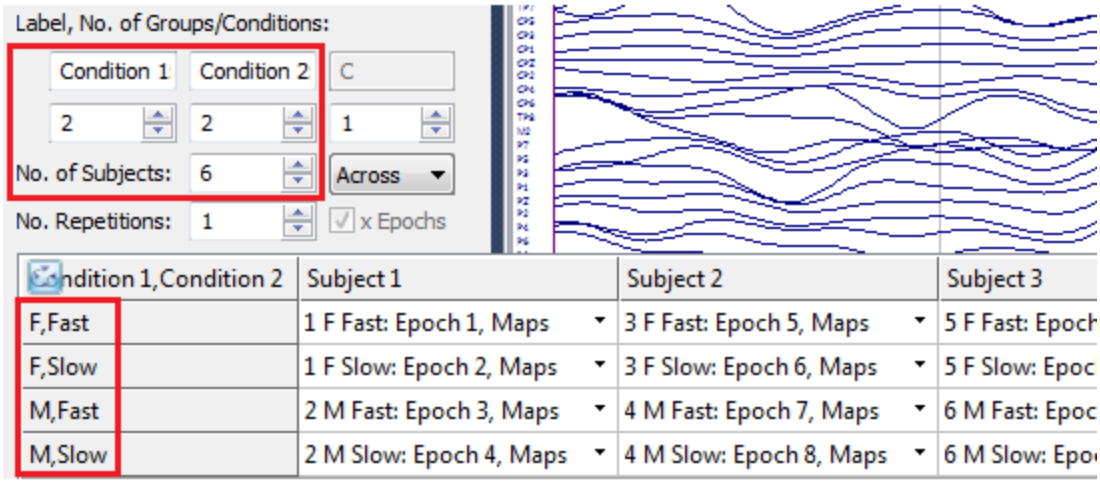
Results. In most cases you will select Results. This option is used for general comparisons of Maps and Dipoles, CDRs, etc.

Latencies. This option allows you to compare one latency range with another, within the same files. This option does not perform an analysis of latency differences between, for example, evoked potential components.

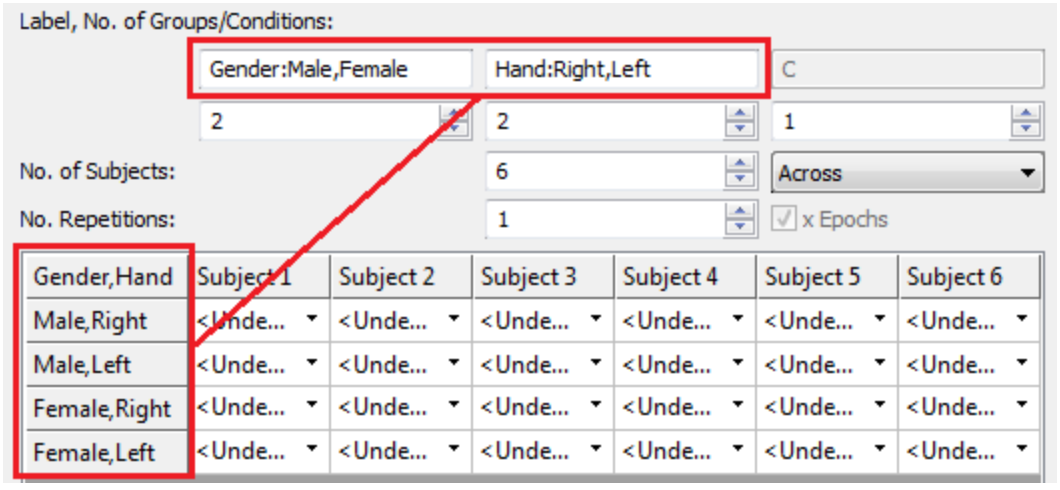
Latencies in Results. This option only makes sense if just two conditions are compared. It then allows to match/compare different latency ranges with each

other. Let's say the brain response of interest to targets is consistently 5ms earlier than the brain response to distractors, and we want to compare latency ranges with each other that are shifted by 5ms. Latencies in Results allows you to feed these data into the statistics calculations. Range 1 and Range 2 below are used to specify the two ranges. Typically this option is used with reasonably small analysis timeranges, not the whole page of data.

Label, No. Groups/Conditions. CURRY will first attempt to determine the Groups and Conditions labels, based on the information contained in the file names. For example, enter the number for Groups (groups are the same as conditions), then Conditions, then Subjects. Click Autofill to fill in the matrix. If the results are acceptable, you do not need to enter anything more here.



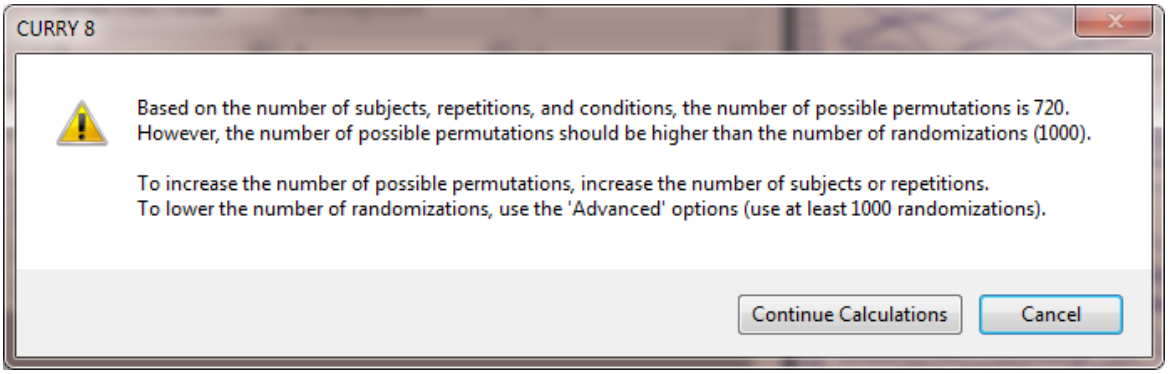
Otherwise, the Label is in the form of **A:X,Y**. You can enter other text, such as Gender, Male, and Female (**Gender:Male,Female**), and the new labels will be seen. In this case, entering the labels manually will make it easier to keep track of the results. The same can be done with the B and C groups/conditions. The labels will be carried through into the results labels.



Groups and Conditions are used more or less interchangeably, since the mathematics are the same. Generally, A will be the Groups, B will be the Conditions, and C will be

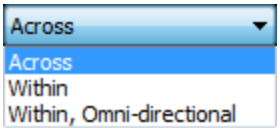
sub-conditions. The three fields correspond to A, B, and C. For example, if you have three groups and two conditions, the fields will be

With certain numbers of subjects and conditions (typically if there are only two groups and few subjects), you may see the following message. This type of statistic is not well suited for simple group to group comparisons; you may need additional subjects or repetitions in order to reach the requisite number of permutations (and randomizations).



No. of Subjects. This is the number of subjects per group (unequal N's per group not supported).

The adjacent field is used to select the type of randomization and comparisons that can be computed. The options correspond roughly to independent versus paired tests, where there are two ways in which paired comparisons can be computed.



If you have independent groups (different subjects, without matching), you would use the **Across** option. Randomizations and comparisons are computed across subjects, and Subjects and Repetitions are interchangeable.

If you have paired groups, i.e., repeated measures on the same subjects, or on meaningfully matched subjects, then you would use either the **Within** or **Within, Omni-directional** option. If you are comparing repeated measures across conditions in the same group as well as between groups (P300 amplitude before and after sleep deprivation in male versus female subjects), there could be differences in the distributions in the maps (maxima in one region and minima in another). If the differences are consistent enough, you may reach statistically significant differences. If the differences occur within the same group/condition, they can more or less cancel each other out, resulting in no significant differences due to increased error variance. This is analogous to the basic ANOVA, where the within group error variance may overpower any between group differences. Significant differences that may occur within individual subjects - regardless of the direction - are not taken into account in the overall results. In the current context, this is the **Within** option. It is analogous to the classic paired statistical

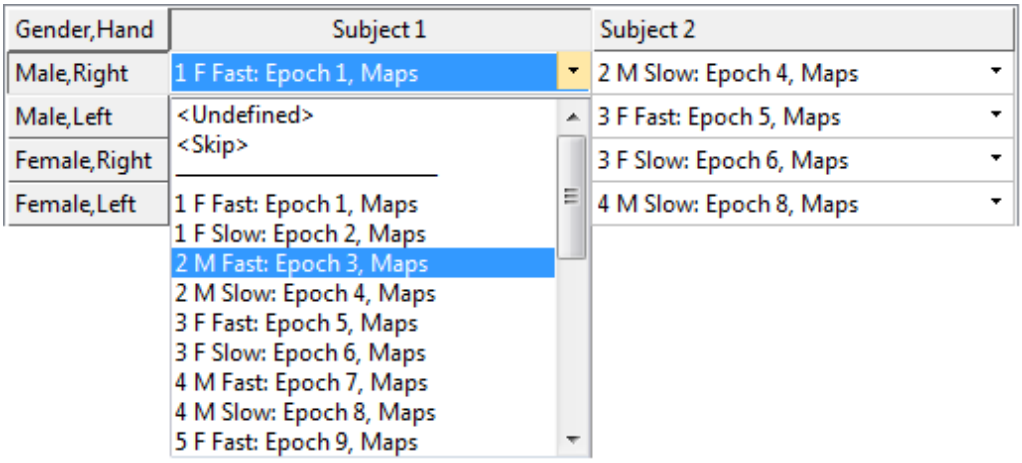
comparisons in parametric statistics. Here, the randomization occurs within subjects and the comparisons are across subjects.

The alternative is to use **Within, Omni-directional**. This takes into overall consideration the significant differences that can occur within subjects, regardless of the direction of the differences across subjects. Significant differences within subjects contribute to the overall p-values, regardless of the direction of the differences (all directions contribute; thus omni-directional). The randomization and comparisons are computed within subjects. Note that just one condition type and one repetition per subject are not enough. One needs more repetitions and/or condition types, otherwise a warning will appear.

No. Repetitions. Repetitions are repeated recordings from the same subject. Repetitions are one way to obtain more data for analysis.

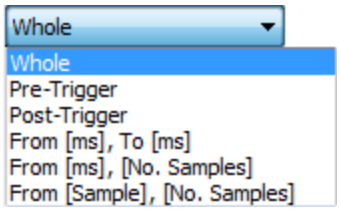
x Epochs. This option is enabled if the data being analyzed have more than one epoch of the same type, and these will be treated as repeated measures (see Repetitions above). This is typically the case for the analysis of individual trials (as opposed to averaged data), or if several averaged data files of the same condition(s) have been pooled together in an epoched file, which may make sense because the number of files to be analyzed will effectively be reduced, and because individual averages can then be deselected using the epoch selection tools. When enabled, all epochs are used.

Analysis Matrix



Latency Ranges
These fields are used to define the latency ranges to be used in the analyses. They are tied to the cursor positions in the Functional Data display. For example, if you have the outer cursor positions placed at 200-400 ms, and select **Whole**, the analyses will be computed over that range, not the "whole" latency range of the epochs.

Range. Select the range to be analyzed.



Whole. This uses the whole range as defined by the outer cursor positions in the Functional Data display.

Pre-Trigger. The pre-stimulus interval will be used.

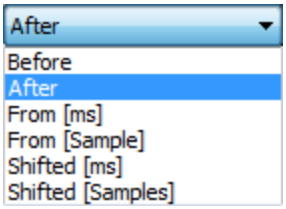
Post-Trigger. The post-stimulus interval will be used.

From [ms], To [ms]. You may define the interval to be analyzed (using ms's).

From [ms], [No. Samples]. The interval is defined by the starting ms latency to a specified number of data samples following it.

From [Sample], [No. Samples]. The interval is defined by a starting sample (data point) to a specified number of data samples.

Range 2. Range 2 will be active if you select **Latencies or Latencies in Results** for **Compare**. In this instance, you are comparing the data samples within one latency range to a second range, within the same data file(s).



Before. Data samples before the starting latency in Range 1.

After. Data samples after the ending latency in Range 1.

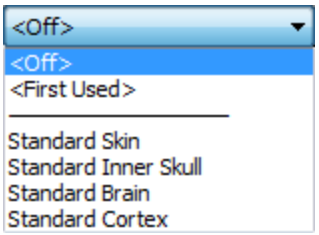
From [ms]. Data samples from this ms point to the same number of samples as selected above.

From [Sample]. Data samples from this sample point to the same number of samples as selected above.

Shifted [ms] / Shifted [Samples]. Sometimes it is easier to use a second analysis time range that is shifted by x ms or x samples with respect to the first (as opposed to entering the global numbers; see **Latencies in Results** above). These new options allow you to do so.

Data Options

Project to. **Project to** is only available for CDR SnPM and used to display analysis results on a different object (surface mesh, points) as opposed to what was used for calculating the CDR. Typically, calculate CDR on a grid, project onto a smoothed brain or a cortex. A nearest-neighbor approach is used to put CDR SnPM results onto the target geometry.



Collapse (Average) Samples. Sometimes you may want to average all input data for the analysis timerange (maps for TANOVA, CDRs for CDR SnPM) into a single map/CDR by means of averaging, and calculate the statistics result only for this single map. This is much faster than doing the calculations per sample, and/but the result will have no temporal resolution. If the analysis timerange is chosen wisely, one can also gain SNR by using this approach.

Normalize. If checked (default), all maps will use the CAR and are normalized before they enter the analysis. CDRs are normalized before entering into the analysis.

If unchecked, all maps will use the CAR before they enter the analysis. CDRs enter as they are.

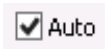
Usually, Normalize is checked. With single subject analyses, you might disable the option if you are looking for significant changes in overall amplitude, such as might happen with changes in arousal level across the recording (as opposed to topography).

Log-Transform Currents. This is something that should be done for CDR SnPM in order to transform input data into a representation with a more favorable distribution of values for statistics. It is therefore activated by default and should normally not be switched off.

Statistics Options

Maximum Frequency (Hz). The "Maximum Frequency" is meant to signify the maximum frequency in the data. This typically is the low-pass filter frequency, e.g. 40 Hz. A new, multiple comparison-corrected significance level can then be calculated based on the desired significance level (typically 0.05), the sampling rate of the data, and the "Maximum Frequency" (see above Wagner et. al. reference under **CDR SnPM / CDR SnPM (incl. Consistency)**. Downsampling the data to the lowest meaningful sampling rate based on the filter settings used is an alternative to using "Maximum Frequency".

Significance Level. Enter the p-value threshold that you wish to use (e.g., 0.05, 0.01, etc.). This value influences the dotted line shown in Maps, and also the analysis of consecutive latencies, but not the computation of p-values themselves.

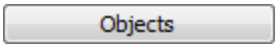
Number of Randomizations. The lower p, the higher the number of randomizations needs to be. For p=0.05, at least 1000 are suggested. Use 

if you are uncertain.

Results

Update Existing Results. Enabling this option will update existing results; if disabled, new results will be created.

Display Results. When enabled, the screens and options needed to select and view the statistical results will be displayed automatically (convenience feature so you do not have to select them manually).

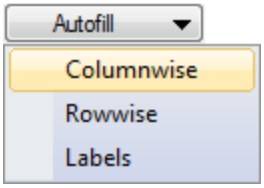
Label. Enable the field and enter a label. This will be seen in the 

list in the 

.

Autofill. The grid will be filled when you click the 

button. You can also select the files manually from the drop-down list to place the files as desired. If only the very first grid entry is defined, everything that follows will be consecutive.



Columnwise. The cells will be filled down the columns.

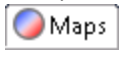
Rowwise. The cells will be filled across rows.

Labels. Selecting this option will leave the matrix contents as they are and will only affect the labels.

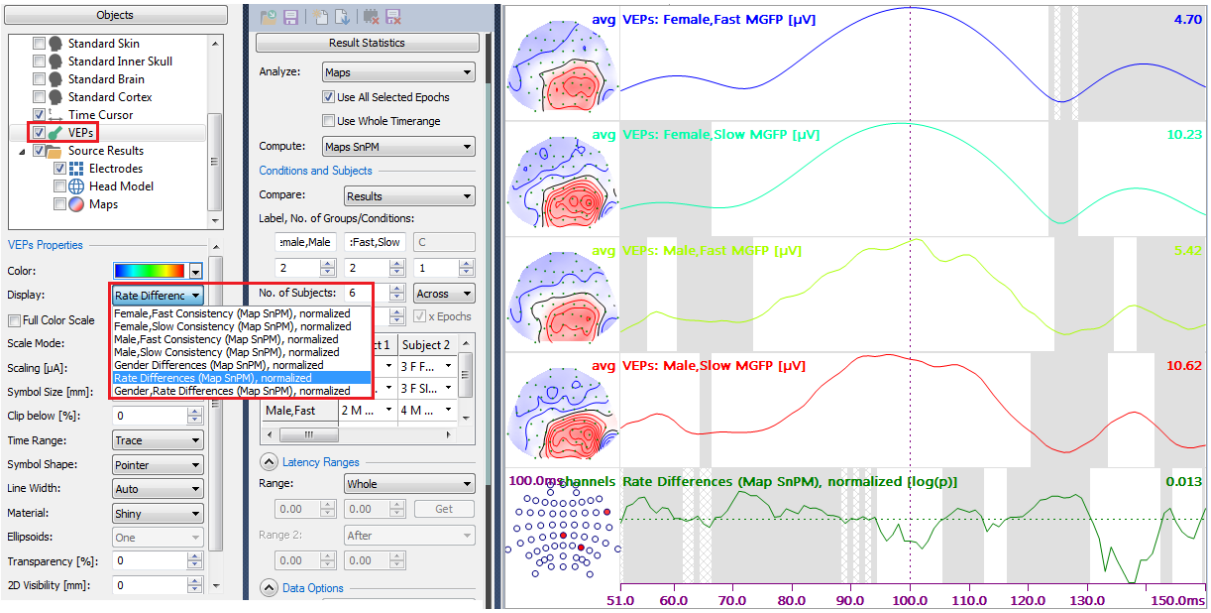
Start. Starts the analysis. The results will be seen in either the **Maps** display, the **3D View**, or both.

Results

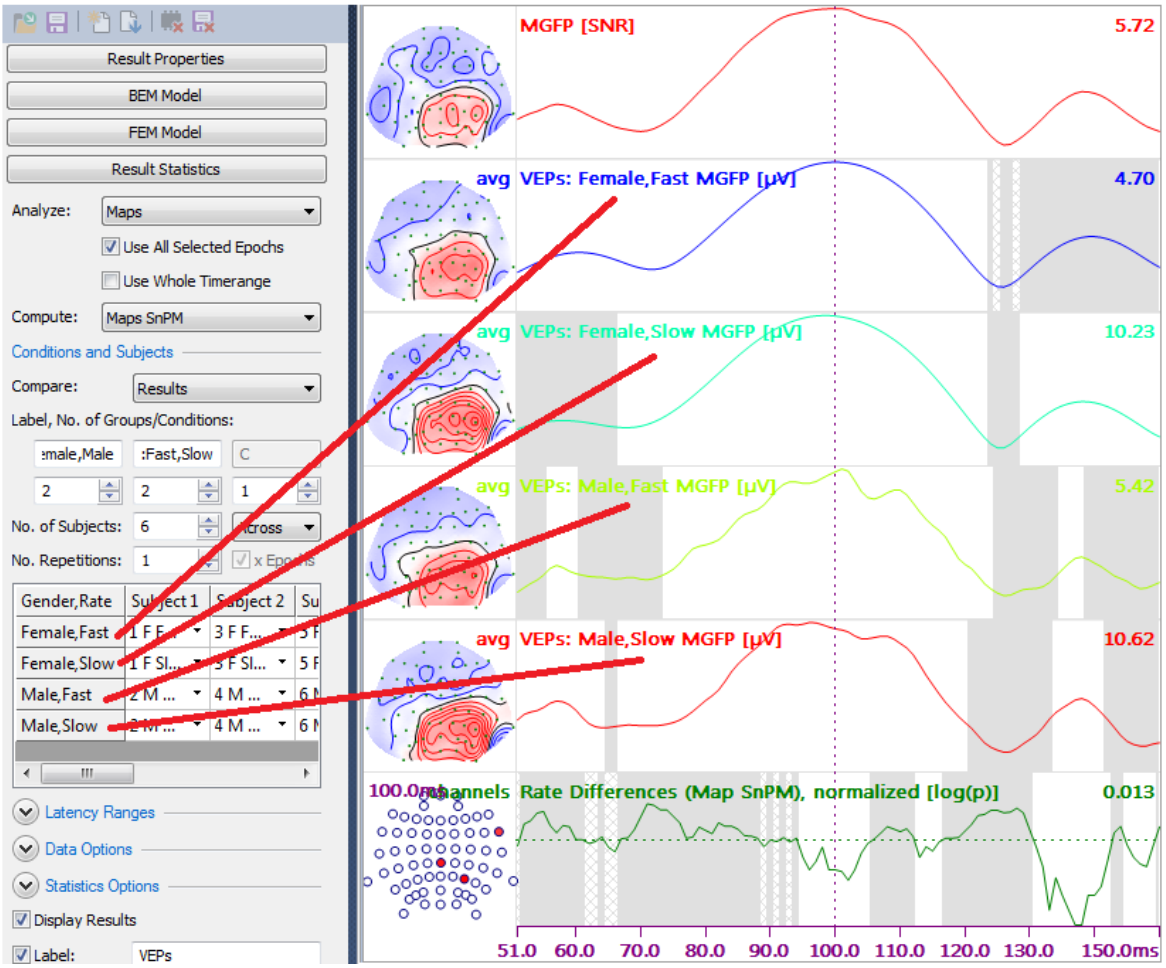
The results are seen in the 

display. What you see is determined by the **Display** option in the Properties of the statistical results (labeled *VEPs* below). The drop-down list lets you select the consistency results for each group, the differences between groups, and the interaction results. In the figure below, the group results for one condition (Rate) are displayed in the lower right field in 

. The dotted line is the p=0.05 level; values below the line are significant at p<0.05. The shaded regions are intervals where the differences were not significant.

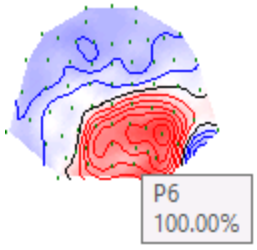


The first line is the overall MGFP for all epochs (enabled from Parameters under Maps). The next four fields above the consistency results correspond to the 4 groups that were defined. The graphs are displaying the MGFP for each group. The 2D Maps are displaying the averaged functional data waveforms for each group.

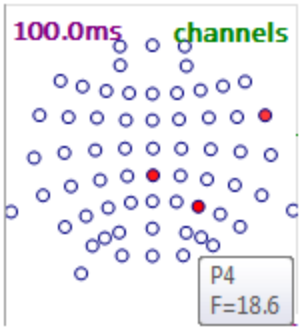


The map for the statistics results (which, when displaying Consistency results, will be the same as for whichever group results have been selected), shows where the differences were most pronounced (the lower left map).

Here is where you see the greatest difference between the basic *TANOVA* results, and the *Maps SnPM* results. With teh TANOVA, t*hese are not significance probability maps*; they are unitless distribution maps. The Tooltip that will appear for each site displays a percentage, where the site that best represents the significant differences has 100%. The others will have proportionally lesser percentages. The significant differences between groups are based on all electrode (sensor) data, and, like an overall F in a complex ANOVA, they do not indicate where the significant differences are occurring on the head - only that across all sites there are significant differences. See the Tutorial examples for more information.



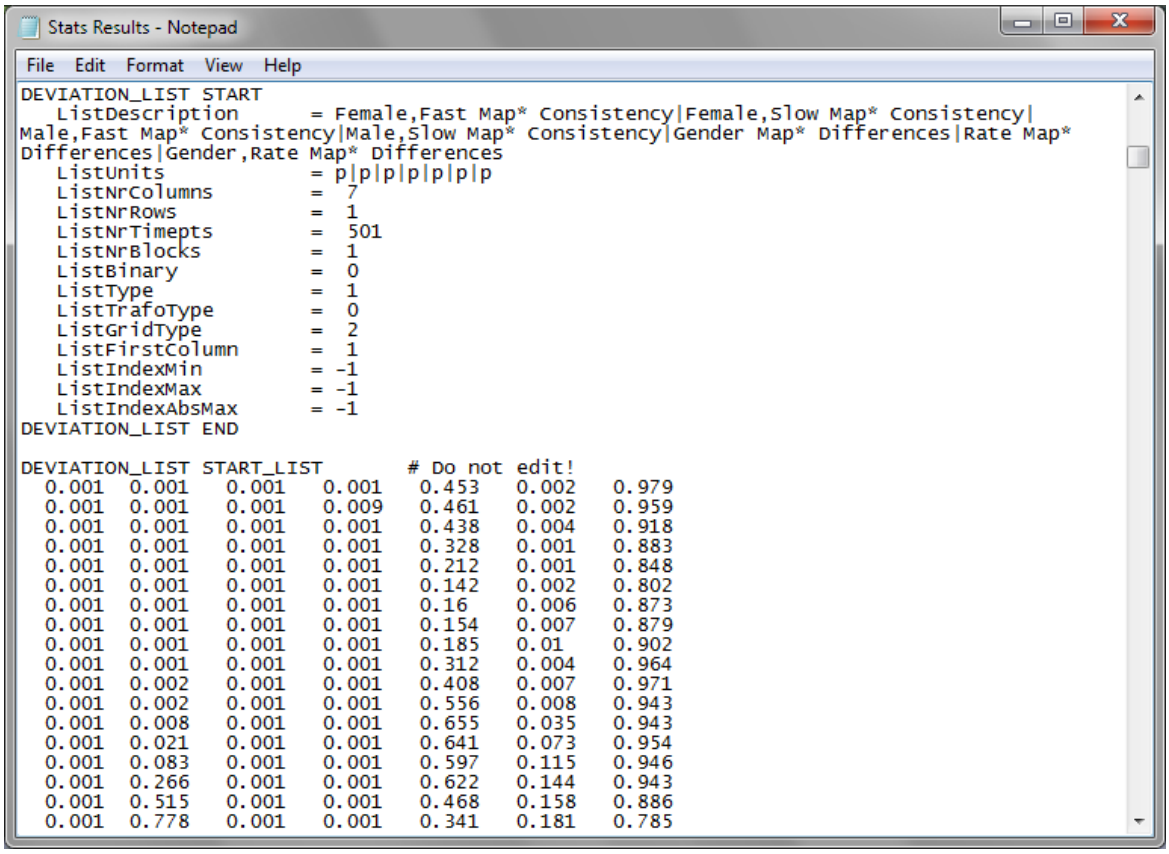
With *Maps SnPM* (and *Currents SnPM)*, however, you do see statistical results for each sensor, in the form of the F. See also the **Output** section for a summary of differences (for both methods).



Saving the Results

The Statistics results are saved from the Results list. *Right click* and select **Save As** (results files have .std extensions; CDR Average files have .stc extensions). To load the files in the future, *right click* on either and select **Load from**. After opening the Study, and before loading the results, you should first set the Timerange in the Functional Data to the same interval as when the statistics were computed. The statistics are seen again in **Maps**, and the CDR grand average is seen in **3D View**.

The .std files are text files that may be viewed in, for example, Notepad. In the Deviation List section of the file, you will see the probability values across time. In the example below, the first 4 columns are the Consistency values for the 4 conditions, followed by the main effect differences and the interaction results, as described on the ListDescription line.



TANOVA Computational Information (see Murray M, Brunet D, Michel C. Topographic ERP Analyses: A Step-by-Step Tutorial Review, Brain Topogr (2008) 20:249–264, and **Electrical Neuroimaging**, Edited by Christoph M. Michel, Thomas Koenig, Daniel Brandeis, Lorena R. R. Gianotti and Jiri Wackermann, Cambridge University Press, 2009).

Within group consistency:

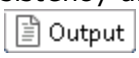
For a given time point,

1. Compute the grand mean across subjects.
2. Compute the GFP of the grand mean.
3. Separately for each group, randomly shuffle the measurements across channels.
4. Compute the grand mean using the randomly shuffled data of the individuals.
5. Compute the GFP of the randomized grand mean and retain it as one instance of the GFP under the null hypothesis (that the GFP of the grand mean before shuffling is about equally as large as after shuffling).
6. Repeat steps 3-5 a sufficient number of times (5000).
7. Compute the percentage of cases where the GFP obtained after randomization is equal to or larger than the GFP obtained in the obvserved data. This is the probability of the null hypothesis.

Between group comparisons:

1. Compute the grand mean across all conditions.

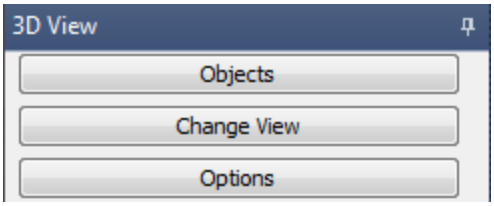
2. Subtract this grand mean across all conditions from the ERPs of all subjects and all conditions/groups to obtain the individual residual maps.
3. For a within-subject factor, compute the grand means of the residual maps for each condition; for a between-group factor, compute the grand means of the residual maps for each group.
4. Compute the observed effect size as the generalized dissimilarity based on the condition- or group-wise grand means.
5. For a within-subject factor, randomly shuffle the residual maps across conditions in each subject; for a between-group factor, randomly shuffle the residual maps across the groups.
6. Recompute the condition- or group-wise grand means of the residual maps after randomization.
7. Use these grand means to compute and retain an instance of the effect size under the null hypothesis as was done for the observed data in step 4.
8. Repeat steps 5-7 a sufficient number of times (5000).
9. Compute the percentage of cases where the effect size obtained after randomization is equal to or larger than the effect size obtained in the observed data. This is the probability of the null hypothesis.

The summarized results for within group consistency and between group differences and interaction are found in the 

display.

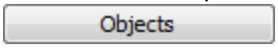
22 3D View

The 3D View window provides an easy and intuitive way for compiling 3D images of anatomical data together with the reconstruction results. Many different types of objects can be plotted. The image can be rotated and zoomed. Plot properties such as color and transparency can be adapted to suit individual requirements.



Note
Most settings can be saved and (automatically or manually) retrieved as **Global Parameters** or **Study Parameters** in the **File** → **Parameters** menu.

The **3D View** options are associated with the 

display (clicking it opens the 

panel).

Position the mouse in the upper left area of the 3D View display to see the 3D View Toolbar icons.

Rotate 360°  . This will rotate the 3D View display one complete cycle in the horizontal plane.

Left, Right, Top, Bottom, Front, Rear Views  . Select one of the standard viewing perspectives.

Timerange Mode  . This toggles between displaying results for a single time point and for all time points within the Timerange.

Ellipsoid Mode  . This toggles on and off the display of the Confidence Ellipsoids (the 1 SD ellipsoid volume displaying the certainty of the source results).

Go To Previous Dipole  . If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the previous dipole.

Go To Next Dipole  . If multiple dipole solutions have been computed, this option will move the Image Data display (slices) to the position of the next dipole.

At the bottom of the 3D View, note that there are options to display 1, 4, 6, or 9 views.

3D Stereoscopy

In order to use 3D stereoscopy in the **3D View**, you will need the following:

- Curry 8.0.0.43 or later
- Operating system that supports DirectX 11.1, i.e. Windows 8.1 or later.
- Latest version of graphics driver that supports "3D Vision" or "3DTV Play" (see below).
- DirectX 11.1 capable **Nvidia** graphics card. Care: Some laptops come with an Intel / Nvidia combination called "Optimus". In that scenario, the Intel card drives the output to the monitor and has to be disabled in the computer's BIOS / UEFI – provided the manufacturer supports this. The graphics board has to support 120 Hz "output".
- **G-Sync** has to be disabled https://en.wikipedia.org/wiki/Nvidia_G-Sync.
- 3D capable monitor, TV, or projector. For monitors, this basically means they have to support a 120 Hz "input" frame rate or higher, TVs and projectors typically bear the label "3D TV".
- Display cable that supports requested resolution and requested frame rate. For instance, 1920 x 1080 @120 Hz require an DVI dual link cable, DisplayPort, or USB 3.0.
- Either (active) shutter glasses or passive polarization glasses, depending on the display used.

"3D Vision"

- Consists of an IR emitter connected to a USB port and *matching* shutter glasses.

- Typically used with 120 / 144 Hz monitors, but also with some projectors.
- IR emitter communicates with glasses to cyclic disable left or right eye
- Display device has to support 3D Vision, Nvidia's setup wizard will take care of the rest.

"3DTV Play"
- Consists of "3D TV" capable display and *matching* shutter or passive polarization glasses.
- Typically used with projectors and TVs.
- Display directly communicates with shutter glasses, no IR emitter required.
- 3DTV Play software required (payware, free of charge for 3D Vision users). www.nvidia.com/object/3dtv-play-overview.html

Setup (Windows 10)
Please complete the following steps to set up 3D functionality.

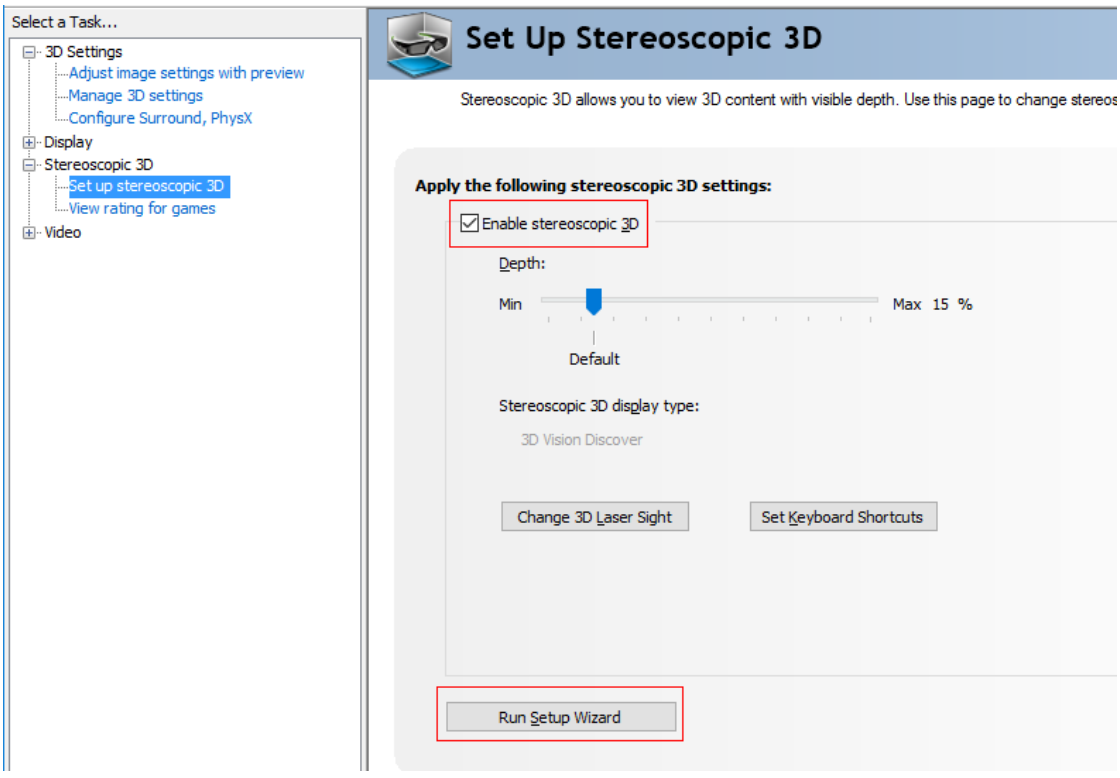
1. *Right click* on desktop and select **Nvidia Control Panel** from the context menu.

2. Expand the tree item **Stereoscopic 3D**.

3. Select **Set up stereoscopic 3D**.

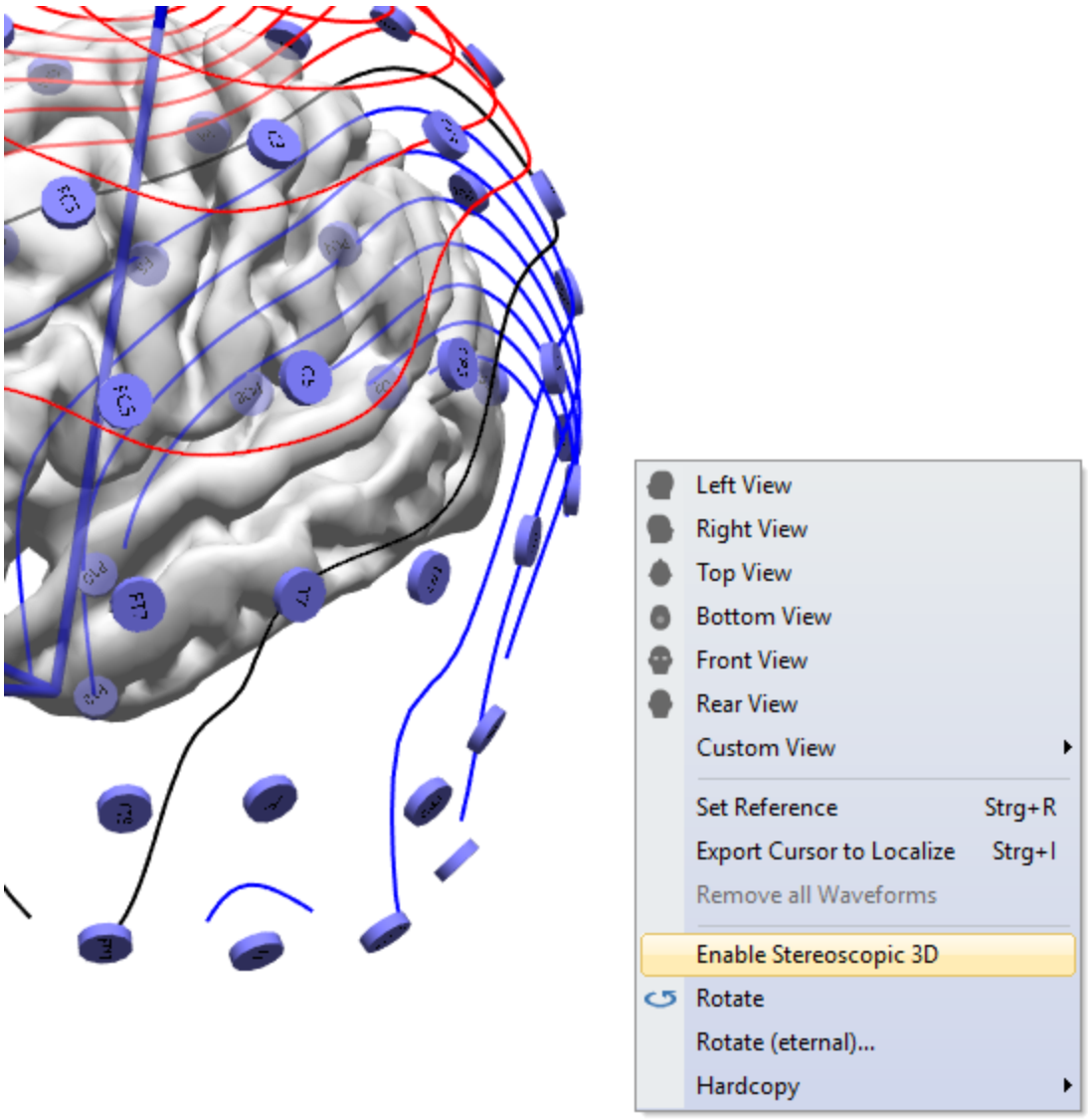
4. Check box **Enable stereoscopic 3D**.

5. Click button **Run Setup Wizard** and follow instructions.

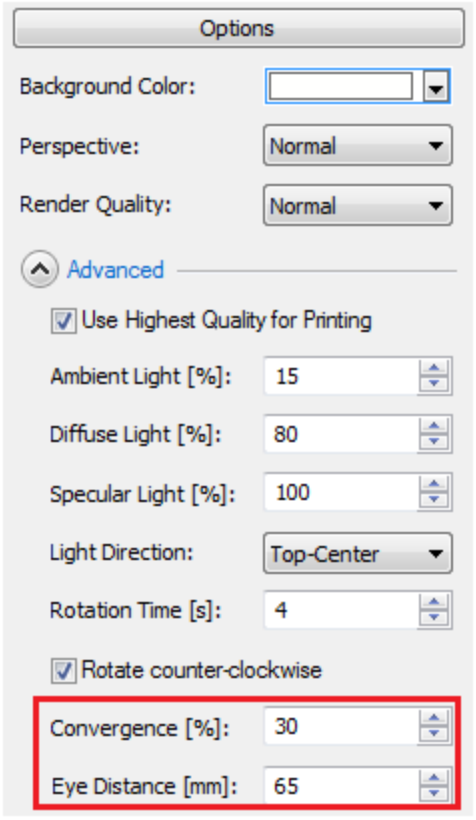


6. Start Curry 8 and load a study.

7. Switch to a rotatable 3D View and select **Enable Stereoscopic 3D** from the context menu.



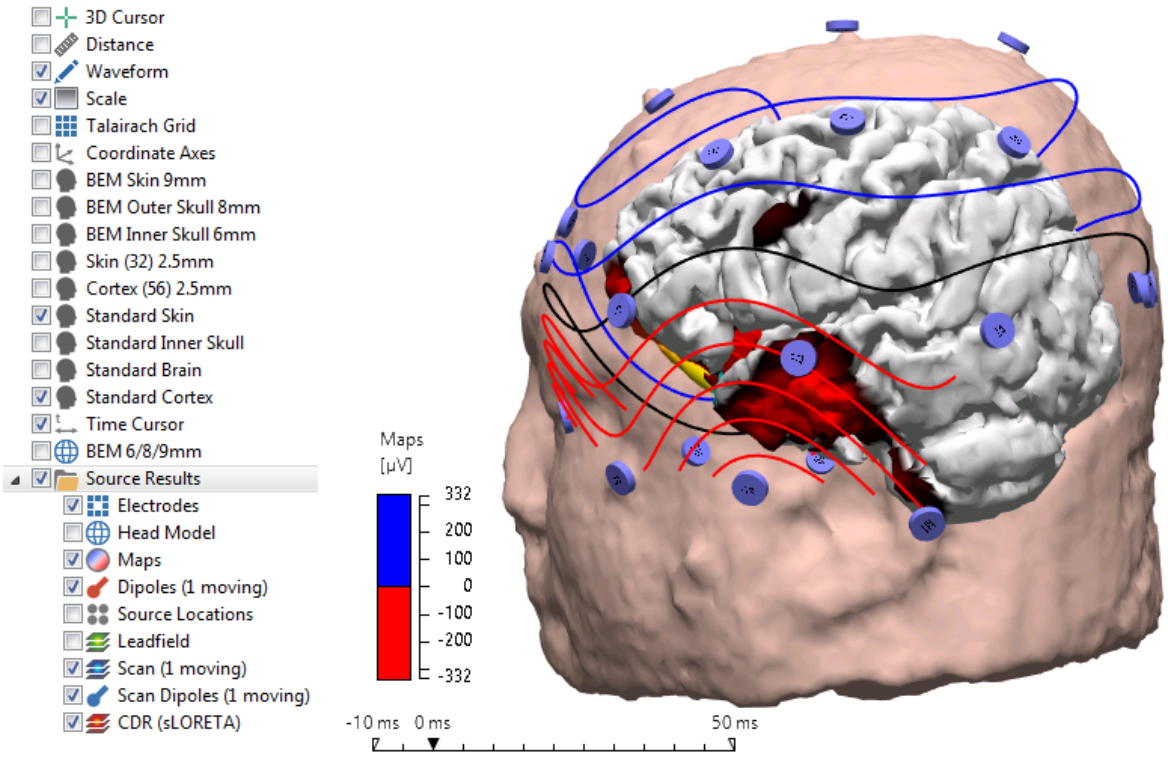
8. You may want to adjust **Convergence** (do so carefully, as it might cause eye strain) in 3D View's **Options**, in the **Advanced** section. (Leave **Eye Distance** in the default setting, unless directed to change it).



22.1 Objects

The Objects list lets you determine what to include in the 3D display. The number of items in the list will be determined by the operations you have completed (such as, creation of a BEM, dipole localization, etc.). Most Objects have their own properties, which typically include color, size, transparency, and other selections.

If you click on an Object in the list, its Properties will be displayed below the list. Alternatively, you can click the Object on the actual 3D Display, and that will also show that object's Properties.

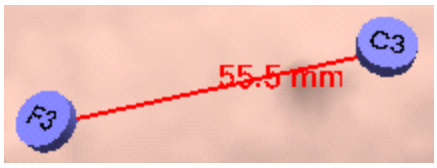


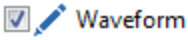
Some of the first objects are present in the absence of any analysis operations.

3D Cursor 3D Cursor . This is the crosshair that is used in conjunction with the cursor position in the iso-images (in the Image Data display). The color, size, and line width are set in the **3D Cursor properties**. The **3D Cursor** has a unique property called **Track Mouse**. With **Track mouse** set to **On**, click on a *surface* in the 3D View and the Image Data cursor will move to that point. It functions as an aid for use with the Cutplanes (described below). The **Localize link** option can be toggled on and off. When toggled on, clicking on a surface in the 3D View with transfer the coordinates to the Localize display, and add the point(s) to the list in the **Localize** panel.

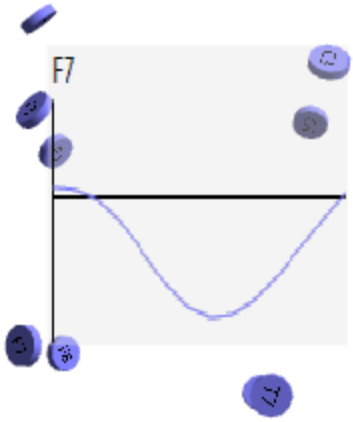
Note
Initially, the **Size** of the 3D cursor is zero and **Track mouse** is **On** in order to establish a link between 3D View and Image Data without displaying the cursor symbol in the 3D View. The default size is 20mm, and the display checkbox is Off initially. (Size ≥ 100mm will always cover the whole display, regardless of window size).

Distance Distance . This option toggles on and off the line representing the distance between two objects, as set using the **Set Reference** option (*Ctrl+R*). Use Set Reference to set the starting point, then click on another surface. If Distance is enabled, you will see the line connecting the two and the distance between. Points can also be selected from the Image Data display. Use the Distance Properties to change the text color, size, and unit of measurement.

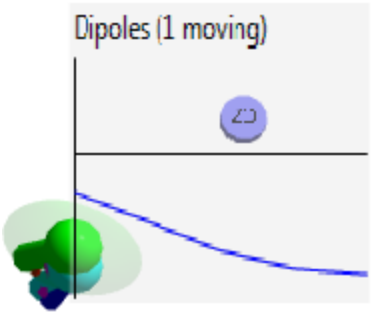


Waveform  . When enabled, you will be able to view waveform information for a selected sensor (electrode or coil) or dipole by using *Ctrl+click*. Remove all waveforms by selecting **Remove all Waveforms** from thew context menu.

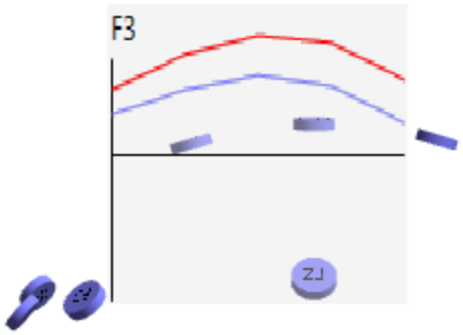
Ctrl+click on a sensor to see the EEG/MEG waveform data for that sensor. *Ctrl+click* again to remove it.



If you have performed dipole source reconstruction, *Ctrl+click* on a dipole to see the Dipole Strengths. *Ctrl+click* again to remove it.

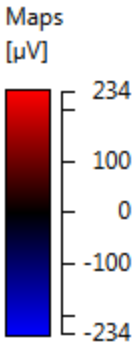


If you have performed dipole source reconstruction, *Ctrl+click* on a sensor to see the measured (blue) and fitted (red) waveforms. *Ctrl+click* again to remove it.

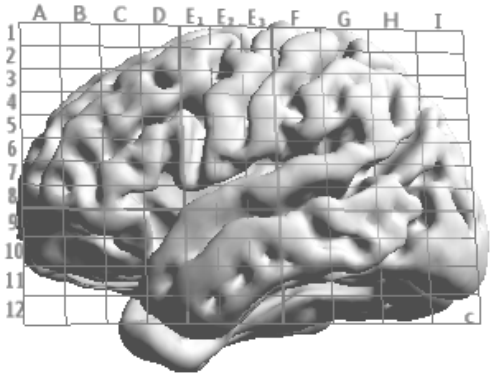


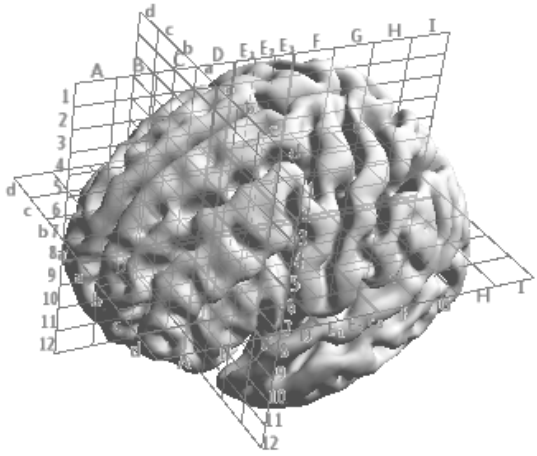
There are options for setting the line and background color; width, height and offset of the waves; line width size and text size; and transparency.

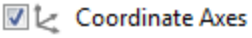
Scale Scale . The color scale can be toggled on or off. The scale only appears in the 3D Display for certain objects: Functional Data, Dipoles and Scan Dipoles (if they are colored according to their goodness-of-fit), Scans, and Currents. These typically have color ranges selected, rather than solid colors. The **Scale** serves as a legend for the colors. The color selected in **Scale properties** is for the text and lines; the scale color is set by object being scaled (such as, the Functional Data).



Talairach Grid Talairach Grid . Enabling this option superimposes the Talairach Grid on the **3D View** cortex (single or triple plane) as well as on the **Image Data**.

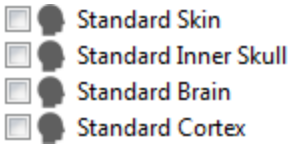




Coordinate Axes 

. These are the XYZ axes that are displayed. The Labels are the "X, Y and Z". You can set the **Color** independently for the Axes and the Labels, vary the length of the Axes, and you can vary the **Text Size**, **Material**, and **Transparency**.

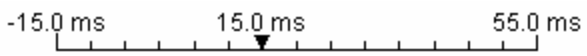
Standard Skin, Standard Inner Skull, Standard Brain, Standard Cortex. These are the compartments and surfaces, computed from the MNI averaged MR data set.



The options for each are described below.

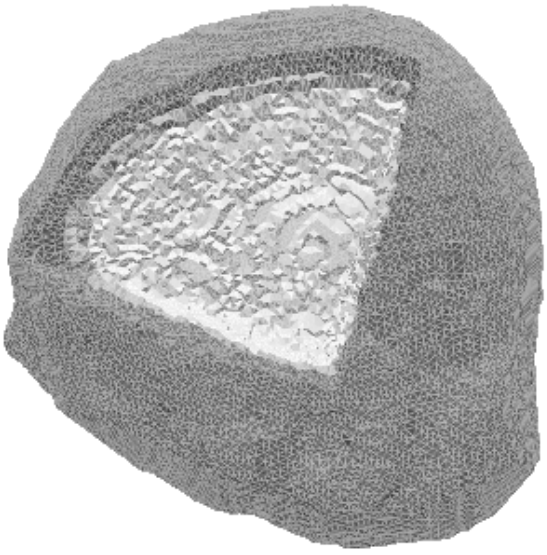
Time cursor 

. The Time cursor is the time range of the selected interval. It may be toggled on and off, and you may select a color for it. You can drag the cursor with the mouse, use the *arrow* keys on the keyboard, or play a Movie (*Alt+M*) to move through the time points.

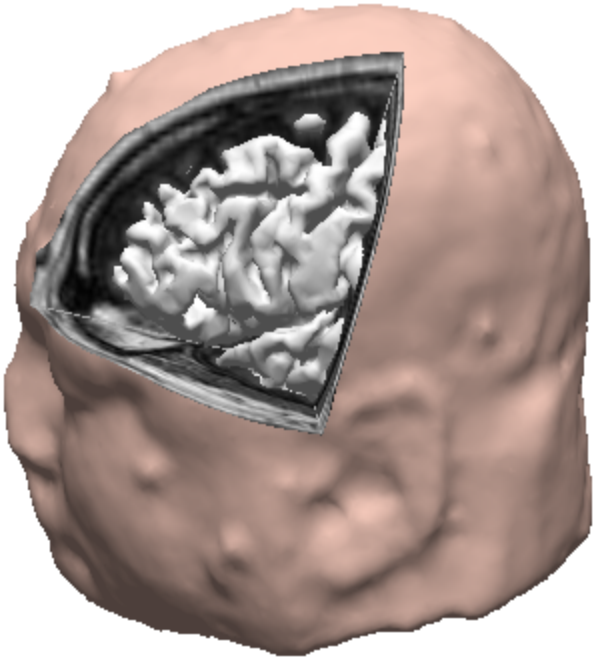


The next set of objects are the BEM surfaces, the segmented surfaces, and the BEM Realistic Head Model(s) that will appear if the surfaces/models have been created.

BEM/FEM Realistic Head Model surfaces. These are the Skin, Skull and Brain compartments used in the BEM and FEM Realistic Head Models. For all of the surfaces in the BEM/FEM Realistic Head Models, you may select the surface Color, Wireframe Color, Wireframe options, Triangles, Material, Inflation, and Transparency from the properties lists (described below). Cutplanes can be used with all of the BEM/FEM related objects (described below).



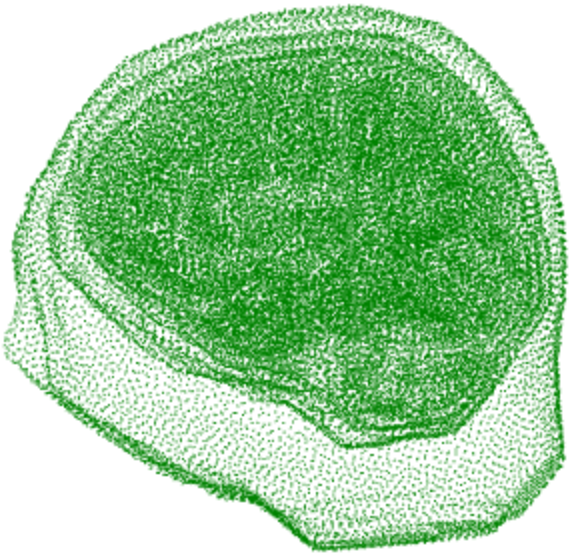
Skin/Cortex. These are the skin and cortex surfaces created when you either segment them manually, or automatically when you use CURRY's automated segmentation routine (left).



Additional Objects

Surface  Surface 3.0mm . This is the result of selecting the **Create a Triangle Mesh** option.

Surface Points  Surface Points 3.0mm . This is the result of selecting the **Create Surface Points** option. Below are the surface points for a BEM model, for example.



Localize Localize . Selecting this will display the points you have selected in the **Localize** display.

Voxel Mesh Voxel Mesh . Selecting this will display the voxel mesh you have created.

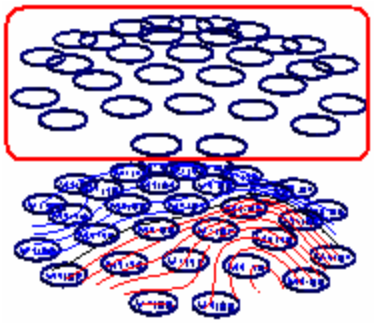
Statistics Statistics . The Statistics Properties are used to display different statistical results.

Source Results. The list of objects under Source Results will vary depending on whether you have performed source reconstruction (and the type of reconstruction); however, some objects will generally be seen regardless.

Functional / Anatomical Landmarks. Toggle the display of the functional (red) and anatomical (blue) landmarks on and off. The Color, Size, Shape, and Transparency can be modified in the properties.

Electrodes. Toggle the display of the electrodes on or off. If you select a color range instead of a solid color, the color of the sensors will reflect the voltage / flux of the currently selected time point.

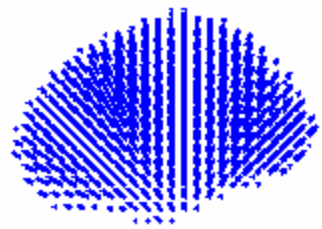
Coils. If you are using MEG data, instead of Electrodes you will see **Coils** in the object list. In addition to the color, size and transparency options, you also have the option to toggle the **Compensation coils** on or off (shown in the red rectangle). Compensation coils are only available with Gradiometers or Reference Coils.



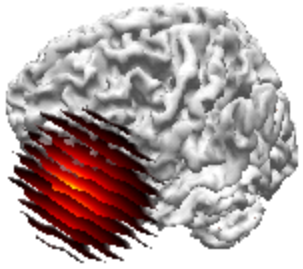
Head Model. Depending on what you selected when you performed the source reconstruction, you will see either the spherical shell(s) or the BEM/FEM head model (described in more detail below).

Maps. Toggle the 3D contour display of the functional data on or off. The Color, Scaling, scaling Increment, Color gradients (solid colors or gradations of colors), and Line width can be modified in the properties.

Source Locations. Enabling this option will display the source locations you selected when you performed the source reconstruction. This could be the 3D Grid, or one of the other surfaces (such as the cortex). You can change the Color, Size, Shape and Transparency in its properties.



Leadfield. This is a visualization of the leadfield (brain current flow) when the source has + voltage and the sink has a - voltage applied. The source and sink electrode sites may be selected individually in the Properties section.



Dipoles / Scan Dipoles / Scans / Currents, etc. Depending on whether you have performed a simple Dipole, Scan, or Current Density Reconstruction, the results will be listed as Dipoles, Scan Dipoles, Scans, CDR Dipoles, or CDR, respectively (described in more detail below).

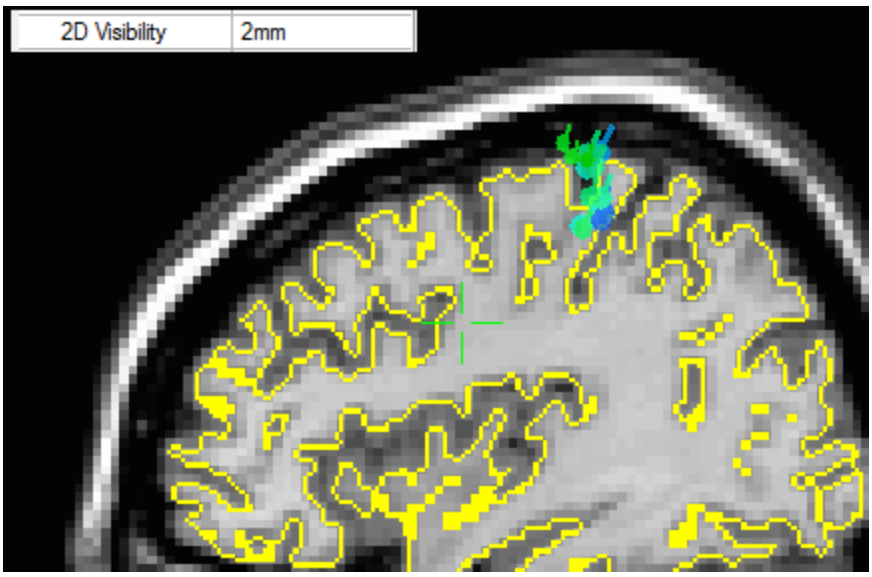
Sensor and Source Coherence. Coherence results among sensors or sources may be toggled on and off. See their individual properties below.

Properties of Objects

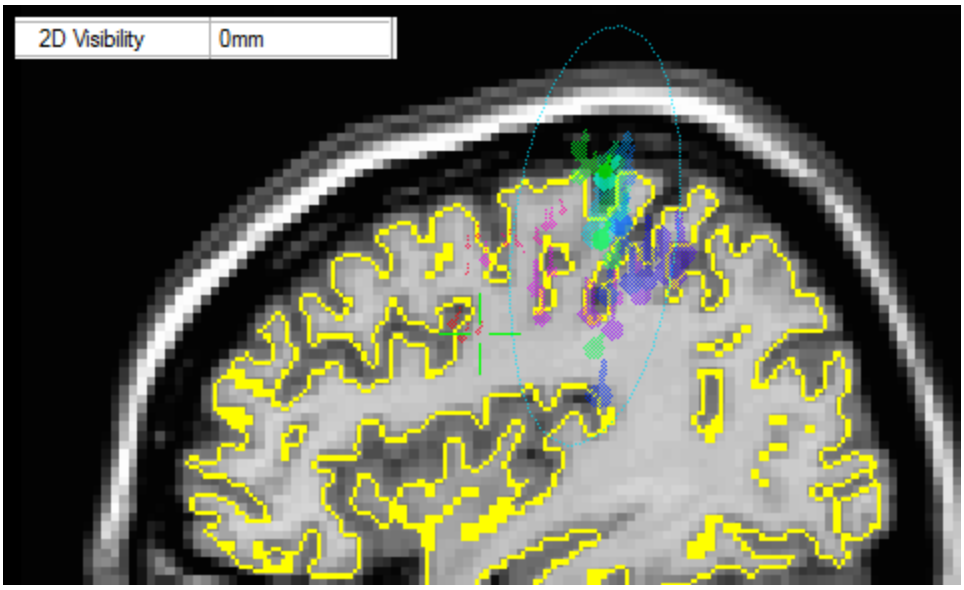
The Objects in the list have associated Properties, shown below the list when you click on an object in the list or the displayed object in the 3D View. Many of the Properties are similar across Objects. The various properties are presented in alphabetical order, for convenience.

2D Symbol Shape. These options are used when displaying dipole results in the **Image Data**. You can change from a color to black and white, and alter the symbol shapes.

2D Visibility. This option occurs in many of the Properties lists. It provides ability to control how many adjacent results are shown in an Image Data cross-section. Enter a mm value > 0. Adjacent objects will be plotted solid, all other objects will not be shown at all. Dipoles are shown below.



A value of zero shows in-slice dipoles solid and all others "dotted".

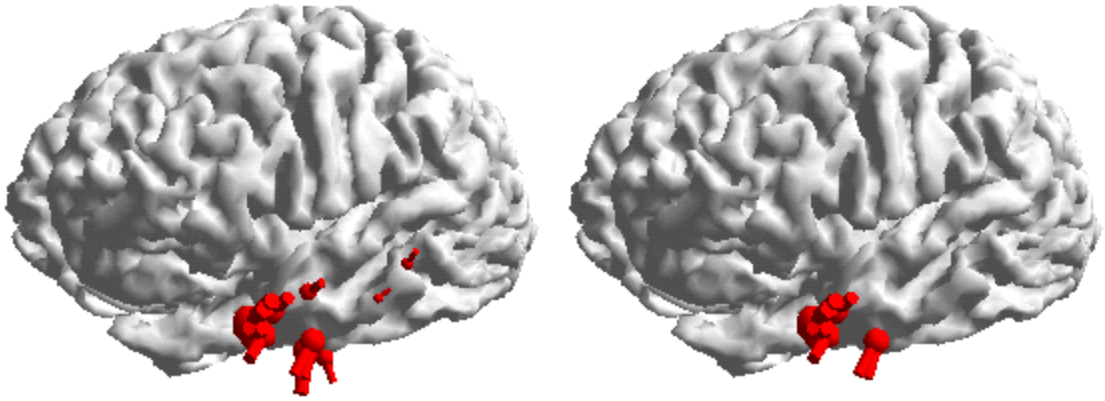


Note that this functionality will not affect the data saved by "Save Image Data", as that is 3D volume data and not a collection of slices.

2D Visibility is available with Dipoles, Electrodes, Localize, Statistics, and Landmarks, as well as Currents, Scans, and Leadfields (in symbol mode).

Axes length [mm]. This controls the length of the Coordinate Axes.

Clip below [%]. This setting lets you set the cutoff threshold for the display of the dipoles, scans, leadfield, and currents. A **Clip below** value of 85%, for example, means that only dipoles having a goodness of fit of 0.85 or better will be displayed. With Sensor and Source Coherence, the coherence values x 100 is used. If **Clip below** is set to a large value, you may not see any solutions.

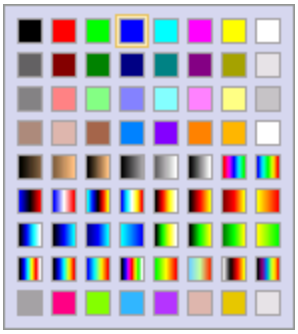


Clip Surface. This option appears with the CDR and Scan currents and the Leadfield. You may elect to **Show** or **Hide** the clipped surface, or select **Auto** to let CURRY determine (e.g., hide values for "grids", and show values for "surfaces"). The clipped surface is comprised of those points with values less than the **Clip**

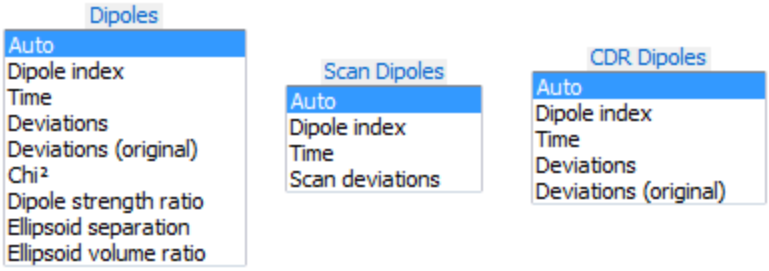
below threshold. If you select **Show**, the clipped surface will be seen in the color you select for **Net color**. If you select **Hide**, the clipped surface will not be seen.

If you select a surface for the **Source Locations** (e.g., the Cortex), the Scan surface will be the cortex. It will be displayed if you select Show, and should not be confused with the Cortex option (Cortex (56) 2.5 mm) in the list.

Color. This also includes **Axes Color**, **2D Color**, **Line Color**, **Wireframe Color**, **Background Color**, **Map Color**, **Current Color**, **Surface Color**, **Scan Color**, **Highlight Color**, and **Label Color**. Colors may be selected for nearly all of the objects: Dipoles, Electrode pads, Coordinate axes, BEM surfaces, etc. Clicking a Color option displays a palette from which you can select a color for the Object.



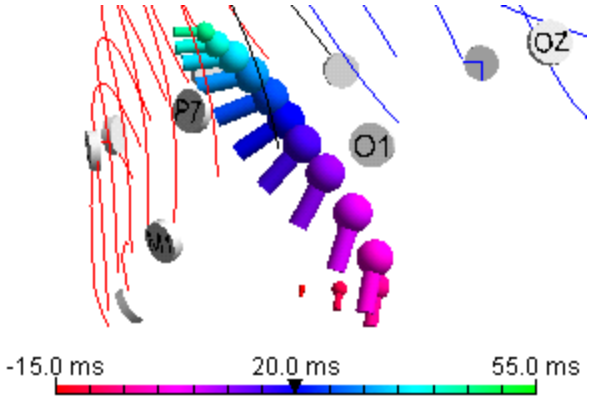
Color Coding. Color coding will be active when you select a color range as the **Color** for the **Dipoles**, **Scan Dipoles**, and **CDR Dipoles** rather than a solid color. Color coding has multiple options. Most of these options are for evaluating underfit or overfit in a 2- or more dipole fit scenario. When viewing the results, it is helpful to select the **Maps** display, with **Strength** and **Deviation** enabled (under **Time-Courses**). The options that are seen depend on which dipoles types have been computed, or if statistics were computed.



Auto. CURRY will select the most likely color coding.

Dipole index. With this option, individual dipoles are displayed with distinct colors, so that dipoles 1, 2, and 3 of a 3-dipole fit can easily be identified. These options are useful in determining whether multiple dipoles are needed to explain the data.

Time. The Time option places a color scale on the Time Cursor. This allows you to see, for example, the temporal progression of a moving dipole based on color.



Deviations and **Deviations (original)**. The Residual Deviation (D) is a measure for the fit quality (how well the source model explains the measured data). D is the root mean square of the difference between measured (Ri) and calculated signals (Fi):

$$D = \mathrm{Sqrt}[\,1 / n * \mathrm{Sum}((Ri - Fi) * (Ri - Fi))] / MGFP$$
$$= \mathrm{Sqrt}[\mathrm{Sum}((Ri - Fi) * (Ri - Fi)) / \mathrm{Sum}(Ri * Ri)]$$

normalized for the measured field (MGFP), which corresponds better to the Signal-to-Noise ratio (SNR) than variances.

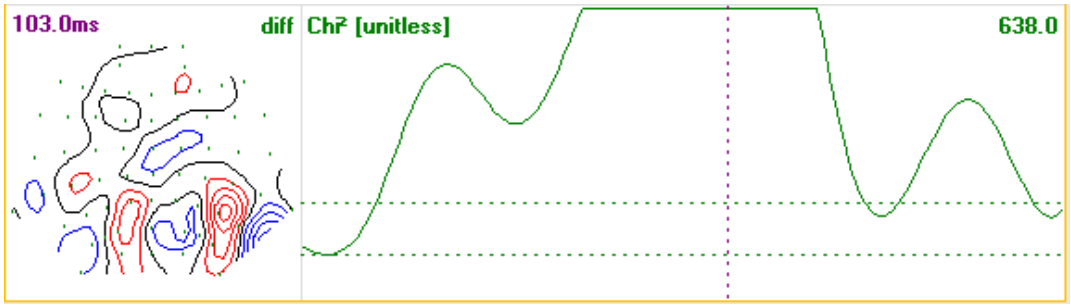
The residual (or "rest") variance V is simply the square of the standard deviation:

$$V = D * D = \mathrm{Sum}((Ri - Fi) * (Ri - Fi)) / \mathrm{Sum}(Ri * Ri)$$

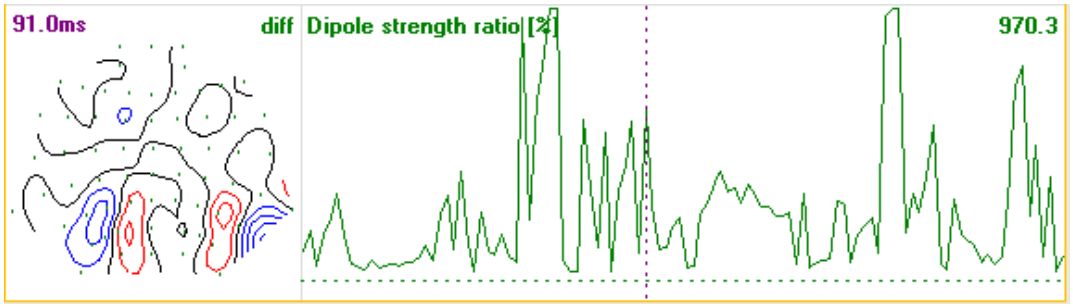
The explained variance is 1 minus the residual variance: EV = 1 - V.

For **Deviations** (normalized) R and F are in SNR units, while for **Deviations (original)** R and F are in μV units.

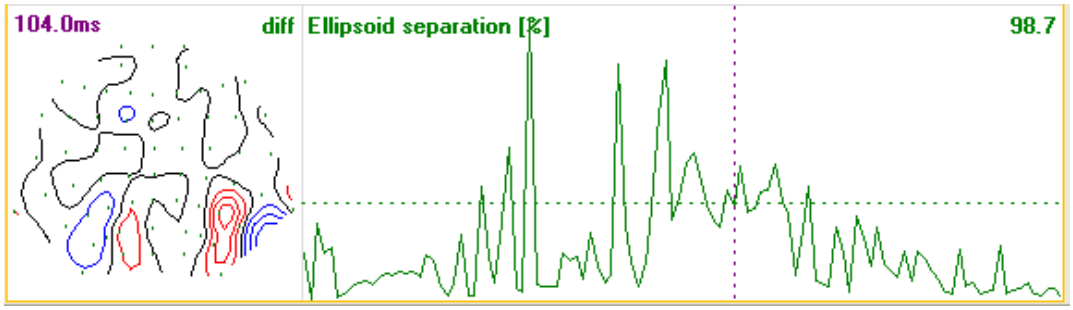
Chi². Chi^2 is computed for the measured versus explained (by the dipoles) data, according to http://en.wikipedia.org/wiki/Chi_square#Definition. See also http://en.wikipedia.org/wiki/Goodness-of-fit. Depending on the number of degrees of freedom, the expected value of Chi^2 is not known. Sometimes the expectation is not met, and this makes the measure useful in detecting over/underfit. The horizontal dotted lines in the plot are the 2.5% and 97.5% intervals for Chi^2 (the desired region).



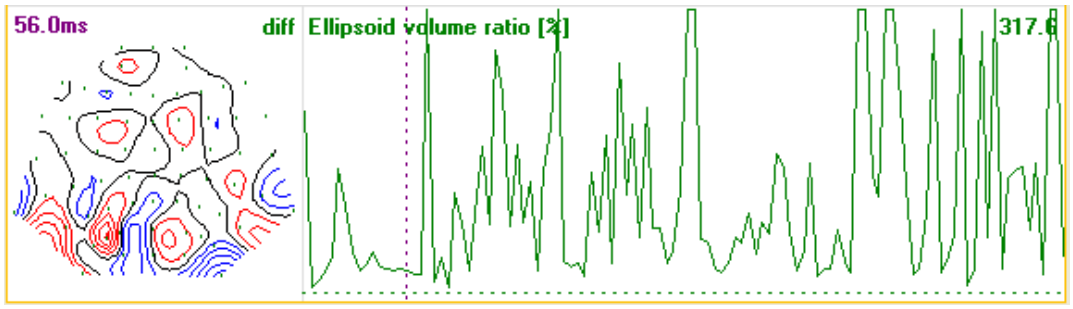
Dipole strength ratio. The ratios of the largest to smallest dipole strengths are displayed (see also the **3D View** color legend and dipoles). The horizontal dotted line is the 100% line (ratio 1:1). When dipole strengths are large, this raises the question as to the need for second or third dipoles.



Ellipsoid separation. This tells you if the ellipsoids overlap spatially (see also the **3D View** color legend and dipoles). If one dipole ellipsoid in largely or entirely within another ellipsoid, you may not need both of them. Ideally, the ellipsoids should be largely non-overlapping. The horizontal dotted line in the plot is the 100% level (higher values have greater separation).



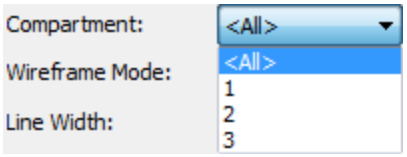
Ellipsoid volume ratio. The ellipsoid volume ratios of largest versus smallest ellipsoids are displayed (see also the **3D View** color legend and dipoles). Larger values have larger ratios between the largest and smallest ellipsoids. The horizontal dotted line is the 100% line (ratio 1:1). The smaller the ratios, the more certain the need is for two or more dipoles.



Color gradient. This is a **Maps** option, used to display the contours in a range of colors, assuming you selected a color range for **Color**.

Compartment. The **Head Models** have a unique option called **Compartment**. The options are **All**, **1**, **2**, **3**, and **4**. **All** displays all shells, **1** displays the first shell

only (typically the Skin), **2** displays the second shell only (typically the Skull), **3** displays the third shell only (typically the brain), and 4 displays fourth shell only (seen with the 4 spherical shell model).

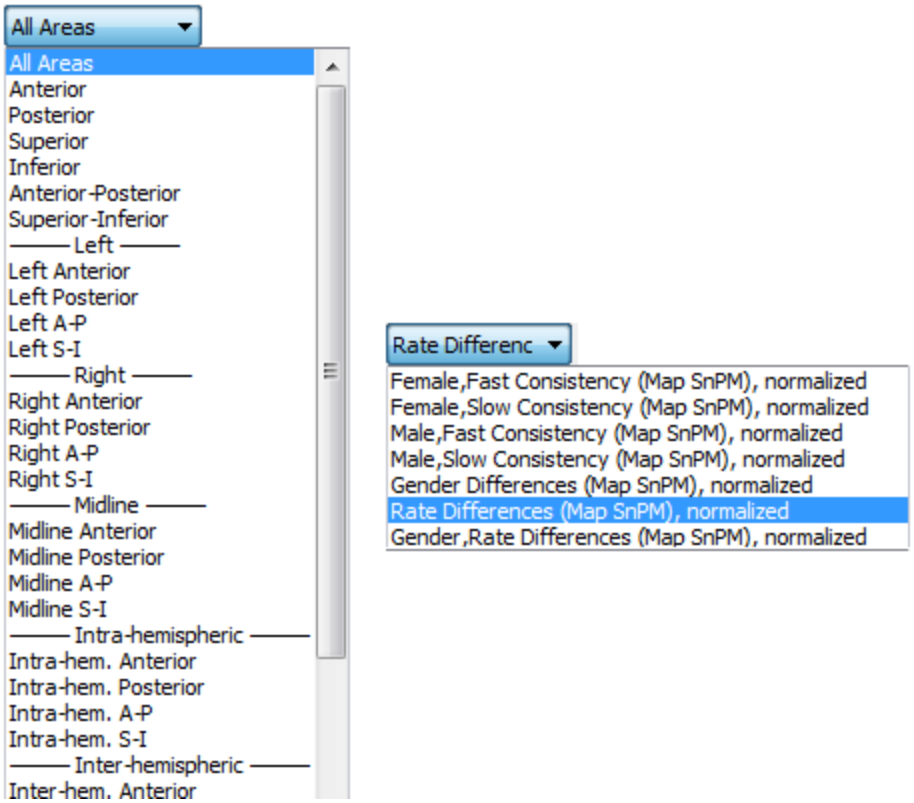


Depth Transparency. See **Transparency** below.

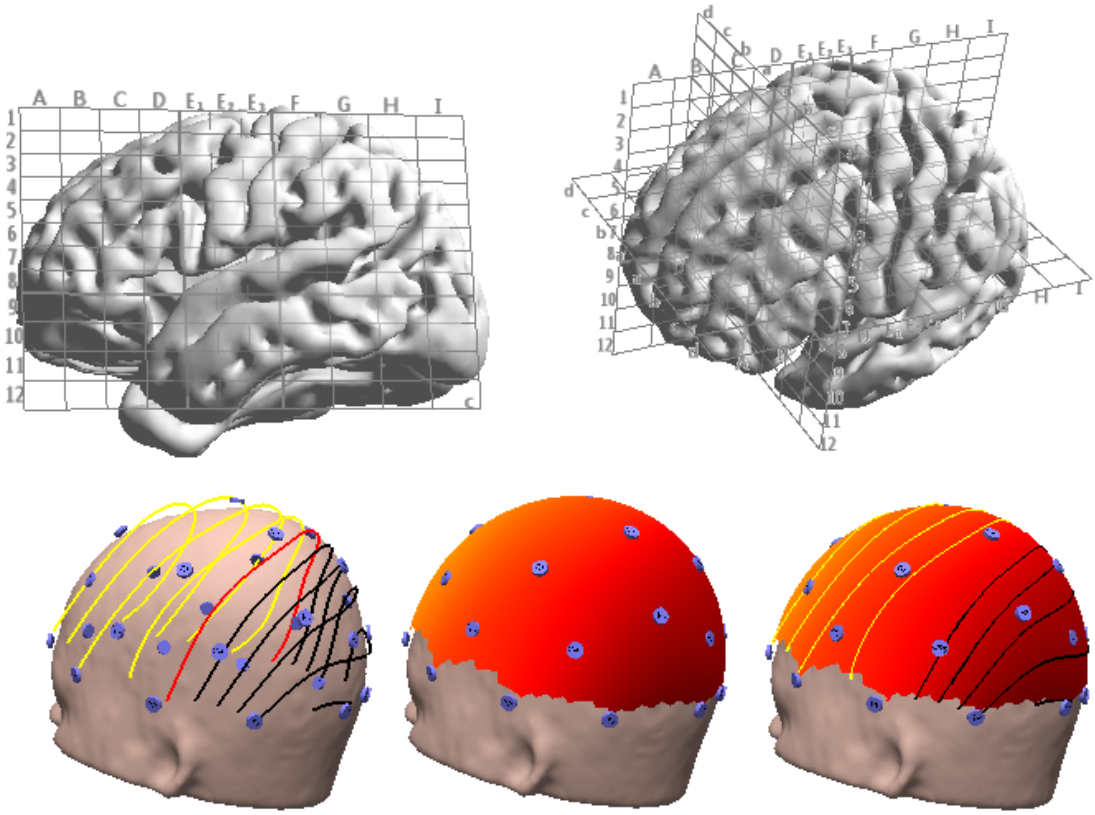
Device Group. This option is present for the contour **Maps** only. If you have multiple devices (EEG, MEG, etc.) you may display the contour maps for any single device, or all devices.

Display. The **Display** option appears with Coherence results (Sensor and Source) and Statistics. With Coherence you may choose to display only certain coherence links by anatomical areas. You can constrain the regions also by using only the **Segmentation Result**, or by using **Stop Markers**, **Pass Markers**, or both **Stop-Pass Markers**.

With **Statistics** the options let you select which result you will see on the lowermost part of the display: internal consistencies, differences for main effects, and differences for the interaction.

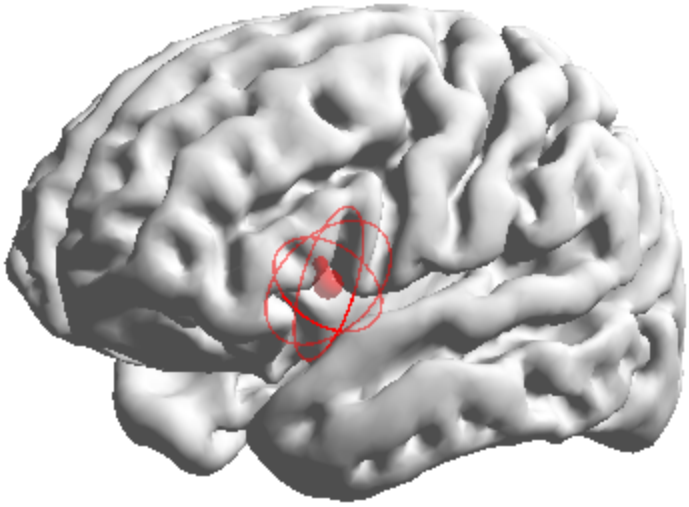


Display Mode. This option is found in **Talairach Grid** and **Maps** Properties. With Talairach Grids, you may display one or three planes. With Maps, you may select between contour lines, maps, or both (Overlaid).



Ellipsoids. This toggles the **Confidence Ellipsoids** On or Off, and displays either the smallest single ellipsoid (**One**), or **All** ellipsoids. The option is present for **Dipoles**, **Scan Dipoles**, and **CDR Dipoles**. Briefly, the ellipsoids show the one SD volume about the most likely source.

Confidence ellipsoids are interpreted in the following way: for all dipole locations inside the ellipsoid, the forward calculated data would not change by more than the amount of noise in the data, compared to the forward calculated data obtained for the best-fit location. This measure is obtained by also allowing all other sources (if more than one dipole is active) to adapt their strengths (and, for moving or rotating dipoles, also their orientations) to yield the best possible fit. It is thus a rather conservative measure for the confidence volume. Volumes obtained by fixing all other sources to their computed values would be smaller than the ones obtained using this approach.



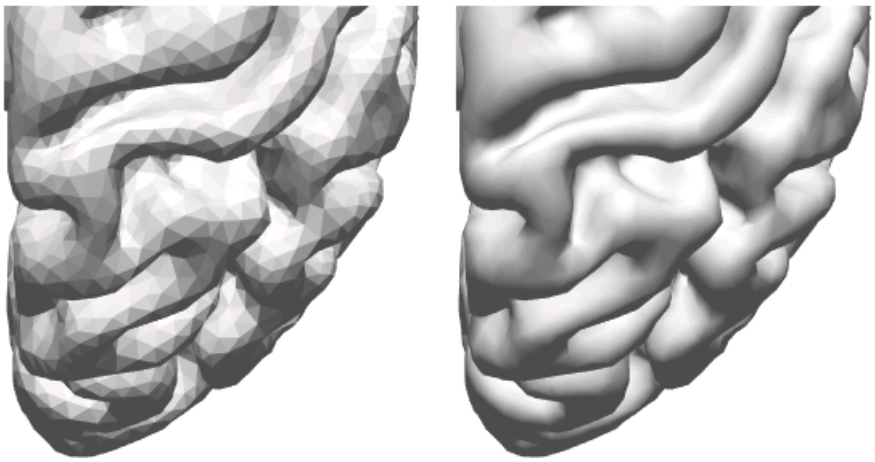
Ellipsoids obtained for sources very near to a BEM compartment border (half a triangle side length) suffer from the same local instabilities as the BEM forward calculations and should be interpreted with care.

The ellipsoid parameters (12 numbers encoding the main axis lengths and their orientations per dipole per timepoint) appear in the deviations list of the .dip file, if results are saved. Please note that they are always saved in the Internal coordinate system.

Dipole confidence ellipsoids are described here.

[Fuchs M, Wagner M, and Kastner J. Confidence limits of dipole source reconstruction results, Clinical Neurophysiology, Vol 115:6 , p1442-1451, June 2004.]

Flat Shading. This option is found with segmented surfaces. When enabled you will see the triangulated surface. When disabled, you will see a smooth surface.



Flat Shading Enabled

Flat Shading Disabled

Flip (Cutplanes). Used to flip the region that is being cut (left to right, or up to down). **Flip On (Top)** constrains the flip to the upper regions (one side to the other). **Flip On** permits the flip in side to side or up and down directions.

Full Color Range. This option is found with Dipoles, Scans, Scan Dipoles, CDRs, and CDR Dipoles. When disabled, the full 0-100% will be used for the color scale. If you enable Full Color Scale, only the range that has values will be mapped, making the color scaling more sensitive. Whether the option is active or not depends on the setting in **Color Coding**.

Grid Sampling. This option is found only with the **Talairach Grid**. The Talairach Grid has discrete points, and the question that arises when the 3D cursor does not hit that point exactly (which is the normal case) is, which point to take? The options (**Centroid**, **Near**, or **Far**) determine which point, or sample, should be used.

Height (and **Width**). Control the size of the **Waveform** displays.

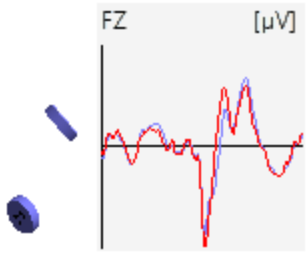


Image Data (Cutplanes). Select the image data set to be displayed within the cut regions.

Inflation. This appears with surfaces, such as the Skin, Cortex, Leadfield, Scans and Surfaces (when a surface, such as the cortex, has been selected for Source Locations). Increasing the field serves to smooth the surface. Initially, rough textures are smoothed, and eventually the surface details are smoothed away completely. The maximum number of inflations is 100.

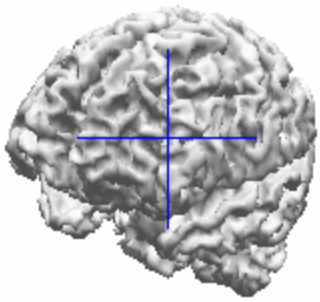
Inflation is described here.

[Mang A, Wagner M, Müller J, Fuchs M, and Buzug T. Restoration of the Sphere-Cortex Homeomorphism, Bildverarbeitung für die Medizin 2006, Informatik aktuell, 2006, Part 4, 286-290.]

Label Size. This option is found with **Localize**, **Surface Points**, and **Source Locations**. This controls the size of the text on the electrodes created in Localize.

Limit Symbols. This option appears with Source and Sensor Coherence, and limits the number of visible arcs, pointers, lines that are seen. Otherwise, the very large number of symbols that may be computed can place CURRY in an apparent non-responding state (since it may take up to a minute per frame to render the display).

Line Width. This sets the width of the Distance line, Maps contour lines, the 3D Cursor (shown), and many other objects. If you select **Auto**, CURRY will adapt the width to the size of the display.



Localize Link. This is used with the **3D Cursor**, and will be active when **Track Mouse** is set to **On**. When toggled on, clicking on a surface in the 3D View with transfer the coordinates to the Localize display, and add the point(s) to the list in the **Localize** panel.

Lowest Scale. This option is used with CDR only. When the Timerange is in "movie" mode, the scale is adapted so that its maximum reflects the largest CDR value for the displayed latency. This can create problems for movies, because for latencies with very low SNR, random garbage is displayed, due to the then very small maximum. This parameter serves as a lower limit for the scale maximum, based on the largest CDR value over the whole Timerange.

Material. The Material option is available for many objects with surfaces. It lets you select from **Dull**, **Shiny** and **Metal** options. These affect the degree of light reflectivity of the surfaces. Metal is the most reflective, and therefore it has the brightest spots where the light strikes.

Minimum Distance. This is used with Sensor Coherence and Source Coherence, and it is the same option as found in the **Parameters** panel for **Maps**. Select the minimum distance between electrodes. Generally, the closer the electrodes are together, the higher the coherence between them, due at least in part to volume conduction. By setting a larger distance between electrode sites, these artificially large coherence links are not displayed.

Minimum Lag. This is used with Sensor Coherence and Source Coherence, and it is the same option as found in the **Parameters** panel for **Maps**. Phase

relationships are displayed in terms of the "lag" between the waveforms at two sites. If you select **0**, all links will be displayed, regardless if any phase shift. If you select **1**, then links where the lag is within 1 sampling point will be displayed, and so on. The values that are available will be determined by the AD Rate. If you have an AD Rate of 500 Hz, the steps will be in 2ms increments.

Maximum Lag [ms]. Maximum lag, along with Minimum Lag, lets you define a range of lag values. If you define a range of, for example, 5-10 ms, then the links will be seen if the signals are in phase, within 5-10 ms.

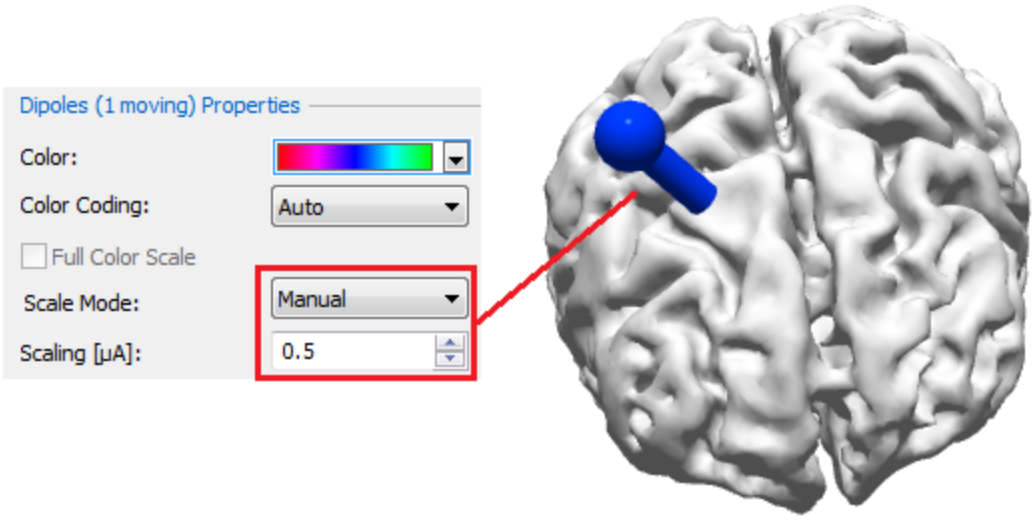
Mode (Cutplanes). Determines the orientation of the cuts (Axial, Coronal, Sagittal, Double, and Triple).

Offset [mm] and **Offset**. (Cutplanes and Waveform). In Cutplanes, this option shifts the level of the cut(s) in the respective direction (depending on the Mode). In **Waveform** properties, the offset moves the displayed waveforms across the screen to make them easier to see.

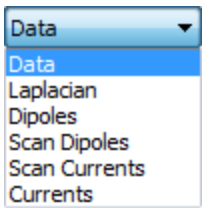
Radial Offset. This option is used with Maps to obtain a better fit of the color maps on the segmented surface.

Scale Mode. This is used to vary the size of the displayed dipoles. The options vary slightly, depending on whether you are looking at Statistics, Dipoles, Scan Dipoles/Currents, CDR Dipoles/Currents, or Maps. In **Auto** mode, the scale for the display of the dipoles will be adjusted automatically as you step through the Timerange. In **Auto [time range]** mode, a fixed display scale is used across points in the Timerange. In **Uni** mode, all dipoles or CDRs are given a fixed size. If you select **Manual** mode, you can vary the size of the displayed dipoles using the **Scale** field.

Scaling and Scaling [μA]. The parameters are similar, but in some case there are no units. This field is used when you select **Manual** for **Scaling**. You can increase or decrease the size of the dipoles. With CDR and Scan currents, you can change the color scaling range.



Show. This is used with Maps only. The contours will reflect the distribution of the selected reconstruction.



Show Compensation Coils. Toggles the compensation coils on and off (Coils only).

Show Labels. This option is used with **Electrodes** and **Coils**, and will toggle the labels on and off.

Show Headshape. This option is found with **Localize**, **Surface Points**, and **Source Locations**, and is used to toggle the digitized head shape on and off (these will be any digitized points beyond the three Landmarks). The Head Shape points will be shown, but will not contribute to the (PAN)-transformation.

Show Pial Surface. The pial surface is a display option for cortical triangle meshes (and derived CDR etc. results) created by "BEM/FEM geometry", and with some of the source reconstruction results. When activated, the outer (pial) layer of cortex rather than a middle layer is displayed. Results such as CDR can be displayed on the pial surface rather than the cortical (middle cortical layer) surface, although they will still have been calculated for the middle cortex layer, as this is where the pyramidal cells are.

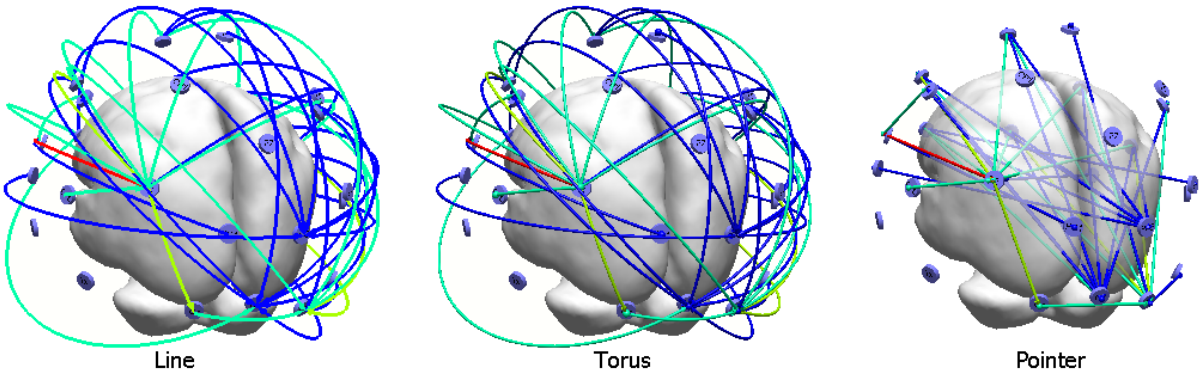
Show Symbols. This option is found in **Scan**, **Leadfield**, and **CDR** Properties, and is used to display the shape you have selected for **Symbol Shape**.

Sink. Site where the sink has a negative voltage applied (seen with the **Leadfield**).

Size [mm]. Sizes of some objects can be specified. The options may be general - small, medium or large - or more specific, as with the millimeter size of electrode pads.

Source. Site where the source has a positive voltage applied (seen with the **Leadfield**).

Symbol Shape. This option is seen with **Sensor** and **Source Coherence**, and the **Leadfield**. The Coherence properties have options for **Line** (plain arcs), **Torus** (3D arcs; default), and **Pointer** (straight lines). The **Leadfield** has options for **Arrow**, **Pole**, and **Sphere**.

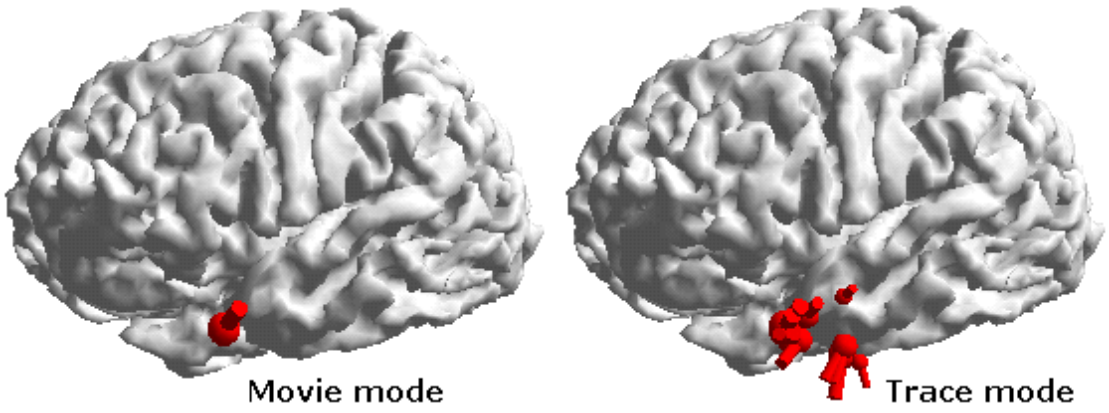


Symbol Size. Used with **Dipoles**, **Scans**, and **Scan Dipoles**, where **Display Mode** is set to **Symbols**. It is also used with **Statistics**. This varies the size of the symbols.

Text Size. This is used to change the size of the text for various labels (Small, Medium, Large, or Off).

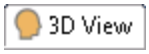
Through (Cutplanes). The level of the cut can be controlled with the **3D Cursor**, it can go through the **Origin** (the 0, 0, 0 point), and the current point can be kept (**Last Used**).

Time Range. For Dipoles, the Time range has **Movie**, **Trace**, and **Trace (Range)** options (also toggled with the  button on the Toolbar, or *Ctrl+Shift+M*). The **Movie** option displays the dipoles one at a time as you move through the Timerange. The **Trace** option displays all dipole solutions at one time. The **Trace (Range)** option displays any dipole that fits into the currently selected Timerange. This makes a difference if you "Keep" your results and switch to a different Timerange.



For CDR and Scan currents, the options are **Movie**, **Maximum**, and **Maximum (Range)**. **Movie** is used to show the changing currents for each time point in the Timerange; **Maximum** displays the maximum range across all time points (and does not change across the Timerange), so that at each location the CDR maximum is visible. Maximum is selected if the Time Range Display Mode (Trace mode) is activated in the toolbar. **Maximum (Range)** scales the CDR so that at each location its maximum (within the Timerange selected in functional data) is visible.

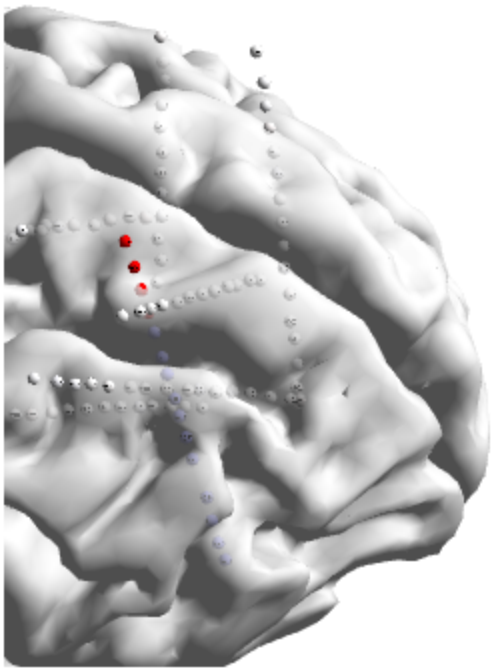
The difference between Maximum and Maximum (Range) becomes apparent if results are Kept, and the Timerange is then changed in functional data, so that it does not match the one the CDR was computed for.

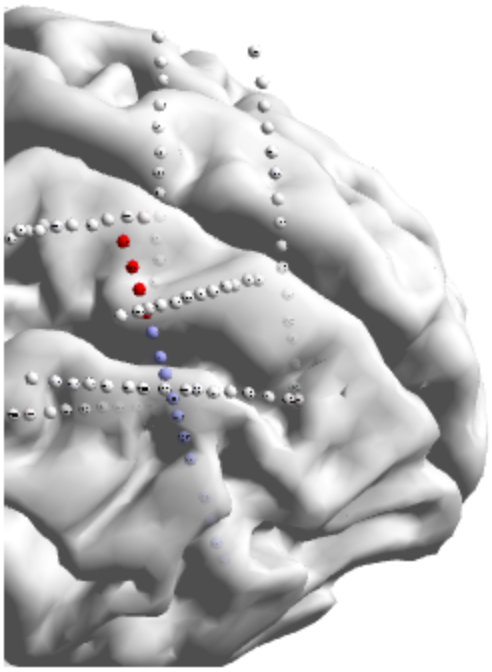
Track Mouse. This is used with the **3D Cursor** only. With **Track mouse** set to **On**, click on a *surface* in the 

and the Image Data cursor will move to that point. It functions as an aid for use with the Cutplanes (described below). The **Localize link** option can be toggled on and off. When toggled on, clicking on a surface in the 3D View with transfer the coordinates to the Localize display, and add the point(s) to the list in the **Localize** panel.

Note
Initially, the **Size** of the 3D cursor is zero and **Track mouse** is **On** in order to establish a link between 3D View and Image Data without displaying the cursor symbol in the 3D View.

Transparency. There are two types of Transparency. One is the basic Transparency that has been part of CURRY for many years. The other is Depth-dependent Transparency. Transparency is shown in the figure on the left. The objects inside the cortex are seen, but not as clearly (0% is opaque; 100% is complete transparency). The objects are uniformly obscured, that is, it does not matter how near or far the "obscured" objects are, they are all equally obscured. In this example, the cortex Transparency was set, in this case, to 30%, with Depth-dependent Transparency turned off. Depth-dependent Transparency is shown on the right. The objects inside are not uniformly obscured, but rather get more obscured the farther away they are, as if fading into a fog. The Depth [%] field, accessible when you select Depth-dependent Transparency, controls how near or far to you the fading begins. This makes it easier to perceive depth when one or more objects are inside another.





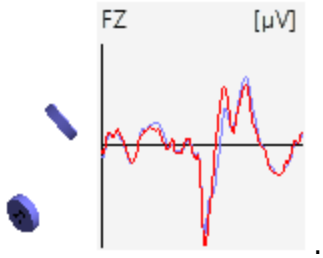
Transparency may be increased for up to *three displayed Objects*. You can increase Transparency for more than three objects, but only three will be displayed. The settings for the ones not displayed will be remembered. To use Transparency on a fourth object, you must reduce one of the other three to 0%.

Note: If your video card is below the minimum specifications, you may be able to have only one transparent object at a time. If you have clicked ***Enable 3D compatibility mode*** *(****Edit*** → ***Options*** → ***Troubleshooting****), you will not see the Transparency options.*

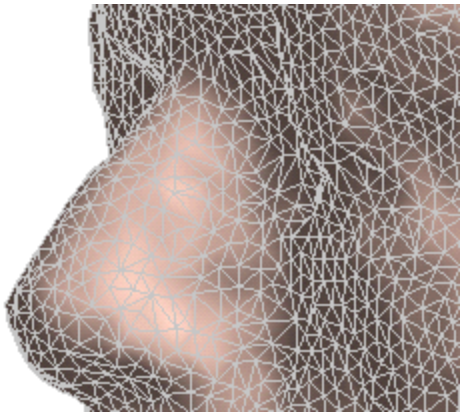
Unit. This option appears with the **Distance** tool and is used to select the unit of measurement.

Use Projected Locations. This option is used with **Electrodes**. When performing source reconstruction, CURRY projects the electrodes onto the outermost compartment of the volume conductor (either BEM surface or shell). These new locations are seen when you enable **Use Projected Locations**. Otherwise, the measured positions are seen (option disabled).

Width (and **Height**). Control the size of the **Waveform** displays.

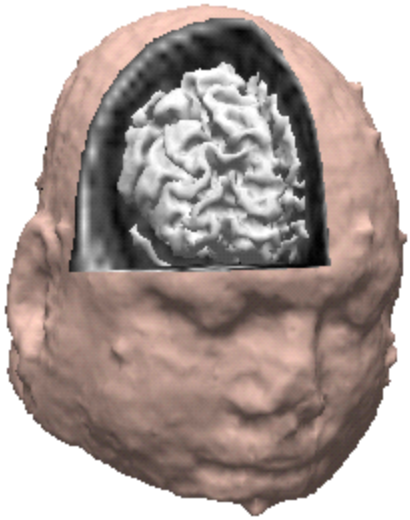


Wireframe Mode. The three options are **Off**, **On**, or **Overlaid**. These determine the face of surfaces. **Off** is a solid surface, **On** is the triangulated surface, and **Overlaid** shows the triangulated surface on the solid surface. The figure to the right shows a closeup where **Overlaid** was selected. The colors of the surface face (**Color**) and the lines (**Wireframe**) are user determined.

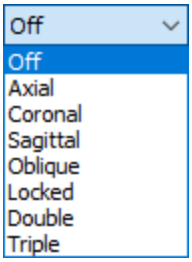


Cutplanes

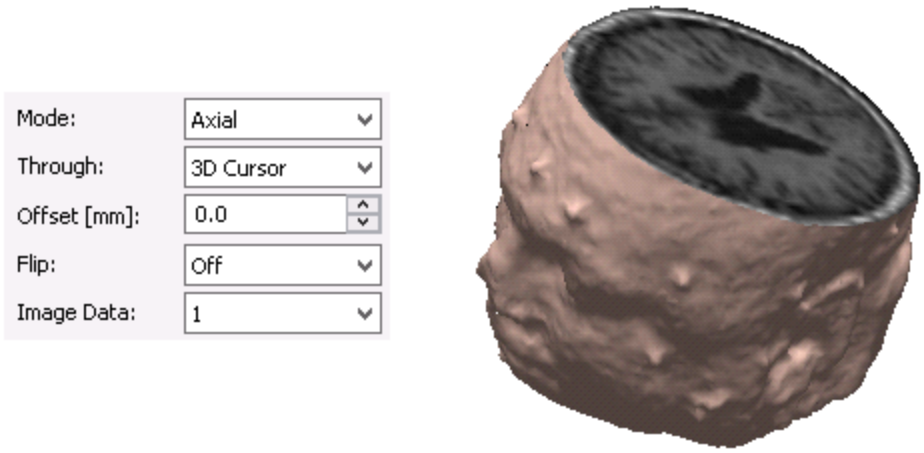
Cutplanes are used to cut away sections of the 3D objects as an aid for visualization. Planes can be cut in 1, 2, or 3 planes at a time.



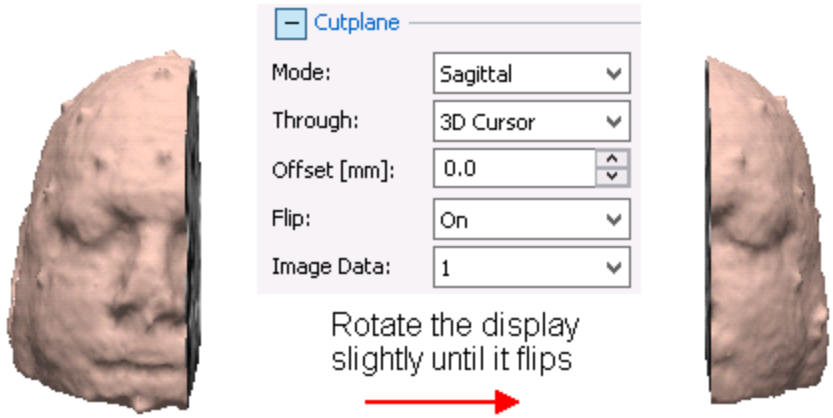
Click **Mode** to access a drop-down list of options (Off, Axial, Coronal, Sagittal, Oblique, Locked, Double, and Triple). Use **Axial**, **Coronal**, and **Sagittal** to make single cuts in the indicated direction. The **Oblique** option lets you set the cut plane in any angle, such as, along the path of a depth electrode. Drag with the mouse to select the desired view and angle, then select **Locked**. You can then change the view without losing the oblique cut plane. Use **Double** to make 2 cuts at once, and **Triple** to make 3 cuts at once (as in the figure shown). Electrodes and Coils are special cases that do not have Double or Triple cuts (see below).



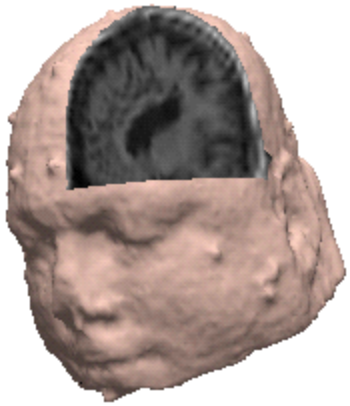
You can use the Cutplanes in the 3D View display, or, sometimes more conveniently, in the Image Data, with the 3D View display selected in the lower right section. Select the Object that you want to cut (e.g., Skin - a segmented surface should already be created), and expand the Cutplane options in its properties field. To make a single cut, select the **Mode** (**Axial** selected below). Set **Through** to **3D Cursor**. Use either of the image data displays that lets you move the cursor up and down in the axial direction. As you drag the cursor up and down, you will see the surface in the 3D View being cut accordingly. In this case, **Image Data 1** was selected, so the image data are seen in the cut.



Note that the direction of the cut will always be in one direction: Axial - from top to bottom, Coronal - from front to back, and Sagittal - from left to right (when the front view is displayed). How do you cut the right side instead of the left side? Cut the left side to the desired depth, then set **Flip** to **On**. Rotate the cut display slightly until it Flips. Then turn Flip **Off** to retain the flipped cut. The same process is used to flip the cuts in the other directions.



To do a Double or Triple cut, the process is basically the same. Select, for example, Triple, and use the cursor in the image data views to set the depths. Use Flip if you need to reverse the cut in one or more of the dimensions.



Mode. Determines the orientation of the slice(s) in either the **Axial**, **Coronal** or **Sagittal** planes, or **Double** or **Triple** planes.

Through. If **Origin** is selected, the cutplane will go through the (0, 0, 0) point. **3D Cursor** controls the position of the cut using the 3D Cursor. **Last Used** keeps the current point.

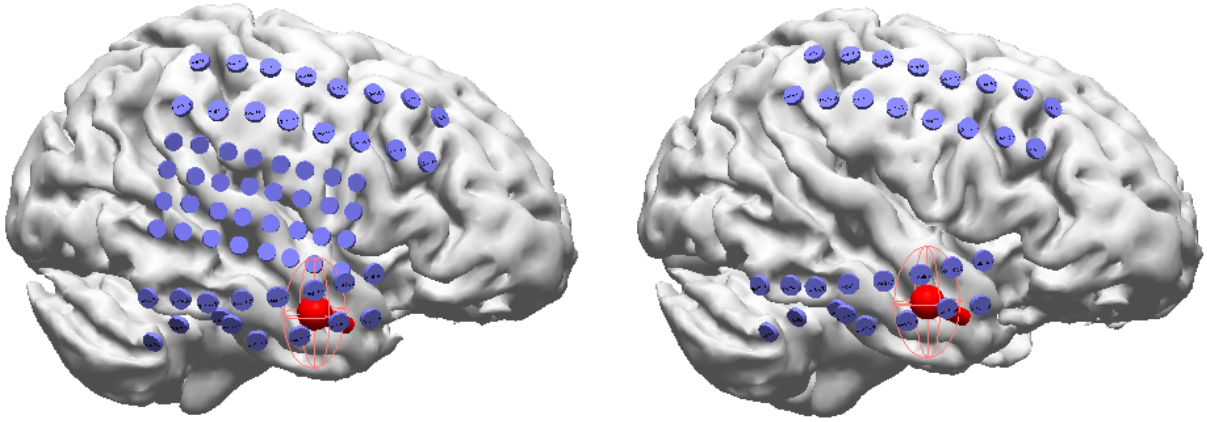
Offset. The cutplane can be shifted along its normal direction. For example, if you are using an Axial cut, the offset value moves the cut in an axial direction.

Flip. Used to flip the cut from left to right, or upper to lower. **Flip On (Top)**, constrains the flip to be in the upper head area only, thus allowing you to change viewing perspectives up and down without the cut flipping to the lower part of the head. **Flip On** has no constraint, and the cut will flip left and right as well as up and down.

Image Data. Allows you to select the image data that will be projected into the cut section (typically Image Data 1, but you will have options for all image data sets that are loaded).

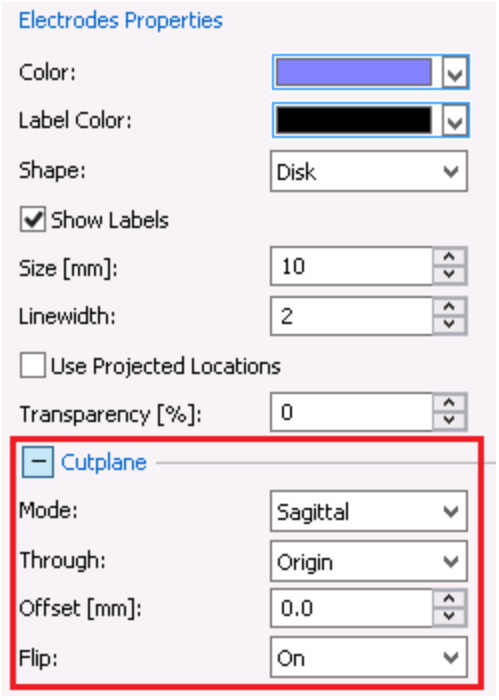
Electrodes and Coils. There are instances, such as in the example below, where you may want to keep the cortex transparent, while at the same time blocking out the electrodes that are on the opposite side of the head.

In this example, there is a 4x8 grid on the left side, two 2x8 grids on the right side, and a dipole solution that is inside the cortex on the right side. If you increase the Cortex transparency so you can see the dipole solution, you also see the grid from the other side (left side of figure). What you want is the transparent cortex without the electrodes on the other side (right side of figure).

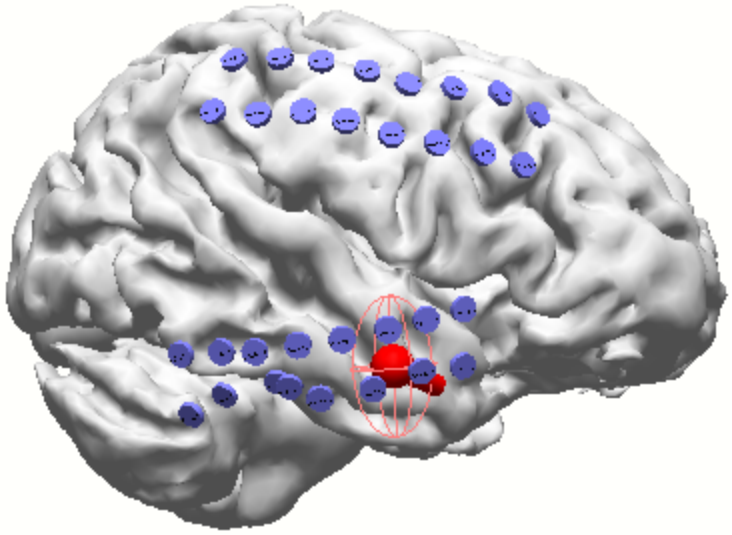


You can do this with the **Cutplane** for Electrodes or Coils.

Starting with the figure on the left (above), set the Cutplane parameters as shown, with a transparent Cortex.

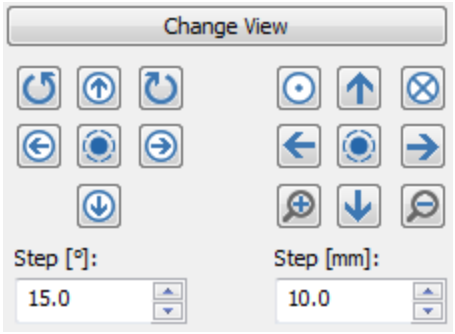


Then increase or decrease the **Offset** value until the "back" electrodes disappear. Alternatively, you can set **Through** to **3D Cursor**, and then click in the 3D View in different places to move to Cutplane to that location, removing the electrodes behind it.

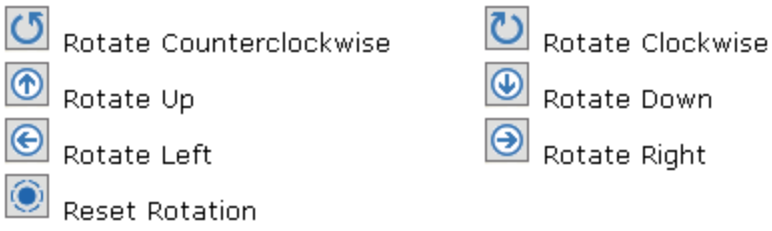


22.2 Change View

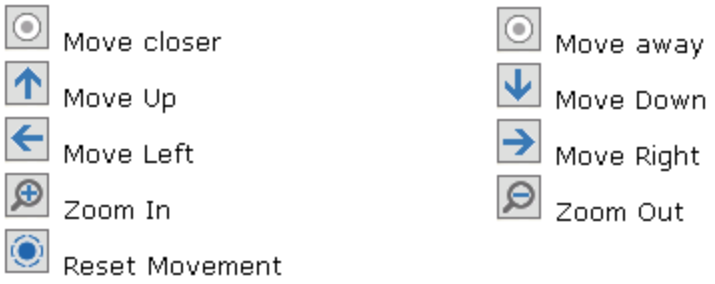
The Change View options provide a means for altering the perspective of the 3D View, and for positioning and resizing the view in the display.



The set of buttons on the left side are used to rotate the view. Clicking a button will step the view in degree increments set in the Step [°]: field, in the direction indicated by the arrows.

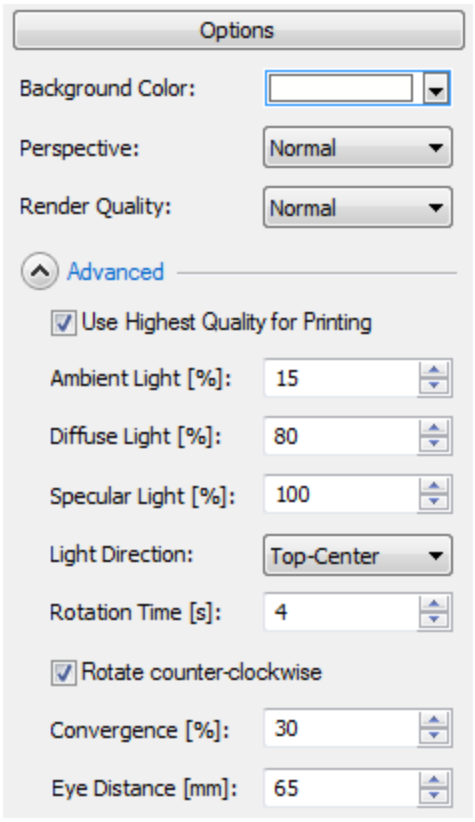


The set of buttons on the right side are used to reposition the view within the display. Clicking a button will either resize the objects or else move the objects in mm increments set in the Step [mm]: field (except the Zoom options), in the direction indicated by the arrows. You can also use *Shift+left mouse* to drag the objects in the display, or use *Shift+cursor arrows* to move the objects incrementally.



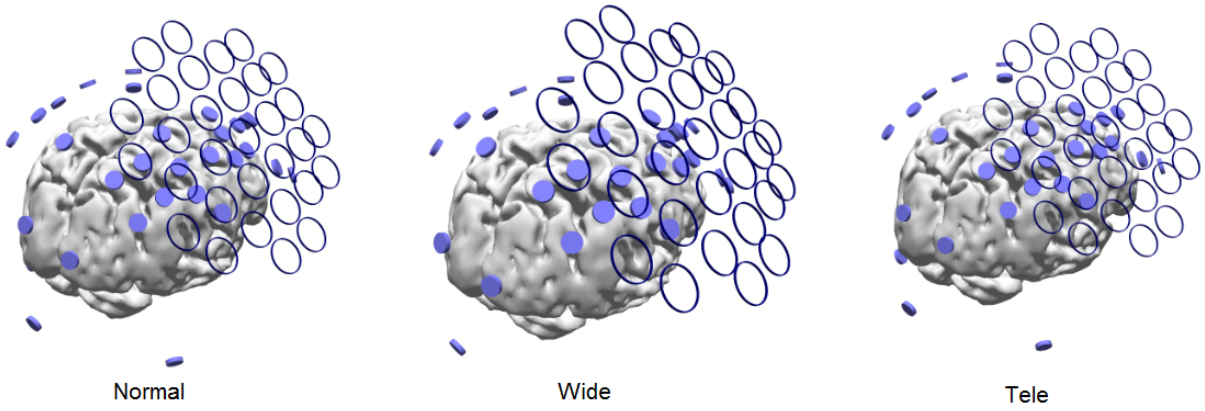
22.3 Options

These options control some common display properties (background color, display quality, views), as well as global lighting settings.



Background color. Click the field to access the color palette to select the background color.

Perspective. You may vary the viewing perspective using the **Wide Angle**, **Normal**, or **Tele** options. The differences are subtle; Wide Angle is closest to the subject.



Render Quality. Select **Low**, **Normal**, **High**, or **Highest** for the rendering quality. The higher the render quality, the slower the replot speed. This influences electrodes, dipoles, and other symbols, as well as contour lines.

Advanced
Use Highest Quality for Printing. If enabled, the highest quality will be used for printing, regardless of the current quality settings.

Ambient light / Diffuse light / Specular light. These settings control the lighting used in the 3D display. To see the effects of Ambient and Diffuse lighting, set Diffuse to 0%, and vary Ambient. The "background" changes. Set Ambient to 0% and vary Diffuse. The details in the display vary. "**Specular light"** specifies the brightness of the "hotspot" of a *shiny* surface. If all visible surfaces are set to "dull", you will not see any difference. If you set specular light to 0%, all surfaces will be "dull", implicitly.

Light direction. Set the direction of the light source to be from the **Top-Right**, **Top-Center**, **Top-Left**, or **Center** direction.

Rotation Time (s). This field controls the time (in seconds) for one rotation of the objects in the 3D View.

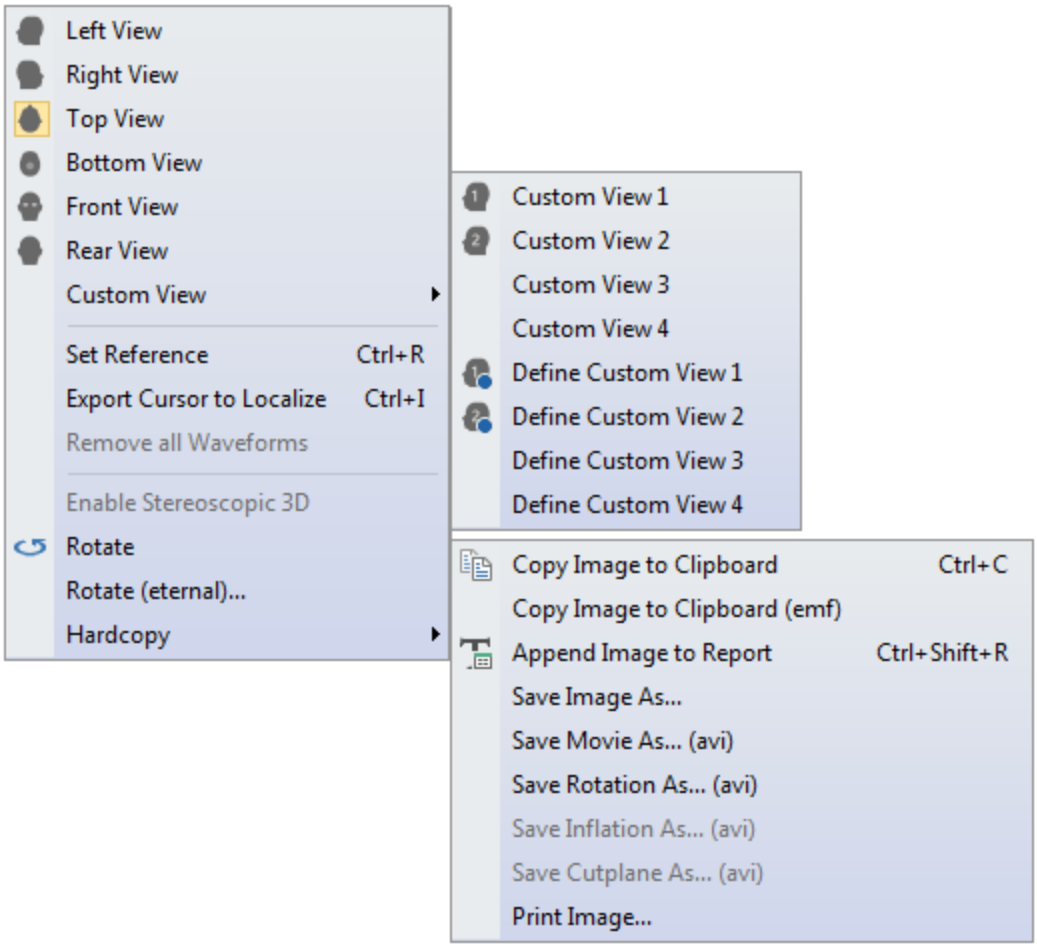
Rotate counter-clockwise. Sets the direction of rotation. Enabled is counter-clockwise and disabled is clockwise.

Convergence [%]. The **Convergence** and **Eye Distance** parameters are used with **Stereoscopic 3D**, described in the **3D View** section above. Use care in adjusting the Convergence parameter, as eye strain could result.

Eye Distance [mm]. See **Convergence**. It is recommended that this parameter not be changed unless so directed.

22.4 3D View, Context Menu

The following options are accessed from the context menu in the 3D View display.

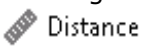


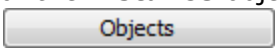
View selection  . These icons are used to select the **Left**, **Right**, **Top**, **Bottom**, **Front**, and **Rear Views**.

Custom View. Custom views are those intermediate perspectives that you wish to use repeatedly.

Custom View 1-4. Display the first through fourth Custom Views.

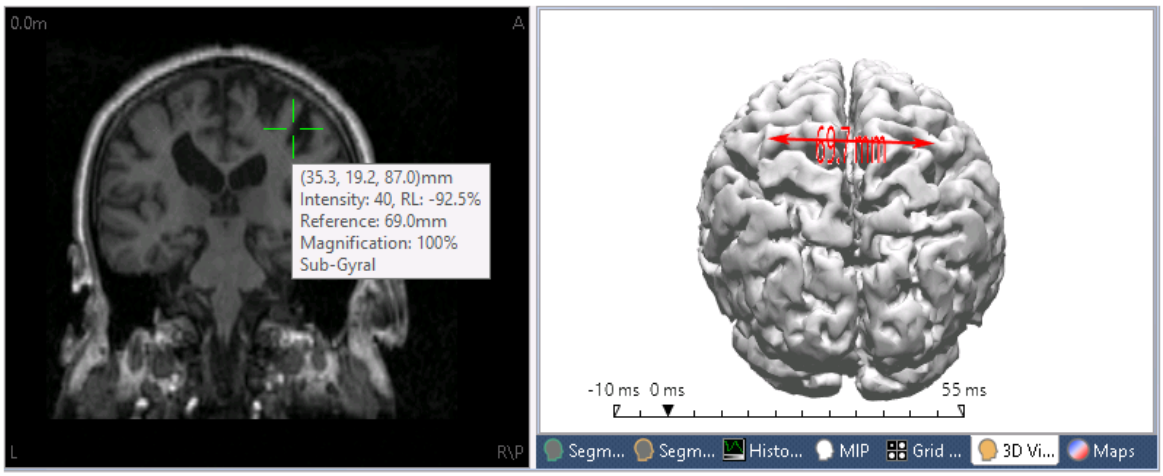
Set Custom View 1-4. Sets the current orientation (size, perspective, etc.) of the display as Custom View 1-4. Select a Custom View at any time to return to it.

Set Reference (*Ctrl+R*). This is the same reference that is set in the Image Data; it also makes use of the **Distance** object in the 3D View. Enable the 

object in the **3D View** 

list (set the Properties as desired). In the Image Data display, select the 

in the fourth pane. Click a position in the Image Data display, and *right click* to select **Set Reference** (in either the Image Data or 3D View display). Then click on a new position or drag the mouse to different positions in the Image Data display. The distance from the Reference is seen in the mouse Tooltip and also as a line in the 3D View display.



Export Cursor to Localize (*Ctrl+I*). Selecting this option (using the cursor position in the Image Data view, or in the MR images in the Localize view) will export the current cursor position to the Localize panel list.

Remove All Waveforms. If you have used *Ctrl+click* on an electrode label to display the corresponding Waveform, you may Remove All Waveforms with this option.

Enable Stereoscopic 3D. Please refer to the **3D Stereoscopy** section above for requirements and operation of 3D stereoscopy.

Rotate / **Rotate (eternal)**. Select **Rotate** (or click the icon on the **3D View** Toolbar, or use *Alt+O*) to rotate the display one 360 degree turn. **Rotate (eternal)** will continue rotating until you pres the *Esc* key.

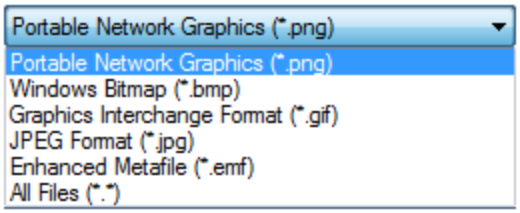
Hardcopy. The following options are seen.

Copy Image to Clipboard. This copies the data channel display (.bmp format) to the Windows clipboard, from which you may Paste it into other Windows applications. This is the same as the icon on the **Standard** and **Report** Toolbars (*Ctrl+C*).

Copy Image to Clipboard (emf). When pasted into other Windows applications (such as Word), individual components of Metafiles can be edited; whereas, BMP files cannot. (In Word, *right click* on the pasted metafile, and select **Edit Picture**).

Append Image to Report. Copies the section of the data display having the focus to the Report. This is the same as the icon on the **Report** Toolbar (*Ctrl+Shift+R*).

Save Image As. This option lets you save the graphic display in any of the formats shown.



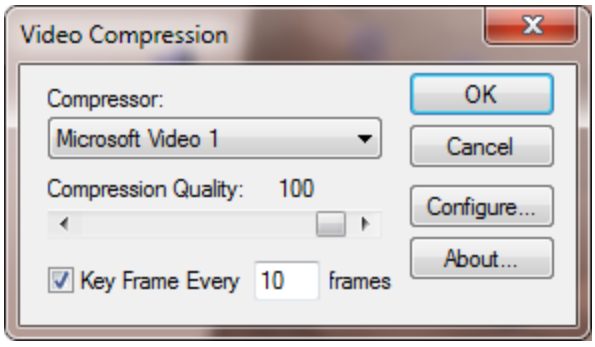
Save Movie As (avi). This option lets you save the Movie in .avi format. (The Movie is across the selected Timerange, and the slices will be adjusted to those that show the dipole solutions).

Save Rotation As (avi). The Rotation may be saved as an .avi file.

Save Inflation As (avi). The Inflation may be saved as an .avi file.

When you save any of the .avi files, you will see options at the bottom of the Save As dialog.

Select Codec. Enable this option to select the type of video compression you wish to use.



Play after saving. If you enable the **Play video after saving** option, the video file will open in, for example, the Windows Media Player and immediately replay the video.

Frame Rate. Higher Frame Rates will replay the movie faster.

Save Cutplane As (.avi). If you manually adjust the cut plane through a progression of slices, for example, you may save the sequence as an .avi file.

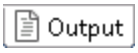
Print Image. The selected pane (that part of the data display that has the focus) will be displayed in the Windows Picture and Fax Viewer, where it can be viewed and printed.

23 Output, Macro, and Report

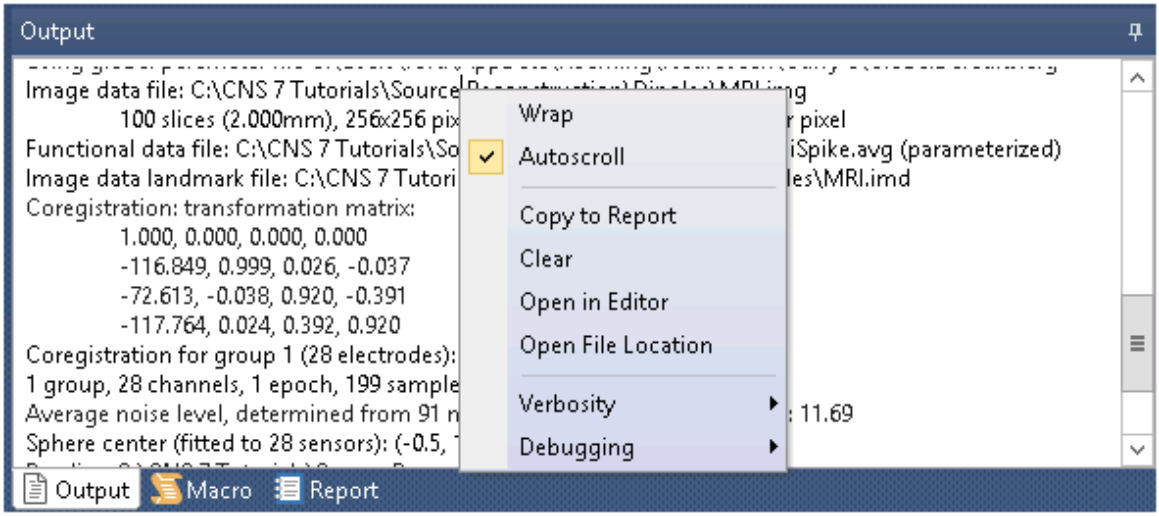
The **Output**, **Macro**, and **Report** tabs 

are initially found in the lower part of the display in their docked position (either autohidden or not). Each is described in the following sections.

23.1 Output

CURRY will create a running log of operations you have performed. This can be seen in the 

panel. *Right click* in the field to access additional options.



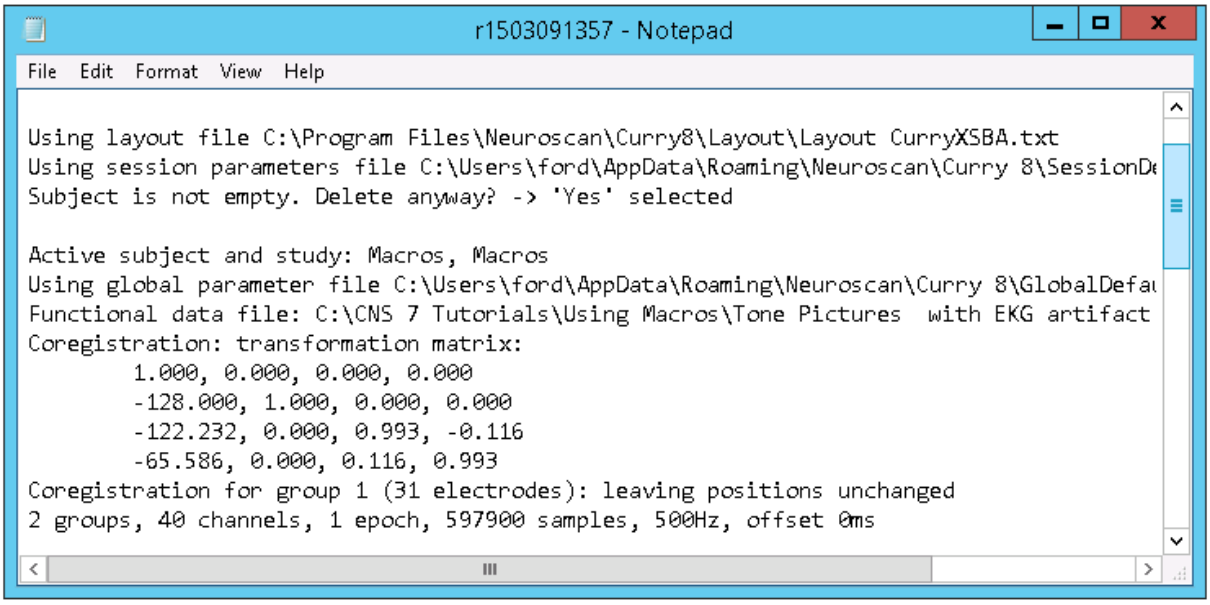
Wrap. If a line in the Output file is too long to fit in the display, clicking **Wrap** will wrap the text to the next line.

Autoscroll. When enabled (default), the display will scroll down to show new information that is added. When disabled, the screen will not scroll down, leaving the previous information in place.

Copy to Report. Highlight a section and click this option to copy it to the Report.

Clear. **Clear** empties the Output field of all contents.

Open in Editor. The contents of the Output window will be displayed in a text editor (e.g., Notepad).



A .txt file is created automatically each time you start CURRY. The assigned file name is a composite of the year, month, day and time. (If you restart CURRY very quickly, you may be asked if you want to overwrite the existing file). Please see the **Target Folders for Windows 7** section.

The contents will of course depend on the operations you have performed, and they should be decipherable will a little study. For example, the results of a CDR are shown below, with additional explanation.

CDR results (minimum L2 norm, misfit 1) for 29849 sources, 10.0 ms:
(max 28194): (-49.2,13.9,14.5)mm, q=3.5864µAmm, (-0.10,0.11,-0.99)
(Inferior Temporal Gyrus)
50%/ 100%: (-40.9,20.1,20.1)mm, q=1619.6µAmm, (-0.08,0.05,-1.00), 2.6ml
(Culmen)
50%/99.9%: (-39.2,18.2,20.8)mm, q=2174.2µAmm, (-0.08,0.06,-0.99),3.9ml
(Inferior Frontal Gyrus)
(perc. 95%): (-36.8,17.3,21.1)mm, q=2706.5µAmm, (-0.09,0.07,-0.99), 5.4ml
(Inferior Frontal Gyrus)
SNR: 9.7, residual deviation (normalized, original): 10.3%, 10.1%, variance: 98.94%, 98.98%
SNR: 9.7, achieved relative deviation: 100% (=9.7x10.3%), lambda (used, fitted): 1.51, 1.51

(minimum L2 norm, misfit 1)
The CDR method and the parameters that were used.

for 29849 sources, 10.0 ms:
The number of sources and the latency reported. CDR results are computed per-latency.

(max 28194):

The number of the largest source (dipole).

(-49.2,13.9,14.5)mm,
Its location.

q=3.5864µAmm,
Its strength.

(-0.10,0.11,-0.99)
Its normal (orientation).

(Inferior Temporal Gyrus)
Its corresponding anatomical/functional atlas labels, if available.

50%/ 100%: (-40.9,20.1,20.1)mm, q=1619.6µAmm, (-0.08,0.05,-1.00), 2.6ml (Culmen)
The same, but for the weighted sum of all dipoles whose strength is larger than 50% of the largest, including the volume they occupy.

50%/99.9%: (-39.2,18.2,20.8)mm, q=2174.2µAmm, (-0.08,0.06,-0.99), 3.9ml (Inferior Frontal Gyrus)
The same, but for the weighted sum of all dipoles whose strength is larger than 50% of the 99.9-percentile of strengths.

(perc. 95%): (-36.8,17.3,21.1)mm, q=2706.5µAmm, (-0.09,0.07,-0.99), 5.4ml (Inferior Frontal Gyrus)
The same, but for the weighted sum of all dipoles above the 95-percentile of strengths.

SNR: 9.7,
The data SNR of this latency.

residual deviation (normalized, original): 10.3%, 10.1%, variance: 98.94%, 98.98%
The normalized (in SNR-space; this value has been used during optimization) and original (in µV-space; this value is typically
reported) deviation (fit error "dev", where goodness-of-fit is 100%*(1-dev)) and explained variance (100%*(1-dev*dev)).

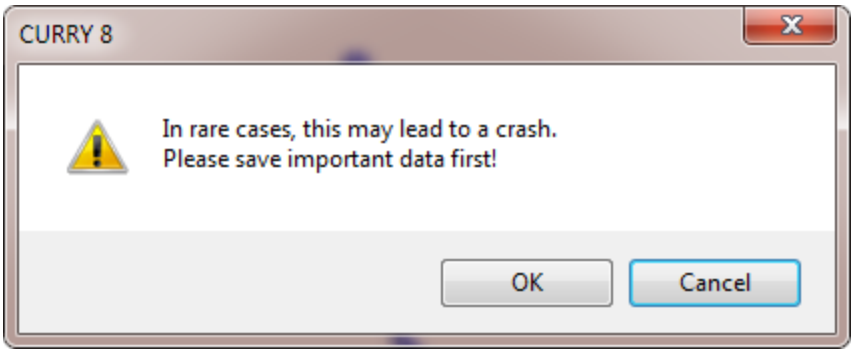
SNR: 9.7, achieved relative deviation: 100% (=9.7x10.3%), lambda (used, fitted): 1.51, 1.51
SNR * residual deviation should yield 100% * misfit. A suggested value for lambda is computed based upon these values for methods like LORETA and Lp-norm and for manual regularization.

Note
The *Application Data* folder may be hidden and you need to enable **Show Hidden Folders** in Windows Explorer in order to see this folder.

Open File Location. Selecting this option opens the Windows Explorer program and displays the contents of the folder where the .txt files are stored.

Verbosity. You may select **Results Only**, **Medium**, **High** or **High (incl. Timing)** **Verbosity** (the amount of detail in the Output field).

Debugging. The **Debugging** option should be left in the **Off** setting unless instructed otherwise by Technical Support. Turning it **On** increases the output load. The **Available Memory** option will find and allocate memory, with the following warning.

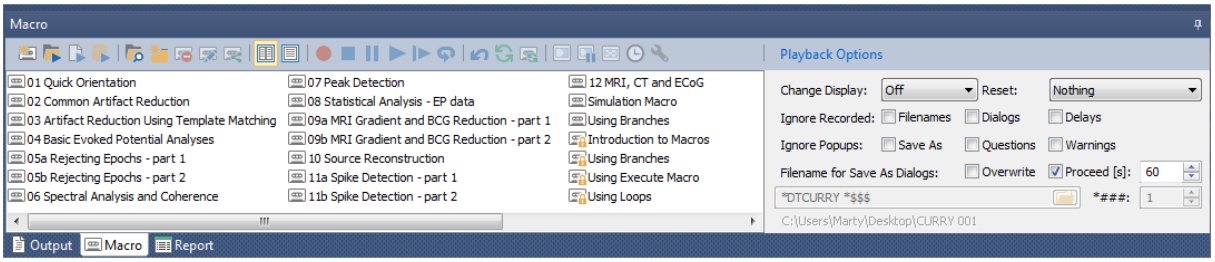


23.2 Macro

The macro recorder in CURRY is used to record the steps you have taken during an analysis. In a sense, it provides a history of what was done with the file. Its primary value lies in the ability to apply those same steps to other like data files that you select. It thus functions as a batch file for automated processing of data. Beyond that, it can be used as a teaching guide for training others in your lab to follow a series of operations. You can use macros to record an entire sequence of operations, or have separate macros for different sequences that you use routinely. Custom created dialog screens can be added to explain operations along the way.

Macros that you have created in earlier versions of CURRY (prior to CURRY 8) should also run in CURRY 8 with the following exceptions. CURRY 8 will only recognize one template under Template Matching, and two Artifact Reduction sequences. Other minor exceptions may also be present. These exceptions may be resolved in future versions of CURRY 8.

To create a Macro you must first have a Study open with a data file that you wish to use. The .mac files that are displayed are saved in the default folder (see **Target Folders for Windows 7**). Until you open a Study, there are limits on how many of the operations are accessible. The simplest place to start is by opening a data file (Study) and then running "An Introduction to Macros", by highlighting it and clicking  .



Note
When using Macros, it is important to understand that they operate within a single Study. Almost anything you can do within a Study can be captured with a macro, including saving result files to a different Study. However, if you wish to operate on the files in the new Study, that requires a separate macro. For example, if you analyze continuous data and save the resulting averaged files to a new Study, you would need a second macro to do further processing with the averaged files. You can set a macro to run when you open a Study, and therefore, with one manual step (opening the Study), you can continue the automated process. It is also possible to loop a macro across Studies under the same Subject (or Files), applying the same macro to all files in the Studies under that Subject. You may also call one macro from within another - see the **Execute a Macro** option below.

Note
Study Parameter files that have been saved with a Study will be recognized before the macro is executed. For example, say you have multiple continuous data files in separate Studies. In each Study you set the SNR Thresholds and save the Study Parameters for each file. If you then loop a macro across the Studies, the Study Parameters are read first, and then the macro is executed.

Macro Toolbar Icons

New Macro  . Create a New macro. A Save As window will appear, in which you can enter a file name.

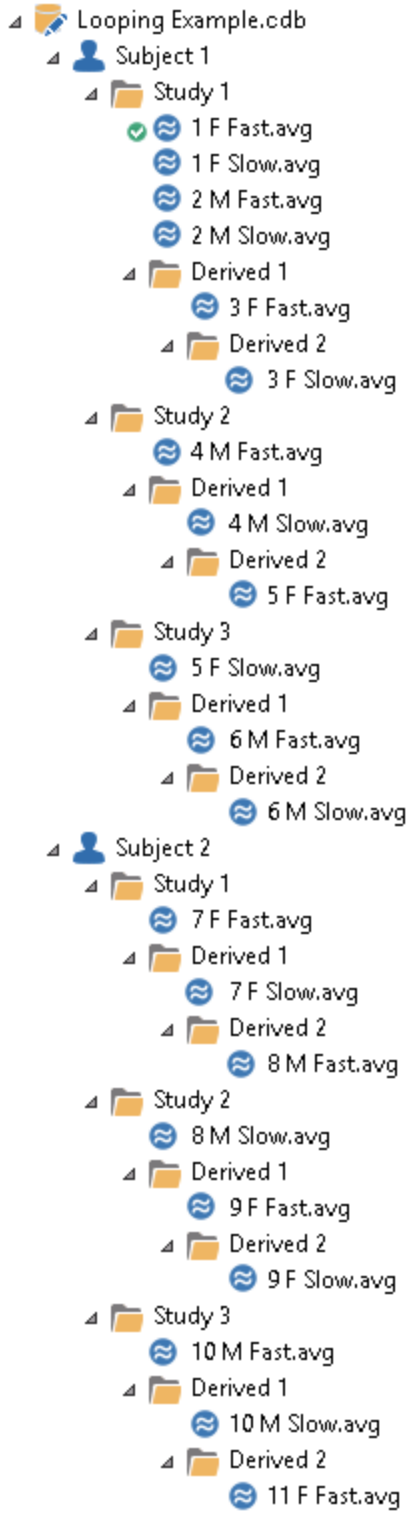
To rename an existing macro file, slowly *double-click* on the file name, or highlight and use *F2*, or use the **Rename** option in the context menu.

New Folder  . This option creates a new folder for your macros.

Select and Play Macro  . This option lets you select and play a macro from folders other than the one where macros are typically held (and therefore appear in the list).

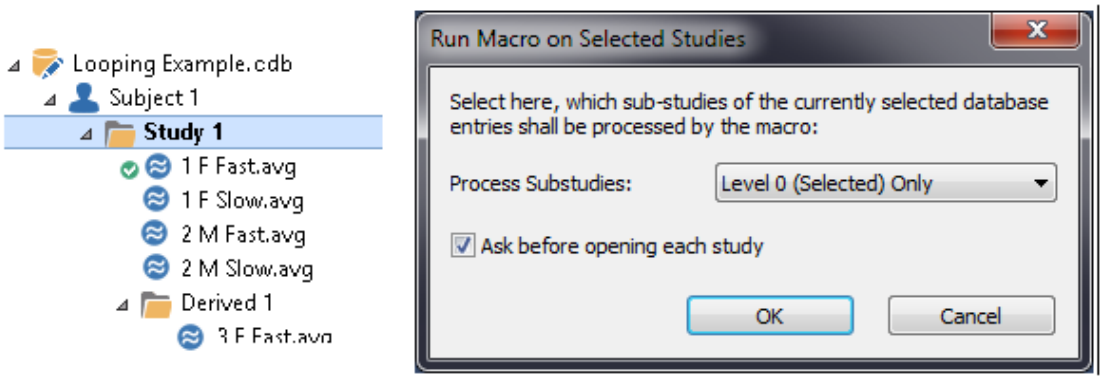
Loop Over Files  . Once you have a macro recorded, you may wish to apply it to multiple data files. Highlight the macro file in the list and click this icon to see an Open File window. Select the files that you wish to use; however, the files must all come from the same folder. If you have files in multiple folders, you can do a file Search in the Windows Explore program, then highlight the files you want to use. Drag and drop these into the Database in a Study you have created. Then use the **Loop Over Studies** option.

Loop Over Studies  . Similar to Loop Over Files except that you select Studies and sub-studies in the Database, rather than individual files. You have considerable flexibility in selecting which files you wish to use. Consider the following Database. There are 2 Subjects, each containing 3 Studies, and each of those contain sub-levels of derived files.

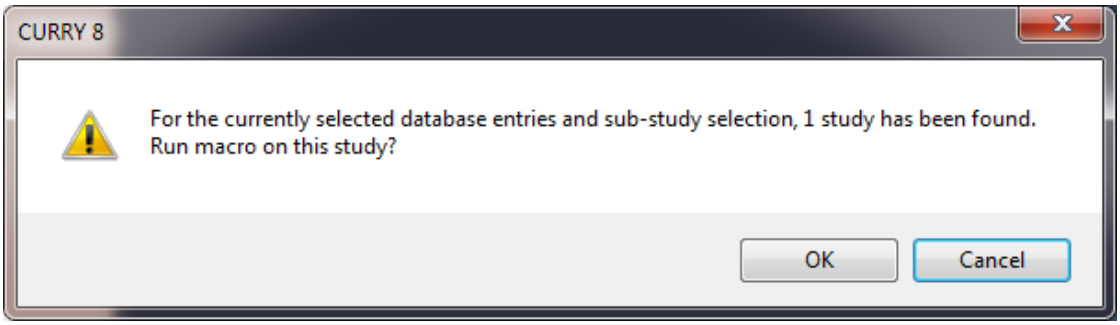


In the simplest example, let's say you want to apply the macro to Subject 1, Study 1, and not the derived folders under it. Highlight Study 1 and click the **Loop Over Studies** button (be sure to select the macro first). In the dialog you see, you have the option to use the **Level 0 (Selected) Only** option. The study you select is

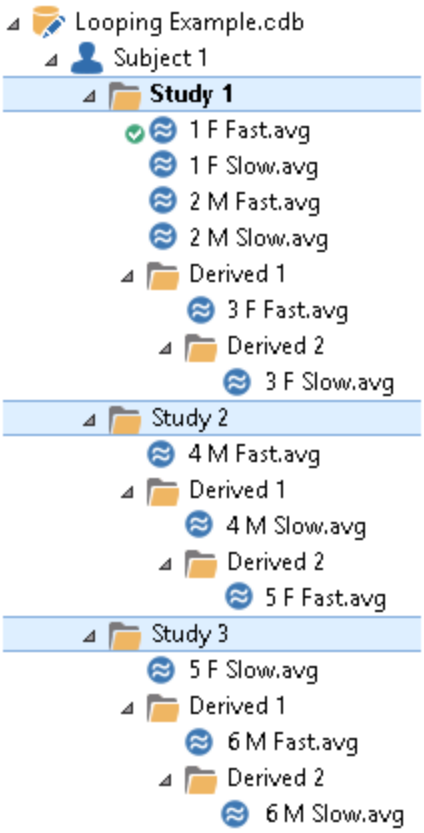
Level 0. If you enable **Ask before opening each study**, you will be asked to confirm that the correct study has been selected. If not selected, the macro will run without interruption.



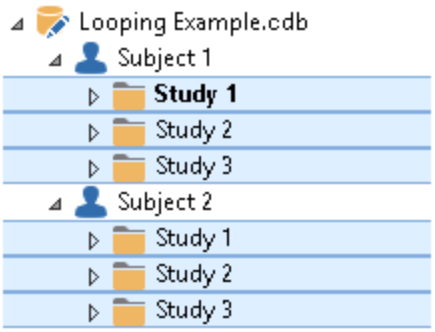
After clicking **OK**, you will see a message telling you how many studies have been found - one in this case. Click **OK** and the macro will be run.



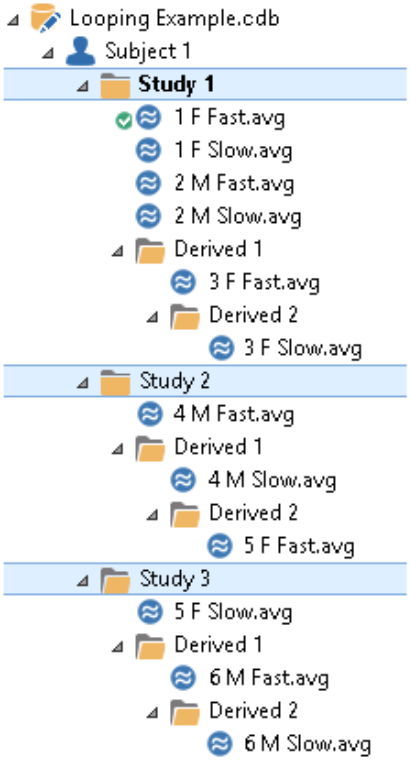
If you instead want to run the macro on all of the studies for Subject 1, and not the derived studies under them, just highlight the studies (*Ctrl+click*) and click the **Loop Over Studies** button. Again select **Level 0**. You will see the message saying 3 studies have been found.

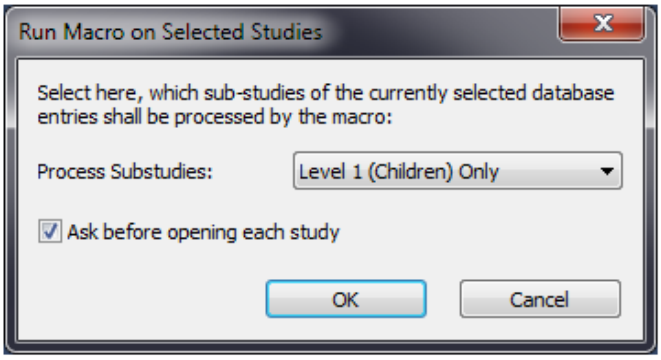


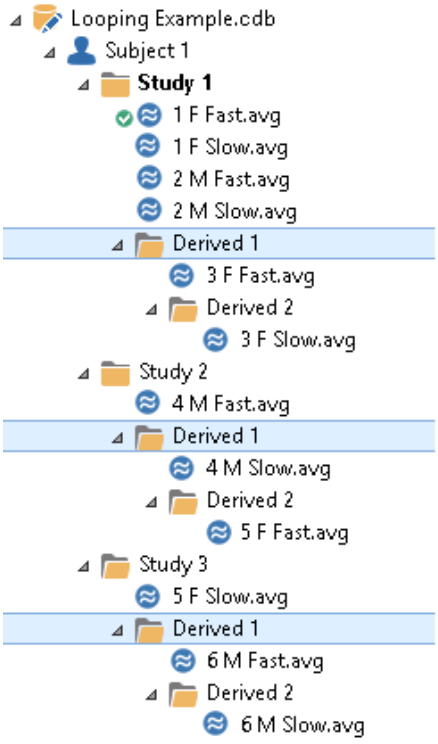
If you want to run the macro across Subjects (and not including derived studies), highlight the studies in each Subject. Click the **Loop Over Studies** button and select **Level 0**. You will see the message saying 6 studies have been found.

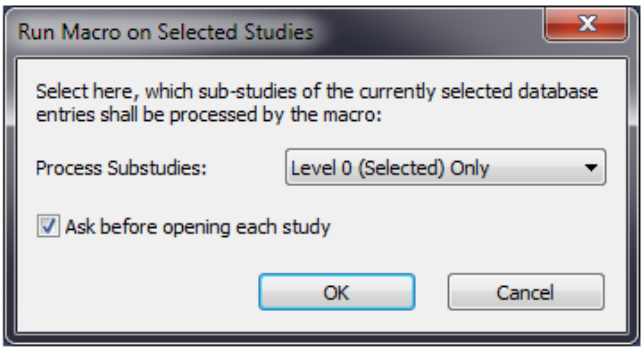


If you want to use only the first level of derived studies for the 3 studies in Subject 1, you can select those studies and then process only the **Level 1 (Children)** substudies, or you can select the derived studies and process the **Level 0** substudies.

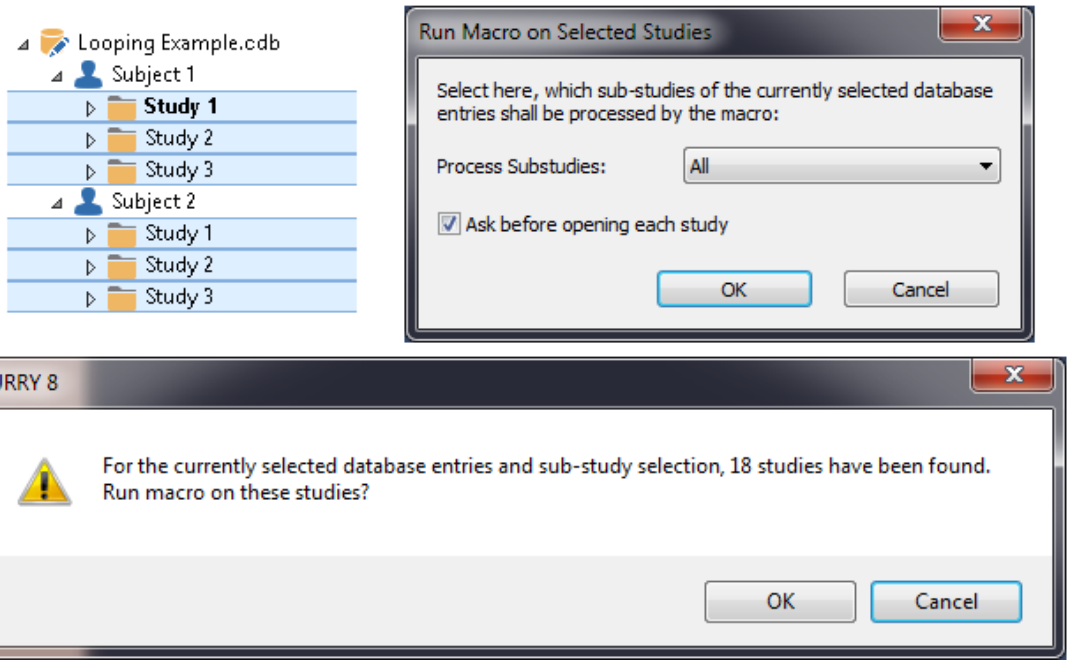

Looping Example.cdb
Subject 1
Study 1
1 F Fast.avg
1 F Slow.avg
2 M Fast.avg
2 M Slow.avg
Derived 1
3 F Fast.avg
Derived 2
3 F Slow.avg
Study 2
4 M Fast.avg
Derived 1
4 M Slow.avg
Derived 2
5 F Fast.avg
Study 3
5 F Slow.avg
Derived 1
6 M Fast.avg
Derived 2
6 M Slow.avg


Run Macro on Selected Studies
Select here, which sub-studies of the currently selected database entries shall be processed by the macro:
Process Substudies:
Level 1 (Children) Only
Ask before opening each study
OK
Cancel

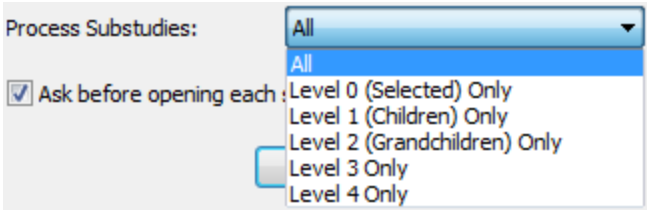

Looping Example.cdb
Subject 1
Study 1
1 F Fast.avg
1 F Slow.avg
2 M Fast.avg
2 M Slow.avg
Derived 1
3 F Fast.avg
Derived 2
3 F Slow.avg
Study 2
4 M Fast.avg
Derived 1
4 M Slow.avg
Derived 2
5 F Fast.avg
Study 3
5 F Slow.avg
Derived 1
6 M Fast.avg
Derived 2
6 M Slow.avg


Run Macro on Selected Studies
Select here, which sub-studies of the currently selected database entries shall be processed by the macro:
Process Substudies:
Level 0 (Selected) Only
Ask before opening each study
OK
Cancel

If you want to process all of the studies in all of the folders, highlight the studies in both Subjects and select **All**. 18 studies will be found and processed.



Using the Process Substudies options, you can select up to 4 levels of subfolders below the current Level 0. These options give you considerable flexibility for choosing which studies you can select for processing.



Open File Location  . Opens the Windows Explorer program to the folder containing the highlighted macro.

Delete  . Deletes the selected macro file.

Edit  . Opens the macro in Notepad for editing (see the section on Editing Macros below).

Duplicate  . Creates a copy of the selected macro file, with "Copy" added to the file name.

List View  . Lists only the file names.

Details View . Lists the file names plus the last date the file was modified and the file size.

Record Macro . Start recording the macro. If you already have a macro file, which you highlight before clicking the Record button, the new operations will be appended to the existing macro.

Stop Macro . Stop recording the macro.

Pause Macro . Pause the execution of the macro.

Play Macro . Start the play back of the macro.

Single-Step Macro . Replay the macro one step at a time.

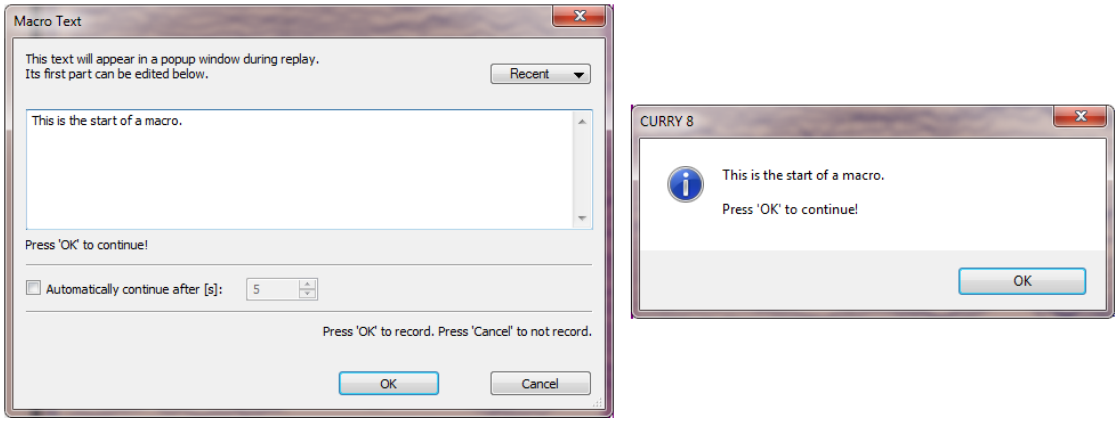
Play Macro Infinitely . The macro will restart and play over and over (for ongoing demonstrations). Press the *Esc* key to stop it.

Undo . Clicking this removes the last step that was recorded. Each time it is clicked, the most recent step is removed.

Record All Interactions . When selected, the UI will be continually updated during the execution of the macro.

UI Update . Inserting this option will update the macro to reflect modifications you have made during the recording.

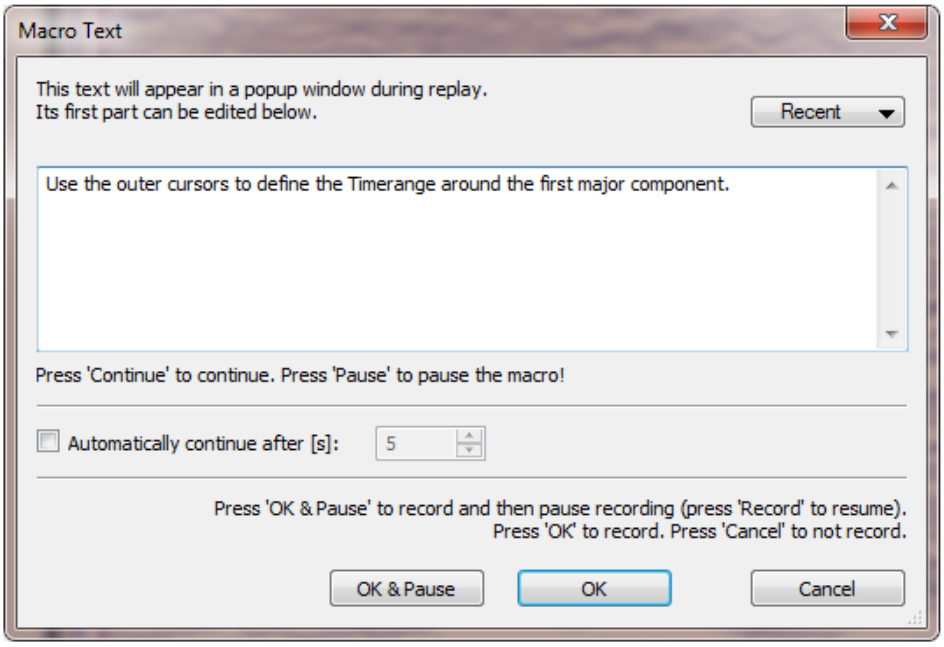
Show Popup Window and Continue . Click this button while recording a macro to see the following screen. Text that is entered will appear in a popup window during replay. If you enable **Automatically continue after [s]**, the popup will countdown the seconds you enter and close automatically.

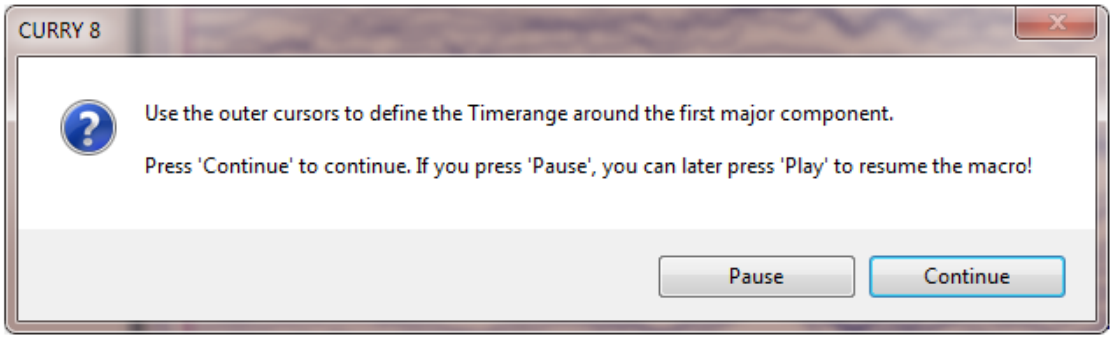


Show Popup Window and Pause or Continue  . This option allows you to stop recording the macro to make changes to the data file, then continue with the recording. On replay, you have the same option to pause the replay to make changes, or to continue without making changes. The **Recent** list displays recently entered text.

During the recording, click **OK & Pause** to stop the recording of the macro, letting you make changes that will not be included in the macro. Click the **Record** button again to resume. If you click the **OK** option, the text you enter will be seen in the replay, and the recording of the macro will continue automatically. If you enable **Automatically continue after [s]**, the popup will countdown the seconds you enter and close automatically.

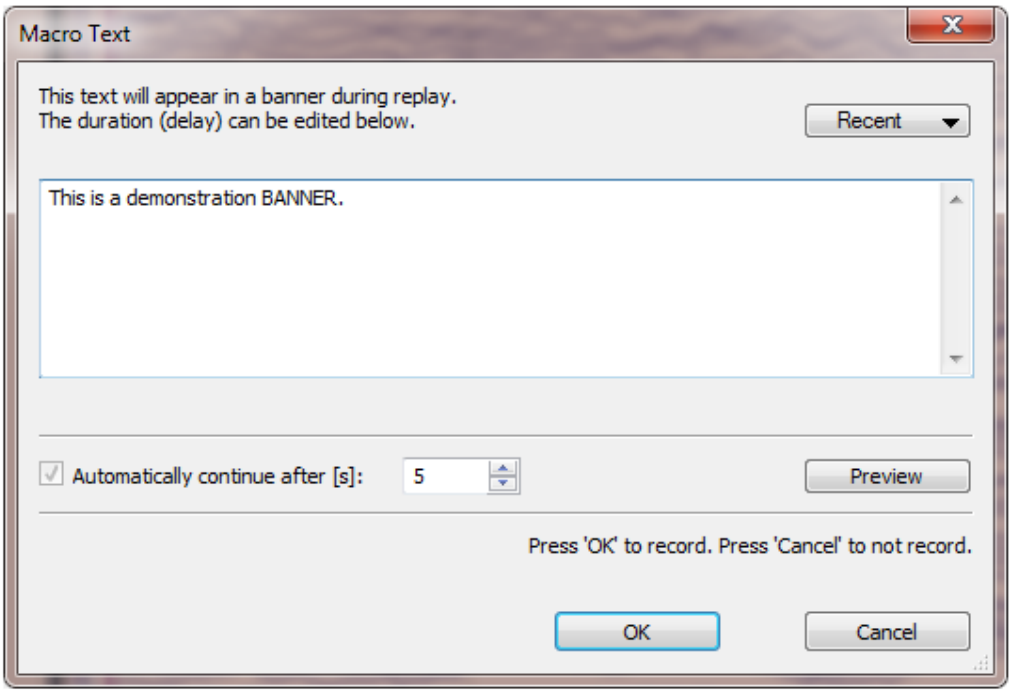
During replay, you will see a popup window with the text you entered. If you click **Pause**, and the replay will pause until you click the **Play** button, thus letting you make manual changes to the file. If you click **Continue**, the replay will continue without pausing.

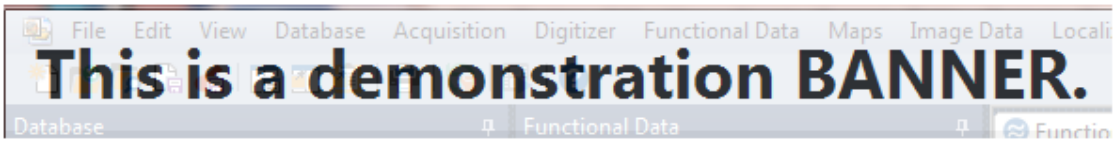




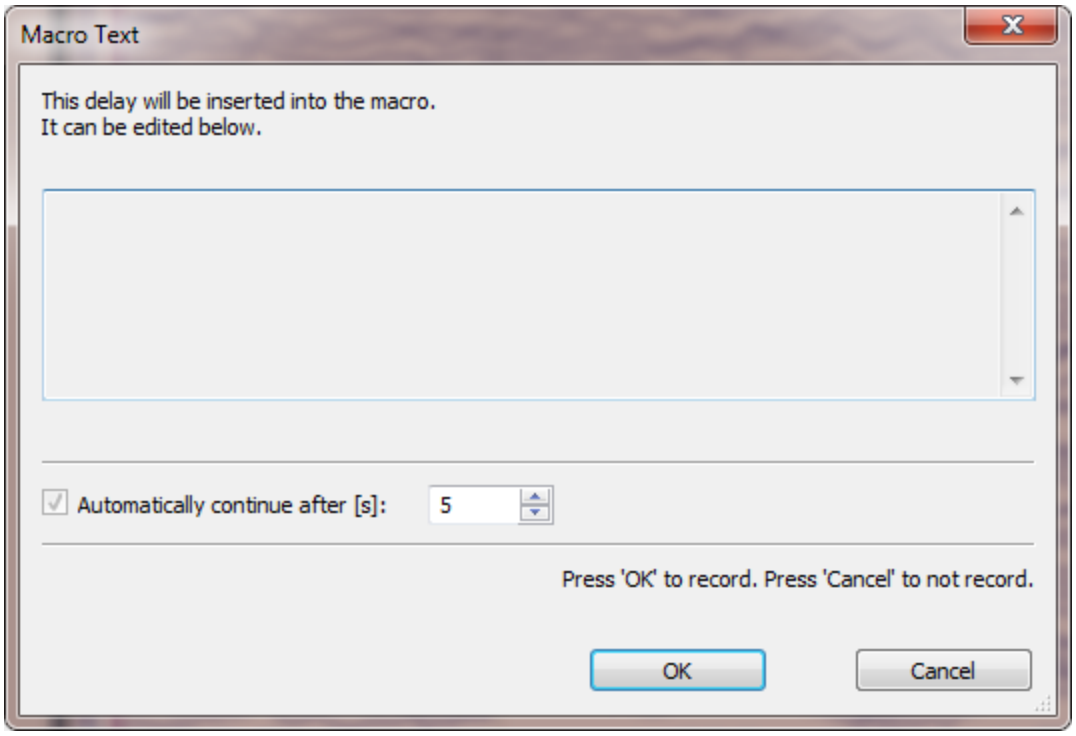
Show Banner  . A custom text "banner" can be created and shown at the top left part of the display. The **Recent** list display recently entered text. The

Preview button will display the banner before it is actually recorded. If you enable **Automatically continue after [s]**, the banner will be removed after the seconds you enter.

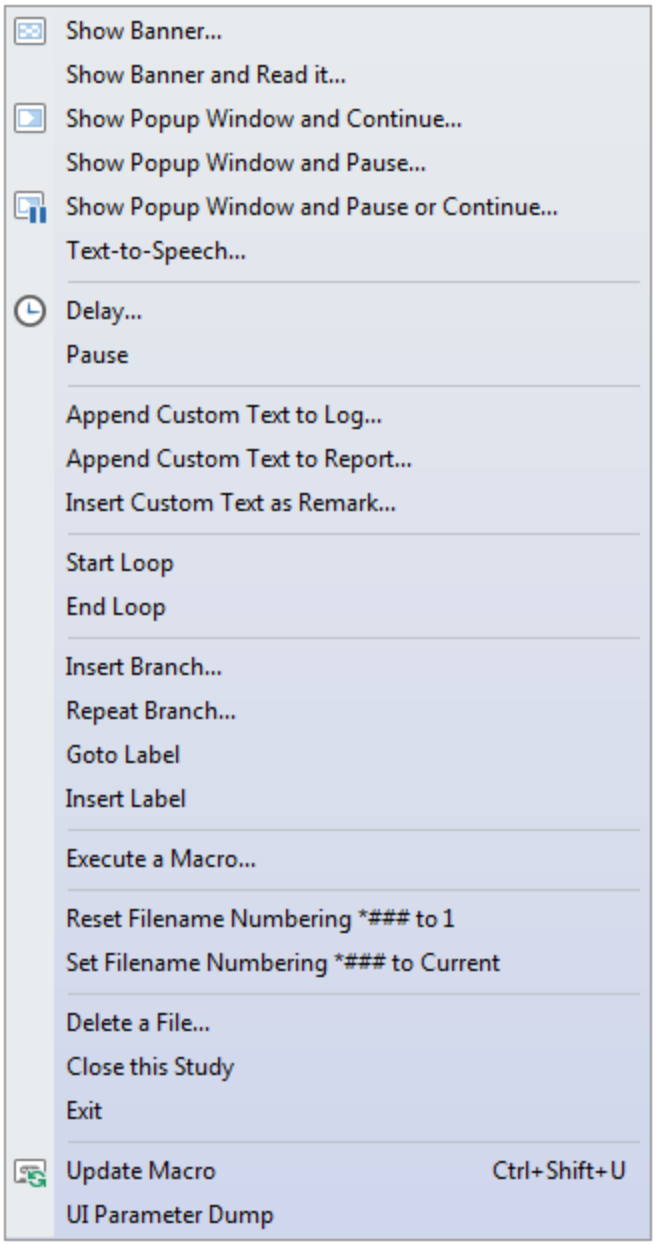




Delay . Determines the duration of the Delay (in seconds) that may be inserted into the macro. On playback, the dialog on the right appears. You can override Delays by selecting Ignore Recorded: Filenames Dialogs Delays in the Playback options.

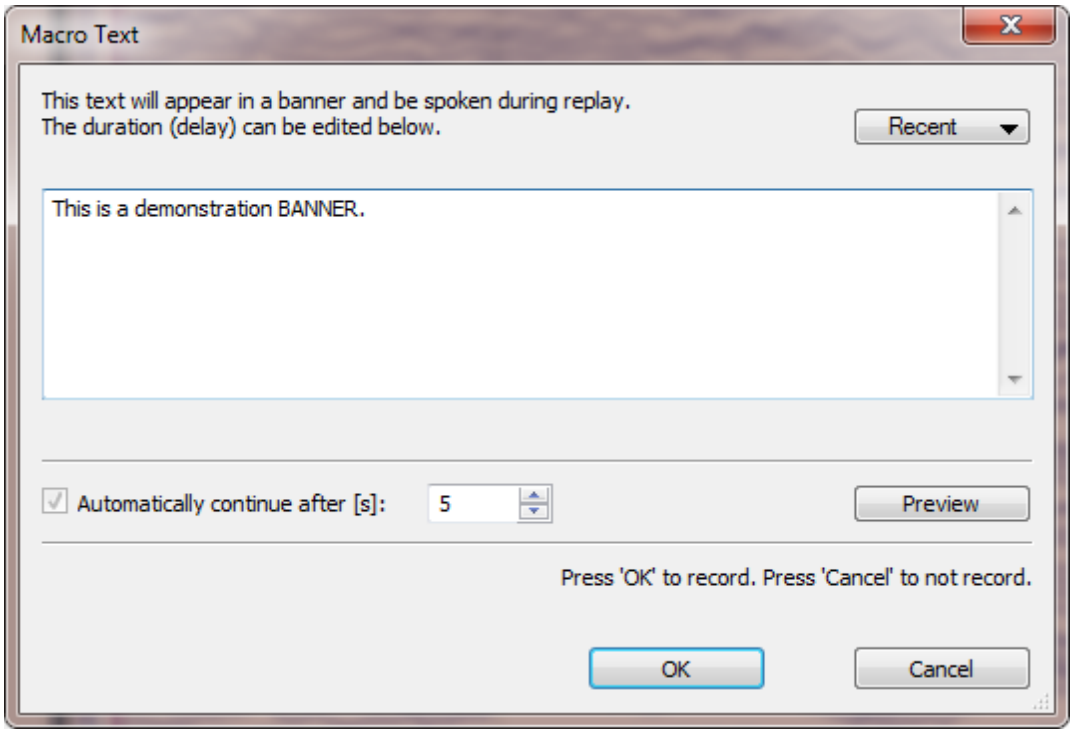


Insert Action  . There are a number of actions that may be inserted into the macro while it is being recorded.



Show Banner. This is the same as the option on the Toolbar described above (**Show Banner**).

Show Banner and Read it. This is like Show Banner except you will hear the text being read.

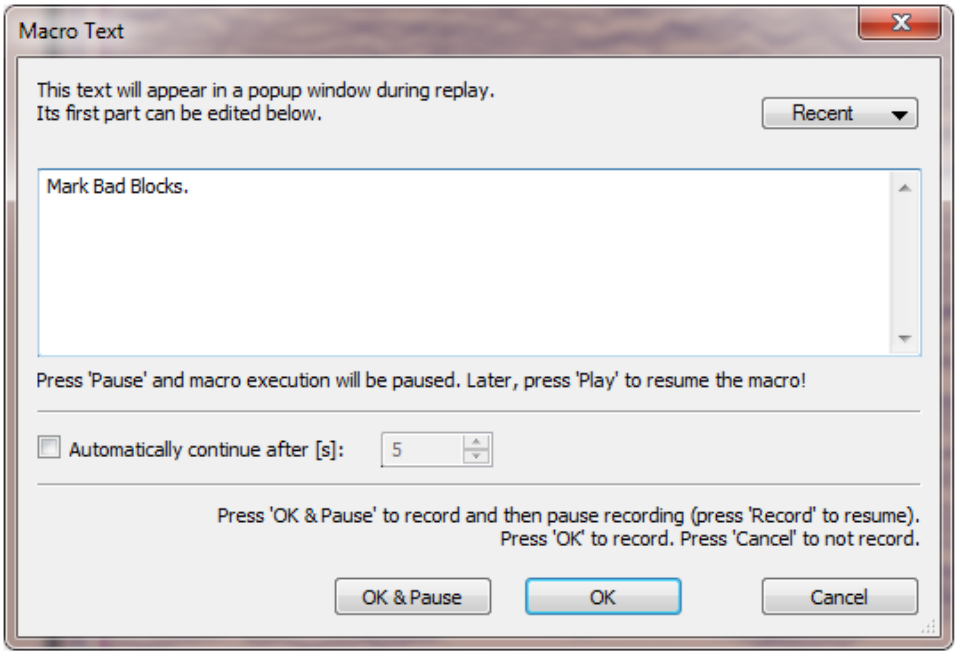


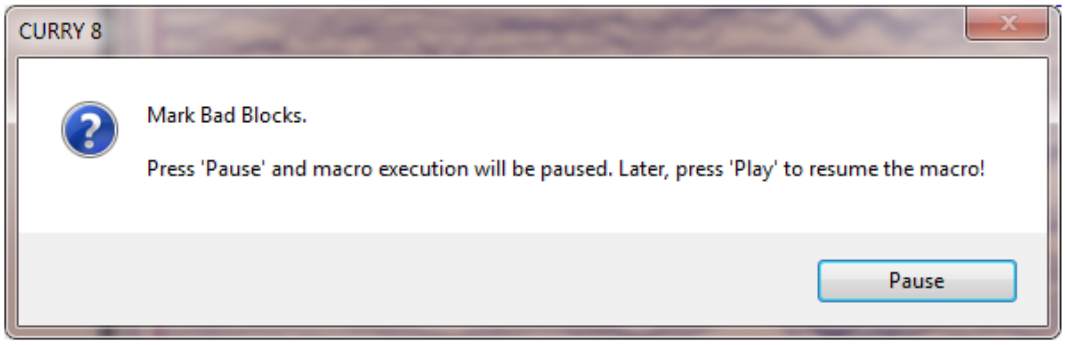
Show Popup Window and Continue. This is the same as the option on the Toolbar described above (**Show Popup Window and Continue**).

Show Popup Window and Pause. This will cause the playback to pause until you click the **Play** icon again. Basically, it is the same as the **Show Popup Window and Pause or Continue**, without the option to Continue during the play back. The **Recent** list displays recently entered text.

During the recording, if you click **OK & Pause**, the recording will stop, allowing you to make manual changes. Click **Record** to continue recording the macro. If you click OK, the message will be recorded in the macro, and the macro will continue recording.

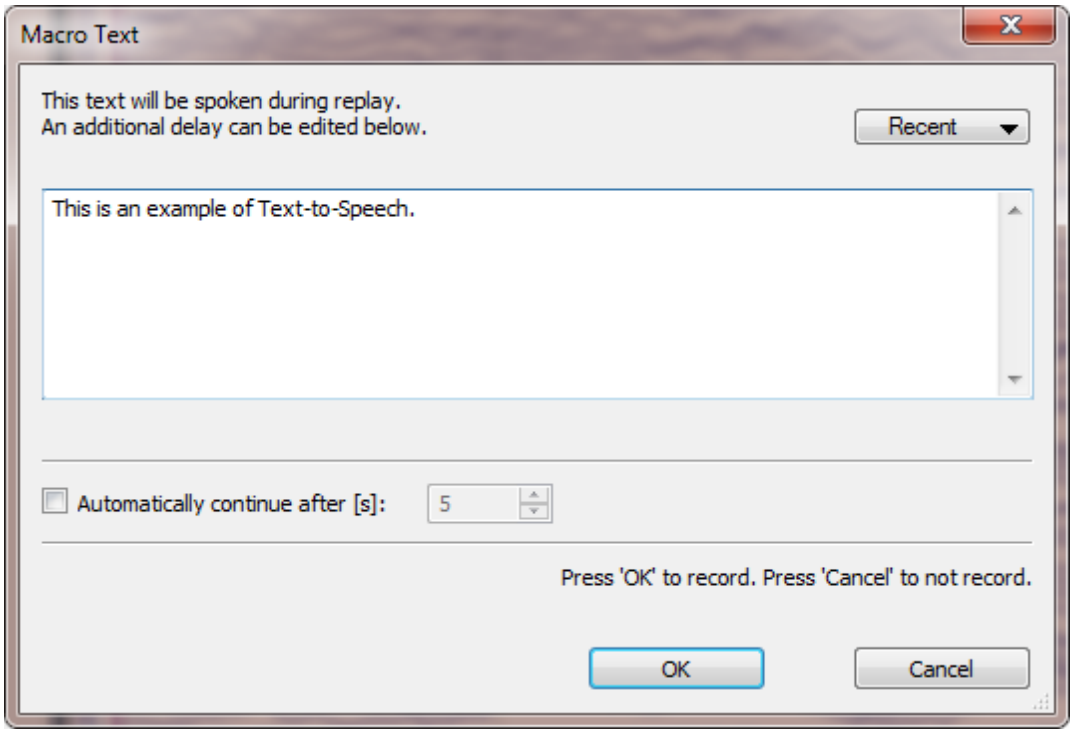
During the replay, the message will appear and the macro will pause. Click the **Play** button to resume the replay.





Show Popup Window and Pause or Continue. This is the same option accessed directly from the Toolbar  , and is described above (**Show Popup Window and Pause or Continue**).

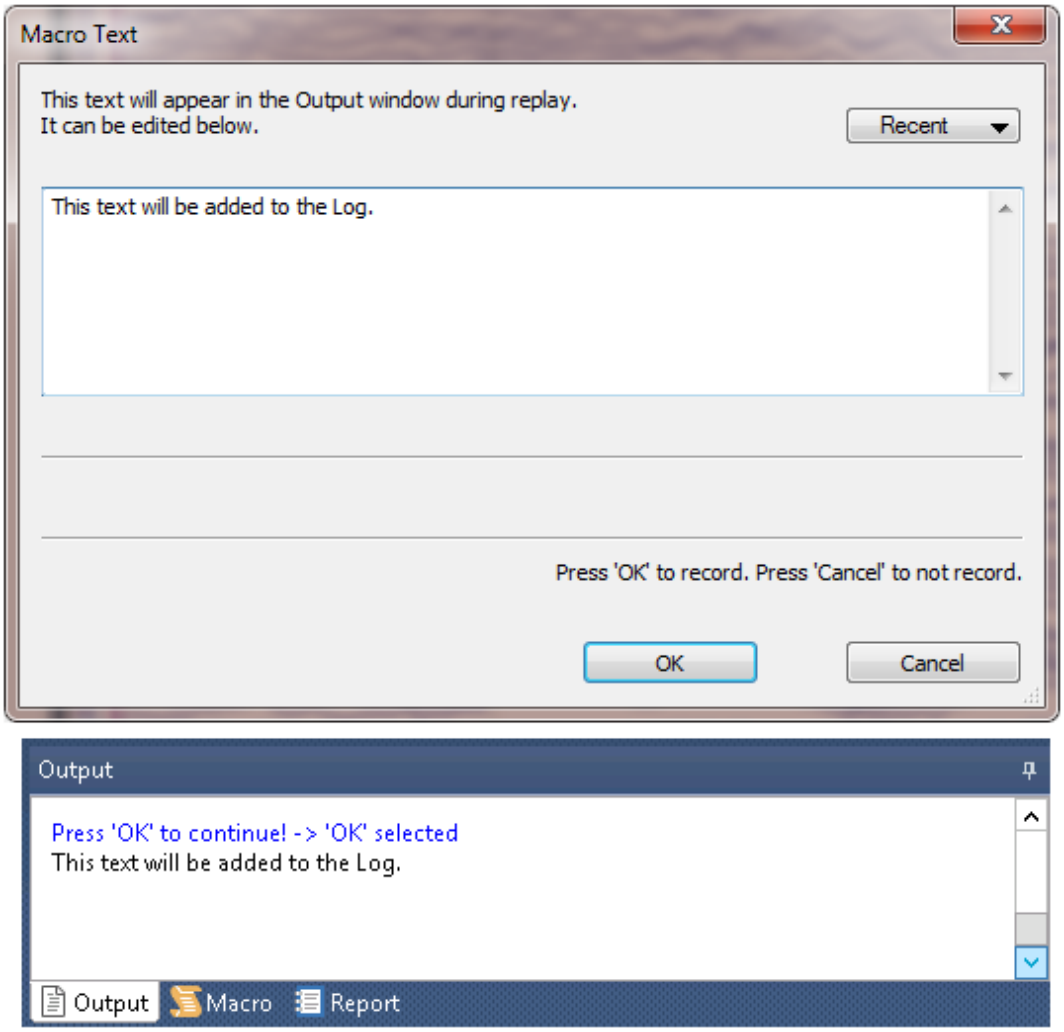
Text-to-Speech. Text that you enter at the time of the recording will be heard via your computer sound system when you replay the macro. You may resume the playback automatically after N number of seconds.



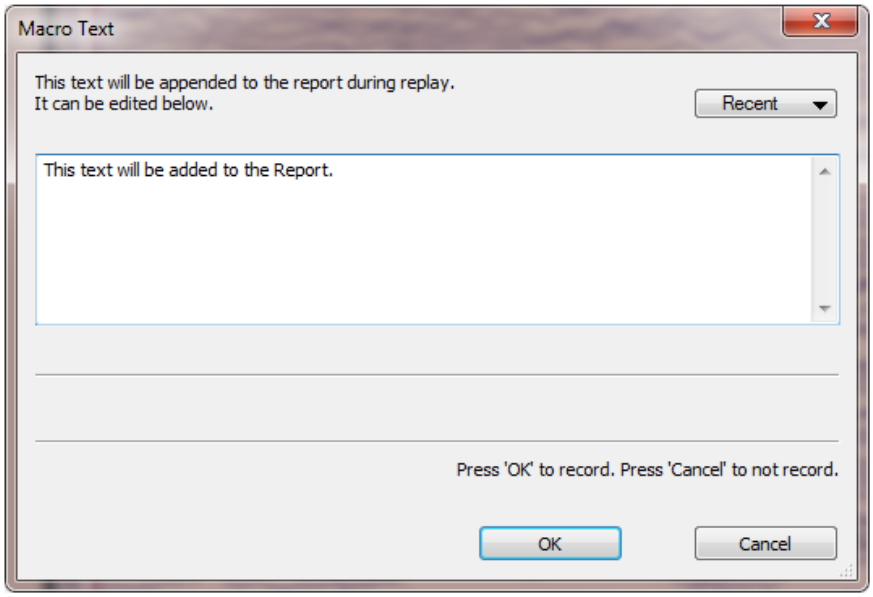
Delay. Inserts a Delay in the playback (same as the **Delay** icon on the Toolbar, described above).

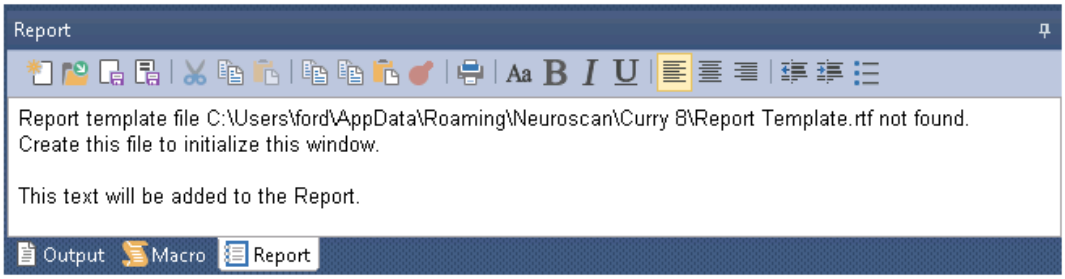
Pause. The playback of the macro will be paused at this point (no dialogs appear). Click the Play button to continue.

Append Custom Text to Log. The Macro Text dialog will appear during recording. Text that is entered will be added to the Log file that is displayed in the Output information.

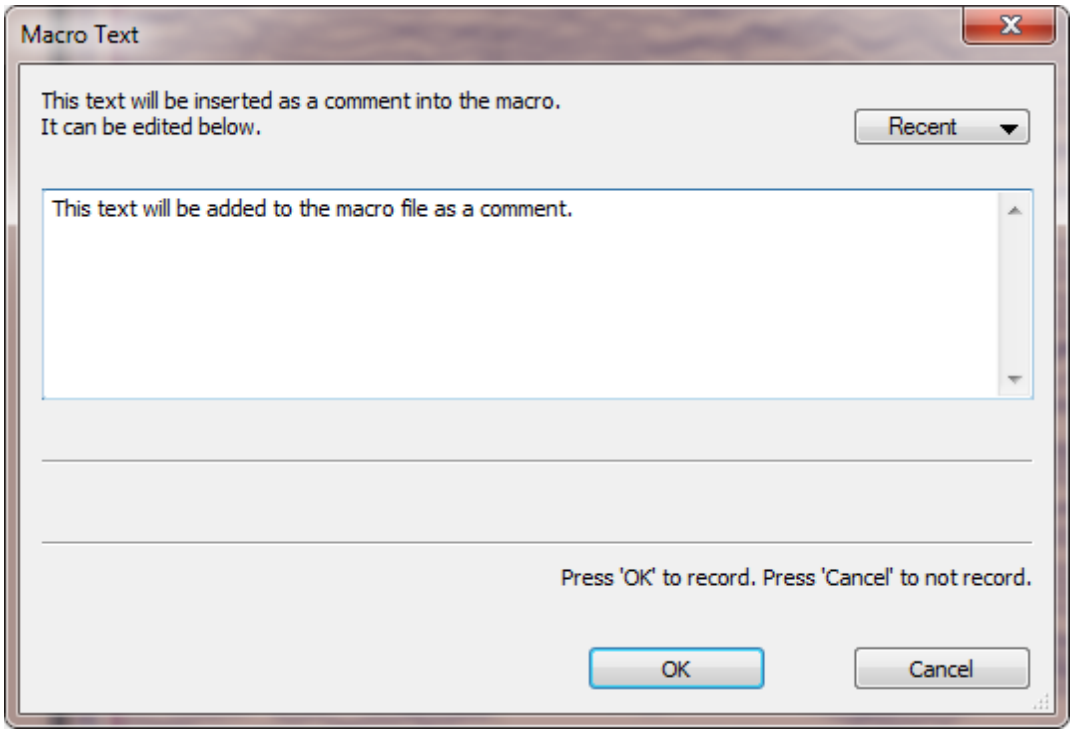


Append Custom Text to Report. The Custom Text will be added to the Report.

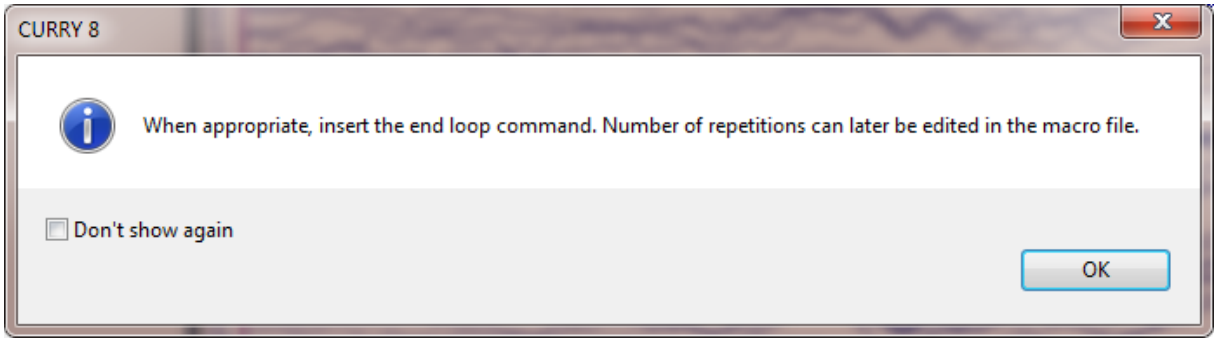




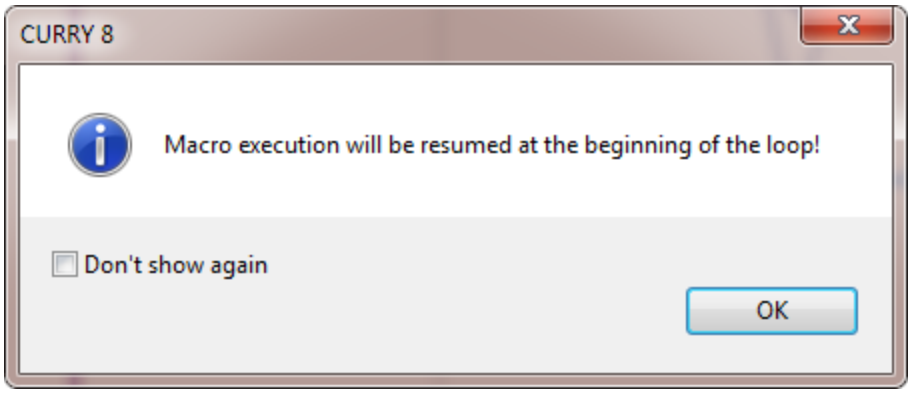
Insert Custom Text as Remark. The Custom text will be inserted into the macro file, which will be seen when you Edit the file.



Start Loop / End Loop. You may create loops within the macro. Click Start Loop where you want the loop to begin. You will see the following message.



Click End Loop at the end of the loop, and see the following message.



To set the number of loops, go into the macro editor  . Change the MacroLoopCounter to the desired number of loops.

```
Mainframe.MacroLoopCounter =  10
```

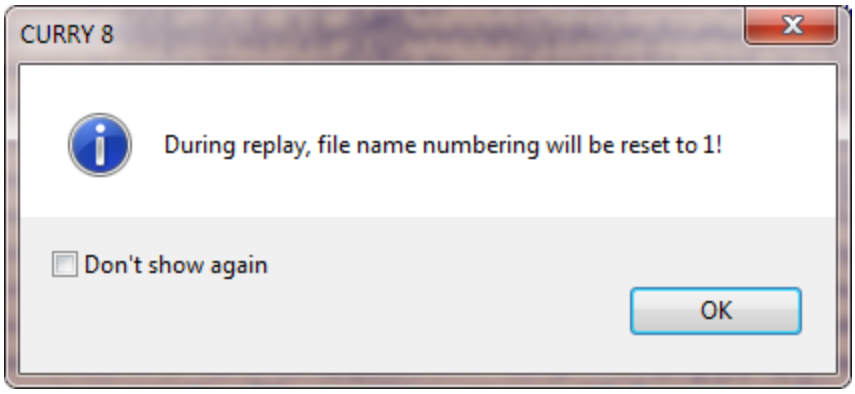
Please see the Using Loops macro for an example. The text of that macro is shown below. The middle section is the loop, where the Start Loop and End Loop commands are seen. In between are the things you want to loop. MacroLoopCounter controls the number of loops.

```
# this is an example where a loop is executed three times

    Mainframe.MacroText       = Next, a loop will be executed three times
    Mainframe.MacroDelay      =  5
    Mainframe.FileVersion     =  8
    Study.Action              = MacroBanner
    STEP END

    Mainframe.MacroLoopCounter =  3
    Study.Action              = MacroStartLoop
    STEP END
    Mainframe.MacroText       = Inside loop (this banner will appear three
    times)
    Mainframe.MacroDelay      =  2
    Study.Action              = MacroBanner
    STEP END
    Study.Action              = MacroEndLoop
    STEP END

    Mainframe.MacroText       = Loop finished
    Mainframe.MacroDelay      =  5
    Study.Action              = MacroBanner
    STEP END
```

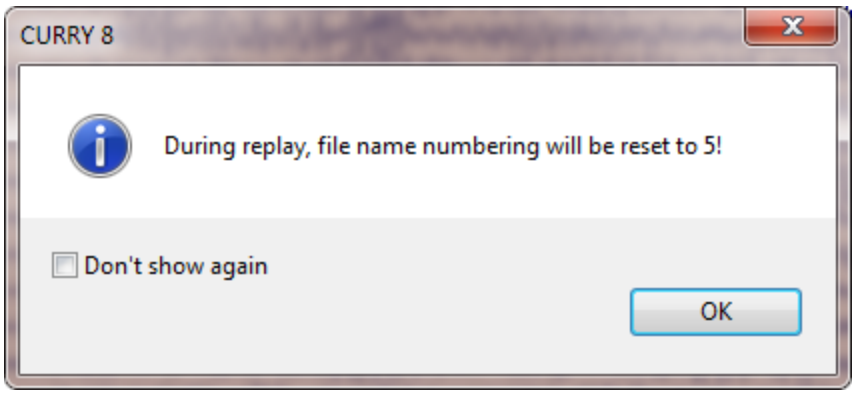
Branching
The branching options in CURRY include **Insert Branch**, **Repeat Branch**, **Goto Label**, and **Insert Label**. These are best explained with some example macros, which are found in the **Branching** section below.

Execute a Macro. This option allows you to call a macro from within a macro. An open file dialog will appear, allowing you to select the macro. The second macro functions like a subroutine.

Reset Filename Numbering *### to 1. Inserting this option will reset the file numbering to 001 when the macro is replayed.



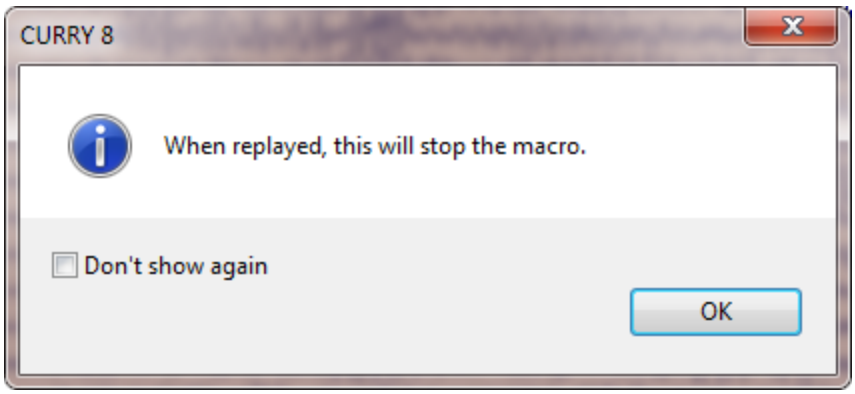
Set Filename Numbering *### to Current. Inserting this option will reset the file numbering to the current value when the macro is replayed.



Delete a File. This option allows you to delete a file from within the macro (generally used for reclaiming space).

Close this Study. This option allows you to close a Study from within the macro.

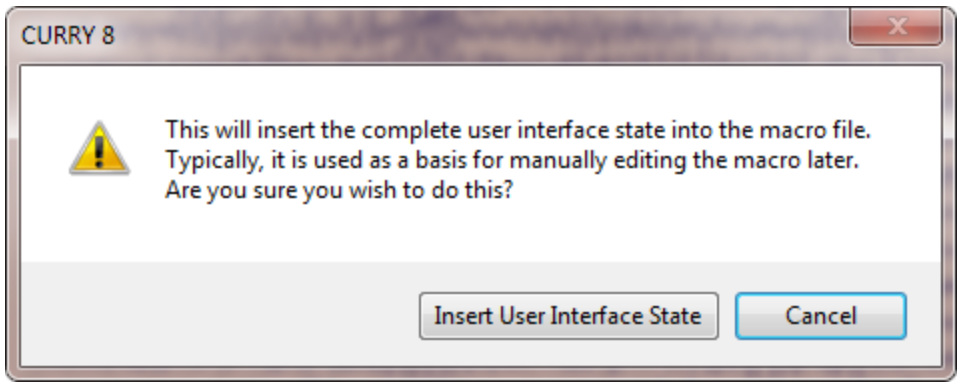
Exit. Use this option to stop the macro during replay.



Update Macro. This is the same option as on the Toolbar. Clicking it will update the Macro to reflect modifications you have made during the recording. These modifications are not always saved immediately to the macro.

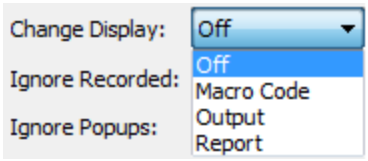
Performing, for example, a Scan will update the macro with all of the previous operations. The UI Update option will "force" the writing of the operations to the macro file.

UI Parameter Dump. Selecting this option will insert the complete set of parameters into the macro file (a lengthy list), whether you have made any changes to them or not. This will allow you to make any modifications to any parameter.



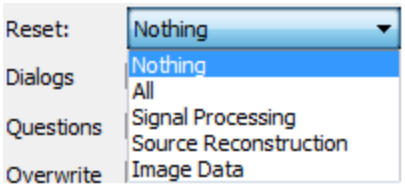
Playback Options. The parameters affect the playback of the macro.

Change Display. This option controls which field will be displayed as you replay the macro.



Selecting **Off** displays the Macro window, showing the progression of the execution of the macro (in percentages). If you select **Macro Code**, you will see the batch code displayed in the **Macro** display window. If you select **Output Window**, you will see the output to the log file in the **Output** display. If you select **Report Window**, you will see any changes made to the Clinical Report in the **Report** display.

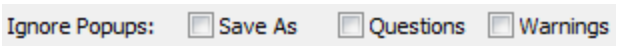
Reset. The Reset option sends a command to all CURRY modules before running the macro. The idea is to start the macro in a well-defined state. **Reset All**, for example, would turn off dipole fits and CDR analysis, delete image data segmentation results and markers, etc. This allows you to run a macro repeatedly and obtain identical results, even if the macro leaves the software in a different state than it was in at the start. **Reset All**, however, can at times have unintended consequences (time points may be reset to 0 ms rather than the original number). It is recommended that you use **Nothing** unless you have reason to use one of the other settings.



You have the options to reset **Nothing**, **All**, **Signal Processing** only, **Fit** only, or **Image Data** only.

Ignore Recorded. You may elect to display or ignore Filenames, Dialogs, or Delays in the Playback of a macro (useful for replaying the macro without any pauses). If you select Filenames, the recorded filename will be ignored, and you will be prompted for the filename, or the file name template will be used. If the template suggests a file that already exists (e.g. because the macro is being run for the 2nd time), the **Overwrite** option (below) allows you to overwrite the existing file (or to be prompted - default).

Ignore Popups. You may elect to display or ignore Save As dialogs, Questions, and Warnings in the Playback of a macro (useful for replaying the macro without any pauses). If you enable the option to ignore the Save As windows, the Filename field will be active. Therefore, rather than the macro pausing for you to enter a name for an output file, you may use the automated file naming option. If the macro pauses, asking if you want to overwrite an existing file, you can enable **Questions**. The popup will not appear and the file will be overwritten automatically.

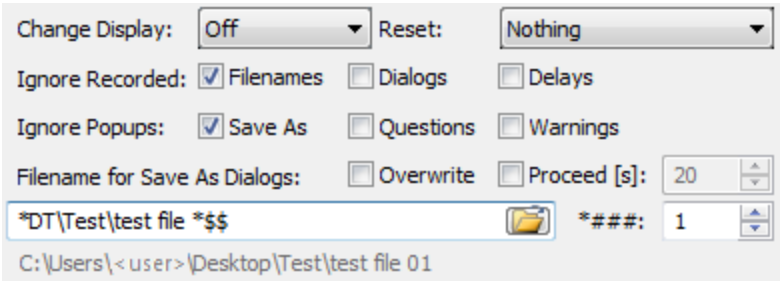


Filename for Save As Dialogs. This field is used to include shortcuts and numerically incremented file names in the macro. This is useful when you are applying the macro to multiple data files, and you need the output files to have unique file names. For this field to be active, you must first enable **Filenames** on the **Ignore Recorded** line, and enable **Save As** on the **Ignore Popups** line. A Tooltip appears when you position the mouse over the Filename label. Shortcuts can be used to simplify the path and filename. Incrementing numbers can be appended to the filenames. You can use a combination of text and substitutions in the paths.

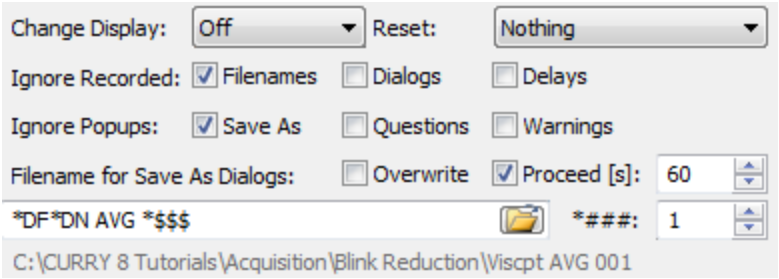
*DT = path to the Desktop
*DB = path to the folder containing the Database file
*EX = Group name (from Database)
*SU = Subject name (from Database)
*ST = Study name (from Database)
*DF = path to the folder containing the Functional Data File
*DN = Data file name
*IF = path to the folder containing the Image Data File
*IN = Image Data File Name

*TI = Unique code based on the date and time
*$$$ = The first three-digit number that is available depending on the files that already exist.
*### = Three (or more) digit number that may be added (this will be incremented based on the number entered in the ***###** field)

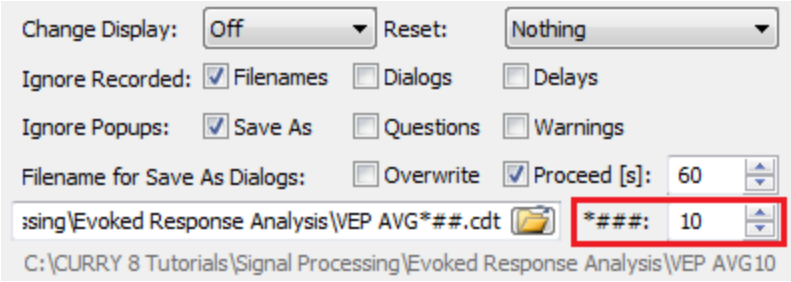
For example, if you want something quick and easy for testing macros, you might use **DT\Test\test file *$$*. *DT sets the path to the Desktop. The "\Test" part will use (or create if needed) a folder on the Desktop called "Test". The actual file name will be "test file 01", and increment on from there (assuming there is not already a test file 01 in that folder, in which case the next available number is used). *$$ controls the numbering. The .cdt extension will be added automatically. The text line below the Filename field displays the actual path and file name.



For example, you want the output file(s) to be placed in the same folder as the Functional Data, using the Data File Name for the root name, followed by "AVG", and an incrementing number for the file name, you would enter *DF*DN AVG *$$$. New saved files will start with the first available number (which may be 001) and will increment by 1.



If you want to select the path manually, but have the file name be added automatically, start by selecting the path using the **Browse** button  . In the Save As dialog, select the path and enter the basic file name you want to use (VEP AVG). Then add *##, for example, after the file name. In this case we also entered **10** in the ***###** field. Files that are saved will start with a 10 at the end, and increment from there (*VEP AVG10.cdt*).

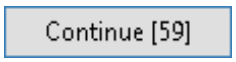


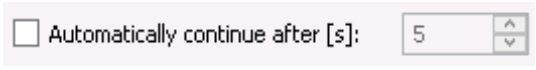
If you record the macro such that the actual paths appear in the FileName line(s), and you want to use substitutions instead, you can edit the macro using the substitutions.

```
Study.FileName      = C:\MACRO Video\Subj 001\tones.cdt

Study.FileName      = *DT*DN
```

Shortcuts such as *SU (subject name) etc. can be escaped by using a backslash, which can be prevented by a double backslash. Examples: *SU is expanded to subject_name, *SU is expanded to *SU, and *SU is expanded to \subject_name. This provides more flexibility in the initial element of the file names.

Overwrite. When enabled, existing files with the same name will be overwritten automatically. Otherwise, you will be prompted to overwrite the file.

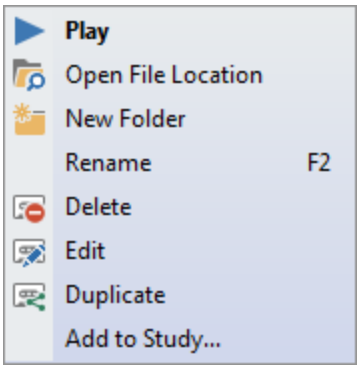
Proceed [s]. This controls the amount of time you see in the countdown clock 

. This supersedes the 

field. Disable the option if you want to use the latter option.

Macro Context Menu

Right click on a Macro area to see the following options. These are alternate ways to access the same options found on the Macro Toolbar or elsewhere, and described above.



Play  . Start the play back of the macro.

Open File Location  . Opens the Windows Explorer program to the folder containing the highlighted macro.

New Folder  . Creates a new folder.

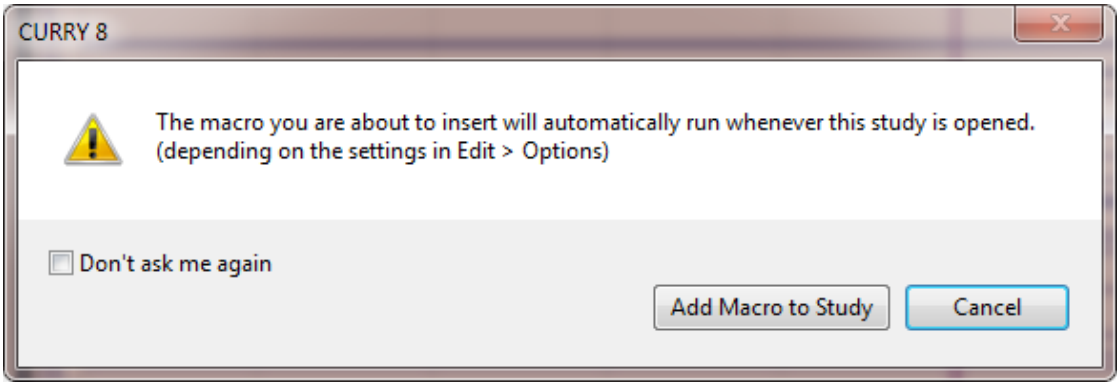
Rename (*F2*). Allows you to rename the selected macro.

Delete  . Deletes the selected macro file.

Edit  . Opens the macro in Notepad for editing (see the section on Editing Macros below).

Duplicate  . Creates a copy of the selected macro file, with "Copy" added to the file name.

Add to Study. This has the same function as **Insert Study Macro**, which may be selected from the Database context menu. The macro may be inserted into the selected Study, and it will be run automatically whenever you open the Study, depending on the **Run Study Macro** selection you have made in **Edit** → **Options**.



Editing Macros. Click the  icon to open the selected macro in Notepad. On first glance, the text of a macro file may seem somewhat complex and baffling. It begins to make sense when you realize that the CURRY software is basically a large set of parameter settings, and these settings are applied whenever you change them. For example, if you change the Timerange, the dipole results are automatically recomputed. Apply an artifact correction, and the results are recomputed without the artifact. It is a dynamic program, constantly reading the settings and applying any changes.

If you perform a **UI Parameter Dump**, as described above, you will see all of the possible parameter settings. These are grouped into models, including, Mainframe, Database, Window, Study, FunctionalData, MapsPca, ImageData1, ImageData2, ImageData3, SourceReconstruction, Localize, Results, and 3DView.

For example, in a macro that you are editing you may see:

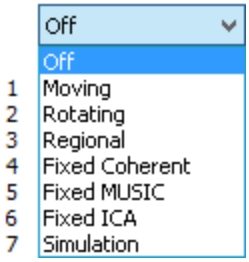
FunctionalData.DataDisplChannels = 31,

which is obvious. There are 31 channels displayed in the Functional Data display.

Others are slightly less obvious, such as:

SourceReconstruction.FitDipolesType = 1.

This is the setting for the **Dipole Type** under **Dipole Fit**. The numerical code determines which dipole type was selected (**Moving** in this case). Numbering will generally be in the same order as the options are listed in the drop-down menus. The lists are zero-based (start with 0 rather than 1).



Let's say you have created a macro that looks like the following. If you study the lines, you'll see that many things make intuitive sense. For example, Timeranges are adjusted, the Butterfly Plot was selected (DataPlotMode = 1), noise estimates were made, source reconstruction was performed, and different objects were selected for the 3D View. STEP END signifies the end of an operation. Now, how do you, for example, add steps to an existing macro?

```
Window.Action            = ViewTab
Window.TabId             = Main
Window.TabLabel           = All
FunctionalData.ProcessDataMode = 3
FunctionalData.StartrangeSample = 97
FunctionalData.ActualSample = 103
FunctionalData.EndrangeSample = 111
FunctionalData.DataPlotMode = 1
FunctionalData.NoiseEstimationMethod = 2
FunctionalData.NoiseEndSample = 94
FunctionalData.DataAmplitude = 68 0 ...
FunctionalData.UserDefinedNoiseLevel = 14.3609 1 ...
STEP END
FunctionalData.DataAmplitude = 140 0 ...
SourceReconstruction.Action = StartFit
SourceReconstruction.FitDipoleChanged = 1
SourceReconstruction.FitDipolesType = 1
STEP END
Window.Action            = GlobalViewLeft
STEP END
Window.Action            = ViewTab
Window.TabId             = Main
Window.TabLabel           = 3D View
STEP END
```

```
Window.Action            = GlobalViewRotate
STEP END
3DView.Action            = ShowObject
3DView.ObjectToSelect     =  31
3DView.ObjectViewStatus   =  1
STEP END
3DView.Action            = SelectObject
STEP END
Window.Action            = GlobalViewRotate
STEP END
3DView.Action            = ShowObject
3DView.ObjectToSelect     =  21
3DView.ObjectViewStatus   =  0
STEP END
3DView.Action            = SelectObject
STEP END
3DView.Action            = ShowObject
3DView.ObjectToSelect     =  22
STEP END
3DView.Action            = SelectObject
STEP END
3DView.Action            = ShowObject
3DView.ObjectToSelect     =  23
STEP END
3DView.Action            = SelectObject
STEP END
```

Let's say you want to add a text Banner at a certain point in the macro. The easiest way to add steps to an existing macro is to *create a new macro that has only the steps that you want to add*. Start recording a new macro and click the Insert Banner  icon from the Macro Toolbar, entering the desired text ("Add this banner to the macro"). In some cases, you may need to update the macro file explicitly by clicking the **UI Update**  icon. The code for adding the Banner appears in the new macro as:

```
Mainframe.MacroText       = Add this banner to the macro.
Study.Action             = MacroBanner
STEP END
```

Now it's just a matter of copying those lines into the first macro. Maybe we wish it to appear after the dipoles were computed. Looking at the first macro, we see lines referring to SourceReconstruction. Paste the banner lines after the STEP END in the original macro.

```
...
SourceReconstruction.Action = StartFit
SourceReconstruction.FitDipoleChanged =  1
SourceReconstruction.FitDipolesType =  1
STEP END
Mainframe.MacroText      = Add this banner to the macro.
Study.Action             = MacroBanner
STEP END
```

```
Window.Action          = GlobalViewLeft
STEP END
...
```

Save the modified macro, and then play it to verify. In this way - creating a second macro with only the steps you wish to add or modify - it becomes fairly easy to edit macros. It is not necessary to understand the actual lines of code - they are created when you perform the desired step(s).

It is obviously a good idea to think through what you wish to include in the macro before you record it, so you can get as much of it as possible in the first pass. At the same time, editing macros is not too difficult either.

Linking and Automating Macros

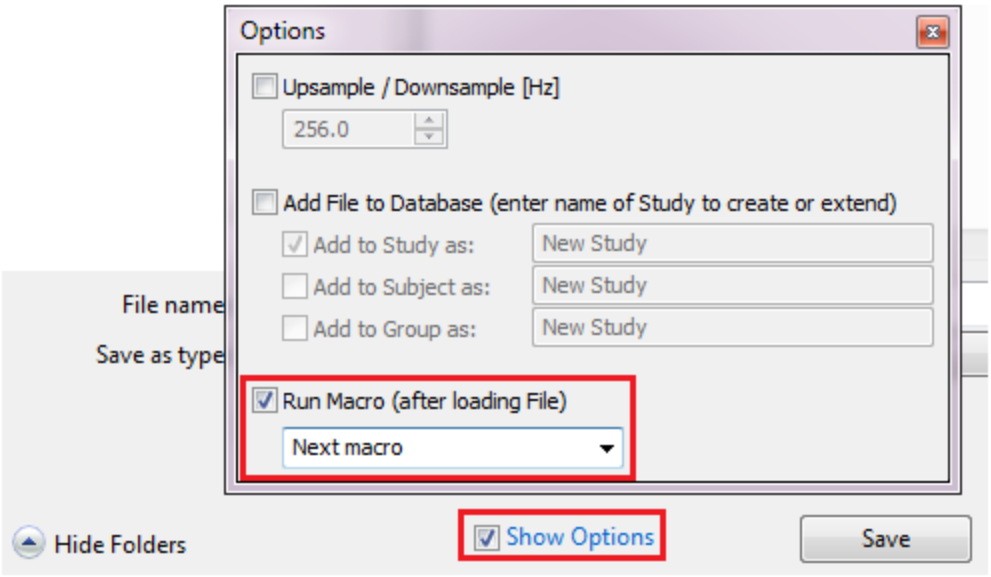
It is not possible in CURRY 8 to start a macro in one Study, and then have it continue on with additional operations in a different Study. For example, if you start with continuous data, and you then create a file containing the epochs, you may have that file open in a new Study. If you are recording those steps in a macro, the recording will stop when the epoched file opens - it is a new Study. You can then continue with a second macro (demonstrated below). You can of course, apply the same macro across a series of studies or data files, but you cannot, for example, save the resulting averages to a new Study, and then open that study and do further processing in the same macro. That requires a second macro. There are, however, ways link macros and to automate their execution.

Run Macro

Suppose you wish to create and save epochs from a continuous file. The epochs file will be saved in a new Study. When you open that Study, you want to run a second macro automatically. Then you want to loop the macros over selected files or studies. The basic steps are:

1. Record the initial macro with one of the data files.

2. When you save the epoched file, you will see a **Run Macro** option at the bottom of the Options window accessed in the **Save As** dialog (when you click the **Save Selected Event Group** button).

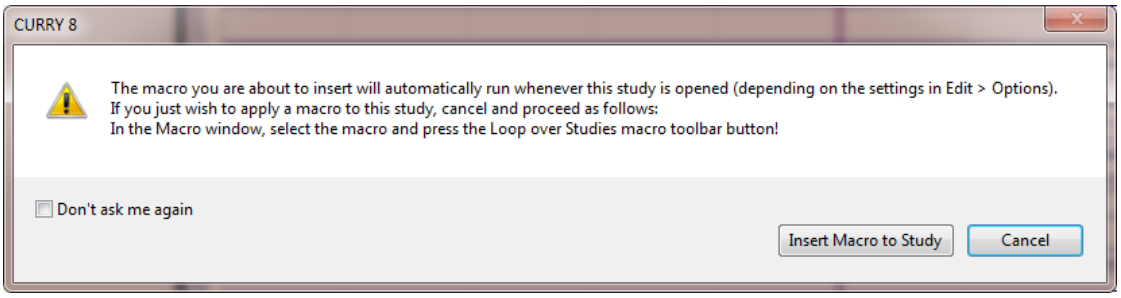


3. Enter the name of the second macro. If you have not created the second macro, enter the name that you will use. If the macro already exists, you may select it from the drop-down list.

4. Record the second macro using that name, starting with the epoched data file.

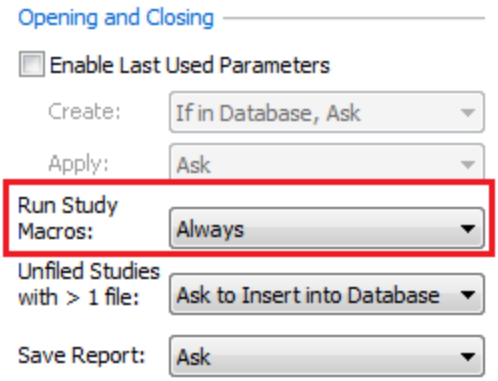
5. When you loop over the files or studies, the second macro will be called automatically.

Insert Study Macro
There is another option for running macros automatically - you may insert it into the Database, and the macro will run when you open the Study (or Subject or Group). *Right click* on the Group/Subject/Study and select **Insert Study Macro**. You will see a confirmation message.



To continue, click **OK** and select a macro (.mac file). These are typically stored in the designated **Target Folders**, or you can store them elsewhere (they will not then appear in the Macro list).

You can control the execution of the macros in these cases using the options under **Edit** → **Options** → **Settings**. You can have the program **Ask** if you want to execute the macro, **Always** execute it, or **Never** execute it.

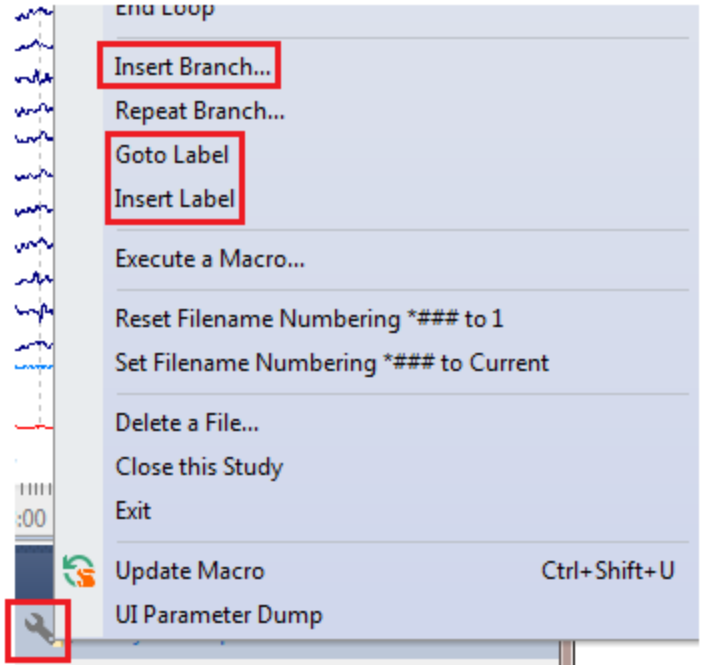


The *Macros* Tutorial demonstrates more of the functionality with realistic examples.

23.2.1 Branching

This section illustrates how to do conditional branching in your macros. The first example is a simple one that shows how to do the basic recording. The second one is more complicated and it includes repeat branching.

Example 1
We will start with a simple real-world example of basic conditional branching, using the **Insert Branch**, **Goto Label**, and **Insert Label** commands. These are accessed during the macro recording from the **Insert Action** list.

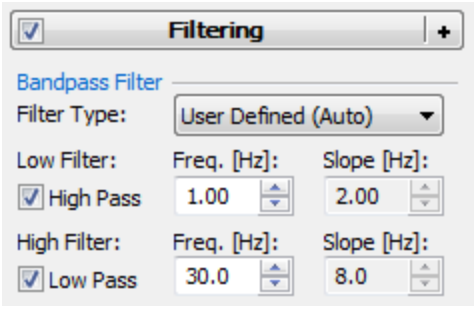


When you are analyzing your data files, some subjects may have a lot of blinks, necessitating VEOG artifact reduction, while others have so little VEOG artifact that there is nothing to correct. In this example, we will do a couple of initial steps, then automatically scan the file visually. We will then create the option to

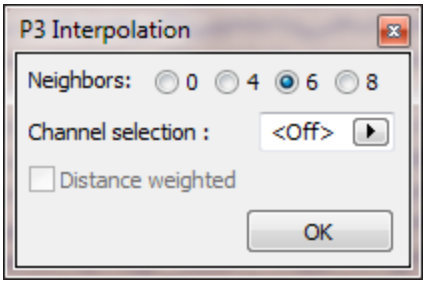
use artifact reduction or not. In either case, the final step will be to create averages of the Type 1 and Type 2 events.

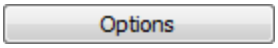
1. After opening one of the data files, we start recording the macro using  .

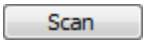
2. We then add **Filtering**.



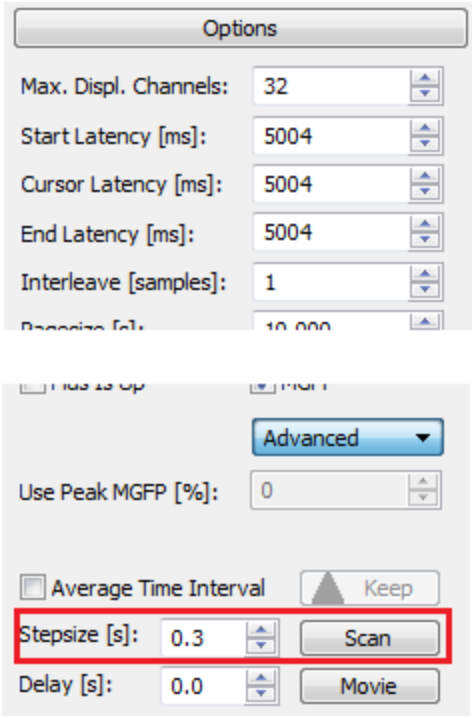
3. We notice that one of the channels has several bad sections in it, and we decide to replace it with an interpolation of the nearest 6 channels (*right click* on the channel label to see the **Interpolate Channel** option).



4. Now we will scan the file automatically to see if there are enough blinks to justify **Artifact Reduction**. The **Scan** option is found in the **Advanced** section under 

. A **Stepsize** of **0.3** seconds provides a quick scan. Then we click the 

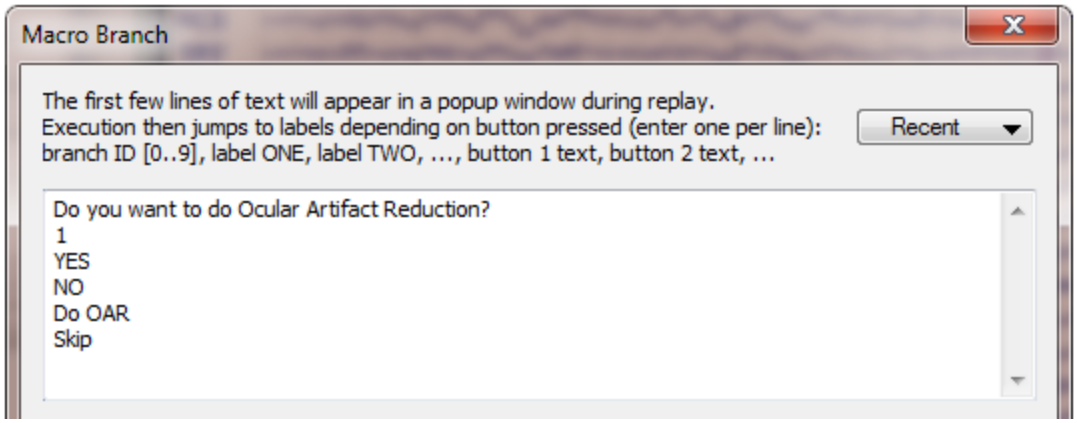
button.



5. The macro to this point looks like the following.

```
Mainframe.Action          = ParameterDialogSelect
Mainframe.MacroParameterDialog = Functional Data|Filtering|0
Mainframe.FileVersion     =  8
FunctionalData.SequenceList = 3 1 0 ...
STEP END
FunctionalData.Action     = FdScanData
FunctionalData.DataStepSize =  0.3
FunctionalData.FilterTypes = 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71
71 71 71 71 71 71 71 71 71 71 71 71 71 71 1 ...
FunctionalData.LowPassFilters = 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1 1 1 1 0 ...
FunctionalData.HighPassFilters = 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1 1 1 1 0 ...
FunctionalData.FilterType = 71 1 ...
FunctionalData.LowPassFilter = 1 0 ...
FunctionalData.HighPassFilter = 1 0 ...
FunctionalData.DataAmplitude = 140 263.687 0 ...
FunctionalData.HighPassWidths = 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
8 8 8 8 8 8 5 ...
FunctionalData.HighPassWidth = 8 5 ...
STEP END
```

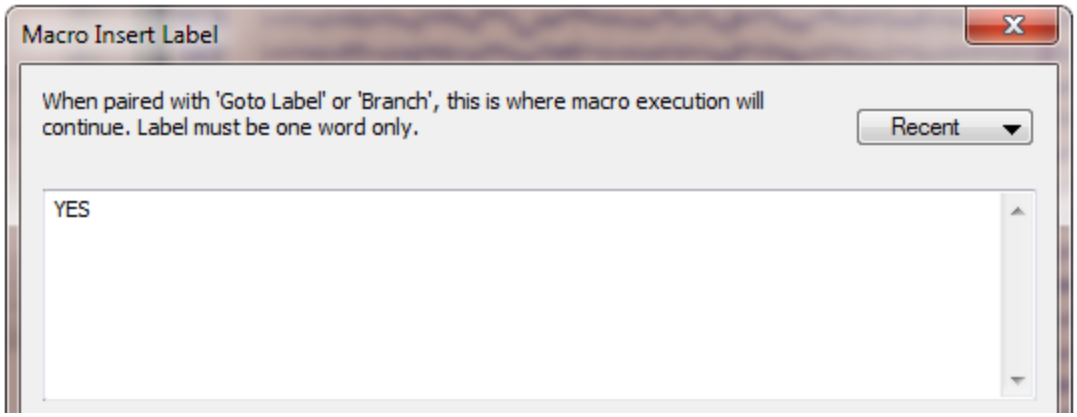
6. Now we are at the point where we want to create the branching. We select **Insert Branch** and enter the text shown. The first line is the text that will be displayed in the popup window during replay. The 1 is the branch ID number. It is not used in this example - the 1 is a place holder. YES and NO are the labels that will be used to define the jump points in the macro. "Do OAR" and "Skip" are what will be seen in the buttons in the popup window.



This adds the following text.

Mainframe.MacroText = Do you want to do Ocular Artifact Reduction?
¶1¶YES¶NO¶Do OAR¶Skip
Study.Action = MacroBranch
STEP END
Study.Action = MacroUpdate
STEP END

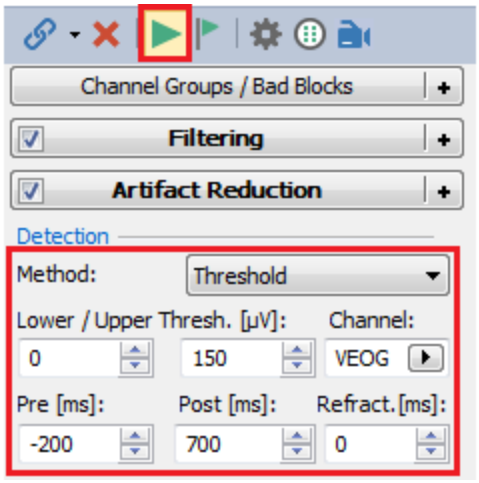
7. Now we need to define YES - the first jump point. Use **Insert Label** to insert the YES label position in the file.



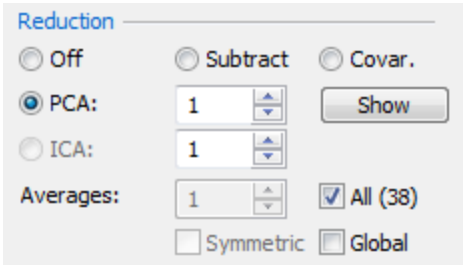
This adds the following text line.

LABEL: YES # must match corresponding goto or branch

8. In the YES branch, the next thing that will happen is to perform the blink reduction, so we add that to the macro, clicking the flashing Scan button when ready.



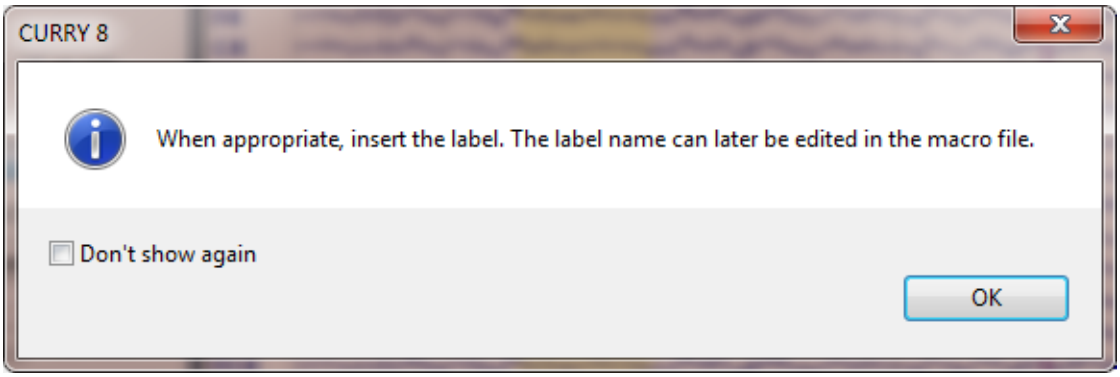
After the Scan is done, we used **PCA** with **1** component and **All** blinks in the average.



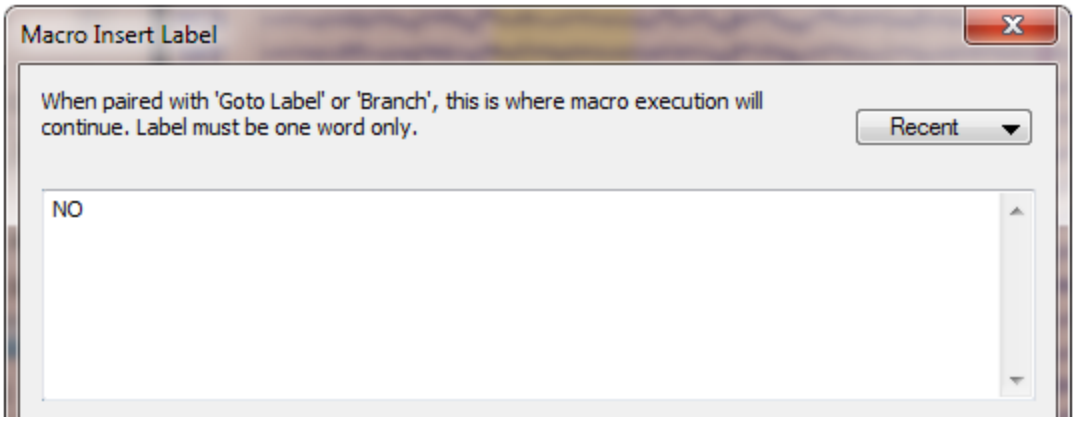
The following text was added to the macro.

```
Mainframe.Action           = ParameterDialogSelect
Mainframe.MacroParameterDialog = Functional Data|Artifact Reduction|0
FunctionalData.SequenceList = 3 1 0 5 1 0 ...
STEP END
FunctionalData.Action      = FdScanArtifacts
FunctionalData.ThresholdChannels = VEOG|<Off>|<Off>|<Off>|<Off>
FunctionalData.ThresholdType = 2 0 ...
FunctionalData.LowerThresholdValue = 0 -200 ...
FunctionalData.UpperThresholdValue = 150 200 ...
FunctionalData.ThresholdPost = 700 500 ...
STEP END
```

9. Now, we want to jump over the steps that we will enter when you select Skip. For now, we just need to add a **Goto Label** command. The actual label will be **CONTINUE**, which we will enter manually when the macro has been recorded.



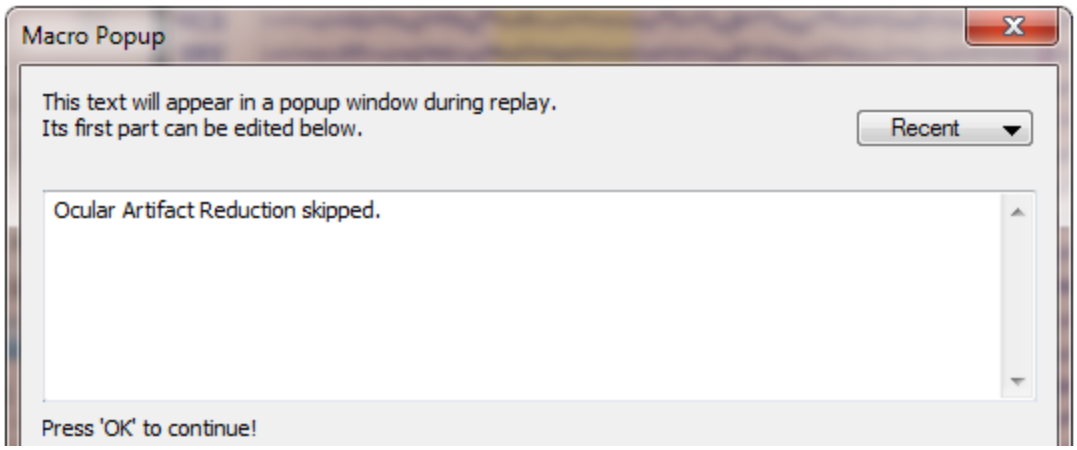
10. Next we need to tell the program where to go if you select Skip. The label, created in step 6 above, is **NO**. So we used **Insert Label** to enter that label.



The line in the macro is:

LABEL: NO # must match corresponding goto or branch

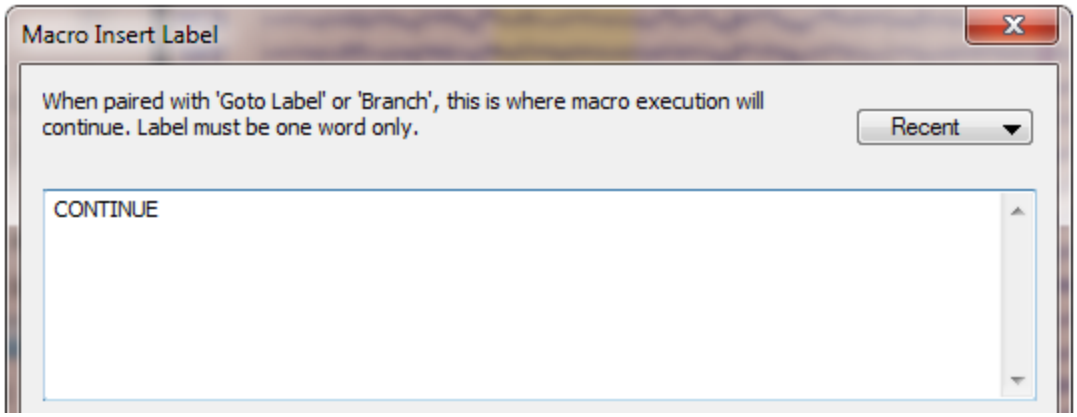
11. If you select Skip, we will add a dialog confirming that. Basically this just illustrates that you may added separate steps to the second branch. For this we will use the **Show Popup Window and Continue** option.

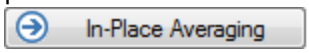


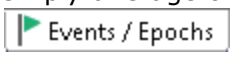
The lines are:

```
Mainframe.MacroText       = Ocular Artifact Reduction skipped.
Study.Action              = MacroContinueText
STEP END
```

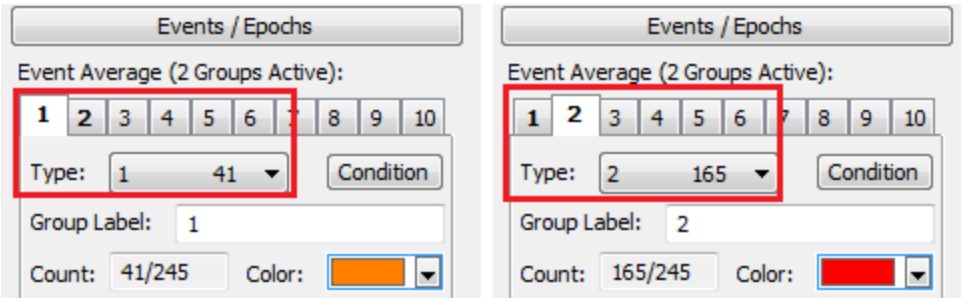
12. Now we need to add the **CONTINUE** line that was planned in step 9. Use **Insert Label** to add that line.



13. We told the "Do OAR" branch to go to the CONTINUE line, and the Skip branch will proceed to that line automatically since it is next in line in the macro. So now all we need to do is add whatever additional steps we want. In this case we will simply average the Type 1s and Type 2s, using 

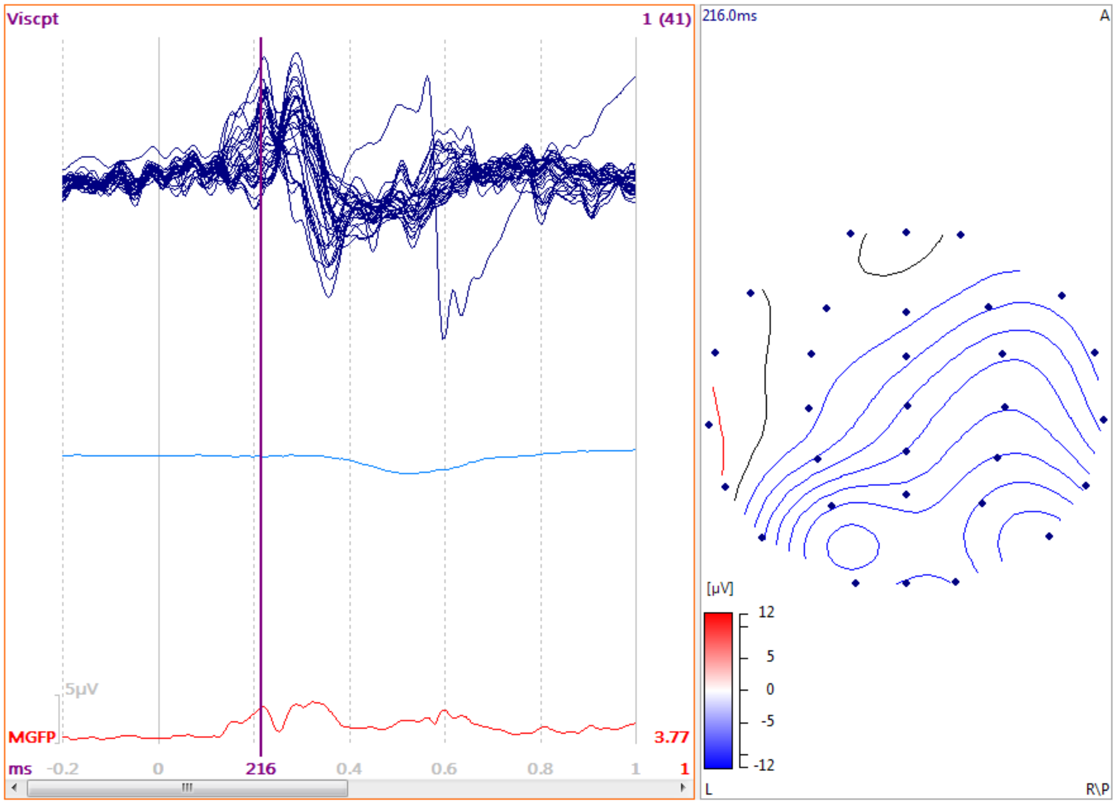
in the 

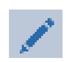
panel. The Groups are set up as usual.



14. After the averages were created, we selected the **Butterfly Plot** and added the 

display. Then stop recording the macro  .



15. Lastly, we need to Edit the macro using  and go to the MacroLabel line. This had a different label, which we replaced with **CONTINUE** and then resaved the file.

Mainframe.MacroLabel = CONTINUE
Study.Action = MacroGotoLabel

The complete text of the macro appears as follows.

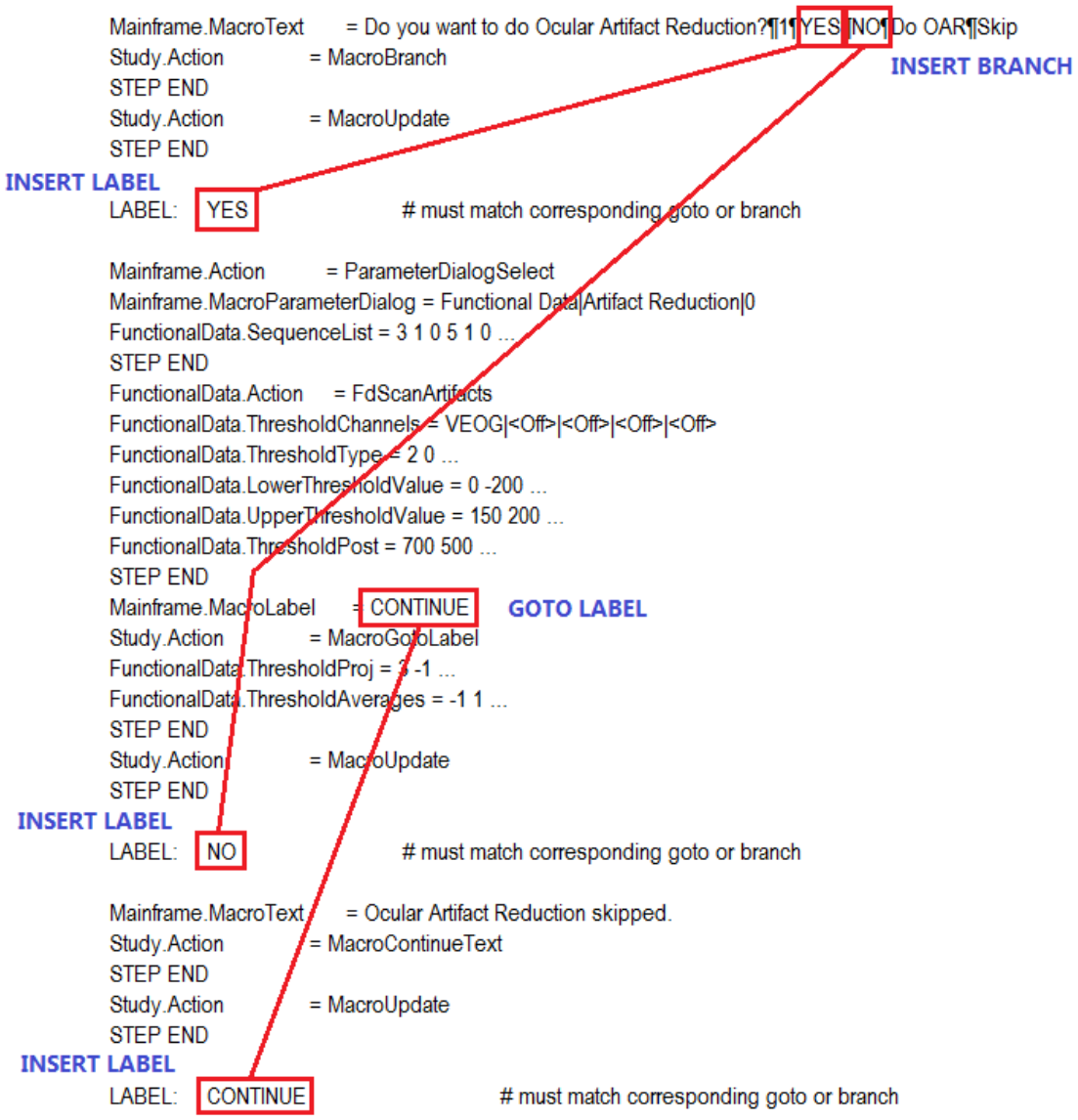
****
****

Mainframe.Action = ParameterDialogSelect
Mainframe.MacroParameterDialog = Functional Data|Filtering|0
Mainframe.FileVersion = 8
FunctionalData.SequenceList = 3 1 0 ...
STEP END
FunctionalData.Action = FdScanData
FunctionalData.DataStepSize = 0.3
FunctionalData.FilterTypes = 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 71 1 ...
FunctionalData.LowPassFilters = 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 ...
FunctionalData.HighPassFilters = 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 ...
FunctionalData.FilterType = 71 1 ...

```
FunctionalData.LowPassFilter = 1 0 ...
FunctionalData.HighPassFilter = 1 0 ...
FunctionalData.DataAmplitude = 140 263.687 0 ...
FunctionalData.HighPassWidths = 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
8 8 8 8 8 8 5 ...
FunctionalData.HighPassWidth = 8 5 ...
STEP END
Mainframe.MacroText      = Do you want to do Ocular Artifact Reduction?
¶1¶YES¶NO¶Do OAR¶Skip
Study.Action            = MacroBranch
STEP END
Study.Action            = MacroUpdate
STEP END

LABEL: YES            # must match corresponding goto or branch

Mainframe.Action        = ParameterDialogSelect
Mainframe.MacroParameterDialog = Functional Data|Artifact Reduction|0
FunctionalData.SequenceList = 3 1 0 5 1 0 ...
STEP END
FunctionalData.Action     = FdScanArtifacts
FunctionalData.ThresholdChannels = VEOG|<Off>|<Off>|<Off>|<Off>
FunctionalData.ThresholdType = 2 0 ...
FunctionalData.LowerThresholdValue = 0 -200 ...
FunctionalData.UpperThresholdValue = 150 200 ...
FunctionalData.ThresholdPost = 700 500 ...
STEP END
Mainframe.MacroLabel      = CONTINUE
Study.Action            = MacroGotoLabel
FunctionalData.ThresholdProj = 3 -1 ...
FunctionalData.ThresholdAverages = -1 1 ...
STEP END
Study.Action            = MacroUpdate
STEP END

LABEL: NO             # must match corresponding goto or branch

Mainframe.MacroText      = Ocular Artifact Reduction skipped.
Study.Action            = MacroContinueText
STEP END
Study.Action            = MacroUpdate
STEP END

LABEL: CONTINUE             # must match corresponding goto or branch

Mainframe.Action        = ParameterDialogSelect
Mainframe.MacroParameterDialog = Events / Epochs
STEP END
FunctionalData.Action     = FdAverageEvents
FunctionalData.GroupLabel1 = 1
FunctionalData.GroupLabel2 = 2
FunctionalData.DataAverageEventType =  1
FunctionalData.SelectedEventAverage =  1
```

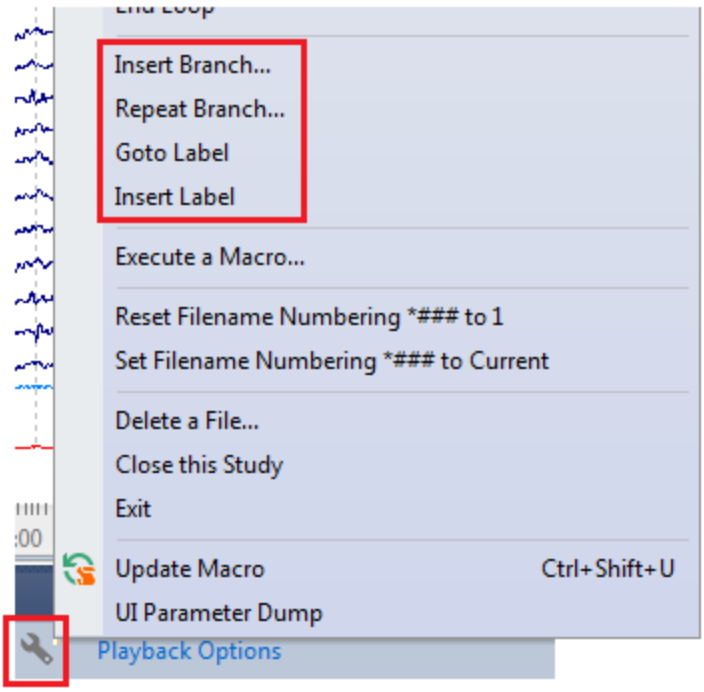
```
FunctionalData.NoiseEpochStartSample =  50
FunctionalData.NoiseEpochEndSample =  50
FunctionalData.SignalStartSample =  50
FunctionalData.SignalEndSample =  50
FunctionalData.EventPreLatency = -200
FunctionalData.EventTypes = 1 2 -4 ...
FunctionalData.SelectedEventTypes = 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 0 ...
FunctionalData.EventLabels = 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 2 0 ...
STEP END
FunctionalData.ActualSample =  104
FunctionalData.DataPlotMode =  1
FunctionalData.DataTimeCursors = 104 ...
FunctionalData.DataAmplitude = 4.8 1.673348 0 ...
Maps.2DCohMinLag          =  0
Maps.2DCohMaxLag          =  5
Maps.2DContourMode        =  2
Maps.2DContourIncr        = 1.4 0 ...
Window.SelectedTab        = Main|FD,Maps
STEP END
 # recording resumed
Mainframe.FileVersion     =  8
STEP END

************************************************************
*
```

The branching parts of the macro are displayed graphically here, showing the "connections". When creating a macro of this type, it is very helpful to have at least a rudimentary flow chart, so you know what labels you will be inserting, and in what order.

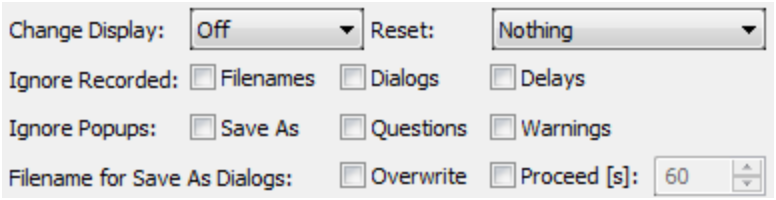


Example 2
The following is a more complex example that uses all of the branching commands. It opens with the option to take one of three paths. It will then tell you the path it took, and ask if you want to start over, return the previous choice, or exit.

The main commands being demonstrated here are accessed from the **Insert Action** list, and include **Insert Branch**, **Repeat Branch**, **Goto Label**, and **Insert Label**.

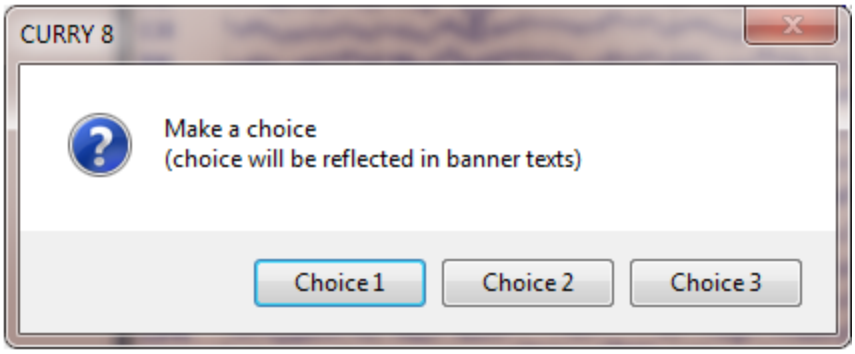


You may create a new Macro and copy/paste the macro code below to it if you wish. To run the macro, you need only to open any Study. To simplify the replay, set the **Playback Options** as shown.

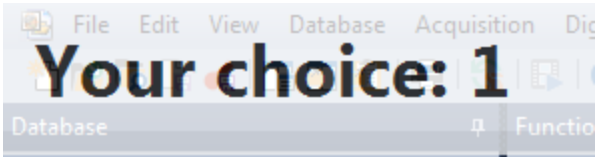


What the Macro Does
When the macro is executed, you will see the following sequences.

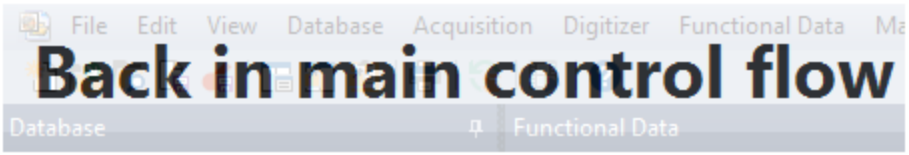
First you see the initial display.



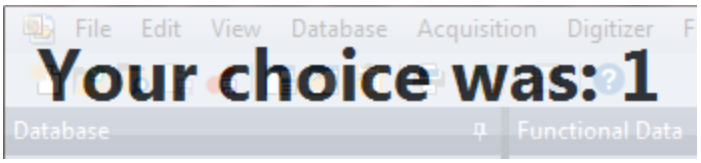
If you choose Choice 1, you will see a Banner showing your choice.



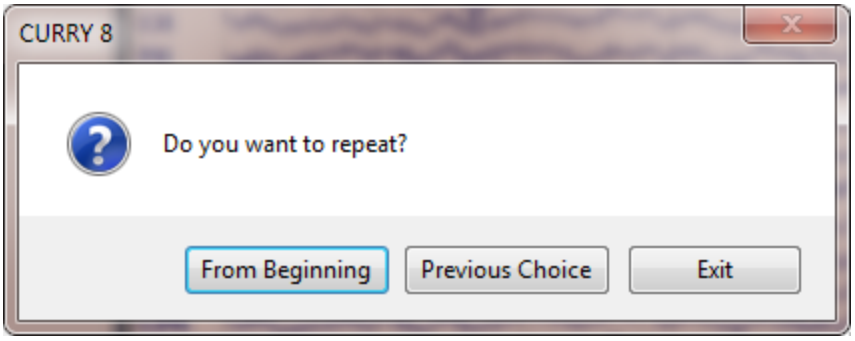
That is followed automatically with the next Banner, showing that the program is back in the main flow.



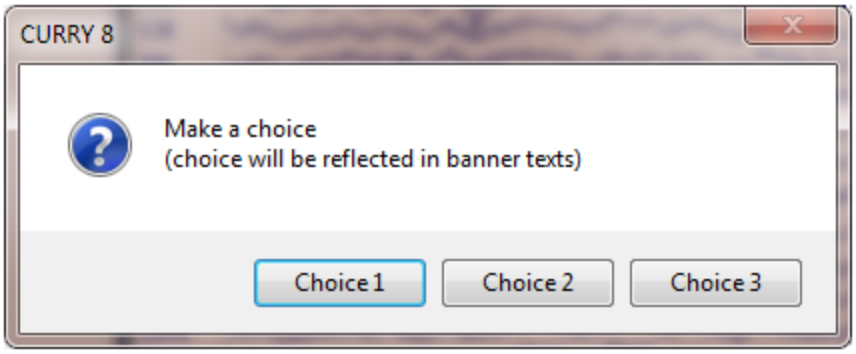
After a few seconds you will see the following Banner, showing you what your choice was. The purpose of this is to demonstrate "rebranching", where this same code will be used again.

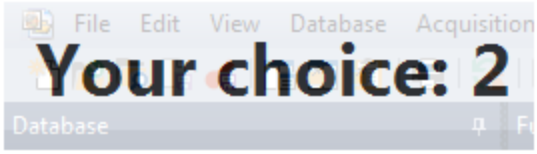


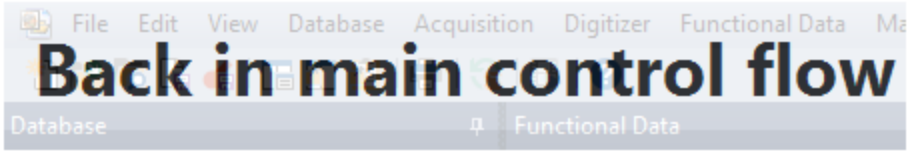
You then see the "repeat" dialog.

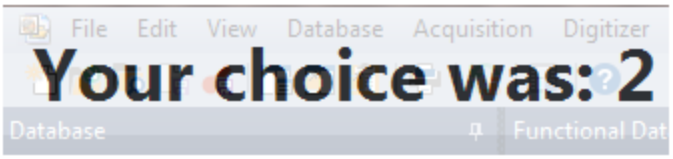


If you click **From Beginning**, you will be returned to the initial dialog. If you now select Choice 2, you will see the expected subsequent dialogs.

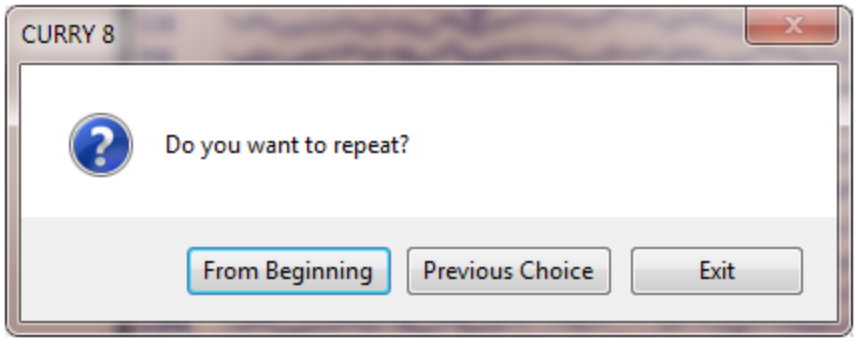


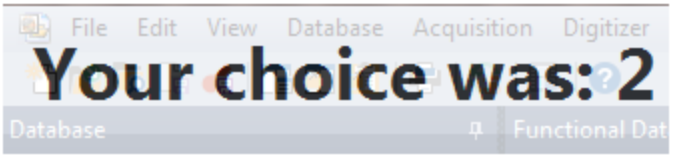




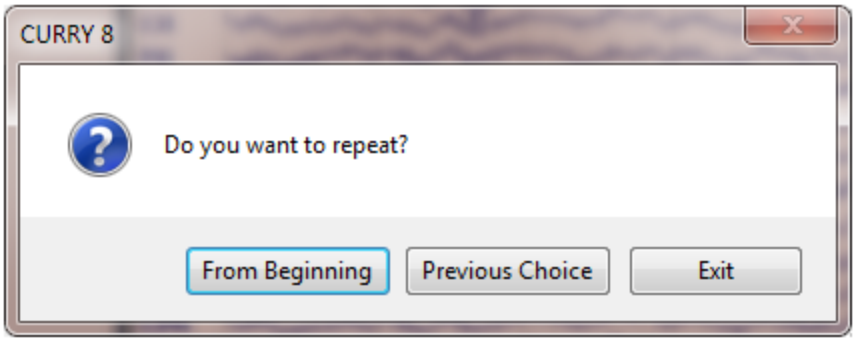


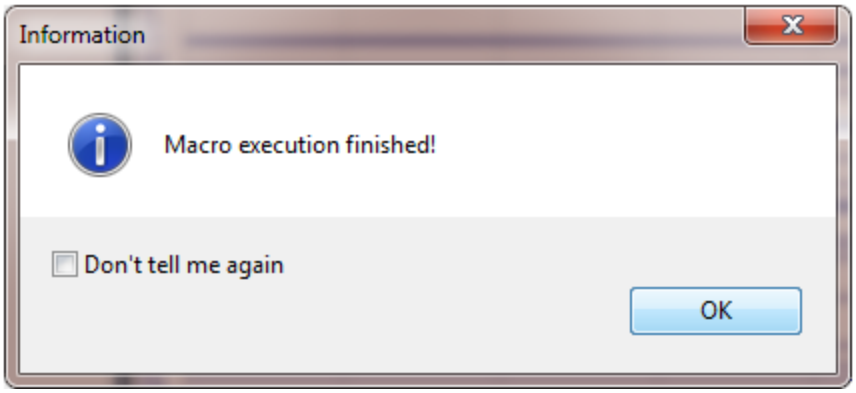
When the "repeat" dialog appears, click **Previous Choice** and you will see the previous Banner, and so on.





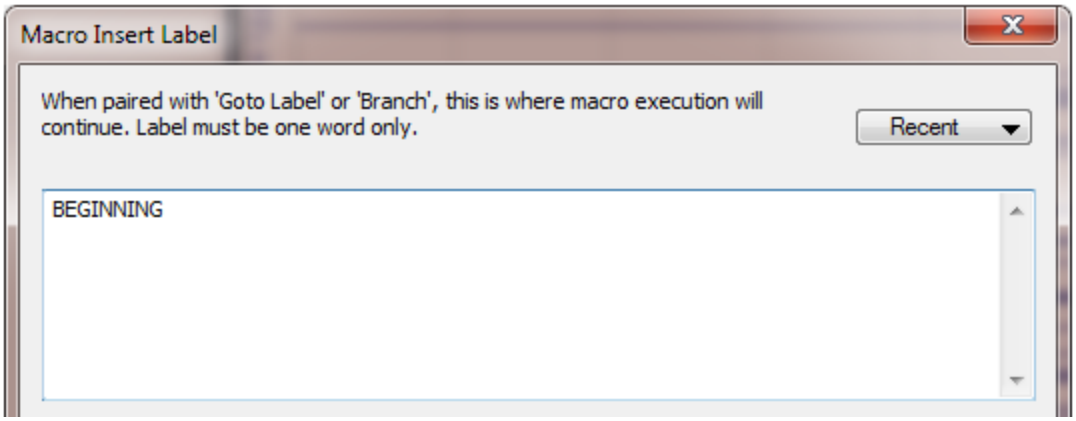
If you select **Exit** from the "repeat" dialog, you will see the message saying the macro execution has finished.





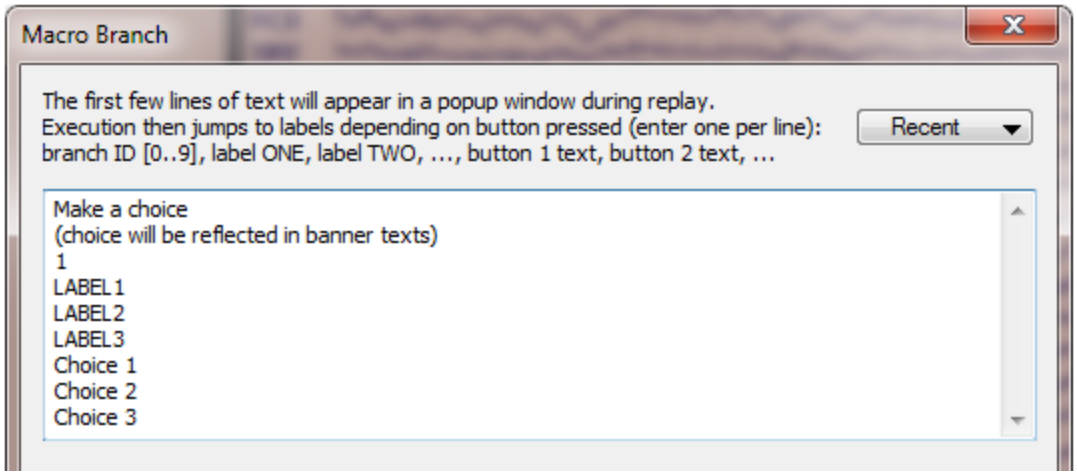
How the Macro was Created
Now look at the macro file below in detail. (Text lines that are preceded by a "#" are comments).

1. The first non-comment code line comes from the **Insert Label** command. Note that labels must be a single word only. This is a point where the macro will branch back to.



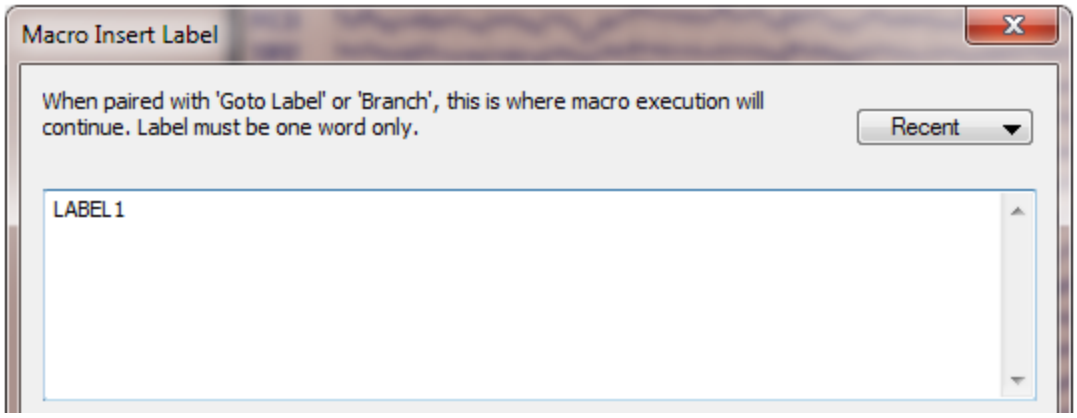
2. Note the next comment lines in the macro. The initial dialog is created with the **Insert Branch** command. The first two lines are text that will be displayed. The number 1 is the ID of this branch and will later be referenced in the MacroReBranch command. The LABELs are targets of the resulting conditional jumps. The Choices are shown on the buttons of the popup window and their order matches the

LABELs. Choice 1 will go to LABEL1 in the macro, Choice 2 will go to Label2, and so on.

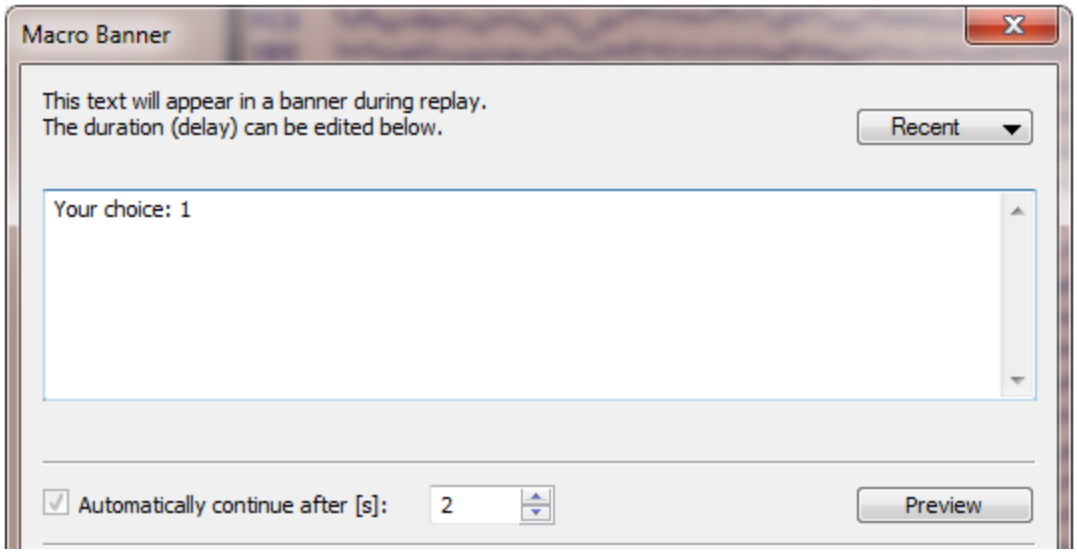


The FileVersion line is added automatically.

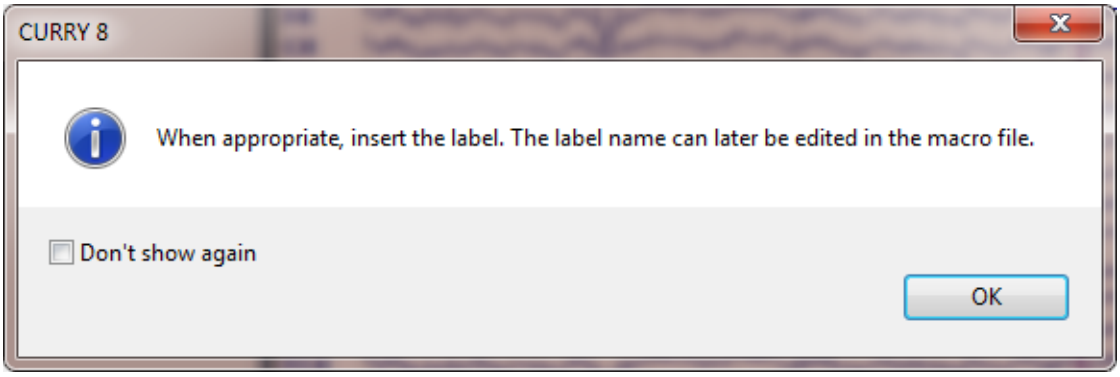
3. Then use **Insert Label** to insert the label: LABEL1.



4. Select **Show Banner** and enter the text to be displayed. Set the timer for 2s.



5. Now we need to tell the macro where to go next. This is done with the **Goto Label** command. You will see the following message. We will need to edit this in the macro, where we change the existing label (DESTINATION in this case) to **CONTINUE**.



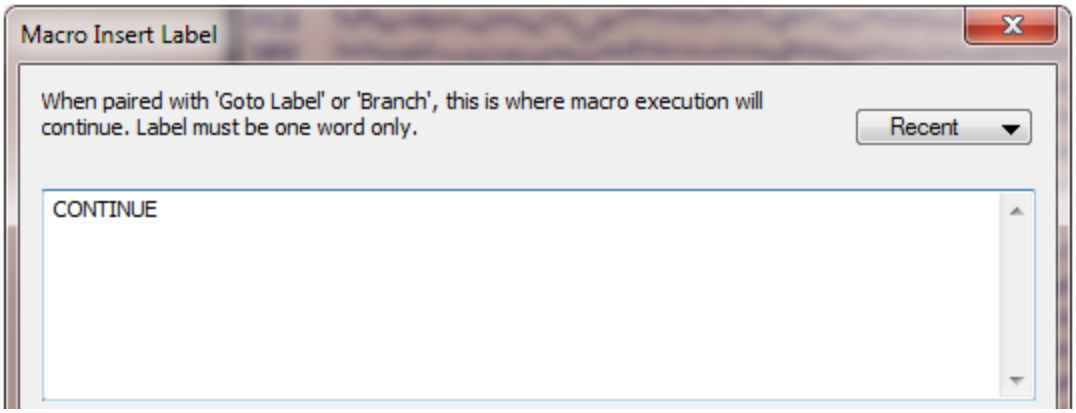
6. Stop recording the macro  and go to its editor  . The most recent steps have created the following lines in the macro. This is where we need to edit the MacroLabel. We will change DESTINATION (in this case) to **CONTINUE**. Similar changes will be made further into the macro, and, if desired, you can make them after the entire macro has been recorded.

```
LABEL: LABEL1          # must match corresponding goto

Mainframe.MacroText       = Your choice: 1
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = DESTINATION
Study.Action              = MacroGotoLabel
STEP END
```

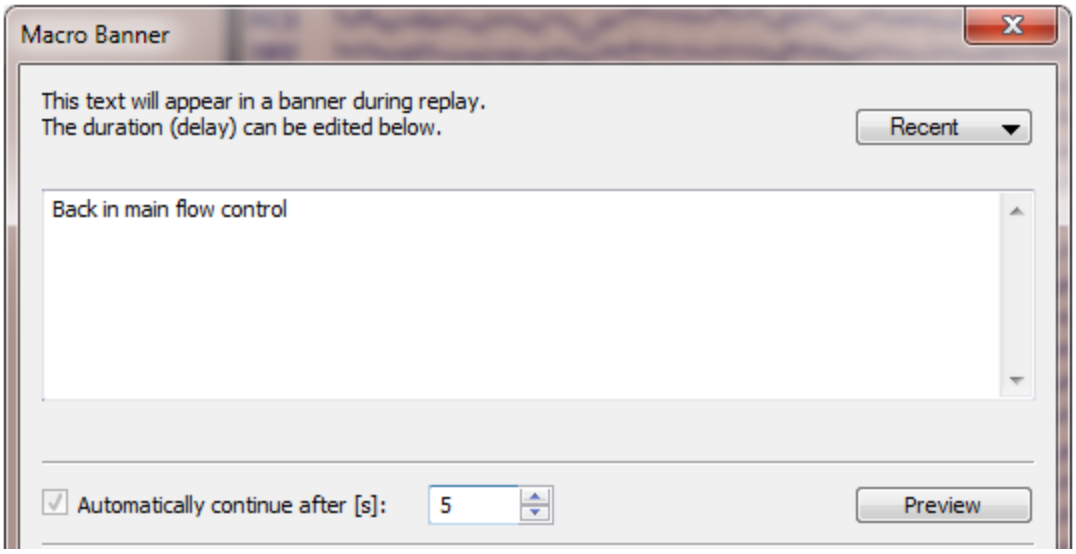
We could repeat the above steps, entering the lines for the second and third choices, or we could do this manually in the macro by copying that section, pasting it twice, and changing the labels and choice text. We then get the three following sections (making sure "CONTINUE" is in the MacroLabel lines).

```
LABEL: LABEL1          # must match corresponding goto

Mainframe.MacroText       = Your choice: 1
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = CONTINUE
Study.Action              = MacroGotoLabel
STEP END

LABEL: LABEL2          # must match corresponding goto

Mainframe.MacroText       = Your choice: 2
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = CONTINUE
Study.Action              = MacroGotoLabel
STEP END

LABEL: LABEL3          # must match corresponding goto

Mainframe.MacroText       = Your choice: 3
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = CONTINUE
Study.Action              = MacroGotoLabel
STEP END
```

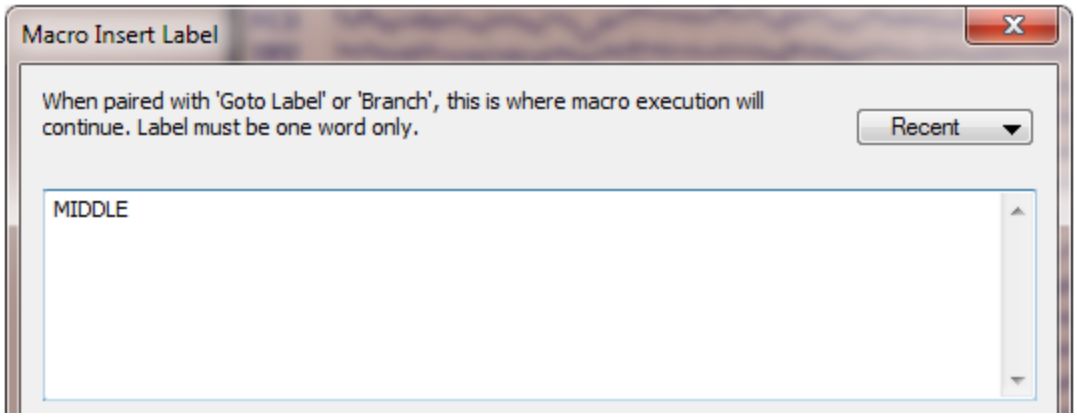
7. Resume recording by clicking the  button. That takes us to the next section, which is designated with the **CONTINUE** label. Use **Insert Label** to enter it.



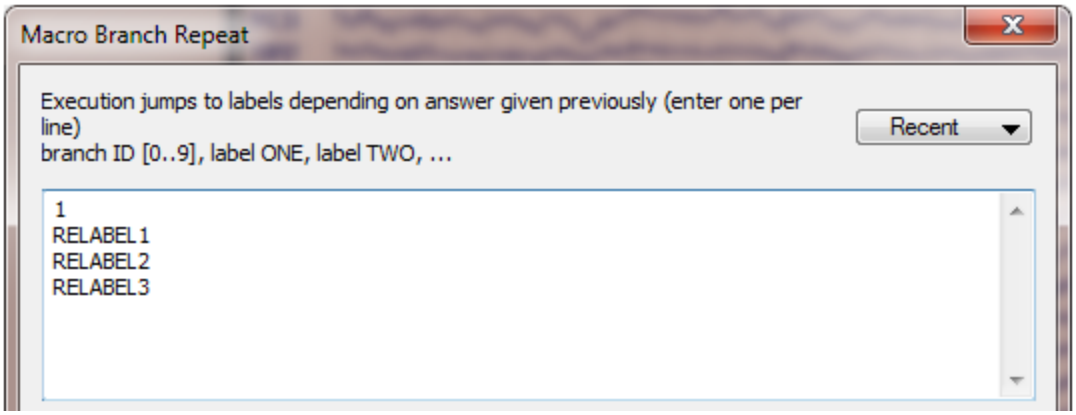
8. Next we will create the Banner that displays "Back in main control flow". Set the time delay for **5**s.



9. Next we will include a "rebranching" section, to illustrate the use of the **Repeat Branch** command. We will designate the start of the section with the label "MIDDLE" for middle part of the macro. Use **Insert Label** to create the label.

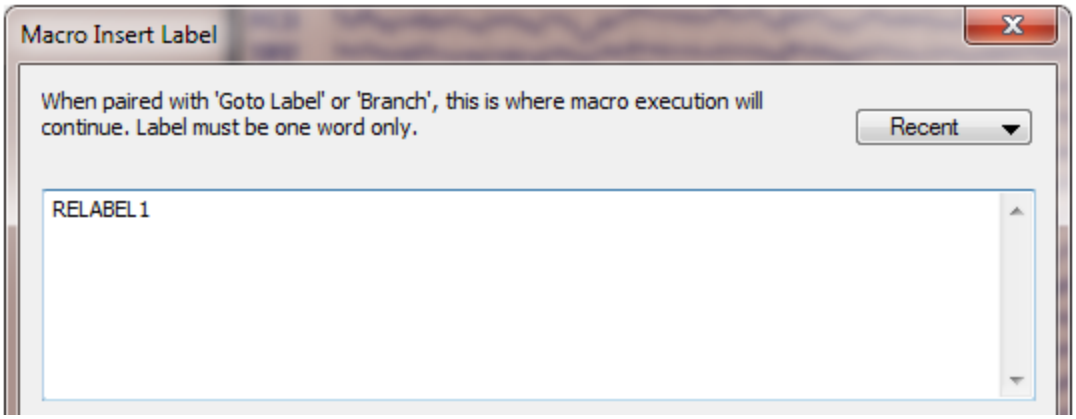


10. Now we want to use the choice that was made on the initial dialog to determine where to go in the rebranching section. This is accomplished with the **Repeat Branch** command. The "1" says to use the choice that was made in the Branch ID 1 command above. The RELABEL labels tell the macro where to jump to, depending on what was selected above.

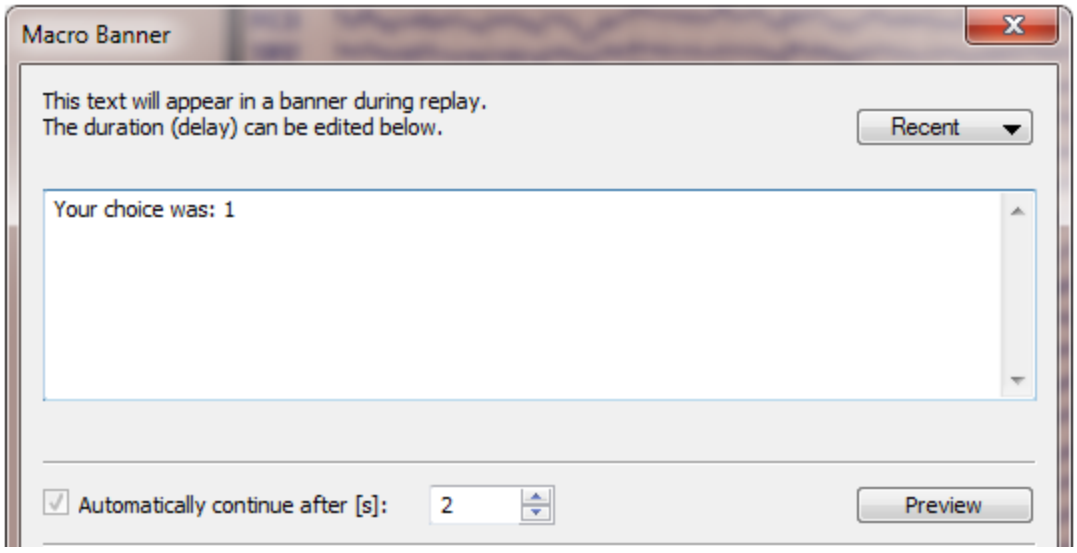


11. We now have to insert the labels and content for RELABEL1, RELABEL2 and RELABEL3.

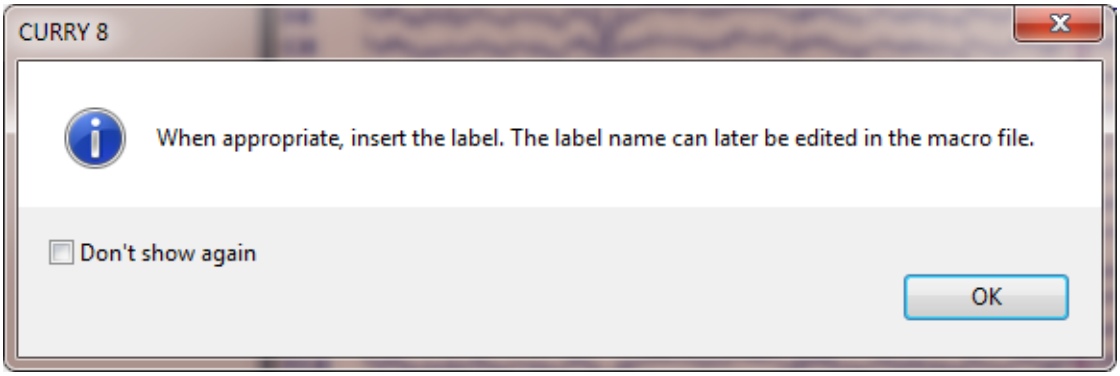
Use **Insert Label** to insert **RELABEL1**.



12. We will create another Banner confirming what your choice was, using **Show Banner**. We'll set the delay back to **2**s.



13. Then we need to direct the macro where to go, so we use **Goto Label**. As above, we will need to edit the macro manually to change the MacroLabel to **RECONTINUE**.



14. Again, stop recording the macro so we can modify the text manually. The recent steps give the following section in the macro. RECONTINUE has already been entered.

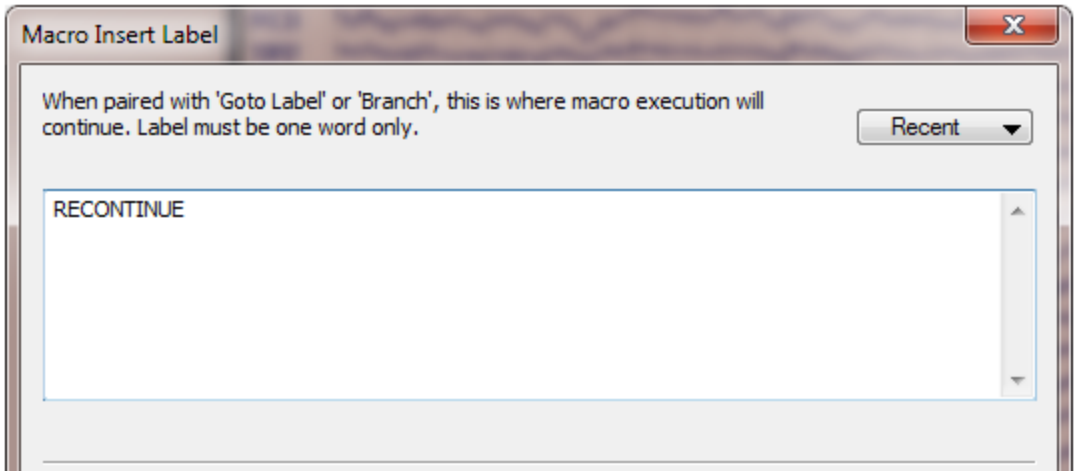
```
LABEL: RELABEL1              # must match corresponding goto or branch

Mainframe.MacroText      = Your choice was: 1
Mainframe.MacroDelay     =  2
Study.Action             = MacroBanner
STEP END
Mainframe.MacroLabel     = RECONTINUE
Study.Action             = MacroGotoLabel
STEP END
```

Use copy/paste and minor editing to create all three sections.

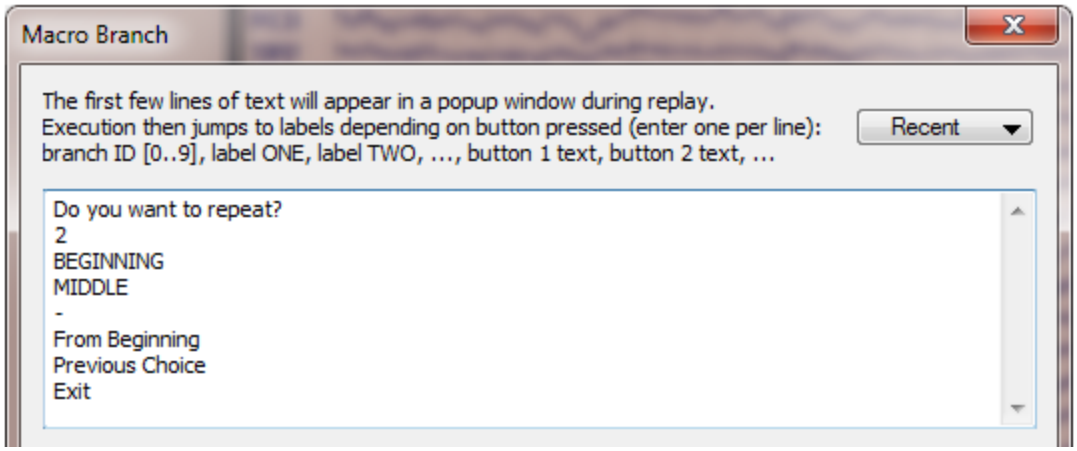
```
LABEL: RELABEL1              # must match corresponding goto

Mainframe.MacroText      = Your choice was: 1
Mainframe.MacroDelay     =  2
Study.Action             = MacroBanner
STEP END
Mainframe.MacroLabel     = RECONTINUE
Study.Action             = MacroGotoLabel
STEP END

LABEL: RELABEL2              # must match corresponding goto

Mainframe.MacroText      = Your choice was: 2
Mainframe.MacroDelay     =  2
Study.Action             = MacroBanner
STEP END
Mainframe.MacroLabel     = RECONTINUE
Study.Action             = MacroGotoLabel
```

```
STEP END

LABEL: RELABEL3              # must match corresponding goto

Mainframe.MacroText       = Your choice was: 3
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = RECONTINUE
Study.Action              = MacroGotoLabel
STEP END
```

15. Resume recording  and use **Insert Label** to insert the label for **RECONTINUE**.



16. Lastly, we will add one final set of branches. Use **Insert Branch** with the following text. The "Do you want to repeat?" line will appear in the dialog. The "2" is just the ID for this branch. The three labels are BEGINNING, which will return to the BEGINNING line near the top of the macro; MIDDLE, which will return to "rebranching" section, and a hyphen "-". The hyphen is a special character that means to continue on with the next section of the macro. In the third position, it is paired with the "Exit" button. Clicking that button with just go to the end of the macro. The hyphen saves you from having to insert a label just to continue on.



Stop recording the macro .

The above macro illustrates the four commands associated with conditional branching.

Macro Code
Below is the full text, with comments, should you wish to copy and paste it into a new Macro in CURRY.

```
**********************************************************

# this macro will give you a choice between three options and continue processing accordingly
# the choice can also be used at a later point
# finally you will be asked to replay macro from the beginning or the middle

LABEL: BEGINNING              # must match corresponding goto

# depending on the user's choice, macro condition branches
# the first few lines of text will be displayed in a popup where the user can make a choice
# the number 1 is the ID of this branch and will later be referenced in the MacroReBranch command
# the LABELs are targets of the resulting conditional jumps
# the Choices are shown on the buttons of the popup window and their order matches the LABELs
Mainframe.MacroText       = Make a choice¶(choice will be reflected in banner texts)¶1¶LABEL1¶LABEL2¶LABEL3¶Choice 1¶Choice 2¶Choice 3
Mainframe.FileVersion     =  8
Study.Action              = MacroBranch
STEP END

LABEL: LABEL1          # must match corresponding goto

Mainframe.MacroText       = Your choice: 1
Mainframe.MacroDelay      =  2
```

```
Study.Action            = MacroBanner
STEP END
Mainframe.MacroLabel    = CONTINUE
Study.Action            = MacroGotoLabel
STEP END

LABEL: LABEL2        # must match corresponding goto

Mainframe.MacroText     = Your choice: 2
Mainframe.MacroDelay    =  2
Study.Action            = MacroBanner
STEP END
Mainframe.MacroLabel    = CONTINUE
Study.Action            = MacroGotoLabel
STEP END

LABEL: LABEL3        # must match corresponding goto

Mainframe.MacroText     = Your choice: 3
Mainframe.MacroDelay    =  2
Study.Action            = MacroBanner
STEP END
Mainframe.MacroLabel    = CONTINUE
Study.Action            = MacroGotoLabel
STEP END

LABEL: CONTINUE            # must match corresponding goto

Mainframe.MacroText     = Back in main control flow
Mainframe.MacroDelay    =  5
Study.Action            = MacroBanner
STEP END

LABEL: MIDDLE              # must match corresponding goto

# depending on a previous user choice, macro execution branches again
# the number 1 is the ID of this branch, retrieving the user's choice from the first
MacroBranch command
# the LABELs are targets of the resulting conditional jumps
Mainframe.MacroText     = 1¶RELABEL1¶RELABEL2¶RELABEL3
Study.Action            = MacroReBranch
STEP END

LABEL: RELABEL1            # must match corresponding goto

Mainframe.MacroText     = Your choice was: 1
Mainframe.MacroDelay    =  2
Study.Action            = MacroBanner
STEP END
Mainframe.MacroLabel    = RECONTINUE
Study.Action            = MacroGotoLabel
STEP END
```

```
LABEL: RELABEL2              # must match corresponding goto

Mainframe.MacroText       = Your choice was: 2
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = RECONTINUE
Study.Action              = MacroGotoLabel
STEP END

LABEL: RELABEL3              # must match corresponding goto

Mainframe.MacroText       = Your choice was: 3
Mainframe.MacroDelay      =  2
Study.Action              = MacroBanner
STEP END
Mainframe.MacroLabel      = RECONTINUE
Study.Action              = MacroGotoLabel
STEP END

LABEL: RECONTINUE            # must match corresponding goto

# depending on the user's choice, macro condition branches
# the first few lines of text will be displayed in a popup where the user can make a
choice
# the number 2 is the ID of this branch
# the LABELs are targets of the resulting conditional jumps, '-' means execution
simply continues
# the Choices are shown on the buttons of the popup window and their order
matches the LABELs
Mainframe.MacroText       = Do you want to repeat?¶2¶BEGINNING¶MIDDLE¶-¶From
Beginning¶Previous Choice¶Exit
Mainframe.FileVersion     =  8
Study.Action              = MacroBranch
STEP END

*****************************************************
```

23.3 Report

The Report function was originally introduced for clinicians who needed a way to create a clinical report, in which you can add figures, text, results, etc. to a template form you create. Additionally, the Report can be used as a form of lab notebook, where you can keep track of operations, results, etc. The report is accessed from the 

tab.

When you initially open the Report display, you will see a Toolbar with blank space below it.

The function of the icons is as follows:

New Report  . Select to create a new report. The *template.rtf* file will be displayed.

Open Report  . Opens window to retrieve existing reports.

Save Report As  . Save the current Report using a user-determined file name.

Save As Report Heading  . Use this option to save the Report Heading you have created.

Cut  (*Ctrl+X* or *Shift+Delete*). Standard Windows Cut option.

Copy Selection to Clipboard  (*Ctrl+C*). Standard Windows Copy option (copies selected image or text to the Windows Clipboard).

Paste  (*Ctrl+V*). Standard Windows Paste option (pastes the Clipboard contents to the Report).

Append Selection To Report  . Copies selected text or image (selected pane) to the report.

Append Data Display to Report  . Copies entire data display (all panes) to the Report.

Append Clipboard To Report  . Essentially the same as **Paste**, although an additional line will be added, as needed (similar to Word's "**paste special → unformatted text**" option, where the text formatting of the report is maintained).

Append Dipole Description to Report  (*Ctrl+Shift+D*). Appends the current dipole description to the Report.

Print Report  . Turns on the printer and prints the Report.

Font Dialog  . Opens the standard Font dialog.

Bold  . Selected text will be **bold**.

Italics  . Selected text will be in *italics*.

Underline  . Selected text will be underlined.

Left Justify  . Justify text at the left margin.

Center . Center the text.

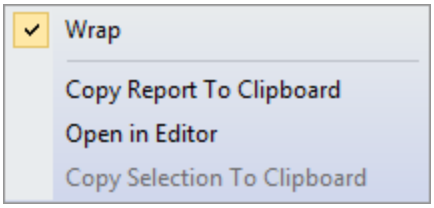
Right Justify . Justify text at the right margin.

Remove Indent (or indent left) . Move text to the left one tab.

Indent to the Right . Indent to the right one tab.

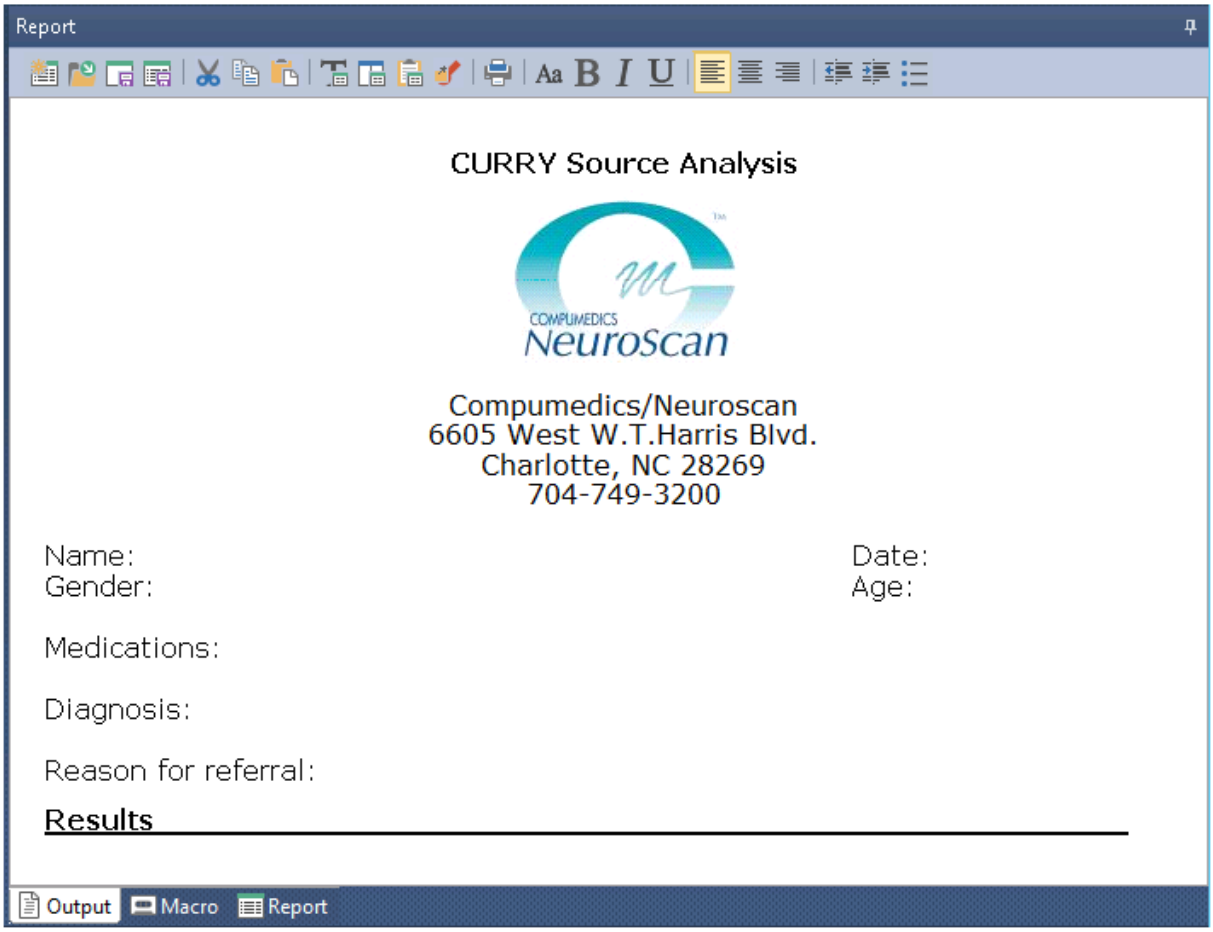
Add Bullets . Add bullets to the selected text.

Report Context Menu. *Right click* in the Report display to see additional options. **Wrap** is the standard function for wrapping the text from line to line. **Copy Report To Clipboard** copies the entire report to the Windows clipboard where it may be pasted into other applications. **Open in Editor** opens the report in a text editor, such as Word. **Copy Selection To Clipboard** copies the highlighted section to the Clipboard.



Using the Report feature

The first step is to create a template in the empty Report window. If desired, you can use **Paste to Report** to add in a graphic logo. A basic example is shown below.



When you have the heading completed, save it as *Report Template.rtf* to the *c:\Documents and Settings\<User Name>\Application Data\Neuroscan\CURRY 8* folder. This is the location where CURRY will look for the template file.

Using the template, add any text information, dipole results, or graphics to the report. (Use any of the related options on the Toolbars or context menus). When completed, save the report using **Save Report As**. Use  to open previously save reports.

Use can use other text editors (Word©, Wordpad©, Notepad©) to create the template, as long as the file is saved in rich text format. Some more complex formatting (wrapping text around figures) may be lost in the .rtf file itself, or when the file is opened in CURRY.

24 Keyboard Shortcut Commands Summary

Many of the commonly used features in CURRY can be accessed more easily by combination keyboard commands using the *Alt*, *Ctrl* and *Shift* keys, as well as the *Spacebar* and other keys. There are two "classes" of keyboard commands - those that use the *Ctrl* key, and those that use the *Alt* key. The *Ctrl+key* commands do not change across displays. The *Alt+key* commands change viewing "properties", and therefore the same key stroke combination may have different actions in different displays. The

commands are summarized below for your convenience (and may be printed for reference).

Most of the commands are seen on the option lists accessed from the Main Menu bar, the Toolbars, or the *right mouse* button. Some of the commands, however, appear only in the documentation, and are thus not otherwise evident. These are preceded by a red asterisk * below.

General commands

Ctrl+C. Copy Selection to Clipboard (the selection may be an image). Same as the Copy icon  (limited application).

Ctrl+P. Accesses the standard Print dialog screen  .

Ctrl+V. Same as the Paste icon  (limited application).

Ctrl+X. Cut to clipboard  .

Shift+Delete. Same as the Cut icon  (limited application).
Ctrl+Z. Undo recent step or entry (limited application).

Ctrl+Shift+C. Copy Data Display to Clipboard  . The entire contents of the data display are copied to the Clipboard.

Ctrl+Shift+R. Append Selection to Report  .

Ctrl+Shift+U. UI Update  . Updates the UI during macro execution.

***Ctrl+Display tab**. If you hold down the Ctrl button while clicking on a Display tab, the current process panel will remain displayed (otherwise, clicking a Display tab will also show the processing panel that is typically used with that display).

***F2**. If you highlight a text field, such as the Subject and Study name, and press the *F2* key, you can then change the name. Other fields, such as the XYZ positions in the localize display function similarly.

***Enter**. Depending on the view that has the focus, the associated parameter dialog tab will be activated.

***Mouse wheel**. Rotating the mouse wheel has different effects in CURRY, depending on which screen has the focus. It increases/decreases the threshold in the **Image Data** and **Localize** displays. It scales data or moves the waveforms in the **Functional Data** display (position the cursor over a label to rescale that channel only, or use + and -). It can be used to change the contour intervals. When a pull down list has the focus, rotating the mouse wheel will cycle through the options in the list. Because of the multiple uses for the mouse wheel, you should be certain which display has the focus *before* you rotate the wheel.
***Shift+Mouse wheel**. Changes number of channels displayed.
***Alt+Mouse wheel**. Scroll up and down through displayed channels.
***Ctrl+Mouse wheel**. Changes number of seconds displayed (continuous data).

***Esc and Break**. The Esc and Break keys will halt many operations, including source analysis, movies, macros, and BEM setup operations that are running in the background.

Database commands

Ctrl+N. Create New Study; access acquisition  .
Ctrl+O. Access Open File dialog for existing Functional Data, Image Data, or Study file  .
***Double-click the data file**. Has the same function as *right clicking* and selecting **Open Study**.
***Up**, **Down**, **Right**, and **Left Arrow** keys. Use the keys to move up/down or collapse/expand folders in the Database tree (standard operation).

Functional Data commands

Ctrl+A. Display all channels.
Ctrl+D. Deselect all channels.

Ctrl+E. Delete Event  .
Ctrl+S. Select all channels.

Alt+B. Butterfly Plot toggle  .

Alt+S. Autoscale data  .
Alt+U. Zoom out.
Alt+Z. Zoom in.

Shift+Left. Go to Previous Event  .

Shift+Right. Go to Next Event  .
PgUp / PgDn. Step through continuous file display screens and epoched file sweeps.
Home / End. Go to the beginning / end of a continuous or epoched file.

Spacebar. Invert polarity, toggle Accept/Reject  .

***Shift+Left Mouse**. Disable Tracking Mode (to place second vertical cursor).
***Double-click left mouse**. Enable Tracking mode (for a single vertical cursor).
***Ctrl+Double-click left mouse**. In the data display, sets the outer two cursors to the first and last points in the display.
***Ctrl+Double-click left mouse**. In the navigation toolbar, moves to the page/epoch where mouse is positioned.
***Ctrl+Drag**. Sets the two outer cursors at the start and end of the section you select, with the middle cursor halfway between.
***Ctrl+Alt+Drag**. Drag mouse to create Bad Blocks.

***Left/Right arrow**. Changes the display latency. In Tracking mode, changes the timepoint.
***Shift+Left/Right arrow, Ctrl+Left/Right arrow**. Changes the beginning of the time range, disables tracking mode.
***Alt+Left/Right arrow**. Changes the end of the time range, disables tracking mode.
***Ctrl+Alt+P**, **Ctrl+Alt+R**, and **Ctrl+Alt+1-4** to select the Filter Sets (online).

Maps, PCA/ICA commands

Ctrl+A. Select PCA  .
Ctrl+D. Deselect all components.

Ctrl+I. Select ICA  .
Ctrl+S. Select all components.

Alt+C. Select Contour Map  .

Alt+D. Toggle Dipole Strengths  .

Alt+G. Toggle MGFP  .

Alt+M. Start Movie  (of 2D contour maps, with one map displayed; a Timerange must be specified).

Alt+P. Toggle Position Plot  .

Alt+R. Toggle Residual Deviation  .

Alt+T. Toggle Thumbnail Plot  .

Image Data and Localize commands

Miscellaneous

Ctrl+D. Delete Localize Entry.

Ctrl+I. Export Cursor to Localize (from Image Data); Import Cursor to Localize (from Image Data).

Ctrl+R. Set Reference.

Alt+C. Display Cursor  .

Alt+D. Display Results  .

Alt+H. Show Segmentation Thresholds  .

Alt+M. Start Movie (a Timerange must be specified)  (from the Standard Toolbar).

Alt+S. Show Segmentation Result  .

***+, -**. Used to change Magnification.

***Shift+Up/Down arrow**. Used to Change Slices.

***Left/Right/Up/Down arrow**. Changes cursor position.

***Ctrl+Cursor keys**. Adjusts oblique view angulation, or (in 3D View) click a grid/strip/depth electrode contact.

***Mouse wheel** in Segmentation Preview/Results display. Changes lower segmentation threshold.

***Alt+mouse wheel** in Segmentation Preview/Results display. Changes upper segmentation threshold.

Segmentation commands

Ctrl+E. Edit Markers.

Ctrl+Shift+Delete. Clear Result and Markers (also  to clear Result and  to clear Markers).

Ctrl+Shift+S. Seedpoint Segmentation  .

Ctrl+Shift+T. Threshold Segmentation  .

Create commands

Ctrl+Shift+B. Create Brain Mask

Ctrl+Shift+I. Create Triangle Mesh  (with a fixed Resolution of 3mm).

Ctrl+Shift+O. Create Overlay  .

Ctrl+Shift+V. Create Voxel Mesh (raw)

Ctrl+L. Create Points (Localize).

Localization

Ctrl+D. Delete Localize Entry.
Ctrl+G. Go to Nearby Maximum / Project to Nearby Maxima.
Ctrl+I. Import Cursor Location
Ctrl+Q. Go to Nearby Maximum (and Export or Import).
***Ctrl+left mouse**. Switches to Append Mode.

3D View Commands

Miscellaneous

Ctrl+I. Export Cursor to Localize
Ctrl+R. Set Reference.

Ctrl+Shift+E. Toggle Confidence Ellipsoids  .
Ctrl+Shift+K. Keep Results.

Ctrl+Shift+M. Toggle Time Range Display Mode  .

Alt+M. Start Movie (a Timerange must be specified)  (from the Standard Toolbar).
Alt+O. Rotate 3D View  .
Alt+V. Save the Movie as an .avi file.
***Shift+left mouse**. Moves the objects as a single unit in the display.
***Shift+arrow keys**. Moves the objects incrementally in the display.
***Double click**. Double clicking in the 3D View display will show the expanded **Objects** list.
***Click on a Surface**. Clicking on a Surface in the 3D View will display its properties beneath the Objects list.
***Left/Right arrow**. Changes the display latency.
***Shift+ Left/Right/Up/Down arrow**. Shifts perspective.
***Ctrl+ Left/Right/Up/Down arrow**. Rotates perspective.
***+,-**. Changes magnification.
***Ctrl+Shift+click**. Used to remove individual electrodes in the 3D View (such as grid, strip or needle electrodes).

Source Reconstruction

Ctrl+Shift+A. Append to Results.

Ctrl+Shift+D. Add Dipole Description to Report  .

Ctrl+Shift+K. Keep Results  .

Ctrl+Shift+P. Pause Fit  .

Ctrl+Shift+Right. Go to Next dipole  (in Image Data).

Ctrl+Shift+Left. Go to Previous dipole  (in Image Data).

Macros

Ctrl+Shift+U. UI Update
Ctrl+Shift+Y. Single Step Macro
F2. Rename

Help Command

F1. Position the mouse and press F1 to access the *User Guide* for the section  .
Click **Shift+F1** to add "?" to cursor, then click to access *User Guide*.

25 Patents

Several parts of CURRY 8 have been patented (and more are pending). Patents as of March, 2011 include the following:

Source Reconstruction

Online Source Reconstruction for EEG/EMG and ECG/MCG Fuchs, Sands
US 7840248 B2, EP 1590037 B1 (Europe), 2004208344 (Australia), 169667 (Israel), 2364329 (Russian Federation), 113325 (Singapore), 4644184 (Japan), 2005/05638 (South Africa), 541620 (New Zealand), 238583 (India), 284059 (Mexico)

Localising and Displaying Electrophysiological Signals Wagner
AU 2006332443 B2 (Australia)

Method and System for Displaying Confidence Intervals for Source Reconstruction Fuchs
US 7840039, HK1083906 (Hong Kong), ZL03820616.1 (China), 4299781 (Japan)

26 Appendices

26.1 Appendix A. Triggering Details

When Using the Older STIM2 System (with the Audio System Unit)

When stimuli are presented or responses are made in the STIM2 system, that information is sent to the CURRY system by means of the "STIM to SCAN" cable (where "SCAN" refers to the prior SCAN acquisition package). The information is sent in the form of TTL pulses (5V square waves with user defined durations).

With the complete STIM2 system, the STIM-to-SCAN cable connects to the back of the STIM Audio System Unit, not to a parallel port on the back of the STIM computer. With the Software Only version of STIM2, the cable does then connect to the parallel port on the STIM PC. If there are no parallel ports, there are USB adapters that will work (contact techsup@neuroscan.com).

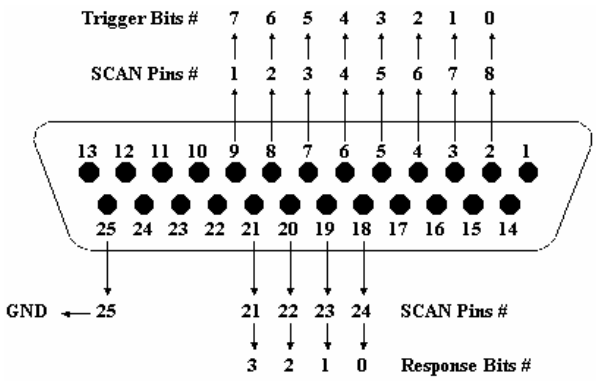
On the acquisition side, the cable connects to the trigger input connector on the System Unit (SynAmps2 and SynAmps RT). With NuAmps, there is an adapter cable that connect to the serial input connector on the NuAmps headbox. For SynAmps Wireless, there is a different adapter cable that connects to the amplifier unit.

TTL Characteristics

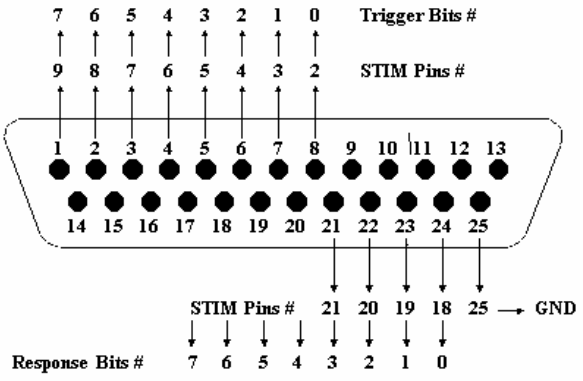
The stimulus TTLs are sent via 8 lines (8 bits) in the STIM-to-SCAN cable (see pinout below). Bit 0 toggles from 0 to 1, bit 1 toggles from 0 to 2, bit 2 toggles from 0 to 4, and so on to bit 7, which toggles from 0 to 128. Therefore, if the TTL is sent on line 8, which is bit 0, that will be interpreted by the acquisition software as an type 1 event (and you will see a 1 in the continuous data file). If the TTLs are sent simultaneously on bits 1 and 4, for example, that would be interpreted as a type 18 event (2 + 16). By combining different bits, you can get events from 1 through 255.

Response events work similarly, although the TTLs are sent only as single bits, not in combination (when using a STIM2 system; otherwise, they can be combined, as with the stimulus bits). With STIM2 Software Only systems, the response lines have been cut.

Note that the wiring of the STIM to SCAN cable is different between the STIM side and the SCAN side (which is why you cannot use an ordinary parallel cable in place of the STIM to SCAN cable). So, for example, if the STIM system sends a TTL using pins 2, 3, and 4, which are bits 0, 1, and 2 (with values of 1, 2, and 4), these are inputted into the amplifier on pins 8, 7, and 6, giving an event code of 7 (1+2+4) in the continuous data file.



Back of STIM Connector



Back of SCAN Connector

The **Duration** of the TTL pulses is set in the STIM2 software. In most cases, a duration of 1ms will be sufficient. You do not want the Duration to be excessively long, especially when the inter-trial-intervals are short. The Duration should be shorter than the ITI, or triggers may be missed.

In list form, the SCAN side connector and pinouts are as follows. Note that pins 14 and 15 carry +5V DC.

1) System Unit Connector: D25 Male, Metal Shell, AMP or equivalent
2) Mating connector: D25 Female, Metal Shell, AMP or equivalent
3) Pinout:

1 Trigger In 07	11 Undefined	21 Response In 03
2 Trigger In 06	12 Undefined	22 Response In 02
3 Trigger In 05	13 Undefined	23 Response In 01
4 Trigger In 04	14 +5VDC	24 Response In 00
5 Trigger In 03	15 +5VDC	25 Ground
6 Trigger In 02	16 Undefined	
7 Trigger In 01	17 Response In 07	
8 Trigger In 00	18 Response In 06	
9 Undefined	19 Response In 05	
10 Undefined	20 Response In 04	

Matching Port Logic
If you are connecting a stimulus system other than STIM2, you will need to match the port logic that is used. Stimulus TTLs use positive logic. This means that the pulses should be at 0V in the Off state, and 5V (at least about 3.5V) in the On state. Response TTLs use negative logic, meaning that the Off state is 5V and the On state is 0V. Generally, it

is best to assume that there must be a return to the Off level between stimulus and response events. With SynAmps RT, this is not a requirement when there are varying stimulus events being sent. For example, if you send a type 1 event followed by a type 2 event, there does not need to be a return to 0V in between. There does need to be a return to 0V if a type 1 follows a type 1.

We do NOT recommend sending voltage triggers through the SynAmps RT headbox. Connecting an external device creates a potential risk to the subject. Do NOT connect any peripheral devices without contacting Technical Support first.

Troubleshooting
Most trigger problems are due to factors that can be resolved, rather than due to hardware failure. These are the common sources of problems.

1. The Duration of the TTL pulses, as set in the STIM2 program, is too short or too long. If it is too short, triggers may be missed, depending on the AD Rate. If it is longer than the ITI, triggers may be missed.

2. If the STIM to SCAN cable is connected incorrectly (such as, to the parallel port on the STIM PC instead of the Audio System Unit), you will see no triggers. Make sure the cable is connected correctly and securely, and that it is a STIM to SCAN cable, and not some other parallel cable. Make sure the Audio System Unit is On.

3. If you are using a system other than STIM2, make sure you are matching the port logic, as described above, and that you are following the "return to 0V" rule between stimuli.

4. If triggers suddenly and inexplicably stop, try restarting the amplifier. Occasionally, there may be a static buildup that places the trigger input port into an atypical state.

5. In some cases, abnormal triggering can occur if the STIM to SCAN cable is in close proximity to a power cable or other source of high EMF.

6. In some cases where you are using a system other than STIM2, you may need to block certain bits or to **Invert** the logic. These options are found in the **Amplifier Control** panel, using the **Trigger Settings** button.

Trigger Settings. This option provides a way to view the incoming stimulus and response triggers from STIM2, or other stimulus presentation software. Clicking the button displays the Trigger Settings dialog, which reads the states of the trigger input board on the amplifier. You must be "connected" to an amplifier or the Simulator for the fields to show anything.

In **Binary**, you are seeing the state of each of the 8 **Stimulus** and **Response** bits, where the bits are from 7 to 0, left to right (i.e., 128, 64, 32, 16, 8, 4, 2, and 1). The resting state of the Stimulus bits is high (positive logic), so the accumulated **Decimal** value is 0. The resting state of the Response bits is high (negative logic), so the accumulated **Decimal** value is 255.

The **Accept** options let you block the input from selected bits. If, for example, there is a malfunction in the STIM2 Audio System Unit, where a stimulus bit becomes stuck On, you can block that bit (disable it by removing the check). This is a temporary solution that will let you continue to collect data until you can have

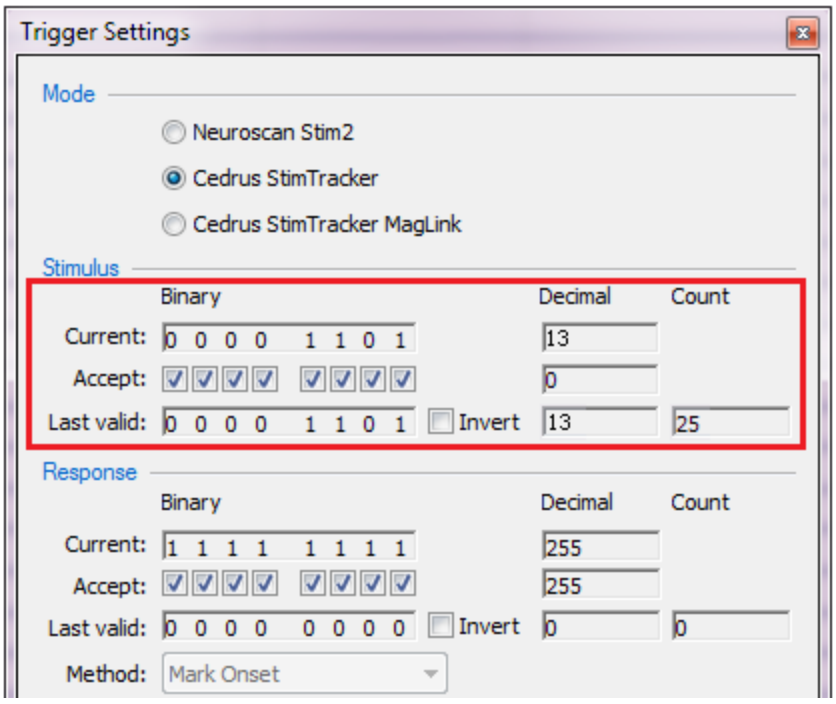
the unit repaired. The stimulus event values will be altered accordingly (the value of the blocked bit will be subtracted). The Accept fields take the place of the Hold Value that was used in the Scan software.

The **Last** fields (Binary and Decimal) display the most recently received stimulus and response events.

The **Invert** fields let you switch the logic for Stimulus and Response bits, if needed. When enabled, this field sets the program to read the inverted TTL values. For example, an inverted "1" will appear as "254". Normally, these fields are disabled (for STIM2 systems). Again, Stimulus triggering uses positive logic (resting is at 0V and active is at 5V), while Response triggering uses negative logic (resting is 5V and active is 0V). Enabling Invert for Stimulus events will then use negative logic, and enabling Invert for Response events will then use positive logic. With some other stimulation systems, you may need to Invert the triggers. As a general rule, if you are using a system other than STIM2 and are not seeing any triggers during acquisition, try enabling Invert.

The **Count** fields show the numbers of Stimulus and Response bit patterns that have been received.

In the example below, TTL pulses have been sent for bits 0, 2, and 4 (right to left), giving a Decimal value of 13 (1+4+8). The Count shows that 25 pulses were received.



To use Trigger Settings diagnostically, *the STIM2 system should be turned on with the stim-to-scan cable connected*. Connect to the amplifiers in CURRY 8 and start one of the STIM2 programs (so it is sending triggers).

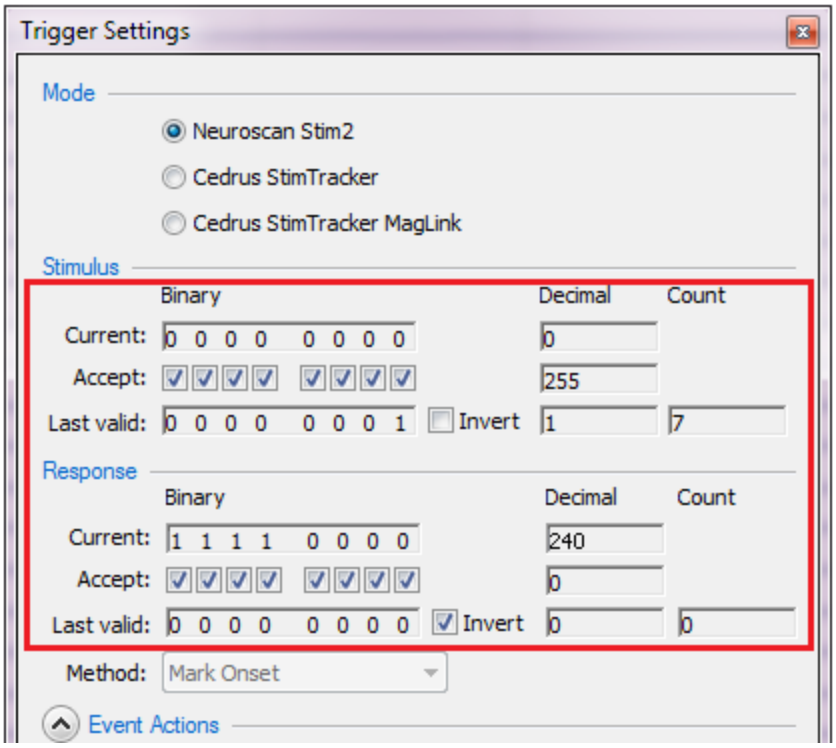
Note

The information here is based on the "normal" stim-to-scan cable. If you have a MagLink system, the response fields will appear a little differently, and if you have a STIM2 Software Only system, the response lines have been cut in the stim-to-scan cable.

Stimulus. The Stimulus fields display the stimulus trigger type codes received. With STIM2 running, you may see only brief flashes in the Stimulus Decimal and Binary fields with each trigger received. If you increase the pulse Duration in the STIM2 software to, for example, 200 ms, you will see the triggers somewhat more clearly. The activated bits will flash in the Binary field, and the type code number will flash in the Decimal field. The Last fields will show that stimuli and responses are being received, even if you do not see them in the Binary fields. (Do not forget to return the Duration to its prior setting when testing is completed).

Response. The Response Decimal field will show the inverted value of the response pad triggers (i.e., 255). Pressing the response pad buttons should show Decimal values of 254, 253, 251, and 247, corresponding to buttons 1-4, and type codes of 1, 2, 4 and 8, respectively. The Binary field will be all 1's until a button is pressed, then the corresponding 1 will become a 0 (uses the 4 columns on the right side of the display). The first 4 columns on the left can be 0's in some situations, and this is not necessarily a cause for concern (they are generally not used).

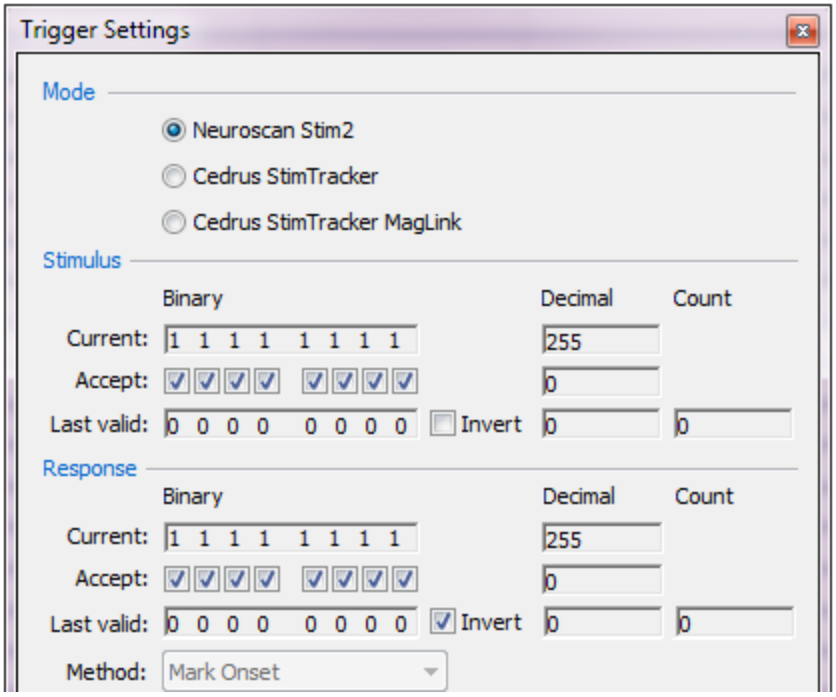
In its "resting" state, note that the Stimulus bits are all low (all 0's), and the last 4 Response bits are held high (1's). Summing the 4 response bits gives the 240 Decimal value.



If you see, for example, one (or more) of the stimulus bits held abnormally high (1), the value of that bit will be added to the type codes you see in acquisition. The cause could be a problem in the STIM box, the stim-to-scan cable, or in the amplifiers.

With other stimulus systems connected, you might see all response bits at 0, or maybe the four left bits at 0. They all need to be high in the resting state. Then it is a question of whether you want to record responses or not. If you do not want responses, then you should not plug anything into those pins on the trigger connector in the back of the System Unit (pins 17-24). The natural resting state of the *SynAmps RT* is high, so they will be OK. If you do want responses, they must use inverted logic, where the resting state is high, and the trigger pulse goes to zero. If pins 17-20 are zero, clip whatever lines are going into those pins - they are not needed for responses (but they do need to be held high).

To help isolate the cause of abnormal bits, disconnect the stim-to-scan cable (or other trigger cable if you do not have STIM) from the back of the System Unit. Select **Trigger Settings**, and you should see the following values.



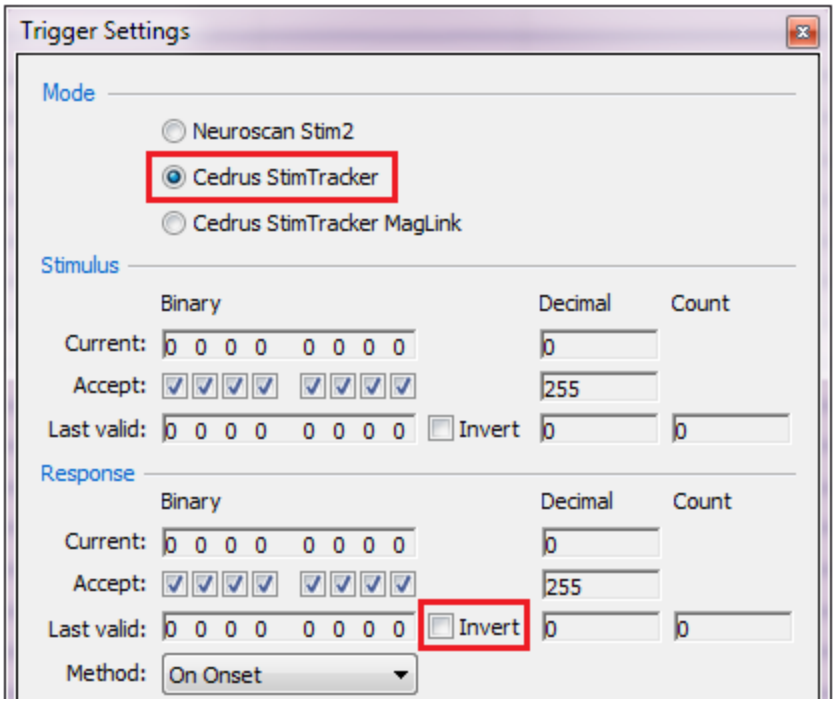
All of the bits should be high. If any are at zero, that points to a problem in the *SynAmps RT* (and a probable return to the service center). If this looks normal, connect the stim-to-scan cable to the *SynAmps RT*, and disconnect it from the stim box. It should still look like the picture above. If it does not, there is a problem in the cable. If it still looks normal, then the problem is likely on the STIM2 side.

Note
With MagLink systems, you will see an "r5" for the scanner trigger events in the data file. The scanner trigger is hard-wired to use Response bit 6. Rather than seeing an r64, the software converts it to an r5 (the r5 is not a combination of response bits 2 and 0).

When Using STIM2 with the StimTracker

Things become a little more complicated when using a StimTracker. The basic information presented above still holds, with the following exceptions.

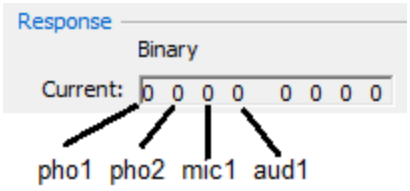
First, when you select the Cedrus StimTracker option, you will note that the responses are no longer Inverted.



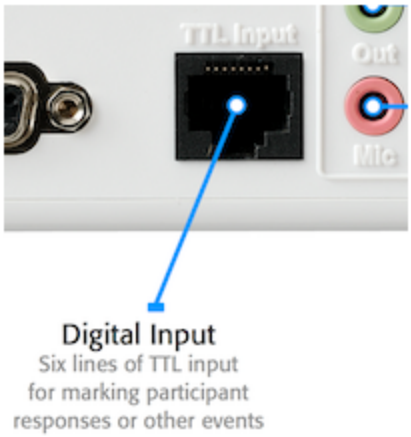
Next, note that some stimuli actually use the Response bits, namely the Audio, Microphone, and one or two Photic Sensors. These are the directly measured audio and visual stimuli, as opposed to the stimuli sent from Stim2 via TTL pulses.

StimTracker Signal	See by Neuroscan as	
Event marker bit 7	Trigger bit 7	128
Event marker bit 6	Trigger bit 6	64
Event marker bit 5	Trigger bit 5	32
Event marker bit 4	Trigger bit 4	16
Event marker bit 3	Trigger bit 3	8
Event marker bit 2	Trigger bit 2	4
Event marker bit 1	Trigger bit 1	2
Event marker bit 0	Trigger bit 0	1
Lightsensor 1	Response bit 7	pho1
Lightsensor 2	Response bit 6	pho2
Microphone	Response bit 5	mic1
Audio L+R	Response bit 4	aud1
TTL input, line 4	Response bit 3	r8
TTL input, line 3	Response bit 2	r4
TTL input, line 2	Response bit 1	r2
TTL input, line 1	Response bit 0	r1

These are seen in the r4-r7 response bit displays.



Responses from the StimTracker response pad actually are sent on Stimulus lines. The 4 TTL Response Inputs refer to the TTL Inputs on the back of the StimTracker, which are generally not used.



Instead, CURRY will convert Stimulus events of 248-255 to Response events of r1-r8. This of course means that you should not use Stimulus events of 248-255, as they will be converted to responses.

If you are using MagLink or Micromag, you will have received a special cable to connect the trigger output from the MRI Trigger Interface to the #2 Photocell jack on the back of the StimTracker.

This uses Response bit 6, which means that you can only use one light sensor in this configuration (inputs 3 and 4 do not work with CURRY or SCAN).

The following figure summarizes the information.

StimTracker Signal	See by Neuroscan as	
Event marker bit 7	Trigger bit 7	128
Event marker bit 6	Trigger bit 6	64
Event marker bit 5	Trigger bit 5	32
Event marker bit 4	Trigger bit 4	16
Event marker bit 3	Trigger bit 3	8
Event marker bit 2	Trigger bit 2	4
Event marker bit 1	Trigger bit 1	2
Event marker bit 0	Trigger bit 0	1
Lightsensor 1	Response bit 7	pho1
Lightsensor 2 /MRI scanner	Response bit 6	pho2 /r5
Microphone	Response bit 5	mic1
Audio L+R	Response bit 4	aud1
TTL input, line 4	Response bit 3	r8
TTL input, line 3	Response bit 2	r4
TTL input, line 2	Response bit 1	r2
TTL input, line 1	Response bit 0	r1

Cedrus Response Pad buttons 1-8 use Stimulus events 248-255 and the corresponding Trigger bits 0-7. CURRY converts stimulus events 248-255 to response events r1-r8. The 248-255 stimulus events in SCAN are converted to response events using a batch file, such as stim2resp.tcl.

The TTL inputs 1-4 refer to the TTL Input jack on the back of the StimTracker, which is not used in the typical configuration.

26.2 Appendix B. MRI Acquisition

A tomographical data record which covers the whole head is required for the correlation of bioelectromagnetic measured data with anatomical structures. In theory, this can be a CT or MR data record regardless of the type of device with which it was obtained. For reasons of radiation and better soft tissue contrast, however, MR images are preferred. The following pages provide general information and propose parameter settings for the imaging of three-dimensional MR image data records.

To help CURRY process MR images, the following criteria should be met:

- Images should have a low noise level. Because the field of view is used in an optimal fashion for sagittal slices, this slice orientation gives the best signal-to-noise ratio for a given acquisition time.
- The relation between anatomical structures and image intensity should remain the same throughout all slices. In some cases, temporal slices have a lower overall intensity than medial slices, which lowers the segmentation quality of temporal lobe structures.
- Cortical structure should be captured with good contrast. White matter should have a higher intensity than gray matter, which should still be well visible. A T1-weighted scan sequence produces such images.
- The whole upper part of the head should be captured, including all skin structures down to the chin or - at least - the nose.
- The data should be stored in DICOM or ACR-NEMA files, whose headers store most of the image parameters CURRY will need.

Preparations for an MR Recording

The subject should be in a comfortable position on the back. In performance planning, remember that the whole head is to be imaged as well as possible (including ears, nose and chin), but that no parts of the shoulders should be captured. Otherwise, the quality of segmentation is adversely affected.

The eyes are to be kept closed when measuring to prevent any movement artifacts due to eyelid movement. Any slope in the position of the head is to be taken care of at planning stage, by appropriate angulation, so that the head is level and central in the layers.
Oil capsules (e.g., vitamin E markers) can be fixed at the appropriate places to mark the position of localization coils, electrodes or other landmarks. These capsules provide a good contrast in the image and are easy to identify later.

The instructions for use of the MR scanner are to be followed.

Care

Although CURRY retrieves the image geometry parameters from the file headers, you should have the parameters documented for counter-checking. Especially, make sure you can tell left from right. Markers should be used during MR acquisition to alleviate this task.

Proposed Parameters

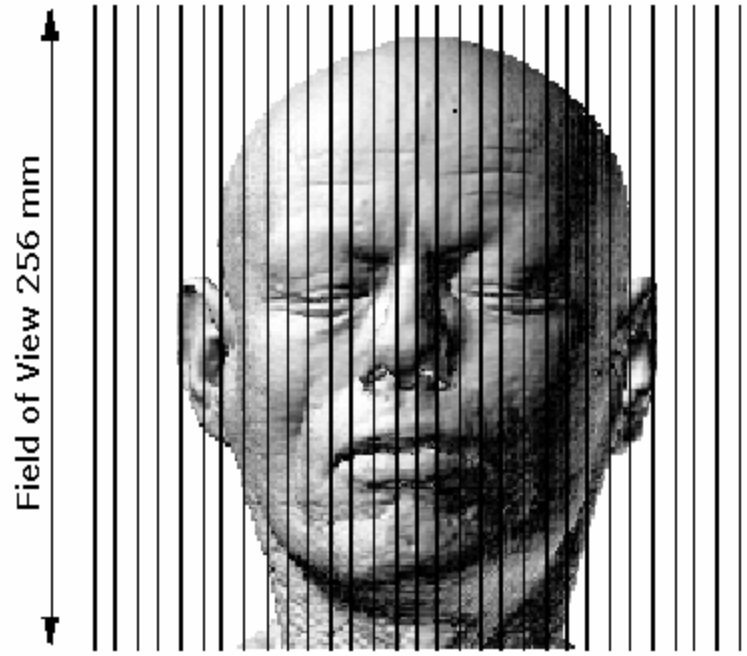
Below are the relevant parameter settings for a 3D volume data record of the head. Experience shows that an excellent image contrast and a low-noise image with good location resolution is produced with these settings—this is essential for the quality of the subsequent segmentation. Starting from a time-optimized T1-weighted 3D standard gradient echo sequence (e.g., 3D FFE), the parameters should be selected using the following list as a basis:

Parameter	Setting
Slice orientation	sagittal
Foldover direction	anterior-posterior
Coil selection	headcoil
Number of slices (subject-dependent)	128...256
Overcontiguous slices	no
Slice thickness (subject-dependent)	1.0...2.0 mm

Parameter	Setting
Field of view (subject-dependent)	256.0 mm
Rectangular FOV	100%
Subject position	head first
Subject orientation	supine
Scan technique	FFE or FLASH
Scan mode	3D
FFE repetition time (field strength dependent)	shortest (approx. 10...15 ms)
Number of echoes	1
Echo time (field strength dependent)	4...5 ms
Flip angle (field strength dependent)	25.0...30.0
Water-fat shift (field strength dependent)	1.5
Contrast enhancement	T1 weighted
Number of signals averaged	1
Scan matrix	256
Reconstruction matrix	256

Acquisition Time

The actual scan time is about 8 minutes in a sequence such as this. In addition there are the measuring times for the orthogonal planning layers (as offered by the system in the preset protocols, 20 - 30 seconds each) and the time for putting the subject in position and preparing the MR system; it usually takes 20 - 30 minutes in total to produce a 3D data record of the head.



Sagittal arrangement of individual images in the MR data record

26.3 Appendix C. File Information

This appendix describes the location, structure, and formats of files related to CURRY.

C.1 CURRY Filenames and Extensions

CURRY 8 reads and writes a variety of files, which are identified by their names and extensions. Due to its Database-driven approach, most input files are preselected via the chosen study. Output filenames are in some cases specified with a file selector chooser. In other cases, e.g., for triangle nets, the filename is determined automatically.

Output files follow a global structuring convention. A file consists of various sections, each of which contains either a list of keyword = value pairs, or an array of numbers.

File Locations and Extensions

The lists below summarize the files read by CURRY or created by CURRY. Consult third party documentation for further descriptions of their files (e.g., BESA, CTF, etc.), or the Neuroscan SCAN manuals for further information (.avg, .eeg,. cnt, and .3dd files).

Data, Digitizer, and Montage Files

.dat	Raw float extension
.bdf	bdf extension
.eeg	Biologic extension
.avr	BESA .avr extension (data file)
.asc	BESA .asc extension (plain ascii)
.ela	BESA .ela extension (label file)

.eps	BESA .eps extension (digitizer file)
.elp	BESA .elp extension (electrode file)
.pos	BESA .pos extension
.sfp	BESA .sfp extension
.vhdr	BrainVision .vhdr extension
.dat	BrainVision .dat extension
.vmrk	BrainVision .vmrk extension
.hdr	BTI .hdr extension
.data	BTI .data extension
.wghts	BTI .wghts extension
.asc	BTI .asc extension
.meg4	CTF .meg4 extension (data file)
.res4	CTF .res4 extension (parameter file)
.hc	CTF .hc extension (digitizer file)
.res	L0ocation result extension
.par	V2 data parameter file extension (old)
.dat	V2 data raw file extension
.ebs	EBS extension
.edf /.edf+	.EDF and .EDF+ extensions
.raw	EGI extension
.trc	MICROMED extension
.eeg	NERVUS .eeg extension
.fif	NEUROMAG extension
.avg	NEUROSCAN .avg extension (averaged data)
.eeg	NEUROSCAN .eeg extension (epoched data)
.cnt	NEUROSCAN .cnt extension (continuous data)
.3dd	NEUROSCAN .3DD extension (electrode, landmark, and head shape data file)
.nxe	NEXSTIM raw extension
.nxa	NEXSTIM avg extension
.eeg	NIHONKOHDEN .eeg extension
.21e	NIHONKOHDEN .21e extension
.lay	PERSYST .lay extension
.dat	PERSYST .dat extension
.sig	STELLATE .sig data extension
.sts	STELLATE .sts parameter extension
.eeg	TELEFACTOR .eeg extension
.dat	TELEFACTOR .dat extension

.erd	XLTEK .erd extension
.etc	XLTEK .etc extension
.snc	XLTE .snc extension
.ent	XLTEK .ent extension

CURRY 8 files

.cdt	CURRY data files
.dap	data parameter file (legacy parameter file)
.dat	raw data file
.rs3	sensor geometry file (legacy parameter file)
.dpa	CURRY 8 parameter file (replaces .dap and .rs3)
.par	data parameter file (CURRY 2)
.dat	raw data file (CURRY 2)
.dig	digitizer file
.dpf	digitizer parameter file (appended to original file: "localize.dig.dpf")
.pom	sensor landmark file (CURRY 2 and newer)
.res	digitizer file (CURRY 2)

Image Files

image.imd	image parameter file
image.img	image data file
image	image data folder
image.iso	isotropic image data file
image.par	image parameter file (CURRY 2)
image.dat	image data file (CURRY 2)
image.ppn	landmark file
image.s00...s99	surface file
image.bo0...bo99	binary overlay file
image.sp0...sp9	points and normals file
image.bd0...bd29	BEM parameter file
image.bt0...bt29	BEM transfer matrix file

Result Files

arbitrary.dip	dipole file
arbitrary.dsc	scan file
arbitrary.dsp	scan dipole file
arbitrary.cdr	current file
arbitrary.cdp	current dipole file
arbitrary.map	measured data and sensor file
arbitrary.dat	exported data file (along with .dap and .rs3 files)
arbitrary.cef	exported event list
arbitrary.ceo	"original" events created during acquisition (same as .cef but will not be overwritten by Functional Data)
arbitrary.pca	exported PCA results file
arbitrary.ica	exported ICA results file
arbitrary.ele	electrode location file
arbitrary.coi	coil location file
arbitrary.std	Statistical results
arbitrary.stc	CDR grand average results

Hardcopy / Print Files

arbitrary.bmp	bitmap image file, true color, lossless, uncompressed
arbitrary.png	portable network graphics file, true color, lossless, compressed
arbitrary.gif	graphics interchange format file, 256 colors, lossless, compressed
arbitrary.jpg	joint picture expert group file, true color, lossy, compresssed
arbitrary.emf	enhanced metafile, true color, lossless, vector-based, uncompressed
arbitrary.avi	movie file, true color, compression depends on selected codec

Other Files

arbitrary.cst	CURRY study file
arbitrary.cfg	parameters file
arbitrary.mdb	Database file
arbitrary.mda	ASCII dump of archive file
arbitrary.pom	location file
arbitrary.rtf	report file
arbitrary.txt	report file
arbitrary.mnt	montage file

C.2 CURRY 7 Generic File Format

Most files that CURRY reads and writes follow a very simple structure, which is nevertheless very general. All parameters appear as keyword = value pairs. Thus, it is very easy to understand the contents of CURRY output files. All CURRY output is formatted in the same way, so that only one general file format has to be learned.

Sections

A file may contain many different sections. Each section holds parameters for a certain purpose. For example, section names in the file default.cfg are:

Example

```
LOG_SETTINGS
DATABASE_SETTINGS
RECONSTRUCTION_SETTINGS
DATA_PARAMETER
SVD_SETTINGS
```

and so on.

Below, an example for the keyword = value structure of a section is given. It is the section that describes the defaults for the Database window as they are used when CURRY starts.

Example

```
DATABASE START
  DataSourceName      = C:\Program Files (x86)\Neuroscan\CURRY 8\Examples\CURRY 8 Examples.mdb
  ProviderClsid       = {DEE35070-506B-11CF-B1AA-00AA00B8DE95}
  OpenDatabase        = 1
  Show FullPath       = 0
  Show Study Subfolders = 0
DATABASE END
```

It can be seen, that the section name is DATABASE_SETTINGS. This section has been created automatically and does not need to be edited by hand. Remarks start with a hash (#). Within a section, certain keywords are recognized. The values to be assigned are on the right. If an unrecognized keyword occurs, CURRY issues a warning. If a recognized keyword is not present, a default value is used.

Arrays

A special type of sections is used for arrays. First, there is a section that describes the properties of the array, then a second section follows that holds the values themselves:

Example

```
LOCATION_LIST START
  ListDescription     = points
  ListUnits           = voxels
  ListNrColumns       = 3
  ListNrRows          = 5
  ListNrTimepts       = 1
  ListNrBlocks        = 1
  ListBinary          = 0
  ListType            = 6
  ListTrafoType       = 0
  ListGridType        = 2
  ListFirstColumn     = 1
  ListIndexMin        = -1
  ListIndexMax        = -1
  ListIndexAbsMax     = -1
LOCATION_LIST END

LOCATION_LIST START_LIST      # Do not edit!
 34  106       44
 34  109       46
 34  109       42
 34  106       44
 34  109       42
LOCATION_LIST END_LIST
```

The (up to three-dimensional) array is identified by its number of rows, columns, and timepoints. The type of contents (integer, floating point, strings) is encoded in the LIST_TYPE entry. This information is used to read the section that is enclosed in the START_LIST, END_LIST pair. Supported types are:

- 0: integer
- 1: double
- 2: character
- 3: float
- 4: short integer
- 5: string
- 6: unsigned character

Compressed Notation

Arrays containing data of type 2 or 6 can be saved in compressed notation, where each byte is represented by a 2-character hexadecimal number. The automatic use of compression can be switched off in the file startup.cfg.

Compound Files

A file that holds, e.g., dipole locations, orientations, and strengths would consist of three such arrays, together with a section that holds the section names for these arrays, a description array, and a transformation matrix which is used to convert locations and orientations into the internal CURRY coordinates. The beginning of a dipole file is:

Example

```
POINT_KEYWORDS START
  PointKeyLocations    = LOCATION_LIST
  PointKeyNormals      = NORMALS_LIST
  PointKeyContrib      = NO_LIST
  PointKeyFlags        = NO_LIST
  PointKeyStrengths    = STRENGTH_LIST
  PointKeyErrors       = NO_LIST
  PointKeyDeviations   = DEVIATION_LIST
  PointKeyFields       = FIELDS_LIST
  PointKeyMgfp         = NO_LIST
  PointKeyAdditive     = NO_LIST
  PointKeyMultiplicative = NO_LIST
  PointKeyComponents   = NO_LIST
  PointKeyColorind     = NO_LIST
  PointKeyChartrafo    = NO_LIST
  PointKeyNumbers      = NO_LIST
  PointKeyNeighbors    = NO_LIST
  PointKeyTriangles    = NO_LIST
  PointKeyRemarks      = NO_LIST
  PointKeyCompressed   = NO_LIST
  PointKeyIndices      = NO_LIST
  PointKeyInflated     = NO_LIST
  PointKeyEllipsoids   = ELLIPSOID_LIST
  PointNrLocations     = 1
  PointNrTimepts       = 2
  PointType            = 2
  PointCoordSystem     = 0
  PointTypeSamples     = 0
  PointPlotFlags       = 20497
  PointPlotFlagsEx     = 0
  PointPlotColor1      = 38
  PointPlotColor2      = 0
  PointPlotColor3      = 0
  PointPlotShape       = 1
  PointPlotSurface     = 1
  PointPlotTranspa     = 100
  PointPlotClipping    = 0
  PointPlotTextsize    = 0
  PointPlotBorder      = 1
  PointPlotAdjacent    = 0
  PointPlotClosed      = 0
  PointPlotType1       = 0
  PointPlotType2       = 0
  PointPlotType3       = 0
  PointPlotInflations  = 0
  PointPlotInfwanted   = 0
  PointPlotRepaired    = 0
  PointTFirst          = 0.01
  PointTDelta          = 0.005
  PointDistance        = 0
  PointArea            = 0
  PointVolume          = 0
  PointSymbolsize      = 15
  PointLinewidth       = 1
  PointPlotDist1       = 0
  PointPlotDist2       = 0
  PointPlotDist3       = 0
  PointPlotPlane1      = (0,0,1)
  PointPlotPlane2      = (0,0,1)
  PointPlotPlane3      = (0,0,1)
```

```
  PointSymbolscale     = 1 -21 1 ...
POINT_KEYWORDS END

POINT_DESCRIPTION START_LIST # Do not edit!
Dipoles (1 moving)
Dipole Fit Results (1 moving) for 1 source, 10.0...15.0 ms (2 samples):
10.0 ms          (-24.5, 24.2, 24.7)mm, q=4788µAmm, (-0.49, 0.04, -0.87), 18.5ml (Uncus, Brodmann area 28)
      SNR: 9.7, residual deviation (normalized, original): 11.1%, 11.6%, variance: 98.77%, 98.65%
15.0 ms          (-27.3, 34.8, 30.7)mm, q=4784µAmm, (-0.65, 0.16, -0.74), 11.6ml (Inferior Frontal Gyrus)
      SNR: 10.6, residual deviation (normalized, original): 10.2%, 10.5%, variance: 98.96%, 98.89%
POINT_DESCRIPTION END_LIST

POINT_TRAFO START_LIST          # Do not edit!
 1    0          0          0
 0   -1          0          0
 0    0         -1          0
 0    0          0          1
POINT_TRAFO END_LIST

LOCATION_LIST START
  ListDescription     = dipoles
  ListUnits          = mm
  ListNrColumns       = 3
  ListNrRows          = 1
  ListNrTimepts       = 2
  ListNrBlocks        = 1
  ListBinary          = 0
  ListType            = 1
  ListTrafoType       = 1
  ListGridType        = 2
  ListFirstColumn     = 1
  ListIndexMin        = -1
  ListIndexMax        = -1
  ListIndexAbsMax     = -1
LOCATION_LIST END

LOCATION_LIST START_LIST        # Do not edit!
 -24.5206        24.1843   24.6584
 -27.3039        34.8362   30.6934
LOCATION_LIST END_LIST
```

and so on...

In POINT_KEYWORDS, general information is given. In POINT_DESCRIPTION, the contents are described, and in POINT_TRAFO the backtransformation matrix is stored. This backtransformation matrix makes it possible to use any coordinate system for the output file and still be able to read it later. Then follow the arrays that have been announced in the POINT_KEYWORDS section: locations, orientations, strengths, deviations, and forward calculated data.

C.3 BEM/FEM Files

BEM description file: *.bd0...29; **FEM description file:** *.fd0...29

Contains the model geometry, sensor locations (if available), conductivities and model parameters. Holds required and sufficient information for creating the full matrix file. For creating the transfer matrix, the complete sensor geometry has to be known.

The file is saved in CURRY 4 generic format.

BEM transfer matrix file: *.bt0...29

The BEM transfer matrix establishes a link between the nodes of the BEM Realistic Head Model and the sensors. This link can be expressed as a matrix, which is stored in binary format. As soon as either the geometry or the BEM parameters or the sensor locations change, the transfer matrix becomes invalid. CURRY detects this situation and sets up a new matrix. CURRY can handle the situation, where only a subset of the sensors represented in the transfer matrix is active.

C.4 Functional Data Files

Free Format and CURRY 8 Data Files *.dat

Data files contain functional data. A variety of formats are allowed. Details are specified in the **Data Parameters** windows.

Data may be in any of the following formats:
- Plain ASCII: 1 value per sample
- Binary (Float): 4 bytes per sample, floating point
- Binary (Short): 2 bytes per sample, integer
- Binary (Double): 8 bytes per sample, floating point
- Binary (Long): 4 bytes per sample, integer

The binary file formats support both Intel and Motorola byte orders, and the ASCII format allows for leading lines and columns to be skipped.

In all of these cases, the layout of the data in the file must be such that
- the outermost loop corresponds to the epochs or trials, while
- the middle loop may either correspond to samples or to channels, and
- the innermost loop will then correspond to channels or to samples respectively.

The outermost loop may be missing in the case of pre-averaged data.

Digitizer Files *.dig

Digitizer files are used for sensor and landmark definition in functional coordinates. Any column oriented ASCII file can be read. The meaning of the columns must be the same throughout the file.

Details are specified in the **Data Parameters** windows.
- Lines containing sensor/landmark coordinates can be selected.
- Columns containing coordinates can be selected.
- Coordinate units may be mm, cm, dm, m, or inch.
- Remark columns can be selected.

C.5 Archive Files

ASCII archive file: *.mda

The ASCII archive file format encodes the contents of a binary archive one to one. ASCII dumps can be made of single subjects or whole archives. ASCII dumps can be added to empty or to existing archives. Examples where the use of the *.dba file format is useful include:

- moving archives between computers with different operating systems,
- merging archives,
- moving subjects between different archives,
- modifying pathnames in archives.

Structure

```
"%%EX",         // begin of experiment
"% LA",         // label
"% DA",         // creation date
"% TI",         // creation time
"% CM",         // comment (multi-line!)
"*",            // comment continued
"%%XE",         // end of experiment

"%%SU",         // begin of subject
"% TI",         // title
"% LN",         // last name
"% FN",         // first name
"% MN",         // middle name
"% DA",         // date of birth
"% GD",         // gender
"% HD",         // handedness
"% CM",         // comment (multi-line!)
"*",            // comment continued
"%%US",         // end of subject

"%%ST",         // begin of study
"% DA",         // date
"% LA",         // label
"% DO",         // doctor
"% CM",         // comment
"*",            // comment continued
"%%TS",         // end of study

"%%FI",         // begin of file
"% TY",         // type (IMAG, MEAS, FLOC, MLOC, DEFS, RESU, etc)
"% FO",         // format guid
"% DA",         // date
"% TI",         // time
"% BN",         // basename
"% FE",         // file extension
"% CM",         // comment (multi-line!)
"*",            // comment continued
"%%IF"          // end of file
```

The ordering of the "%" lines within a group (or block) is irrelevant, but only "% CM" lines may be continued using the "* ..." tag.

Studies on the Same Level versus Derived Studies (nested)

```
Same level:     Subject
                   Study1
                   Study2

%%%ST            // begin of Study1
[content]
%%%TS           // end of Study1

%%%ST            // begin of Study2
[content]
%%%TS           // end of Study2

Derived Studies:  Subject
                     Study1
                        Derived Study2

%%%ST            // begin of Study1
[content]

%%%ST            // begin of Derived Study2
[content]
%%%TS           // end of Derived Study2

%%%TS           // end of Study1
```

In the former *.dba format, the paths are stored in Unix-like fashion (//C/Programs/Neuroscan).

In the current *.mba format, the paths are stored in Windows-like fashion (C:\Programs\Neuroscan).

C.6 Supported CURRY 2 File Formats

Functional Data Parameter File: *.par

Structure

parameter file version (must be 10... 12)
function mode (0=epoch, …)
number of SynAmps (32 channel amplifiers)
number of samples per trial /epoch
number of trials / epochs
original sampling frequency [Hz]
subsampling frequency [Hz]
averages flag (any value will do)
storage flag (any value will do)
trigger value (any value will do)
trigger flag (any value will do)
time delay between epochs [15.625 msec]
trigger offset [msec]
randomization delay between epochs [15.625 msec]
    number of channels in SynAmps
        display, gain, highpass, lowpass, notch, scale, calibration factor, device number
        … (for all channels)

… (for all SynAmps)

Care

Rectangular brackets [ ] in the section below indicate optional entries.
measured data byteorder (0: SUN, 1: PC). This entry is ignored; data must be in PC byte order!
number of SYNAMPS (1...4)
number of devices
device mode (0, 1: cryostat 0/1; 10, 11: electrode set 0/1)
number of sensors, sensor order (0, 1, 2), baselength in mm, diameter in mm, [<option A>]
channel numbers (one line)
2D field of view: xmin, xmax, ymin, ymax in mm
2D field of interpolation limits: xmin, xmax, ymin, ymax in mm
contour line qualities: nxl, nyl, nxm, nym, nxh, nyh
device parameters (as below)
… (for all devices)

Where <option A> refers to:
diameter2 in mm, ishelmet (0/1), derivative (0=axial, 1=planar), shape (0=circ, 1=rect), center x,y,z in mm

Structure of magnetic device parameters (mode = 0 or 1)
relative 3D coil coordinates: x, y, z in mm, [Sensor Number]
… (for all sensors)
… (for all coil types, e.g lower, upper)
3D sensor normals: nx, ny, nz in mm
… (for all sensors)
crosstalk compensation matrix (upper triangle, line-wise)

Structure of electric device parameters (mode = 10 or 11)
2D electrode coordinates: x, y in mm
… (for all electrodes)
3D electrode coordinates: x, y, z in mm, [Sensor Number]
… (for all electrodes)

Note

display yes=1, no=0 applies only to data acquisition
highpass, lowpass, notch and scale apply only to data acquisition
calibration factor is in units of pT/LSB (MEG/MCG) or of nV/LSB (EEG/ECG)
device number applies only to data acquisition

Note

Optional entries in this part are only available for parameter file version number -12 and following.

Example

```
-12
0
2
128
10
10000
```

```
      1000
      0
      3
      1
      1
      64
      -20
      0
      32
            1 1 0 6 0 10 1000.0 3
            1 1 0 6 0 10 1000.0 3
…
      32
      1 1 0 6 0 10 1000.0 3
…
1
3
1
10
80 0 0.00 0.00
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65
66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 /* this is a single long line */
-10.000 1010.000 -10.000 210.000
0.000 1000.000 0.000 200.000
29 9 44 14 59 19
30.0 30.0
…
30.0 30.0 30.0
…
```

Raw Data File: *.dat

Measured EEG/MEG data files in CURRY 2 format store data in an epoch-channels-samples fashion. The file has as many data block as there are epochs. Each block has as many sub-blocks as there are channels. In each sub-block, samples are contiguous. Each sample is a 2-byte unsigned integer. Scaling factors are in the parameter file. The byte order must be PC (Intel) style.

Structure of raw data file (binary)

```
                  measured field/potential
                  … (for all timepoints in epoch)
            … (for all sensors)
      … (for all epochs)
```

Functional Localization File: *.res

Structure

Number, x, y, z in mm, dev[%], label
… (for all localized coilsets)

A rigid transformation (translation and rotation) is performed. All coordinate units must be in mm. At least three transformation points must be specified. The deviation value is not taken into account.

Example of unity transformation: no_loc.res

```
1  1.0  0.0  0.0  0.0  0.0
2  0.0  1.0  0.0  0.0  0.0
3  0.0  0.0  1.0  0.0  0.0
4  0.0  0.0  0.0  0.0  0.0
```

MEG

Number is number of coilset.

Example

```
1 123.1 67.8 53.5 0.23 coilset 1
2 114.3 53.4 97.0 0.28 coilset 2
3 152.8 49.1 54.4 0.18 coilset 3
4 148.4 61.0 25.3 0.19 coilset 4
```

EEG

Number >= 0: Entry is electrode position. Ordering of electrode positions corresponds with ordering in electrode group. Number != 0: Entry is transformation point. Number of corresponding entry in anatomical localization file *.pom is the absolute value of the point number.

Example

```
-5 206.05 134.77 120.12 0.0 PAL,      fifth transformation point
-4 49.80 138.67 124.02 0.0 PAR,       fourth transformation point
-1 123.05 47.85 152.34 0.0 NAS,       first transformation point
-2 125.98 223.63 83.98 0.0 INI,       second transformation point
0 156.25 230.47 120.12 0.0 O1         (electrode nr 1)
0 100.59 235.35 120.12 0.0 O2         (electrode nr 2)
0 194.34 194.34 132.81 0.0 T5         (electrode nr 3)
3 181.64 214.84 171.88 0.0 P3         (electrode nr 4), AND third
transformation point
0 131.84 233.40 192.38 0.0 Pz         (electrode nr 5)
0 75.20 222.66 176.76 0.0 P4          ...
0 59.57 201.17 135.74 0.0 T6
0 208.98 146.48 151.37 0.0 T3
0 192.38 169.92 211.91 0.0 C3
0 132.81 181.64 241.21 0.0 Cz         - Vertex
0 69.34 172.85 215.82 0.0 C4
0 45.90 150.39 156.25 0.0 T4
0 195.31 94.73 171.88 0.0 F7
0 181.64 107.42 216.80 0.0 F3
0 129.88 106.45 240.23 0.0 Fz
0 75.20 110.35 216.80 0.0 F4
0 58.59 99.61 175.78 0.0 F8
0 153.32 60.55 186.52 0.0 Fp1         ...
0 97.66 62.50 187.50 0.0 Fp2          (electrode nr 19)
```

Anatomical Localization File: *.pom

Structure

x, y, z in mm
... (for all entered points)

Example of unity transformation and shift: no_loc.pom **(cf.** no_loc.res**)**

```
129.0 128.0 128.0
128.0 129.0 128.0
128.0 128.0 129.0
128.0 128.0 128.0
```

MEG

```
128.00 177.33 248.00 coilset1
208.00 168.00 186.67 coilset2
```

```
180.00 228.33 191.33 coilset3
174.67 120.00 229.33 coilset4
```

Image Data Parameters: *.par

Structure

Image format (binary)
Image orientation
Field of view in mm
Number of slices
Number of first slice
Slice interleave
Slice-to-slice distance in mm
First slice offset in mm
Number of valid slices
Raycast segmentation top gap in mm
Raycast segmentation center (x) in mm
Raycast segmentation center (y) in mm
Raycast segmentation center (z) in mm
Raycast segmentation threshold
Light source direction (x)
Light source direction (y)
Light source direction (z)

Parameter values

Image format:

bits 0,1:	0: sagi, 1: coro, 2: hori
bit 2 set:	<-> x, y
bit 3 set:	invert z
bit 4 set:	invert y
bit 5 set:	invert x
bit 6: 0:	linear, 1: gauss-Interpolation

Field of view:

positive:	slice shift off
negative:	slice shift adjusted

Number of slices:

positive:	256 x 256
negative:	512 x 512
negative, < -10000:	128 x 128

Example

```
0
0
256.0
128
1
1
1.8
13.7
128
10.0
128.0
128.0
128.0
30
-1.0
```

- 1. 0
1. 0

Point list: *.sp0…9

Byte assignments

byte	type	contents
0...7	double	field of view [mm]
8...11	int	number of points
12...14	unsigned char	first point: location x,y,z [voxels], multiply with (field of view)/256 to obtain [mm]
15...17	unsigned char	first point: surface normal nx+128,ny+128, nz+128 [a.u.], subtract 128 to obtain nx,ny,nz
18...23	unsigned char	second point
24...29	unsigned char	third point
...	...	...

Triangle list: *.s00…99

Byte assignments

byte	type	contents
0...3	int	number of bytes to follow
4	unsigned char	type (0: polygons)
5	unsigned char	nr of vertices (3)
6	unsigned char	bytes per coordinate (1)
7	unsigned char	shading (0: light source, 1: net, 2: map)
8	unsigned char	side length [voxels]
9.11	unsigned char	reserved
12...15	float	max. current density [uAmm]
16...19	float	patch volume [mm^3]
20...22	unsigned char	first triangle, first point: location x,y,z [voxels], multiply with (field of view)/256 to obtain [mm]
23...25	unsigned char	first triangle, first point: surface normal nx+128,ny+128,nz+128 [a.u.], subtract 128 to obtain nx,ny,nz
26...31	unsigned char	first triangle, second point
32...37	unsigned char	first triangle, third point
38...55	unsigned char	second triangle
56...73	unsigned char	third triangle
...	...	...

Tetrahedra list: *.s00…99

Byte assignments

byte	type	contents
0...3	int	number of bytes to follow
4	unsigned char	type (1: tetrahedra)
5	unsigned char	nr of vertices (4)
6	unsigned char	bytes per coordinate (1)
7	unsigned char	shading (0: light source)
8	unsigned char	side length [voxels]
9..19	unsigned char	reserved
20...22	unsigned char	first tetrahedron, first point: location x,y,z [voxels], multiply with (field of view)/256 to obtain [mm]
23...25	unsigned char	first tetrahedron, second point
26...28	unsigned char	first tetrahedron, third point
29...31	unsigned char	first tetrahedron, fourth point
32...43	unsigned char	second tetrahedron
44...55	unsigned char	third tetrahedron
...	...	...

26.4 Appendix D. Glossary

Anatomical Landmark
A uniquely defined anatomical location.
Archive
A collection of data etc. Also, a place where the data is stored.
Artifact, also: Artefact
A signal present in EEG or MEG data, but not generated by the brain itself (e.g., movement artifacts).
Auricular
Of, relating to, or received by the sense, or organs of hearing.
Axial
For a line: along an axis; for a plane: perpendicular to an axis. In CURRY, the axis used is the vertical axis, and axial slices are thus horizontal slices.
Axon
The long thread-like extension of a nerve cell that conducts nerve impulses from the cell body. Can be compared to a 'Dendrite' (see 'Dendrite').
Bioelectrical
Electric phenomena caused by biological currents.
Biomagnetic
Magnetic phenomena caused by biological currents.
BTI
Biomagnetic Technologies Incorporated. MEG system manufacturer.
Byteorder
The order in which bytes are presented.
Cardiac
Of, or relating to the heart.
Cardiophysiological
Of, or relating to the physiological behavior or properties of the heart.
Closing
Result of performing a dilation operation (see 'Dilation') followed by an erosion operation (see 'Erosion').
Coilset

A set of orthogonal coils whose location can be localized exactly by an MEG system. Coilsets are attached to the skin for co-registration of sensor and anatomical coordinates.

Constellation
A group of something, e.g., dipoles that are active together.

Contiguous
Touching along the side or boundary; in contact. Physically adjacent; neighboring.

Coronal
Short for Coronal suture; of, or relating to a corona or coronal (a crown-like structure, such as the top of the head).

Crosstalk
Unwanted signals in one channel of a communications system as a result of an (inductive) coupling of channels.

CTF
MEG system manufacturer.

Dendrite
Any of the short branched, thread-like extensions of a nerve cell, which conduct impulses towards the cell body. Can be compared to an 'Axon' (see 'Axon').

Digitizer
A system to determine the location of the tip of a special pencil or other instrument in 3D-space (Fastrak, Vicra).

Dilation
Operation, or procedure which enlarges a shape. Thin structures become thicker and more robust from the operation. It can be compared to inflating a balloon.

Electroencephalograph (EEG)
An instrument for recording the electrical activity of the brain, usually by means of electrodes placed on the scalp. Used to study brain waves and identify many other conditions of the brain.

Encephalogram
An EEG recording.

Erosion
Operation, or procedure which deflates a shape. Large structures connected by thin structures are 'cut loose' by the operation. It can be compared to deflating a balloon.

Gaussian
Related to the theories of numbers and applied mathematics to astronomy, electricity & magnetism and geodesy developed by German mathematician Karl Friedrich Gauss (1777-1855).

Gouraud Shading
Method of triangle shading, where the vertex colors are interpolated across the triangle's area.

Gradiometer
Arrangement of coils used to measure spatial derivatives of a magnetic field.

Halfspace
Space on one side of a plane.

Hardcopy
Computer output printed on paper, as opposed to machine readable output, such as magnetic tape, or output to the screen.

Headcoil
See coilset.

Highpass
Allowing the passage of high-frequency information, but sufficiently attenuating frequencies below a certain threshold value.

Hounsfield Scaling

A method of mapping image intensities to colors, where an arbitrary intensity range is mapped linearly to a given color range. Intensities outside this range are assigned the extremal colors.

Inhibitory
Acting in a manner so as to hinder, or restrain something.

Inion
The most prominent point at the back of the head, used as a point of measurement in craniometry (the study and measurement of skulls).

Isofield
Region where a field is constant, in 3D normally a closed surface, in 2D a closed line.

Isopotential
Region where a potential is constant, in 3D normally a closed surface, in 2D a closed line.

Isotropic
Having uniform physical properties in all directions. Also, in biology, not having predetermined axes.

Isotropization
To cause something to become isotropic.

Landmark
A location used for measurements.

Leadfield
The term leadfield comes from the observation that when you enforce a voltage difference between two leads (=electrodes), ie inject a current, you will obtain a distribution of currents throughout the head, which is called the leadfield. Reciprocally, if you place a current dipole inside the brain, you will obtain a distribution of currents throughout the head resulting in voltage differences at the leads. This (linear) relationship between a current dipole moment (for a dipole with fixed location and orientation) and the resulting voltage topography can be written as a vector. For many dipoles, it can be written as a matrix - the leadfield matrix. Typically it has #sensors x (#sourcelocation x 3) entries (three orthogonal dipoles per source location). The leadfield matrix thus describes the linear relationship between dipole moments and voltage maps, but also (reciprocally) between imposed voltage differences and resulting current flow in the head. The latter can be visualized in 3D View when displaying the lead field.

Legendre
Adrien Marie Legendre (1752-1833). French mathematician, noted for his work on the theory of numbers, the theory of 'elliptical functions' and the method of 'least squares.'

Localization
Specification or determination of a location.

Lowpass
Allowing the passage of low-frequency information, but sufficiently attenuating frequencies above a certain threshold value.

Macro
A sequence of actions that are performed automatically.

Magnetoencephalogram (MEG)
As EEG, but the biomagnetic fields are recorded.

Magnetoencephalographic
Of, or relating to the use of magnetoencephalograms.

Meta
Indicates change, alteration, or alternation.

Meta-trial
A virtual trial which is computed from a collection of trials by averaging.

Montage
A recipe for placing sensors which normally also includes the referencing strategy. In CURRY, the sensor layout in arbitrary coordinates, together with landmarks in the same

coordinates and the measured data type. A montage plus the data themselves plus the anatomical locations of the landmarks completely define a measurement.

Multi-modal
A combination of several (measuring) modalities, e.g., EEG, MEG, and MR.

Nasion
A craniometric (of the study of skulls) point where the top of the nose meets the ridge of the forehead.

Neuro-
When preceding another word, indicates association with a nerve, or the nervous system.

Neurology
The study of the anatomy, physiology and diseases of the nervous system.

Neuroimaging
Producing images of neuronal activity.

Neuromag
MEG system manufacturer.

Neuromagnetic
Magnetic fields caused by neuronal activity.

Neuron
A cell specialized to conduct nerve impulses; consists of a cell body, axon (see 'Axon') and dendrites (see 'Dendrite').

Normal
A line perpendicular to another line (in 2D) or plane (in 3D).

Opening
Result of performing an erosion operation (see 'Erosion') followed by a dilation operation (see 'Dilation').

OptoTrak
A 3D localizer system or digitizer. By means of cameras, the location of a pencil in 3-space is determined.

Overcontiguous
Highly-contiguous, overlapping.

PAN
See PPN.

Parietal bone
Either of the two bones forming part of the roof and sides of the skull.

Pixel
Elementary, quadratical or at least rectangular picture element in a 2D image.

Polhemus
A 3D localizer system or digitizer. By means of magnetic fields, the location of a pencil in 3-space is determined.

Postscript
A page description language. Many hardcopy devices understand Postscript.

Polylines
Connected line segments.

PPN
Pre-auricular point- and nasion-based. PPN coordinate systems are defined by these landmarks.

Pre-auricular points
Points near the ear, identifiable by pressing a finger against one's cheek while moving the jaw.

PSP
Post-synaptic potential (see Synapse).

Realistic head model

A model of the head that is closer to reality than a spherical approximation. Realistic head models use at least some shape properties of the head.

Reference
The zero definition of a measurement. In EEG measurements, there can e.g., be single reference electrodes, a common average reference, and 'linked earlobe' references.

Reflectivity
A measure of the ability of a surface to reflect radiation, equal to the reflectance of a layer of material sufficiently thick for the reflectance not to depend on the thickness. Also, the quality or capability of being reflective.

Re-Referencing
Changing the reference, normally by means of re-computing the signals.

Sagittal
Straight, resembling an arrow. Of, or relating to the sagittal suture (see 'Sagittal suture'). Also, situated in a plane parallel to the sagittal suture (see 'Sagittal suture').

Sagittal suture
Serrated line on top of the top of the skull that marks the junction of the two parietal bones (see 'Parietal bone').

Seedpoint
The location from where an algorithm starts. Downhill fit algorithms and region growing algorithms are e.g., seedpoint-dependent.

Segmentation
The definition of a shape.

Spherical model
A model that comprises spheres.

Subsampling
Capturing a spatial or temporal signal by means of samples which are distributed less dense in space or time than the original signal.

SynAmps
Multi-channel amplifier used to measure EEG signals. SynAmps systems are distributed by Neuroscan.

Synapse
The point at which a nerve impulse is relayed from the terminal portion of an axon (see 'Axon') to the dendrites (see 'Dendrite') of an adjacent neuron (see 'Neuron').

Thresholded
Kept above or below a specified threshold, or between two threshold values.

Tomographical
Of, or related to 'tomography.'

Tomography
Any of a number of techniques used to obtain an image of a selected plane section or volume of the human body, or some other solid object.

Triangulation
Method to create triangles connecting given points in 2D or surface points in 3D (surface triangulation), or to create tetrahedra connecting points in 3D (3D triangulation).

Voxel
Elementary, cubical or at least rectangular picture element in a 3D image.

Wiener
Norbert Wiener (1894-1964). U.S. mathematician, who developed the concept of cybernetics.

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