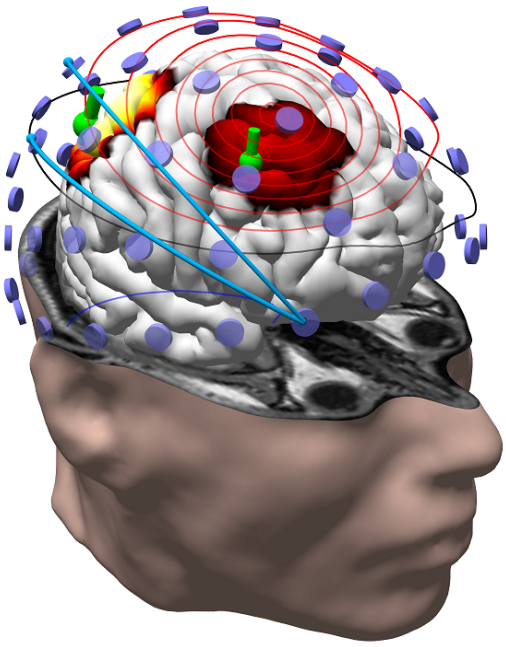

CURRY 8

Tutorials

Multi-modal neuroimaging

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CE 0413

Year of Manufacture: 2017

COMPUMEDICS NeuroScan™

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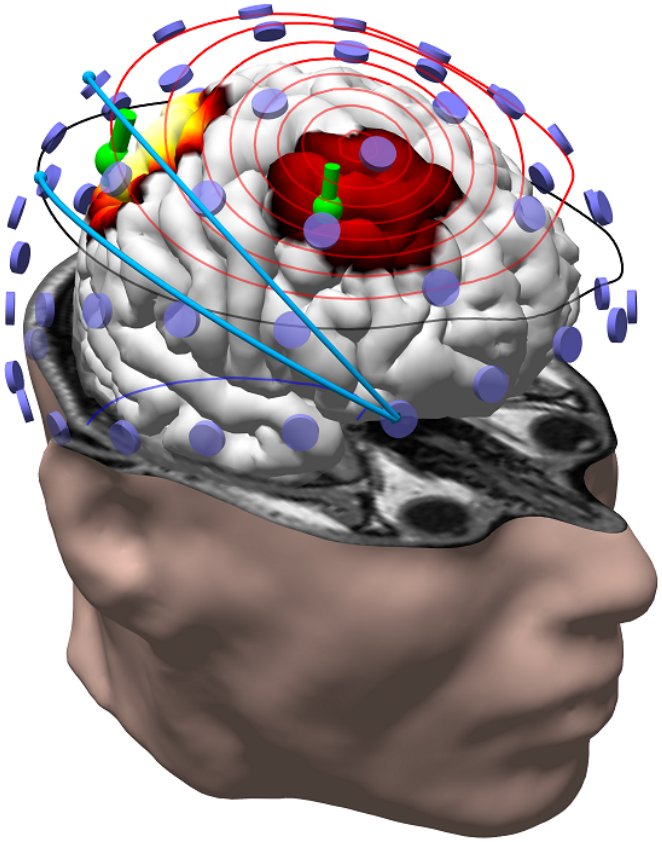
1 CURRY 8

CURRY 8

Tutorials

multi-modal neuroimaging



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Year of Manufacture: 2017

COMPUMEDICS NeuroScan™

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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**.

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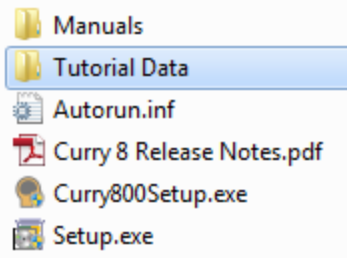
CURRY 8 Tutorials [6501C]
2017-7-7

2 CURRY 8 Tutorials

We have made a concerted effort to provide a variety of ways to help you become familiar with the extensive functionality that is contained within CURRY. The Tutorials below provide one method, and all users of CURRY - old and new alike - are encouraged to go through them. The Tutorials are organized largely in the order that you would use CURRY, assuming you have a complete license. That is, they start with configuring the program to acquire EEG data. They then go on through basic analysis of the EEG/MEG data. Image data applications are covered next, followed by source reconstruction examples.

If you have something other than a full license, you will not see or have access to all of the functionality that is described. Focus on those sections that are included with your license, and ignore sections that are not. (It is easy to upgrade to more inclusive licenses by purchasing them and then adding the license to your HASP dongle).

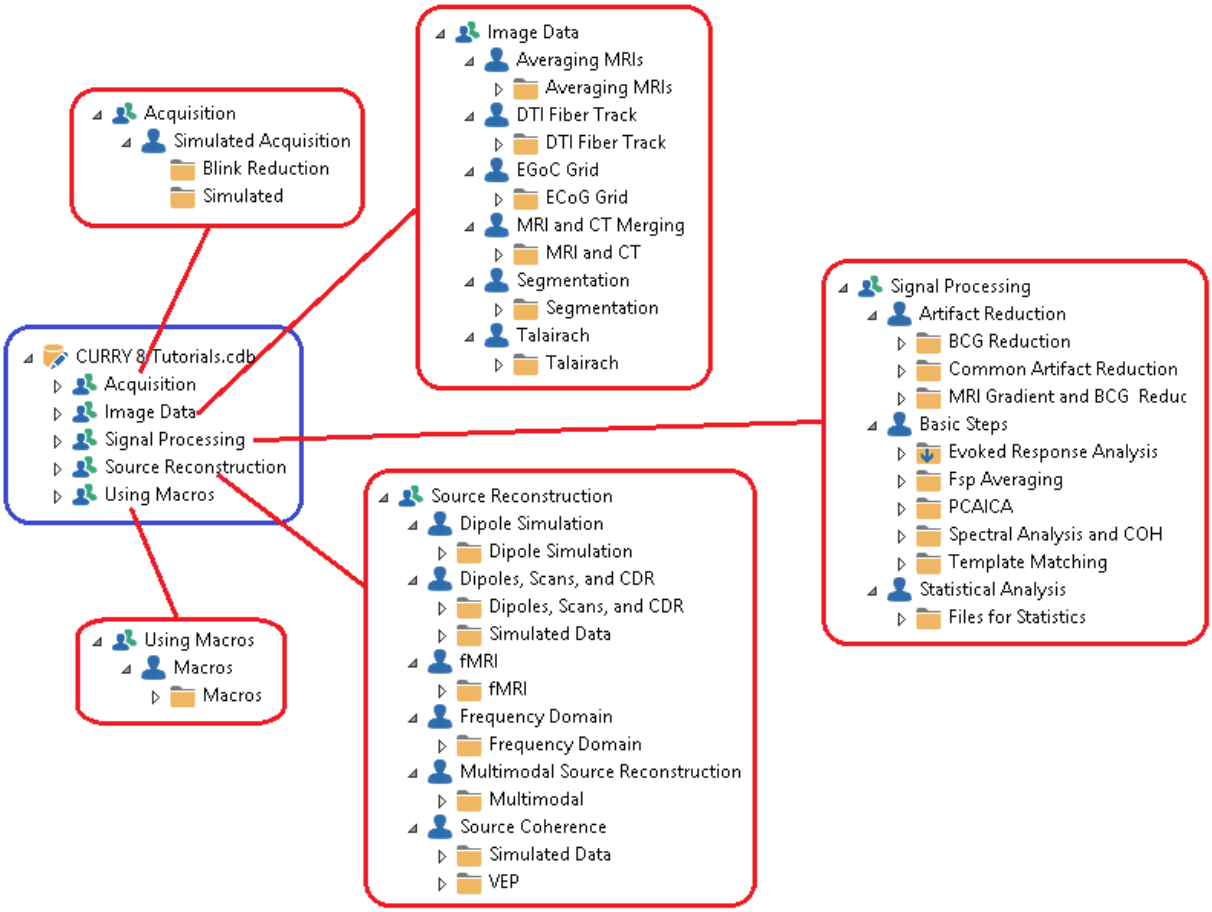
The Tutorial database and data files are included on your DVD/thumb drive with the CURRY installation. To install them, go to the *Tutorial Data* folder on the DVD/thumb drive, and run the CURRY8Tutorials.exe file, extracting the files to the default *C:* location.



Or, you may download the files by going to **Help** and select **Download Tutorial Data**. Run the .exe file, extracting the files to the default *C:* location.

The Database is called *CURRY 8 Tutorials.cdb*. If you open CURRY and find no Database has been loaded, go to **Database** → **Open** and select the *CURRY 8 Tutorials.cdb* file from the *C:\CURRY 8 Tutorials* folder. Shown collapsed, on the left, you can see that it is divided into the major functional modules of CURRY. The expanded view for each major module is shown. There is a Tutorial for each entry, and the files that are used are in the various Studies. The installation on the hard drive more or less mirrors the same hierarchical structure.

It is assumed you have some basic knowledge of CURRY. If you go through the tutorials more or less in order, you should pick up the basics that you will need later on. The later tutorials assume you know, for example, where most things in the user interface, or at least how to find them using the Workflow.



In addition to the Tutorials, we are compiling a library of Macros within CURRY to demonstrate various operations. These will be included with the installation, although more will be created in the future, and these will be found online.

Lastly, we provide live online assistance either via shorter targeted sessions using shared desktops and GoToMeeting, or more formal CURRY Schools that can be online or in person. Watch the web site for upcoming schools, or contact curry8help@neuroscan.com.

2.1 Conventions

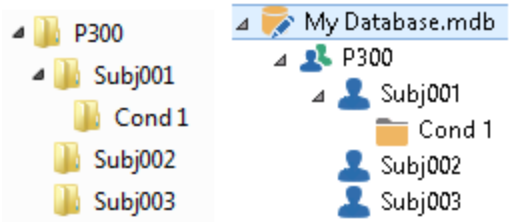
The following sections describe some of the more commonly used conventions in CURRY.

2.1.1 Substitutions for Paths

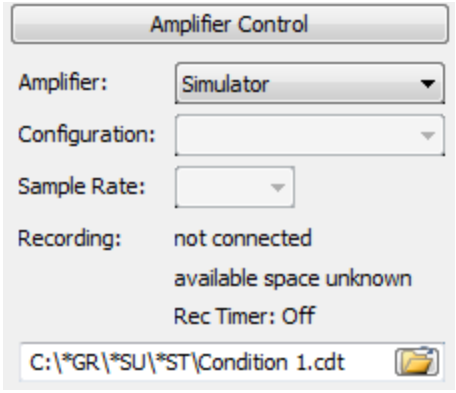
There are several places in CURRY where you have the option to save files using Substitutions for the paths and file names. These are included for your convenience - you can use different paths and file names as desired, or not at all. Examples of these include online data files being recorded, the Average Configuration dialogs (online and offline), and files created with Macros.

For example, let's say you are recording data files, and you have already created an organization scheme for where you want the files to be stored on your hard drive (left). Maybe you have a folder called "P300" for the experiment (Group) you are

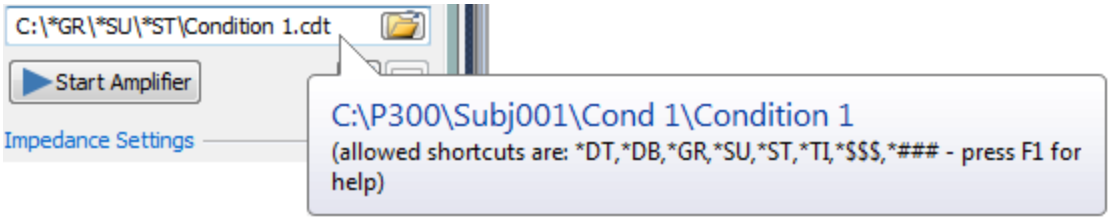
running, and below that are subject folders, such as "Subj001". For each subject, you have a subfolder called Cond 1. The file that you want to record for that subject is called *condition 1.cdt*. In CURRY, you create a Database that mirrors the hard drive organization (right). This is for convenience only (not a requirement).



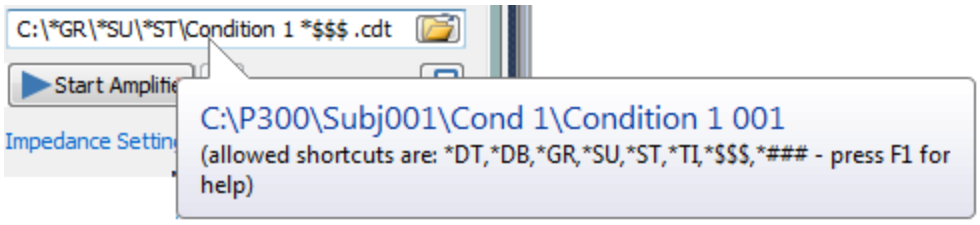
Now examine the Recording field below. After entering the drive, C:\, we have entered *GR for the Group name, *SU for the Subject name, and *ST for the Study name. *Condition 1.cdt* will be the file name.



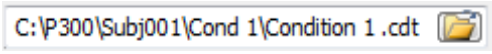
A Tooltip will assist you in using the substitutions. Positioning the mouse over the field, and clicking in the field displays the Tooltip. It shows the allowed shortcuts, as well as the current path, which in this case is *C:\P300\Subj001\Cond 1\Condition 1.cdt*. The recorded file will be placed in that folder with that file name.



If we are expecting multiple continuous files to be recorded in this session, we could add *Condition 1 *$$$.cdt*. The *$$$ adds a number starting with 001 (or whatever the next free number is) to the file name, and it will increment automatically from that point on with each file you save.



If you save the path/file name with the **Global Parameters** (or Study Parameters, in which case you will need to always use that file), you will not have to make any changes in this field.

Of course, you can use the Browse button to select the target folder and enter the file name manually, if preferred 

.

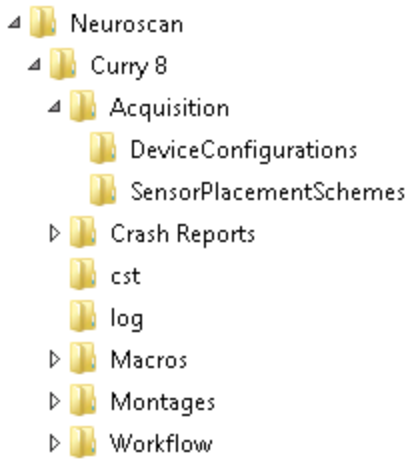
These options have particular value when you are using Macros in which multiple files are created and saved. If you want the macro to run all the way through, without any user input, you will need a way to automate the file names/path selections. See the *CURRY 8 User Guide*, *Macros* section, for details regarding substitutions. See also the **Macro Recorder** tutorial for similar information.

2.1.2 Target Folders for Windows 7 (and newer versions)

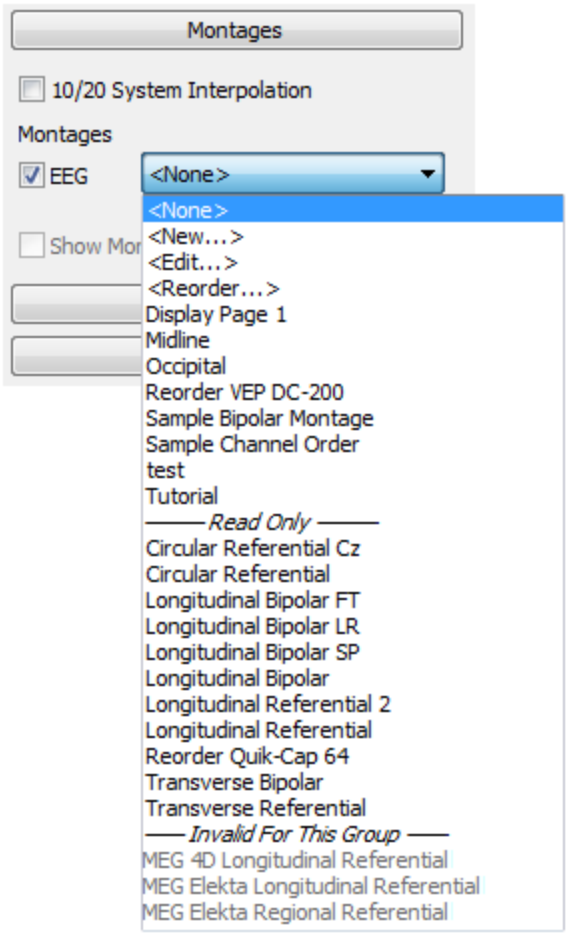
There are multiple places in the CURRY 8 where you may retrieve files supplied by Neuroscan, as well as similar files that you create. For example, there are Configuration Files for acquisition that we supply, and these can be modified and saved with a different name, or created from scratch. The files supplied by Neuroscan are installed into certain folders. Those that you save are stored, by necessity, into different folders (a Microsoft requirement).

The folder is: *C:\Users\<User Name>\AppData\Roaming\Neuroscan\Curry8\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, log, macro, and montage files have their own folders.



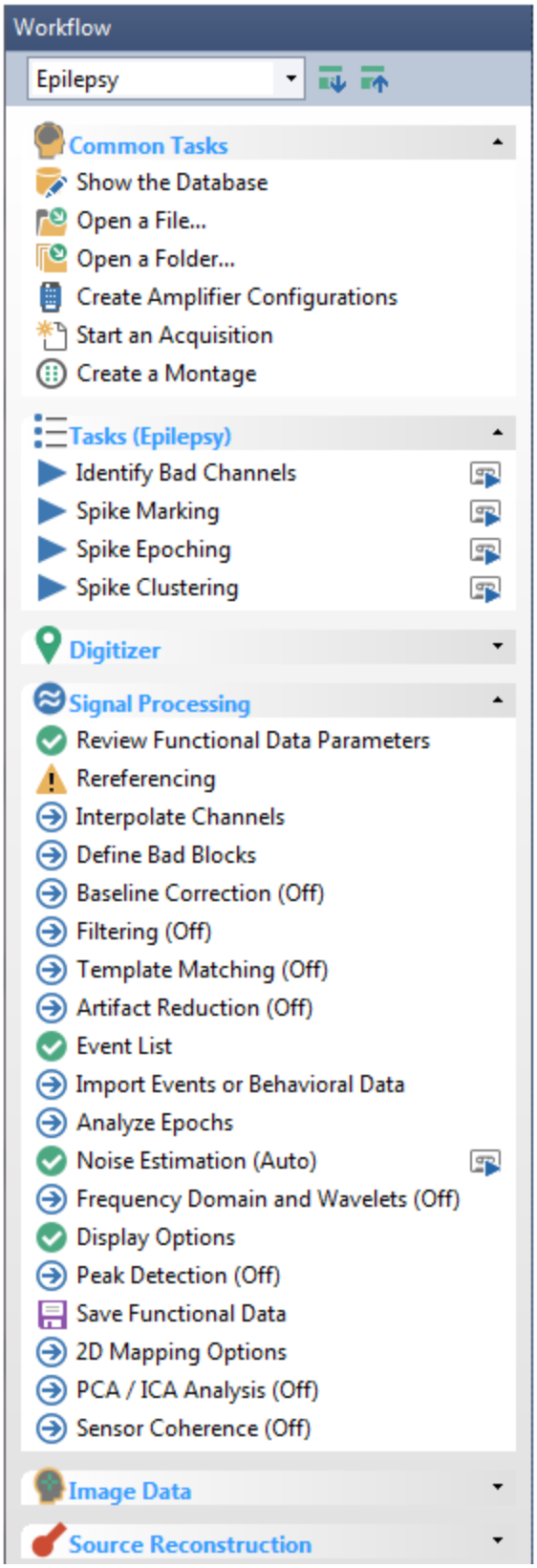
Wherever this distinction occurs, you will see a drop-down list that has files in three sections. Those above the *Read Only* line are ones you have saved. The ones we supply are *Read Only* files. You can modify them, but not overwrite them. Save them with a different file name. They will be saved to 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). Click the **<Open Install File Location>** line to go directly to this folder.



2.1.3 Workflow

The concept of the Workflow was added to CURRY primarily as an aid in familiarization to the program. You can do everything in CURRY without ever using the Workflow, but in the beginning it is helpful to have something that takes you immediately to the part of the program that lets you do what you want. In some cases, you will be taken to different parameter panels and displays. In others, you may see a brief macro that will provide helpful information. The button means that there is a macro to play.

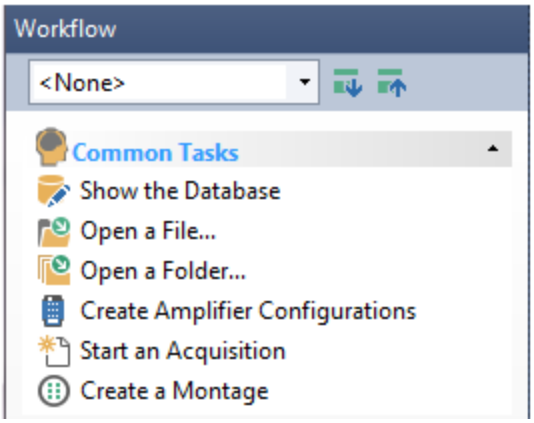
You will see different sections and items in the Workflow depending on what state the program is in (Acquisition or Analysis), what license(s) you have, and what steps have already been completed. You may expand or contract the sections, as desired.


Workflow
Epilepsy
Common Tasks
Show the Database
Open a File...
Open a Folder...
Create Amplifier Configurations
Start an Acquisition
Create a Montage
Tasks (Epilepsy)
Identify Bad Channels
Spike Marking
Spike Epoching
Spike Clustering
Digitizer
Signal Processing
Review Functional Data Parameters
Rereferencing
Interpolate Channels
Define Bad Blocks
Baseline Correction (Off)
Filtering (Off)
Template Matching (Off)
Artifact Reduction (Off)
Event List
Import Events or Behavioral Data
Analyze Epochs
Noise Estimation (Auto)
Frequency Domain and Wavelets (Off)
Display Options
Peak Detection (Off)
Save Functional Data
2D Mapping Options
PCA / ICA Analysis (Off)
Sensor Coherence (Off)
Image Data
Source Reconstruction

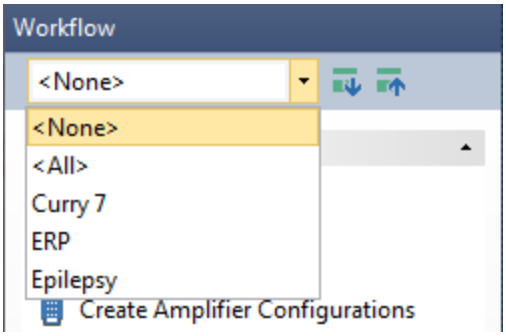
1. You can access the Workflow at any time by clicking the **Workflow** tab in the lower left part of the CURRY 8 display

.

2. When you first open CURRY 8 and display the Workflow, you will see the following options. Basically, the program is asking you, what do you want to do? The symbols before each option let you know there is an icon on the Toolbar that will provide the same functionality.

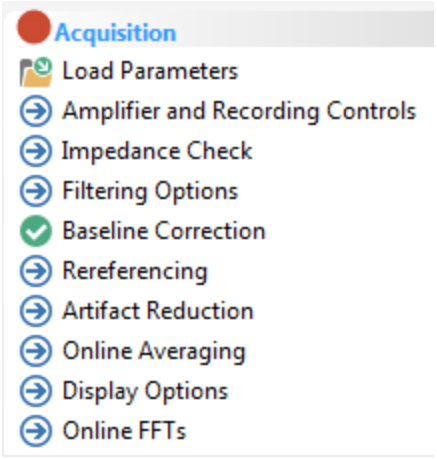


The field at the very top allows you to select a **Scope**. **Scope** modes contain preset parameters for common uses of CURRY, as shown. If you select one of the Scope options, those parameters will be entered in various parts of CURRY, such as, the epoch intervals. You can always change them, if needed, and then save the changes as new Scope Parameters or as Study Parameters.

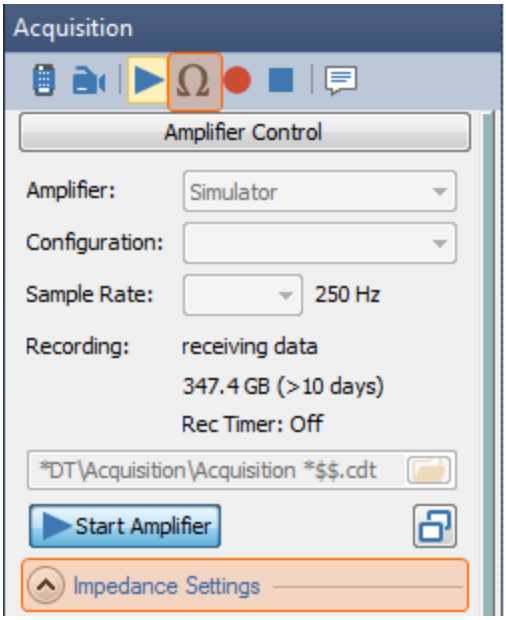


The **Common Tasks** items are self-explanatory. Click on one to go to that part of the program.

3. Once you connect to your amplifier, or begin to replay a file in the Simulator, you will see additional acquisition options.



If, for example, you want to perform an **Impedance Check**, click that line, and the program will take you to the proper panel and flash the Impedance button.

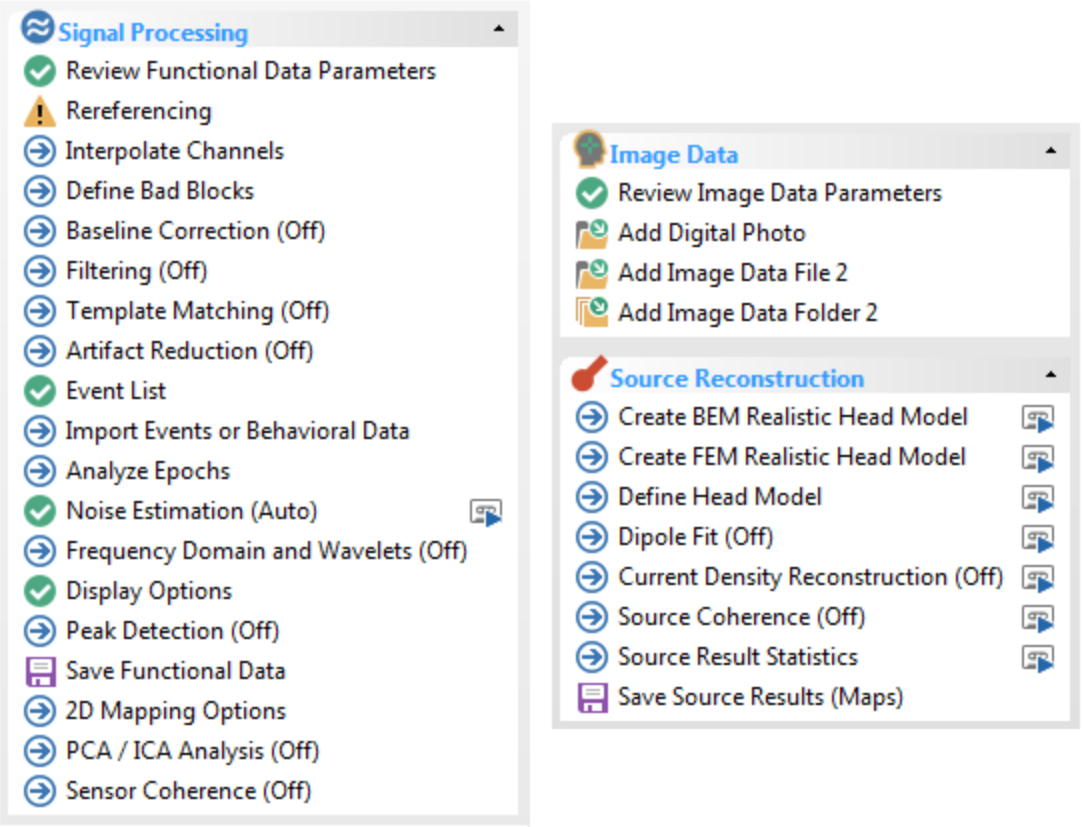


If you want to perform **Artifact Reduction**, clicking that line will display the **Artifact Reduction** panel, and so on.

While many of these are options are the same as are contained in the Acquisition parameter panels, there may be times where you have on panel open, then wish, for example, to re-reference the data display, and not recall where that option was. Clicking the Workflow line takes you there immediately.

Note that some items are preceded by a and others have a . The blue arrow means that this parameter has not been changed. The green check mark means that the option has been changed, but can be reviewed. The information in parentheses (when present) tells you the current setting, status, count, etc. for the particular item. The button means that there is a macro to play for more information.

4. If you are analyzing the data offline, you will see more items in the list. Again, some take you to a parameter panel, some take you directly to the specific option, and others may only play a macro that contains more information. There are workflow sections for Signal Processing, Image Data, and Source Reconstruction. Again, the content will change depending on what steps you have completed (and what licenses you have).



Note that there are several "Save" options. There is occasional redundancy in the CURRY program. There can be three or four different ways to do the same thing. Some of the more frequently used "Save" options are included in the Workflow to make them easier to find. They have the same function as other Save options. For example, **Save Functional Data** is the same as **File** → **Functional Data** → **Save Data**, and **Functional Data** → **Save** → **Save Data**, and from the **Results** list, **Functional Data** → (*right click*) **Save As**.

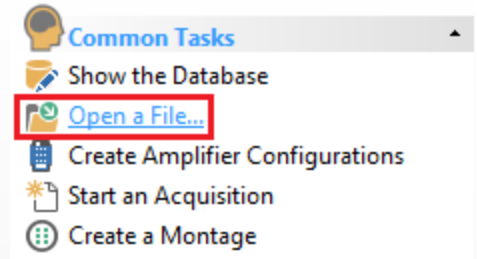
2.1.4 Database

A Database defines the files that you will be using, and places them in a hierarchical structure. The Database does not actually contain the files, rather, it points to the files that will be used. If you will be recording data from multiple subjects in a research study, and you wish to impose an organization on the files you will be using, you would then use a Database. If during the course of your analysis you create additional files, such as averaged data files, configuration files, parameter files, source reconstruction files, etc., it will be easier to keep them organized if you use a Database.

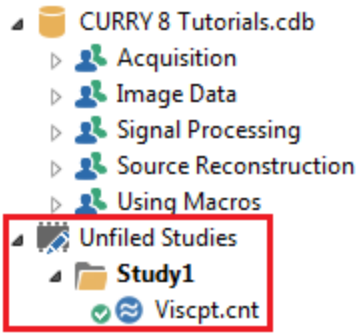
Prior to CURRY 8, CURRY used *.mdb Database files (MS Access), and CURRY 8 will still read those files. However, the preferred file type in CURRY 8 is .cdb (SQLite).

If you are not using a Database, you may still access acquisition and analysis from within CURRY.

1. You can open a file from the **Workflow**, or select **File** → **Open** and then select a data file (see the *Files of Type* field for options), or click the **Open** icon .



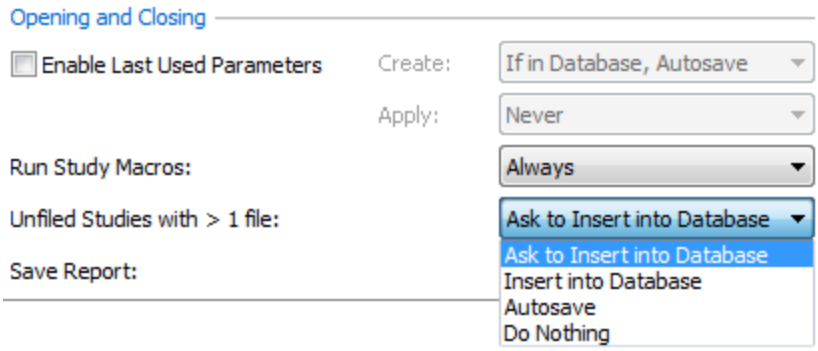
If the file has not been opened before (or if there is missing information, such as sensor positions), the **Functional Data Import Wizard** will be seen (see the **Functional Data Import Wizard** tutorial). After completing the steps in the Wizard, the file will appear. If you are simply opening a file, an *Unfiled study* is seen at the bottom of the Database with that file name in it. (Some MEG data files are "complete", and you will not see the Wizard at all).



2. After performing the desired operations and closing the Study, the Unfiled Study will be removed.

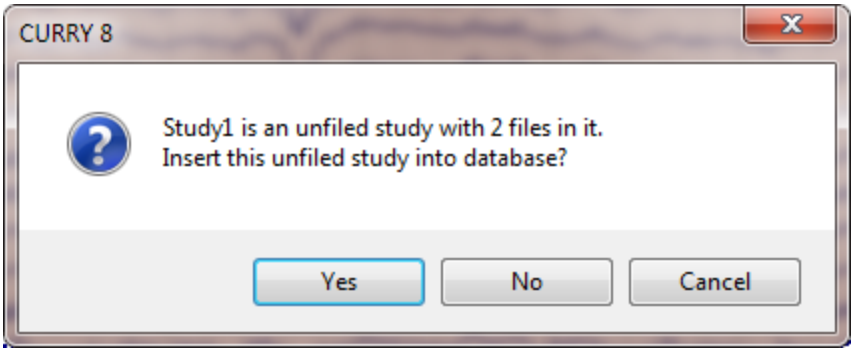
3. If you want to keep an Unfiled Study, you may drag the Study (drag **"Study1"** in the figure above) to an existing Subject in whatever Database you have open and drop it there. You may also use **File** → **Save Study As...** to save the study apart from a Database (.cst files). You can then open the Study later using **File** → **Open** with *Files of Type* set to *CURRY 8 Studies*). The Study will be opened again as an Unfiled Study (which can then be added to a Database by dragging and dropping to a Subject).

4. You can set the program to treat Unfiled Studies in different ways when you close CURRY. These options are found under **Edit** → **Options** → **Settings**, in the **Opening and Closing** section.

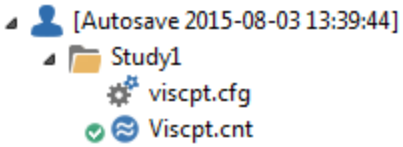


Unfiled Studies with > 1 file. The rationale here is that if you are just opening a data file for some fairly simple purpose, there will likely be no additional files created, such as, study parameter files. In that case, the program will simply close. If you have added one or more additional files to the Unfiled Study, there is a greater chance that you will want to save these. Therefore, you can set the program to do different things if there is more than one file in the Unfiled Study.

Ask to Insert into Database. You will be asked if you want to insert the Unfiled Study into the currently open Database.



If you say **Yes**, you will see the Study saved under a new Subject, with the data and time that it was saved.



Insert into Database. The Unfiled Study will be inserted into the Database automatically under an Autosaved Subject, as shown above.

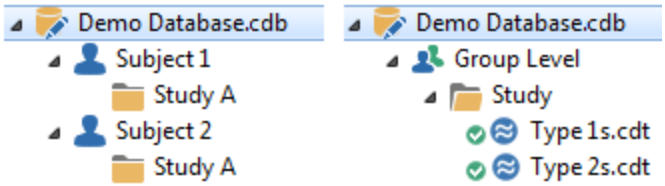
Autosave. The Unfiled Study will be saved automatically (as a .cst file).

Do Nothing. The program will close without saving the Unfiled Study.

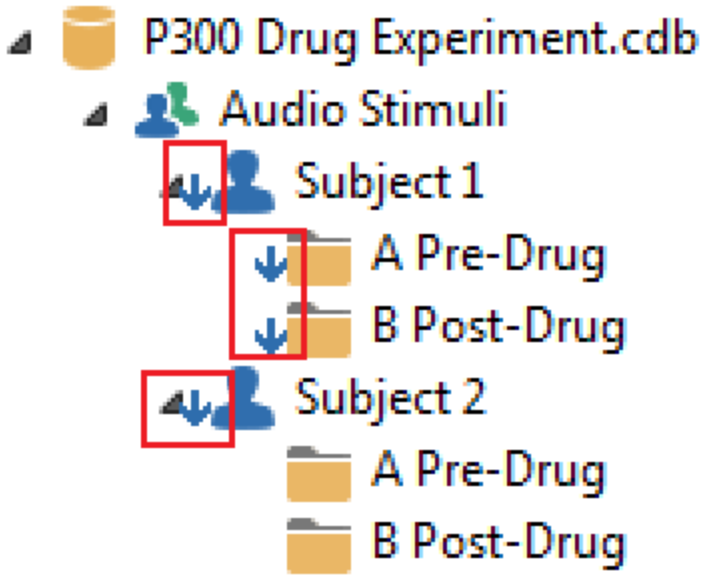
Using Databases

The easiest way to approach the idea of the Database is to realize that it has a familiar hierarchical structure, similar to that seen in Windows Explorer. There are folders with subfolders with more subfolders. The intended use is for the Database to be comprised of one or more Groups (or none). Each Group can contain one or more Subjects (or none). Each Subject can have one or more Studies (or none). The data files are listed in the Study folder(s). Files that are created in the analysis process (such as averaged EP files) are often placed in "Derived Study" folders, which are just subfolders.

If that does not fit your particular needs, you can organize the Database in other ways, such as, you can omit the "Groups", or omit "Groups" and "Subjects", etc. (Group, Subject, Study, and Derived Study folders can all be renamed as desired using *F2*).



You may notice that sometimes there are down arrows that are part of the Subject and/or Study symbols (Study shown below). The arrow indicates that **Inherit Parent Parameters** has been enabled (accessed by *right clicking* on the Subject or Study). When enabled, it means that the parameter file in the parent folder will be applied to the child folder(s). See the **Using Parameter Files** tutorial for more information. By default, the Inherit Parent Parameters option is enabled for Subjects and disabled for Studies.

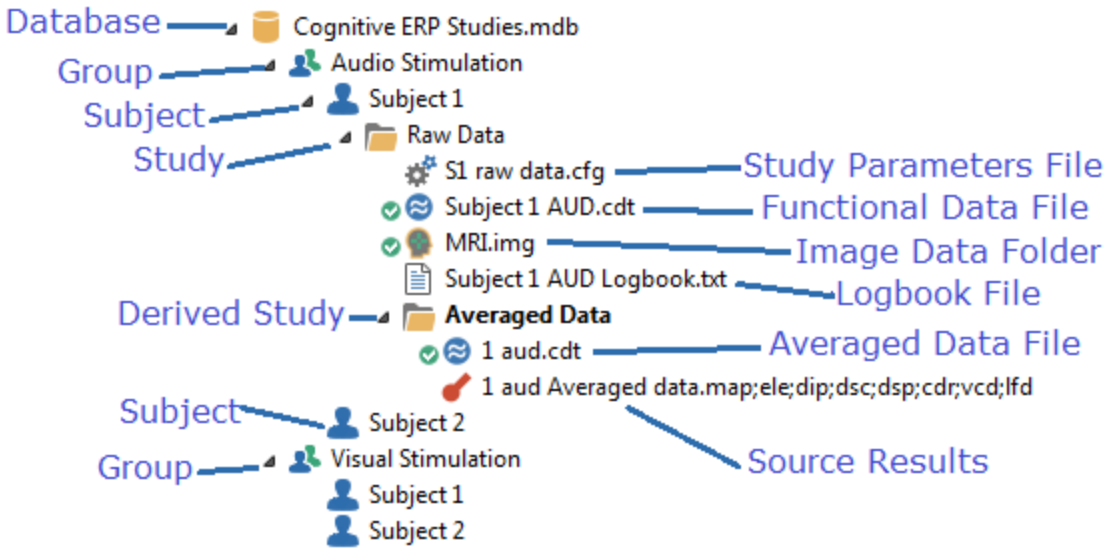


Database

It is a good idea to give some thought to the Database structure before starting to collect data for a particular project. Say, for example, that you were going to conduct a research study in which you will record basic auditory and visual P300 sessions. To

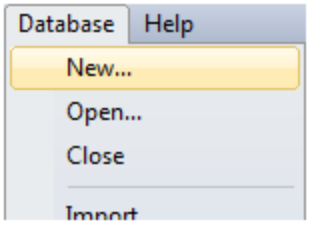
make it interesting, let's say you are recording P300s in pre-drug and post-drug conditions. You have the MRI data for each subject.

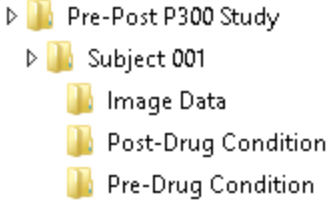
The basic Database could be organized as follows. The overall Database was created. One experiment is for auditory stimulation, the second is for visual stimulation. There are multiple subjects for each. Each subject has a folder (Study) for the raw data and the averaged data. The functional, imaging, configuration, etc. files have been inserted.



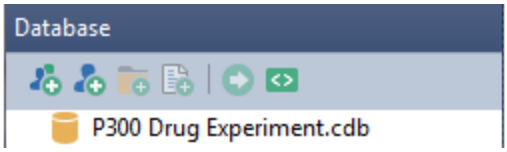
Creating a Database is a simple process:

1. After opening CURRY, go to **Database** → **New**. In the Create New Database dialog, you may select or create a folder, and a file name (*P300 Drug Experiment.cdb*) to save the Database. Typically, this will be a dedicated folder that will also contain the data files, organized in subfolders (figure on the right is from Windows Explorer).



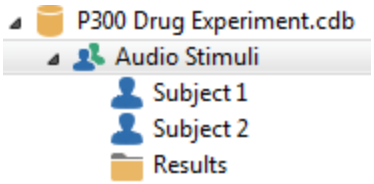


2. The Database will then be seen in CURRY. The first two icons will then become active.

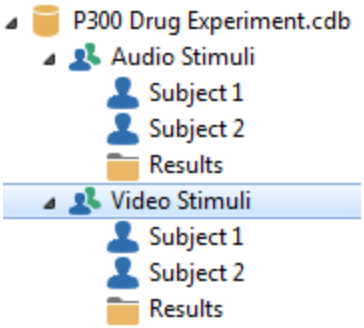


3. There is no inherent correct or incorrect way to organize the Database. Organize it in whatever way best fits your design. For example, you do not need to have any Groups at all. These options are included to facilitate the structure, when needed. In this example, we will create separate Groups for the Audio and Visual sessions. *Right click* on the Database and select **Add New Group**, or click the **Add Group** button . The "New Group" will be seen, and you can rename it as desired (*Audio Stimuli*). You can rename the Groups, Subject and Studies at any time by highlighting one and pressing the *F2* key on the keyboard, or by *right-clicking* on the entry and selecting **Rename**.

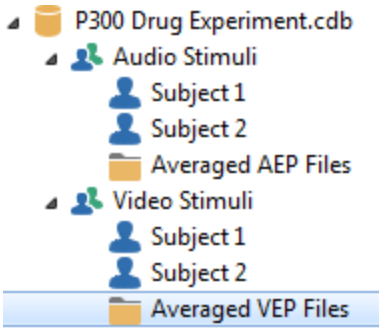
Note that two Subjects and a Results study have been created automatically. CURRY is anticipating that you may want more than one Subject. The results folder has been created directly under the Group, anticipating that you may want to have a separate folder where you can save, for example, all of the averaged data files you will create. These all need to be in a single folder when you go on to create a grand average of all averages files.



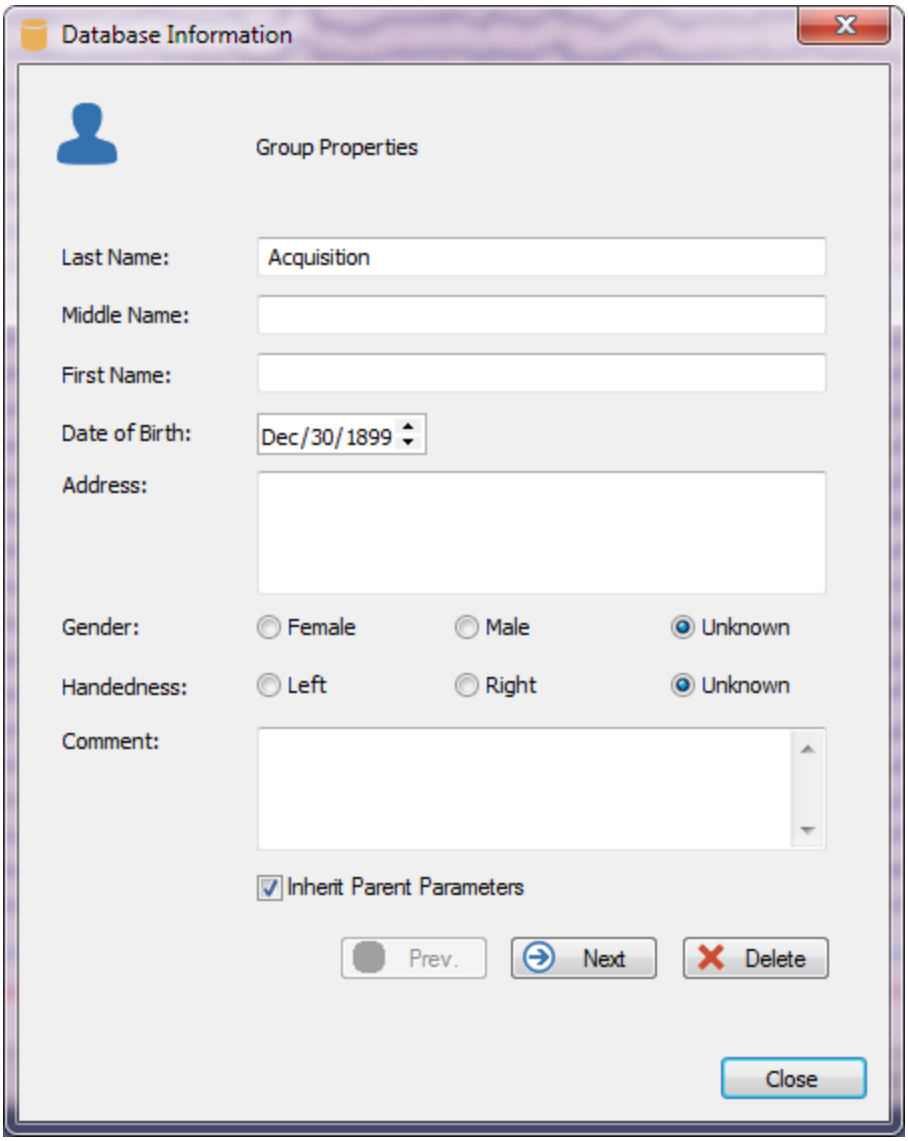
Repeat the process to add the second Group (*Video Stimuli*). (You may also use **Database → Add New Group**).



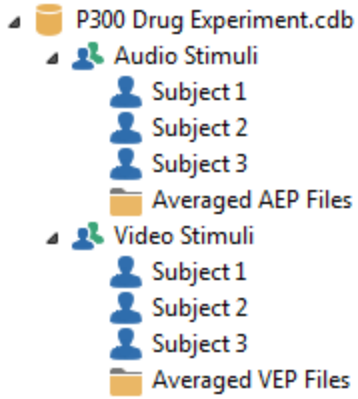
Relabel the Results folders so they will be meaningful later on. Click on the first one to highlight it, and press the *F2* key on your keyboard (or *right click* on the Study and select **Rename**).



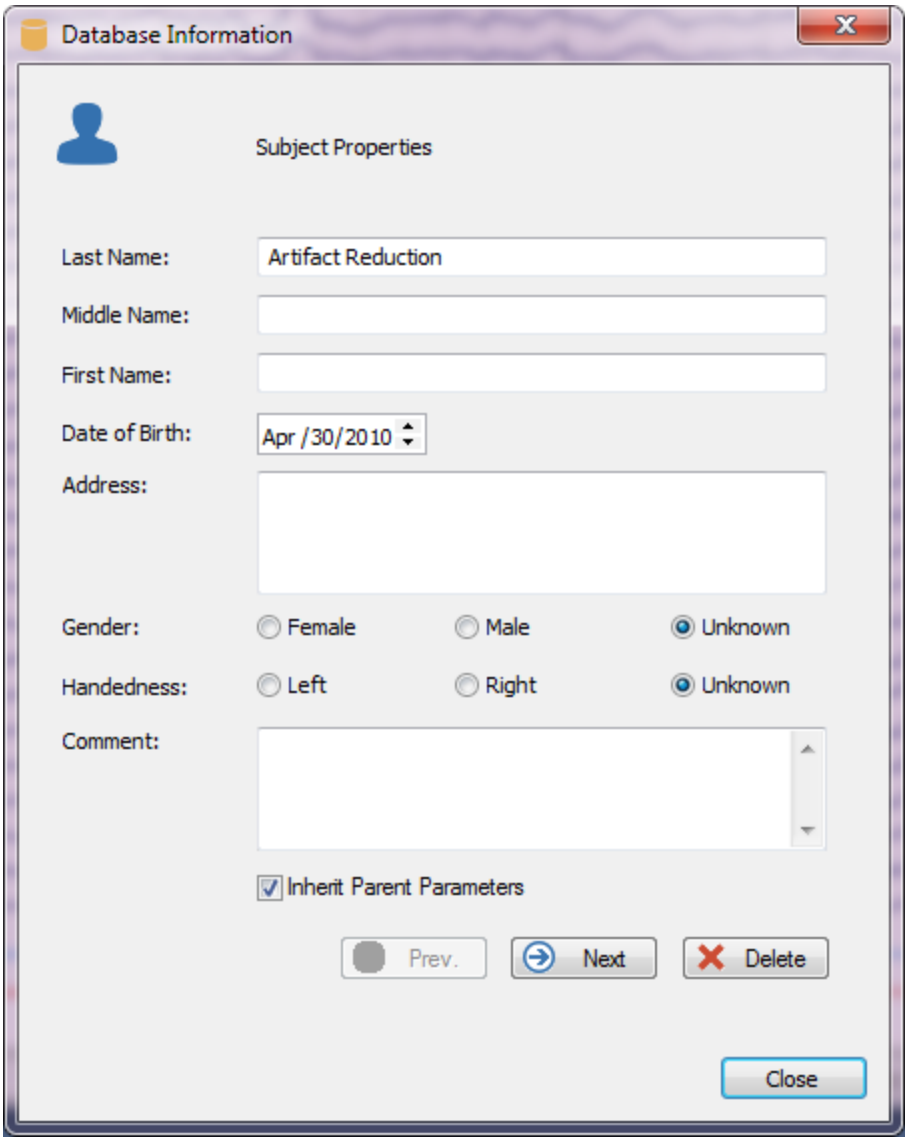
Another option you can include is to *right click* on the Group (or any entry) and select **Properties**. Use the fields in any way desired to help keep track of the procedures you were using, the subject characteristics, and so forth.



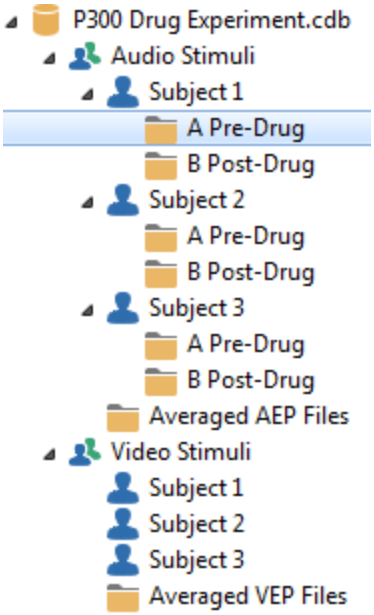
4. Next, we will add an additional **Subject** to each Group. You do not need to add folders for all of them at the beginning - this is just to demonstrate how it is done. Each Group may contain one or more **Subjects**. To add a Subject, highlight the desired Group and click on the **Add Subject** icon on the Database Toolbar, or *right click* on the **Group** and select **Add New Subject**. You will have the opportunity to rename the Subject at that point. Delete the "New Study" lines that are created automatically.



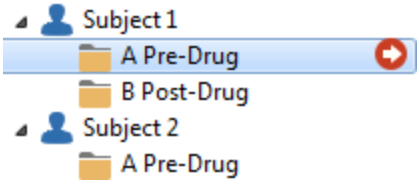
If you *right click* on the Subject and select **Properties**, you will see the following window in which you may enter additional information about a particular Subject, if desired.



5. Next we will add **Studies** to the **Subjects**. (CURRY was closed and reopened to show the final order). In this design, each Study will have a Pre-Drug and Post-Drug Study. *Right click* on the Subject and select **Add New Study**, or highlight the Subject and click the **Add Study** button . You will have the opportunity to change the Study name. Since the studies are listed alphabetically, and we want the pre to come before the post, we'll add an A and a B to the Study names. Repeat for all Subjects. Note that you may drag and drop the Studies, copying them from one place to another.

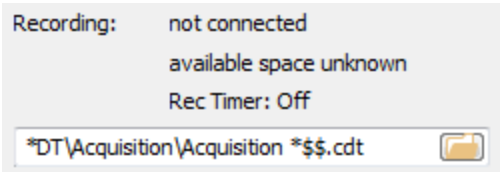


6. Now, if we were going to acquire data, the next step would be to highlight the Pre-Drug Study and click the **Start Acquisition** icon that appears to the right of the study , or *right-click* on the Study and select **Open**, or just *double-click* on the Study. Any of the methods will access acquisition.



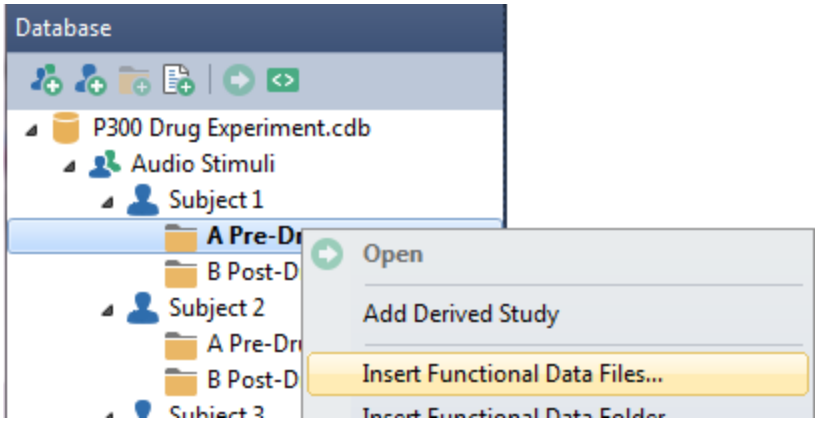
The acquisition part of CURRY will open. This would be a good time to select the folder where you wish to store the EEG data you will be acquiring (in the Recording section of the

panel). This is where the data file will be stored on your hard drive. In the Database, it will appear in the Study you have open. You can use the wildcard substitutions for saving the file (see the **Substitutions for Paths** tutorial), or the browse button, or a combination of both.



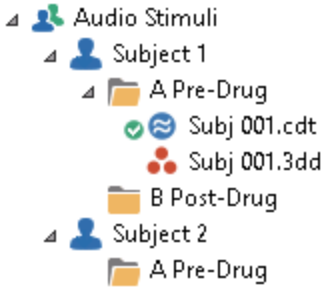
7. If you already have the data recorded and just wish to load the file into the Database, you can *right-click* on the Study and select **Insert Functional Data Files**. Use can also use the **Insert File** icon from the Database Toolbar. The file will be inserted into the selected Study. You can also open Windows Explorer, locate the data file(s) there, and drag and drop them into the desired Study. Use

the standard *Ctrl+click* and *Shift+click* to select multiple data files to drag and drop.



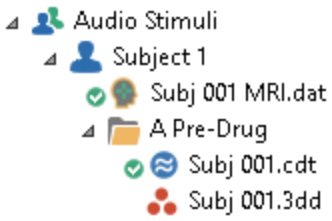
If you are loading the data for the first time, you will need to import the file(s) via the *Functional Data Parameters Wizard*, which will be described in a later Tutorial.

8. For this example, we have included the sensor position file (*Subj 001.3dd*). This is a file that was created (in SCAN) using the Fastrak Digitizer, which contains the XYZ coordinates of the electrodes, as well as the coordinates for physical landmarks on the subject's head. They are loaded similarly to functional data files. *Right click* on the Study and select **Insert Digitizer File**. You may also select the digitizer file from within the Functional Data Import Wizard.

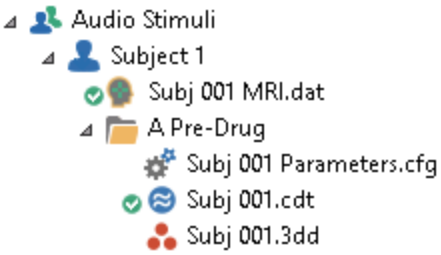


9. If you have image data (MRI, CT, etc.), you may load it in the same way. The data (either a single file with all of the slices, or a folder containing individual files for individual slices) will be entered. In this case, since we will be using the same MRI for both Studies, we can load it at the Subject level (or in each Study - both will work). If you are loading the image data for the first time, you will need to import the file(s) via the **Image Data Parameters** windows, which will be described in a later Tutorial.

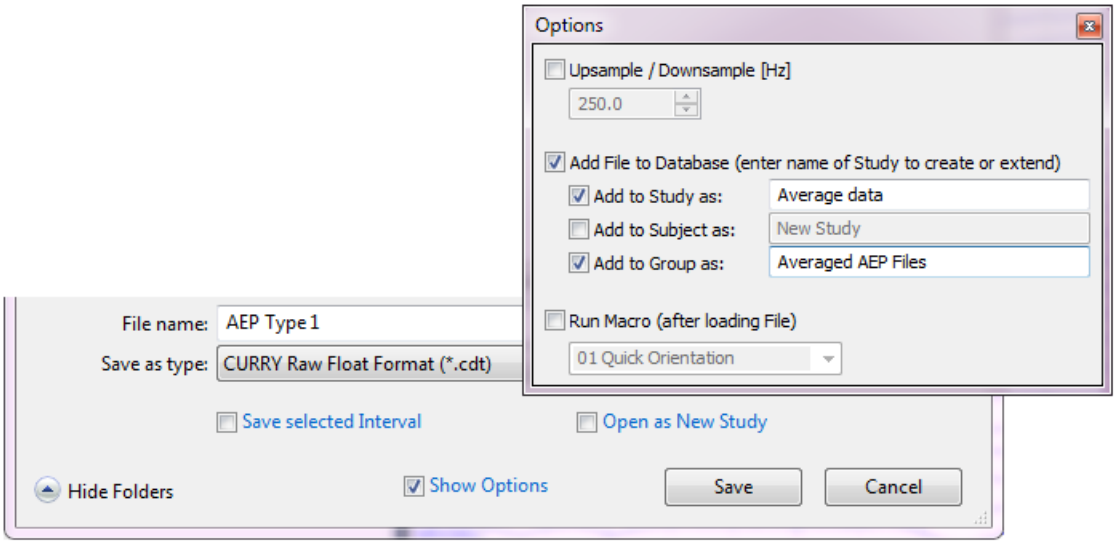
In the example below, we have loaded the Pre-Drug EEG file, the single .3dd file, and the MRI data file (loaded at the Subject level).



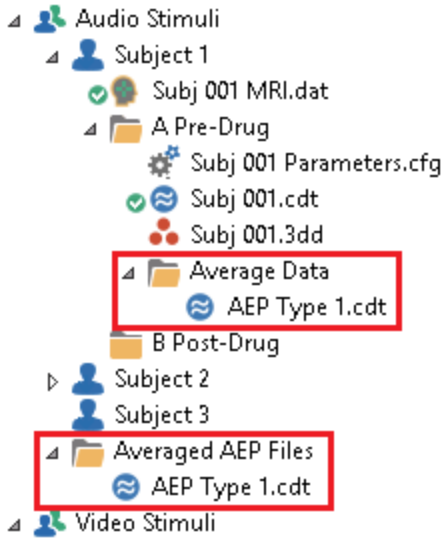
10. You can continue the same structure using multiple Subjects, all within the same Database. You will likely have saved the **Study Parameters**, and these will be seen as .cfg files in the current Study.



11. When you process the data files, you will in most cases have results files, such as, averaged evoked response data. When you save the new data file (**Functional Data → Save → Save Data**), you will see multiple options on the Save As screen. Specifically, there are options to save the average file to the Database (click **Show Options**). In this case, we are creating a new Derived study (sub-folder) called Average Data. This will be placed below the currently Open study. Also, since we will eventually want to create grand averages of all like data files (these must all be in the same Study), we will also add the file at the Group level, using the folder that was created when we first added the Group, and relabeled Averaged AEP Files.



The Database now appears as shown below. The same file now appears in two places. This saves the step of having to move the file manually to a folder containing all files to be averaged for the grand average.



Recall that the data files themselves are not contained in the Database. The entries in the Database merely point to the files on the hard drive. Therefore, if you make changes to the averaged data file, and resave it to the hard drive, you do not need to do anything else at any level in the Database (unless you change the file name).

Using Multiple Files in the Same Study
If you insert multiple continuous data files in the same study, the study will open with the files concatenated automatically. The files must be comparable, such as, they must have the same number of channels, the same labels, the same sampling rate, etc. CURRY will treat the concatenated files as if they were a single continuous data file.

Averaged data files are frequently inserted into a single Study, as that is the procedure for creating an average of the averaged files. The files must all have the same number of channels, the same labels, the same start and ending latencies, and the same sampling rate. When the Study is opened, the individual files will be seen as a sequence of epochs. Operations that you apply, such as rereferencing, filtering, channel interpolation, peak detection, the Timerange you select, etc., will be applied to all of the average files (epochs).

This concludes the Tutorial describing the general use of the Database.

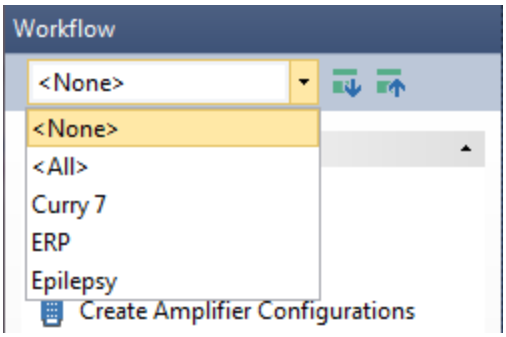
2.1.5 Using Parameter Files

If you find yourself frequently entering the same parameter settings over and over in the course of data acquisition or analysis, you can simplify the steps by using the various types of Parameter files. (Another option is to use macros, see **Macro Recorder**).

To make the best use of the options in CURRY, you need to understand the various types of parameter files and how they are used. CURRY uses a different approach from our SCAN software, one that has been used in the CURRY program for many years. Instead of thinking about serial steps that are performed to analyze the data, think instead of a constellation of parameters, that is, all of the parameter settings that are contained in the body of the program. *Changes to the parameter settings are applied instantly* in many cases. You do not have to create separate files along the way. If you have averaged data (such as EPs or averaged epileptic spikes), and you are doing source reconstruction, any changes you make to the data files - the Timerange you are analyzing, the type of dipole analyses, and so forth - are reflected immediately source results. At various points you may take a snapshot, so to speak, of all of the current parameter settings (the **Study Parameters**) and save them with the Study you are working with (or recording). When you open that Study again, the parameters are applied, and you are then back where you were when the Study was last closed (with certain exceptions). You can take the Study Parameters used with one data file, and apply them to other like data files, thus reducing the duplication of effort. The result is a much faster and more efficient way to configure acquisition and perform the analyses.

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 always use, you can save these as Global Parameters and they will be applied to all data files when you open the Study. Global Parameters contain only a relatively small subset of all possible parameters. If you find you cannot save some settings as Global Parameters, use Study Parameters instead.

Scope Parameters. At the top of the **Workflow** are the Scope Parameters you may select. Scope parameters are simply those preset parameters that are used most often with ERP Analysis, Epilepsy evaluations, or Source Analysis. The Curry 7 option uses the Curry 7 defaults values. When you select one of these, those parameters will be inserted at the various places in CURRY. These are simple conveniences to save you time. If you find that you need to modify the Scope Parameters, then set the parameters the way you want them and save them as Study Parameters. Study Parameters supersede Scope Parameters.

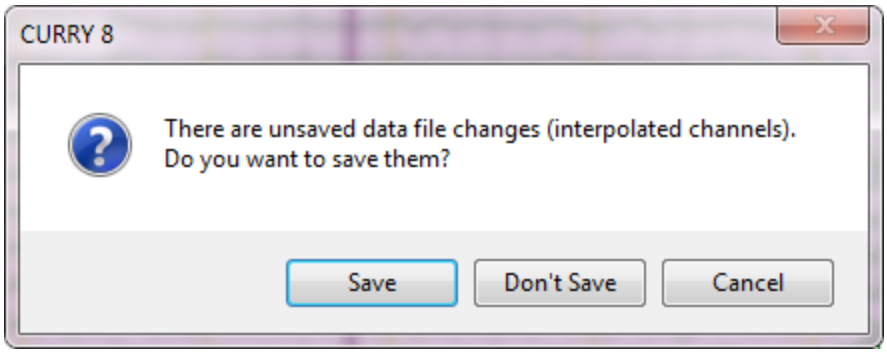


Study Parameters can be applied to the particular Study, or, if placed in a higher level, they can be applied to files in all or selected lower Studies. The Study Parameters file contains those changes that have been made to the Global Parameters or to the Scope Parameters. When you start CURRY, the Global Parameters are read first, then the Scope Parameters if any were selected, and then the Study Parameters. The Study Parameters therefore take precedence over the Scope and Global ones.

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, then Study Parameters in descending order. 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 Parameters are applied.

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**, where you can enable their use (with options), or not. A "Last Used" .cfg file is created, similar to the Study Parameters.

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.

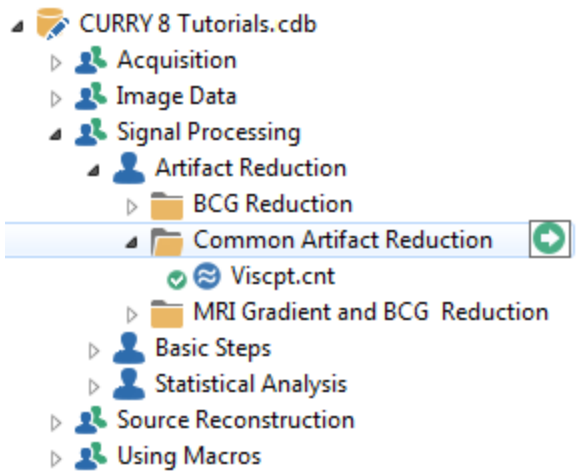


If you save the changes, they will be applied automatically when you reopen the Study.

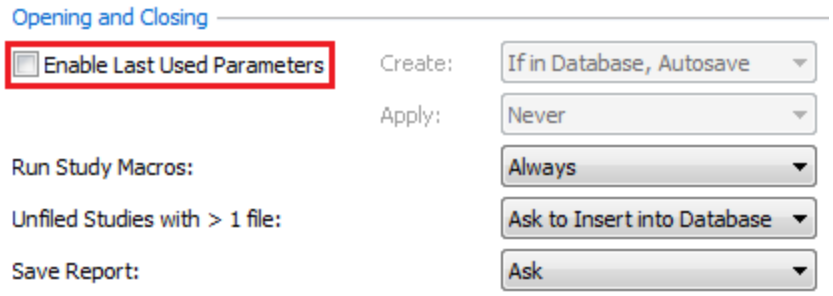
Inherit Parent Parameters. With Subjects and Studies, you have the option to inherit the parameter file from the parent folder, if it exists. For example, you may have a Subject folder that has multiple Studies below it. Instead of placing parameter files in each Study, you can place one parameter file in the Subject folder, and designate some or all Studies to inherit the parameter settings. Similarly, you can place a parameter file at the Group level, and apply it to all or only selected Subjects and Studies below it. The option is accessed by *right-clicking* on the Subject or Study and selecting/deselecting **Inherit Parent Parameters**. The default setting for Subjects is to have the option enabled; for Studies the default setting is off.

This tutorial uses the Study shown below to illustrate parameters. If you have already a .cfg file for this Study, *right click* on it and select **Remove File from Study**. *This does not delete the file from the hard drive*; it only removes it from the Study in the Database. If you do not see the *CURRY 8 Tutorials* Database, go to **Database → Open** and select the file from the *C:\CURRY 8 Tutorials* folder. If you do not see that

folder, you will need to download the tutorial Database and files from **Help → Download Tutorial Data**.

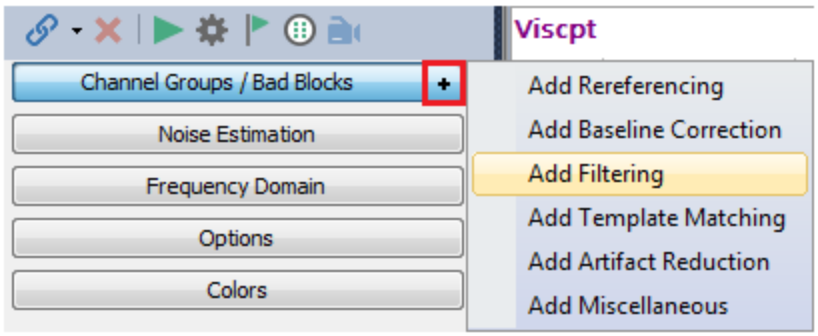


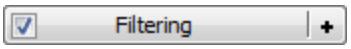
Go to **Edit → Options → Settings** and make sure that **Enable Last Used Parameters** is disabled.



1. Open the Study. The parameters that you see - the color, the number of channels displayed, and so forth - are all dictated by the **Global Parameters**, and they will be the same for every file you open (unless superseded by other parameter files).

Click the **+** sign at the end of the **Channel Groups / Bad Blocks** title bar, and select **Add Filtering**.



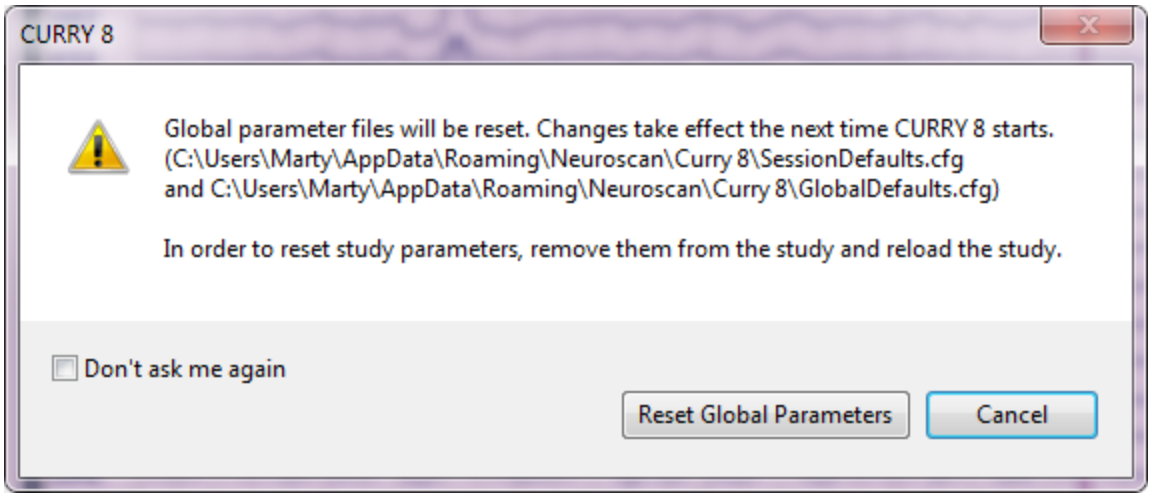
In the  panel, select **User Defined (Auto)** for the **Filter Type**, and set the **Low Pass** filter to **10 Hz** (to see the filtering effect easily).

Click the button on the Toolbar to invert the polarity (position the mouse in the upper left area to see the Toolbar). A Tooltip will give a brief description.

2. If you want *all data files* to appear with these filter parameters, and with the inverted polarity, click **File → Parameters → Save Global Parameters** (click it). You will see a confirmation message. Click **Save Global Parameters**. (if you have already saved Global Parameters that you wish to retain, skip this step).

Close and reopen the Study. The data appear as when the Study was closed. Any other file you open will have the same filtering and polarity setting.

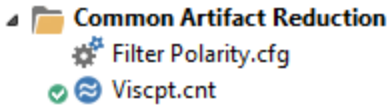
3. Now click **File → Parameters → Reset Global Parameters**. This restores the default parameters. Click **Reset Global Parameters** to the message.



Close the Study, exit CURRY, and restart CURRY. Now you see a different Database (*CURRY 8 Examples.cdb*), which is the default one. To return to the Tutorials Database, go to **File** and select the *CURRY 8 Tutorials.cdb* file in the recently opened files/Databases list. Open the Study again and see that the original parameter settings have been restored.

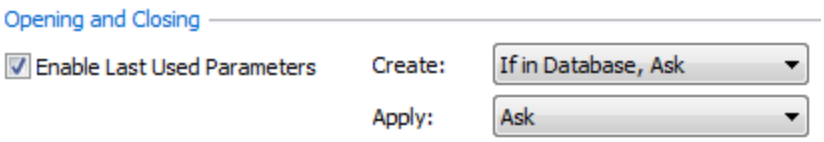
Global Parameters, again, are settings you want to apply across all data files, all of the time. Not all parameters can be saved as Global Parameters.

4. Select the Filter settings and invert the polarity , as before. Save the Study Parameters by clicking the **Save Study Parameters** icon on the Toolbar (or, use **File → Parameters → Save Study Parameters**). You will see a Save As window where you can enter a file name and folder (use *Filter Polarity.cfg* for the file name, to keep track of the settings that were changed). Click **Save** and the .cfg file is then added to the current Study.



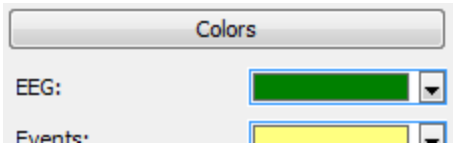
5. Close the Study.

Go to **Edit → Options → Settings**. In the **Opening and Closing** section, click **Enable Last Used Parameters**, set **Create** to **If in Database, Ask**, and set **Apply** to **Ask**. (This is preparation for the next step, in order to illustrate Last Used Parameters).

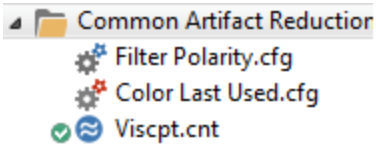


Click **OK** and open the Study. The filtering and polarity changes that were made are seen when the data file is opened again.

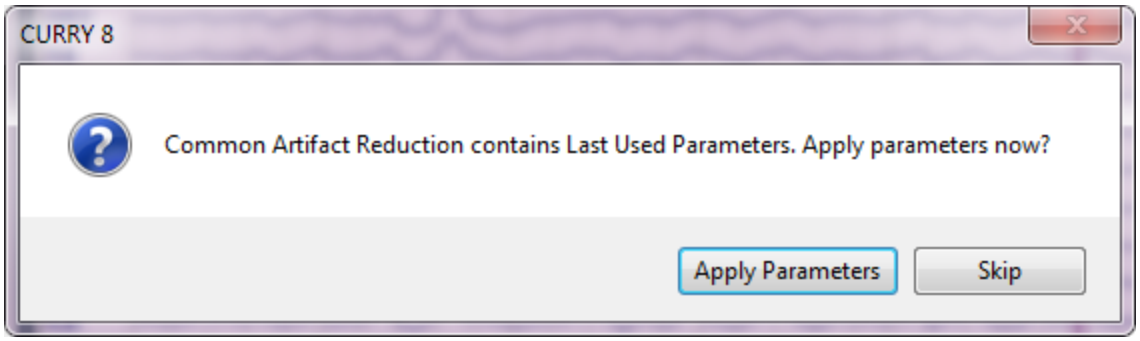
Now expand the Colors panel (for **Functional Data**) and select a different color for the **EEG** waves. Do not save this change with the existing Study Parameters.



6. Close the Study. Because we set the **Create** field to "If in Database, Ask", CURRY sees the existing *Filter Polarity.cfg* file in the Study, and then asks if you want to save the **Last Used Parameters** file. Use *Color Last Used.cfg* for the file name, and click **Save**. Now there are two .cfg files in the Study.



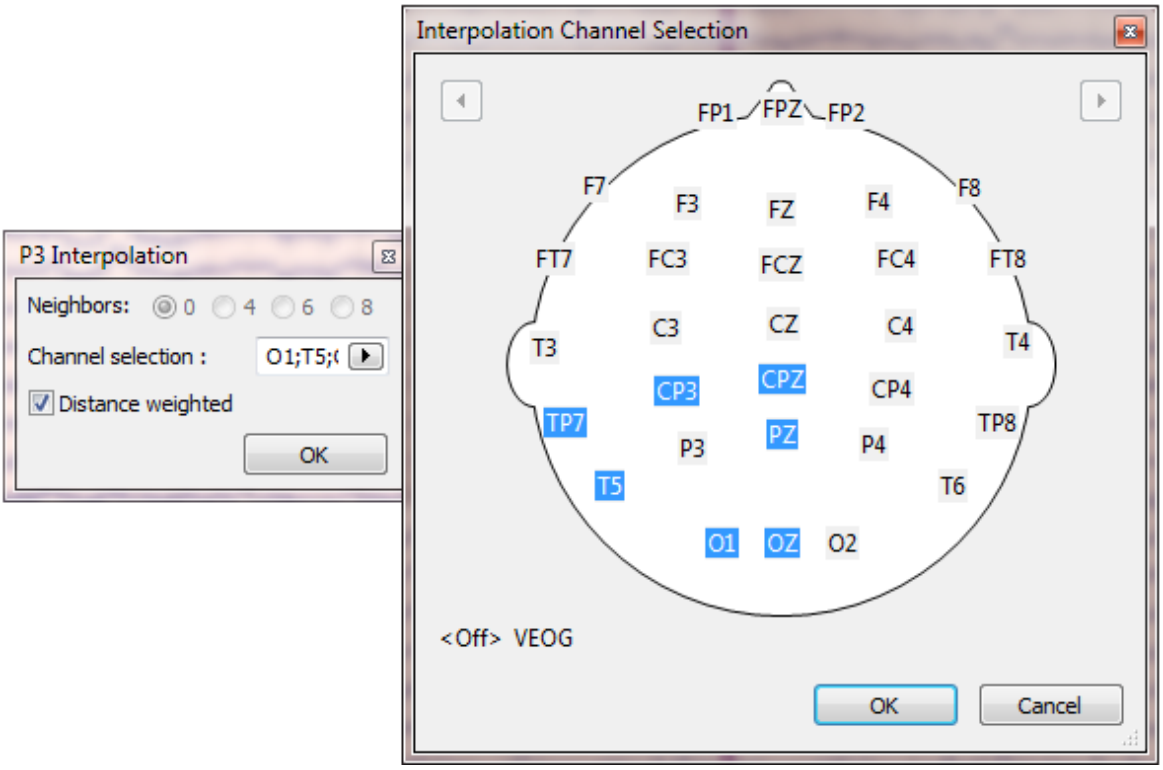
Open the Study again. Because the **Apply** field was set to "Ask", the program will ask if you want to apply the Last Used parameters. Before saying **Yes**, note that the *Filter Polarity.cfg* parameters have already been applied (the file has been filtered, and positive is up). Click **Apply Parameters** to apply the Last Used parameters.



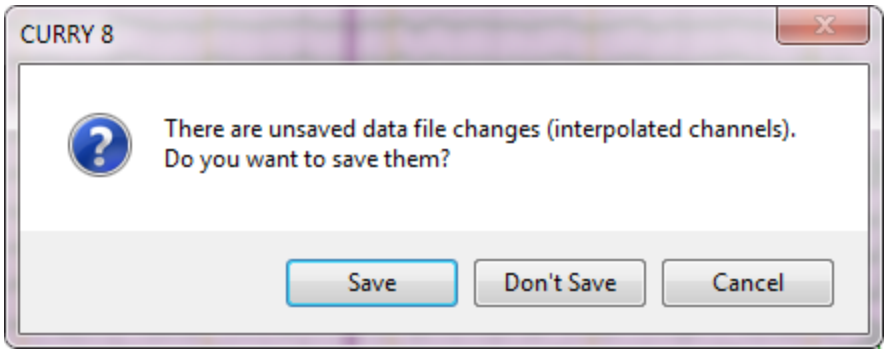
The Color change is then applied.

Last Used Parameters take precedence over **Study Parameters**. Last Used Parameters are used to save settings that are specific to the current file. **Study Parameters** are generally used to save the settings for all data files that you will be working with. **Global Parameters** are used for all files, all of the time. If you were to remove the *Color Last Used.cfg* file from the Study, the parameters from the *Filter Polarity.cfg* file alone would be applied. If you also remove that file, the Global Parameters would be applied.

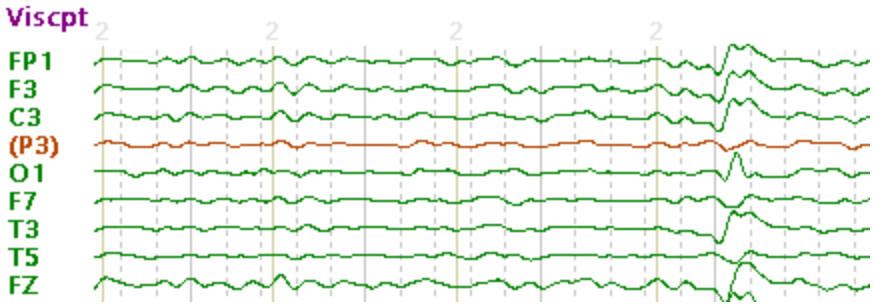
7. Move to the 49th second in the file, and note the large artifact mainly at P3. We decide to replace the P3 channel with an Interpolated channel. *Right click* on the P3 label, and select **Interpolate Channel**. In the P3 Interpolation window, display the **Channel Selection** window. Use the *Ctrl*+ combination keystroke option to select the electrodes surrounding P3. Click **OK**, select **Distance weighted**, and click **OK**. (The P3 channel is now seen in a different color, and the label is in parentheses).



Interpolation, **Bad Blocks**, and **Deselected Epochs** are special cases involving changes that will be applicable to the current data file only. If the Study Parameters included these settings, and you saved them and then applied the parameters to another data file, you would get unintended results. Instead, these special cases are detected automatically, and you will have the option to save them in the .dpa parameter file, mentioned at the top of this tutorial. Close the Study to see the following message.



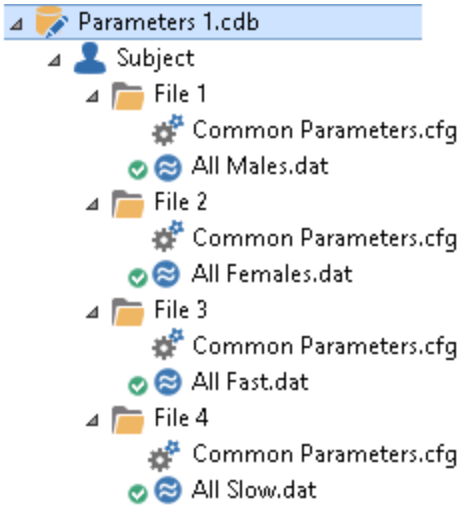
Click **Save** to save the changes. Open the Study again. Click **Apply Parameters** to apply the Last Used Parameters. Now you see the file with all of the parameters being applied: the filtering, the polarity inversion, the color change, and the interpolated channel.



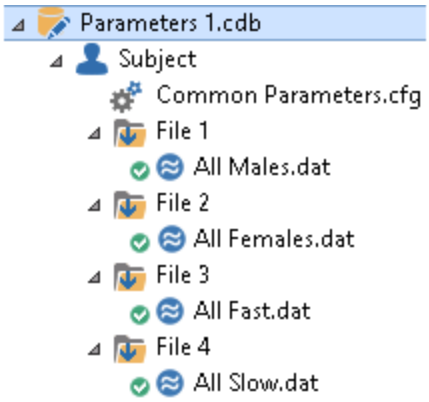
To review, what you are seeing are the Global Parameters, the Study Parameters (which are changes you have made), the Last Used Parameters (more recent changes), and the special case interpolated channel.

Close the Study. Go back to **Edit** → **Options** → **Settings**. In the **Opening and Closing** section, deselect **Enable Last Used Parameters**. We will now look at some of the remaining options involving parameters.

8. Now we will digress for a moment. Let's say you have a Subject with four different Studies, each with a continuous data file. You want to process the files in the same way. You can analyze one file, save the Study Parameters, and then drag-and-drop the parameter file into the other three Studies. In this case, there are four averaged data files. In the first one, we performed a baseline correction, filtered the data, inverted the polarity, and selected the Butterfly Plot. The Study parameters were saved as *Common Parameters.cfg*. That file was dragged and dropped (copied) into the other Studies. When each of those is opened, the same parameters will be applied.

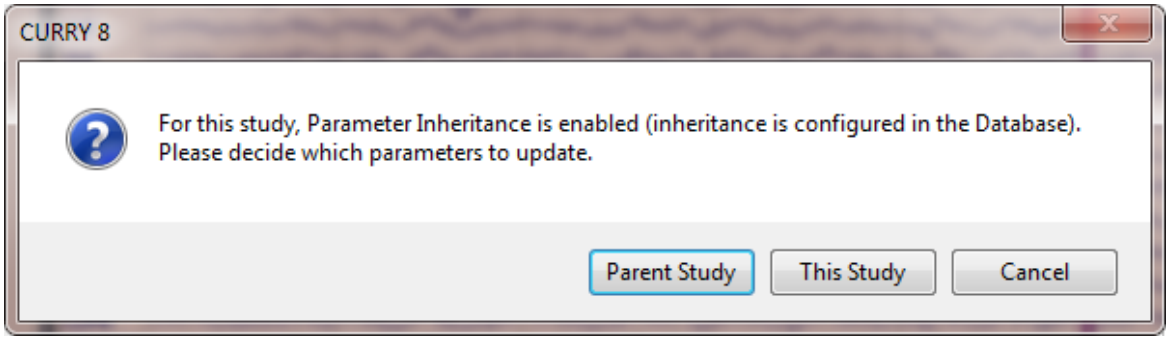


Alternatively, we could Move (*Ctrl+drag and drop*) the parameter file under the Subject, where it can be applied to all Studies below it (simple drag and drop will Copy the file). To receive the inherited parameters, you must enable the **Inherit Parent Parameters** option for each Study (*right click* on the Study to access the option). A down arrow appears in the folder symbol to let you know that the inheritance channel is open. If you leave Inherit Parent Parameters disabled, only the Global Parameters would be applied to the Studies.



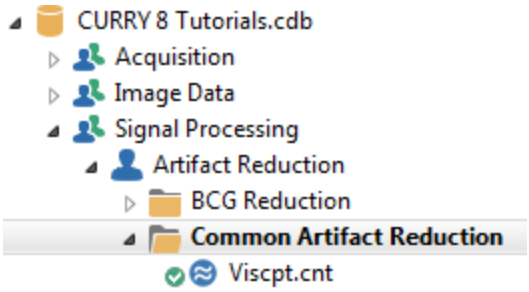
You can thereby control which Studies inherit the parent parameters. You can, of course, have Study Parameters (or Last Used Parameters) in the Studies, and these will take precedence. In practice, it is unlikely that there would be a conflict between parameter files in the Subject level versus those in the Study level, but if there were, the Study level would overrule the Subject level.

In the example above, we created the *Common Parameters* file while working with the first Study, and then physically dragged-and-dropped it to the Subject (and Removed it from File 1). If we had enabled **Inherit Parent Parameters** for File 1 first, we would have seen the following message when we saved the Study Parameters from the Toolbar. Here we have the option to save the parameters file with the Parent folder, or with the current Study. If we had selected **Parent Study**, the parameter file would have been saved with the Subject, in this case.



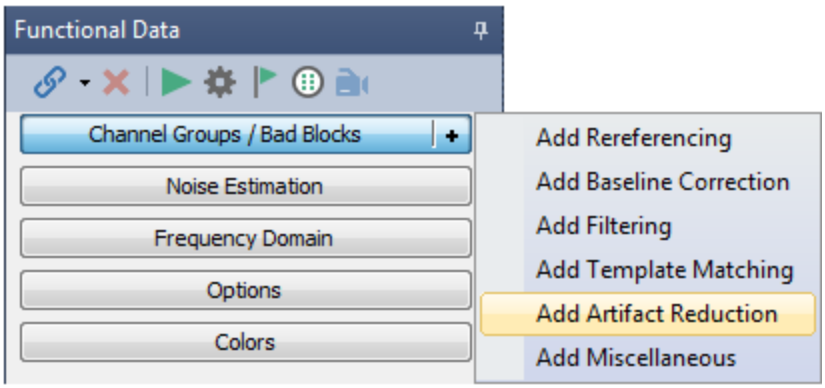
Now we will point out some of the limitations with parameter files.

9. Continuing with the *CURRY 8 Tutorials* Database we have been working with, go back to **Edit** → **Options** → **Settings** and disable ☐ Enable Last Used Parameters, if you have not already done so. Remove the .cfg files from the *Common Artifact Reduction* study (context menu option). Then open the *Common Artifact Reduction* study again.

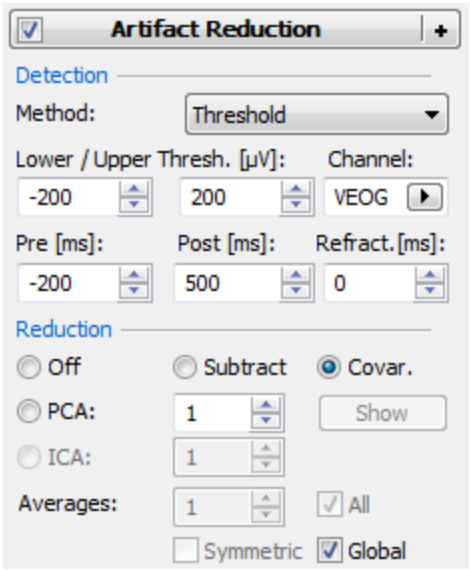


Note that the P3 channel remains interpolated. This is because that change is saved with the .dpa parameters file. If we wanted to remove that, we could either remove the interpolation manually, and then close the Study, which would then give the option to save the change to the .dpa file, or, we could *right click* on the data file in the Database and select **Delete Legacy Parameter Files (.dap,.rs3)**. We would then need to go through the import Wizard to recreate the parameter files. Leave the channel interpolated.

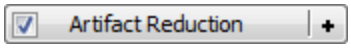
10. Add **Artifact Reduction** to the processing list by clicking on the + sign at the end of **Channel Groups / Bad Blocks**.



Expand the **Artifact Reduction** panel and enter the values shown. Then click the flashing **Scan Artifacts** arrow at the top .



11. Save the Study Parameters, using *Blink reduction.cfg* for the file name. Save the file and close the Study, then reopen it.

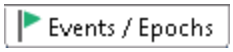
12. The Detection parameters are seen in the 

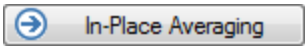
panel. However, the blinks are still in the data file. Note also that the **Scan Artifacts** arrow at the top is flashing again.

This illustrates an important point about saving parameters. Parameter *settings* are saved, but not *operations*. "Scans" are operations. If you want to save the parameters, you can save them, but you will still need to click the Scan button(s), and other similar operations, manually when you apply the parameters to a different file (or the same file again). If you want to save the entire procedure that you are using to analyze the data, you can do that using macros (macros include the various settings as well as the operations).

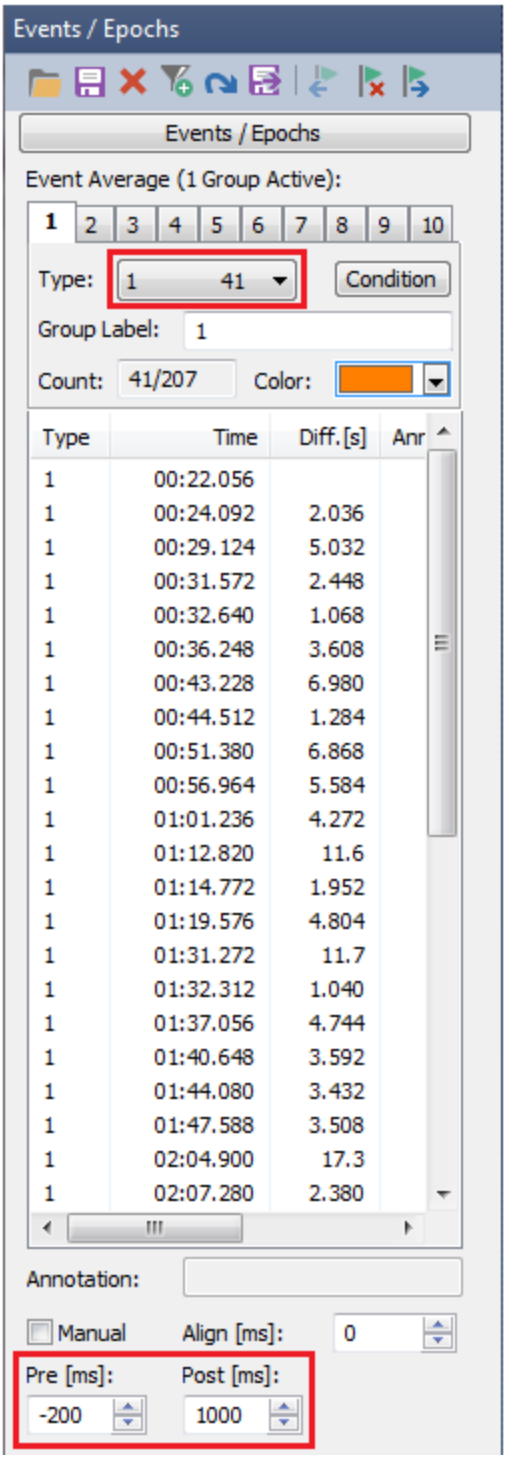
Note
If your analysis sequence includes the creation of averaged data files, you should save the Study Parameters before you actually create the average(s). Once the average is displayed, CURRY is in a different state, so to speak. Saving the Study Parameters at that point will be ineffective. You can, of course, save the average data, open that Study, and save its own parameter file.

In this particular file, we would need to click again to get back to where we were. Close the study. Remove the .cfg file from the Study.

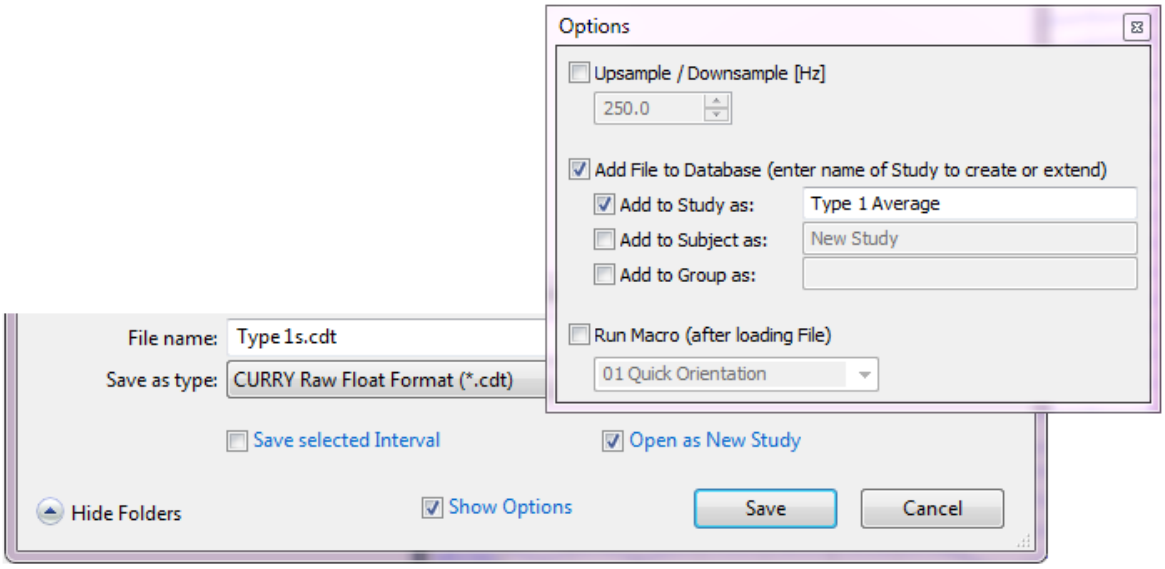
13. Open the Study again, and display 

(below the Database), or click the **Open Events** icon at the top of the **Functional Data** parameter panels. Set **Type** to **1**. Enter **-200** for the **Pre [ms]** field and **1000** for the **Post [ms]**. field. Click the 

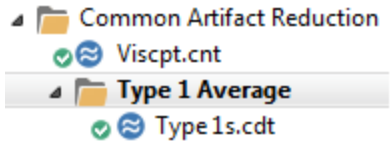
button to create an average of the Type 1s.



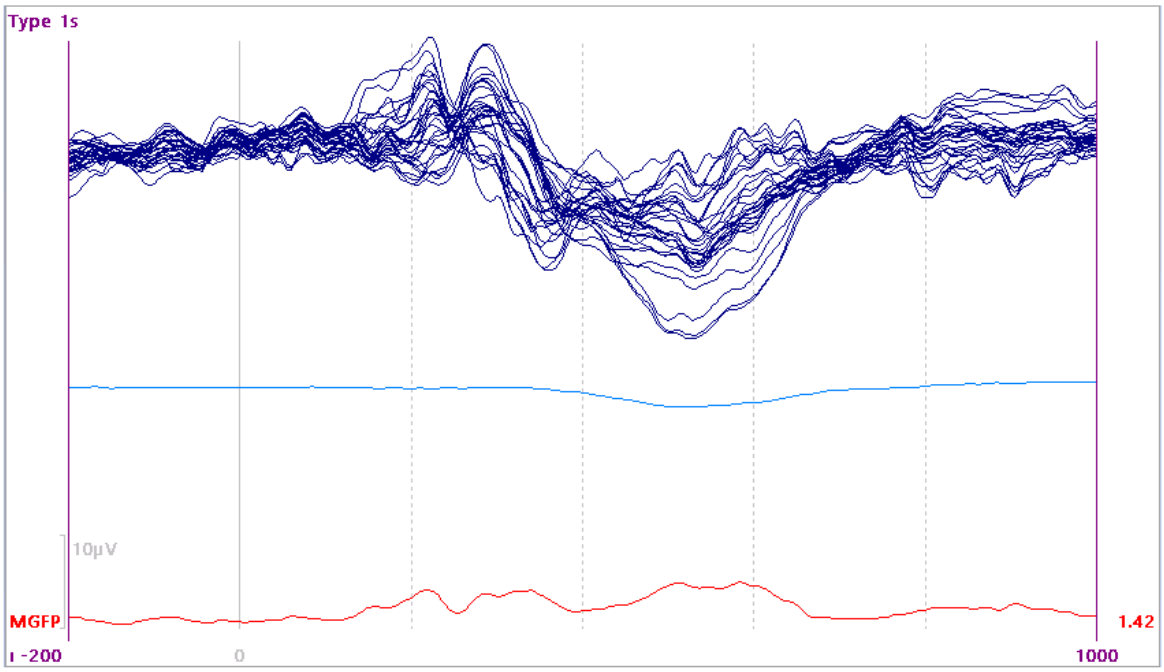
After the average appears, select **Functional Data → Save → Save Data**. Enter *Type 1s* for the file name. Select the **Add File to Database** option, and enable the **Add to Study as** option. Enter *Type 1 Average* as the new Study name. Enable the **Open File as New Study** option. Click **Save**.



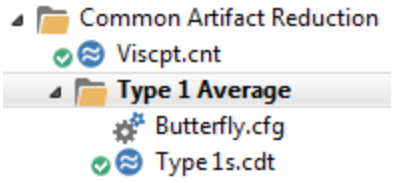
14. The new Study has been added to the Database, as a subfolder to the current folder.



15. In the data display, *right click* in the data display and select **Butterfly Plot**. This gives the following display of the average data. (If your waveforms look different, you may have the CAR selected).

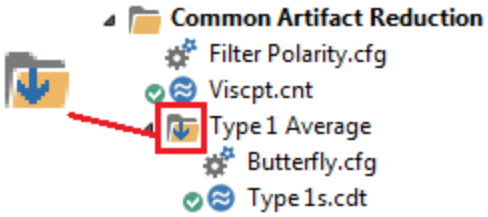


16. If we want to see this same display the next time we open this Study, we can save the Study Parameters. Click the **Save Study Parameters** icon on the Toolbar . Save the file as *Butterfly.cfg*. The file will be added to the Derived Study.



Close both Studies.

17. Lastly, *right click* on the *Common Artifact Reduction* folder, and select **Insert Parameters**. This is another way to add parameter files to the same or different Studies. Select the *Filter Polarity.cfg* file. Since we want (for demonstration purposes) to include the parameters from the *Filter Polarity.cfg* file with the averaged data file, *right click* on the derived Study (*Type 1 Average*), and select **Inherit Parent Parameters**. A small down arrow will appear on the folder, indicating that the parameters will "flow down" into that Study.



Now when you open the *Type 1 Average* study, both sets of parameters are applied. Close the study.

Care

Be careful when you save the parameters. *All* changes you have made will be saved. If you are not careful when you save the parameters, you may save changes from many prior steps, including some that you did not mean to save. With **Global** parameters, open a Study, make the changes that you want to be applied to all files, and then continue. With **Study** and **Last Used Parameters**, recall all of the changes you have made before saving the parameters to be sure you really want to save all of them.

There are a few conventions to be aware of when using Study Parameters.

1. There are limits to how far you can go in the analyses and still save the settings in the Study Parameters. If you have continuous data to start with, and the goal is to perform additional analyses with the averaged data that are created from the continuous data, it is important to understand that the Study Parameters you use with the continuous data are not carried over once you have averaged the data. For example, let's say your processing steps include Baseline Correction, Filtering, Artifact Reduction, and SNR based epoch rejection prior to averaging the selected events. If you save the Study Parameters at this point, all of the settings will be

applied to the continuous data when you open the file again (you will still need to Scan the data), or if you apply the same settings to another like data file. The next step in the process would be to average the selected events. In essence, CURRY has switched to a different Study (or state), and the parameters for the continuous data no longer apply to the averaged data. In fact, if you try to save the Study Parameters again, you will find that the Save Study Parameters option is grayed out. When you obtain the average, you need to save it and open that Study in order to save the Study Parameters for the average file.

The typical way to manage the Study Parameters is to have the averaged data in a derived folder below the continuous data. 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.

2. The next convention to know is that the Study Parameters in a child folder always take precedence over those in the parent folder. If there were no averaged Study Parameters in the example above, CURRY will attempt to apply the continuous Study Parameters to the averaged data. 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 would then be applied to all of the continuous data files, if they are set to inherit the parent parameters.

3. 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 set will be applied to the subsequent data files. 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.

4. When you have the Study Parameters created for one data file, and wish to apply them to another data file, you can simply drag and drop the .cfg file from one Study to another. Alternatively, you can *right click* on the target Study and select **Insert Parameters** from the context menu. Then select the desired .cfg file.

Once you understand these few conventions, you will find that Global and Study Parameters can save you a lot of time by "remembering" the settings that you wish to use frequently.

Please see the section on Global and Study Parameters in the *CURRY User Guide* for more information.

2.2 EEG Acquisition

IMPORTANT REMINDER

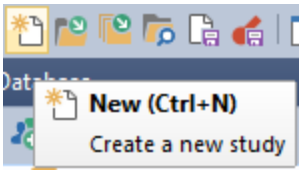
Before you start recording data for a project, *always* run a few pilot subjects first, and go through the *entire* analysis sequence to ensure that everything will work as you intend. Every so often we hear from a user

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 the situation.

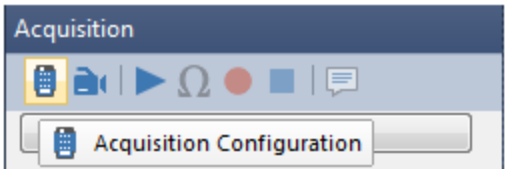
When acquiring data, you can begin by saving the file to the hard drive, without using a Database, or you can create a Database and access acquisition from an empty Study, as described above (see the **Database** tutorial).

If you are setting up the program for the first time, the next step is to configure the amplifiers, sensor positions, and montages. You can use one of the supplied configurations, making changes as needed, or create one from scratch. The settings may then be saved and used in future recordings. If you make changes to an existing configuration file, you should save that as a new file, leaving the original supplied file unchanged.

Here it is important to understand the difference between configuration files and parameter files. Configuration files (.xml extension) are used to save the settings you make in the screens accessed from the Create Amplifier Configurations option in the Workflow, or by clicking the **New** icon.

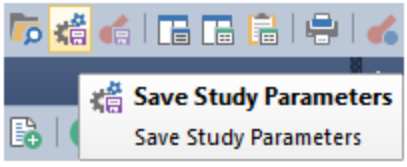


From there, click the Acquisition Configuration icon at the top of the Acquisition parameters panels.



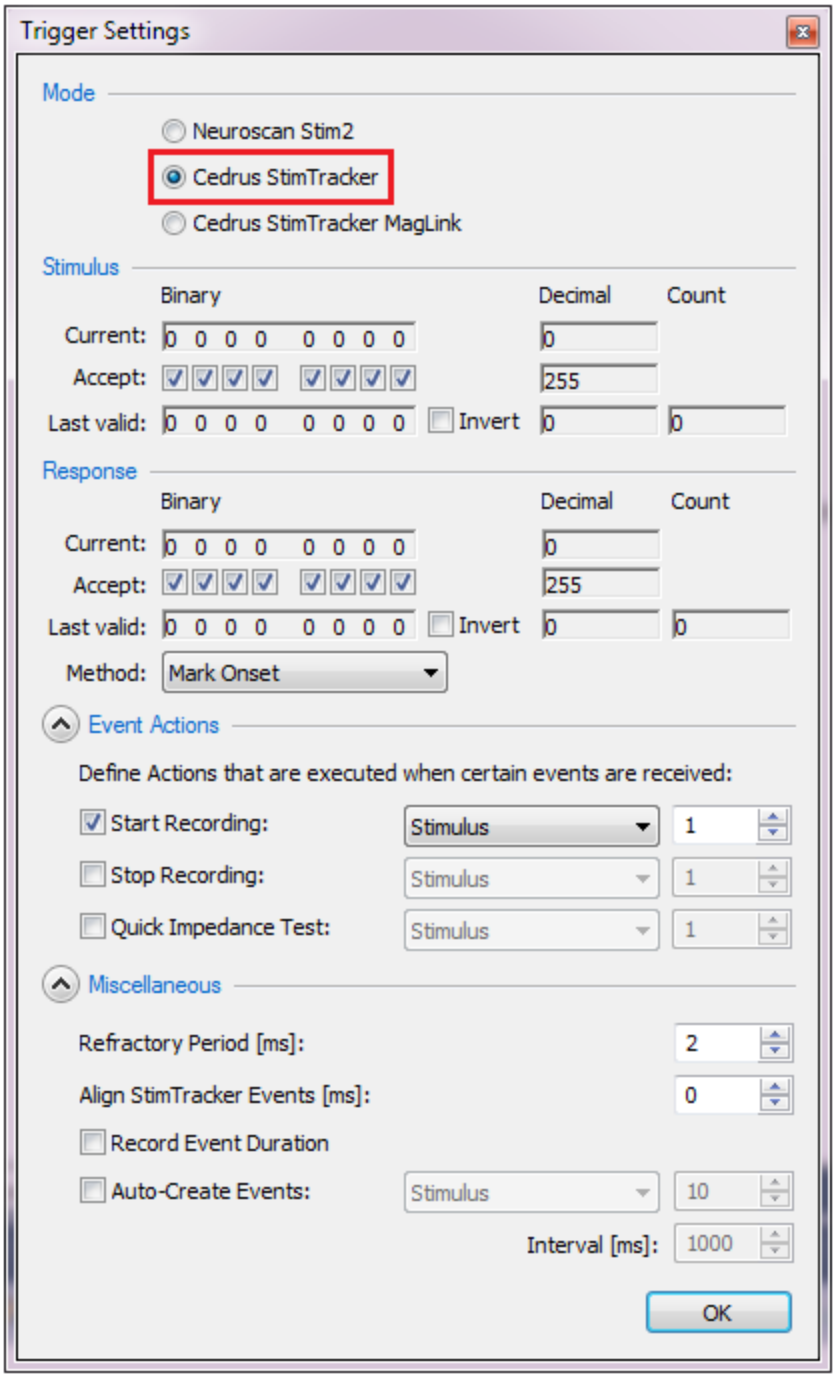
The configuration files are retrieved from the initial Acquisition Configuration screen, or from the Amplifier Control panel.

Parameter files contain the selections you make in any of the Acquisition panels (Amplifier Control , Filter Parameters , etc.). These are saved by clicking the **Save Study Parameters** icon on the Toolbar. These can be retrieved and applied when acquiring more data files.



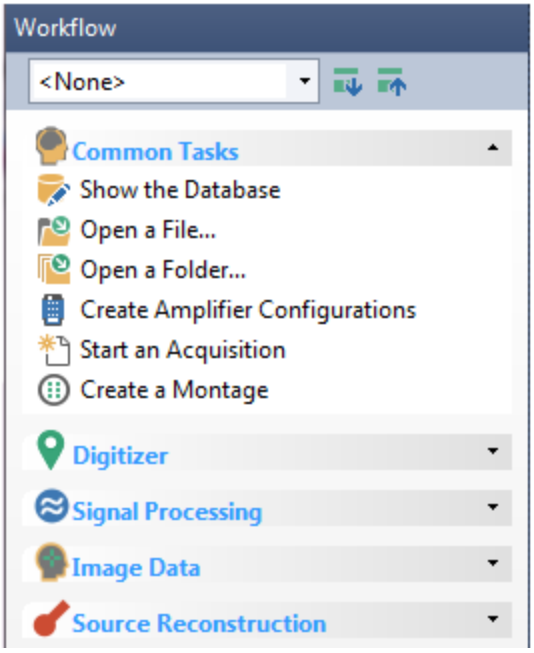
Using the StimTracker

If you are using the StimTracker system, be sure you have selected it from the Trigger Settings options, found at the bottom of the **Advanced** section under Amplifier Control. For more details, please see the **Amplifier Control** section in the *CURRY User Guide*, and the **StimTracker Test** section in the *STIM2 User Guide*. If you are using the StimTracker and a MagLink or MicroMagLink system, select that option.



Using the Workflow list

When you are first getting familiar with CURRY 8, you may find the Workflow lists to be helpful in finding the things that you want to do. You will see different options depending on where you are in CURRY. See the **Workflow Tutorial** for more information, or the Workflow sections in the *User Guide*.



2.2.1 Initial Configuration, Create Montages

Before you start acquiring data, you need to configure the system to operate in a desired way. Once you have completed the process, you can save the settings to a configuration file. This saves you from having to reenter all of the settings each time you acquire data. You can have more than one configuration file. Some basic configuration files are supplied with the software. If you wish to modify these, you should start with an existing configuration file, make changes, and save it as a new file, (the program will not let you overwrite the original configuration files).

The configuration files are *.xml* files, and these are stored in one of two folders. Please see the **Target Folders for Windows 7** section for more information.

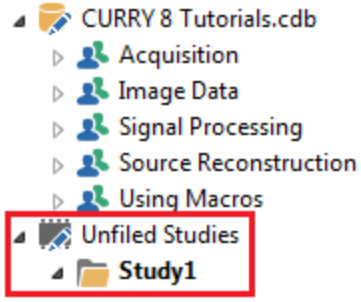
When you access a list of configuration files in CURRY, you will see both sets of files. Those above the horizontal line are ones you have created; those below the line are the ones that have been supplied with the program.

The steps in this Tutorial represent a subset of the options that are available for acquisition. Additional functionality is contained in the subsequent Tutorials, as well as in the *CURRY User Guide*.

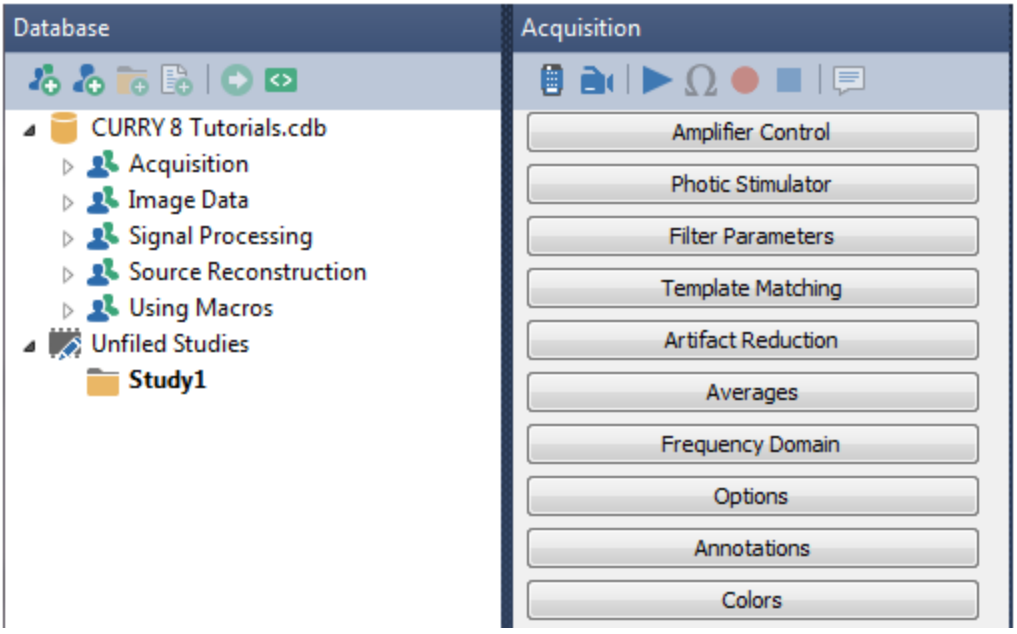
One of the first decisions you need to make is whether or not to use a Database. You can acquire data with or without a Database. A Database imposes organization, and they are very useful if you are acquiring multiple data files where you need to keep track of the files - both during acquisition and later during analysis. If you are

recording a single or a few data files in isolation, you may not need to use a Database, although you still can. We recommend that you use Databases in order to become familiar with them and understand how they function, then decide whether or not to use them based on your immediate need. See the **Database** tutorial for more information.

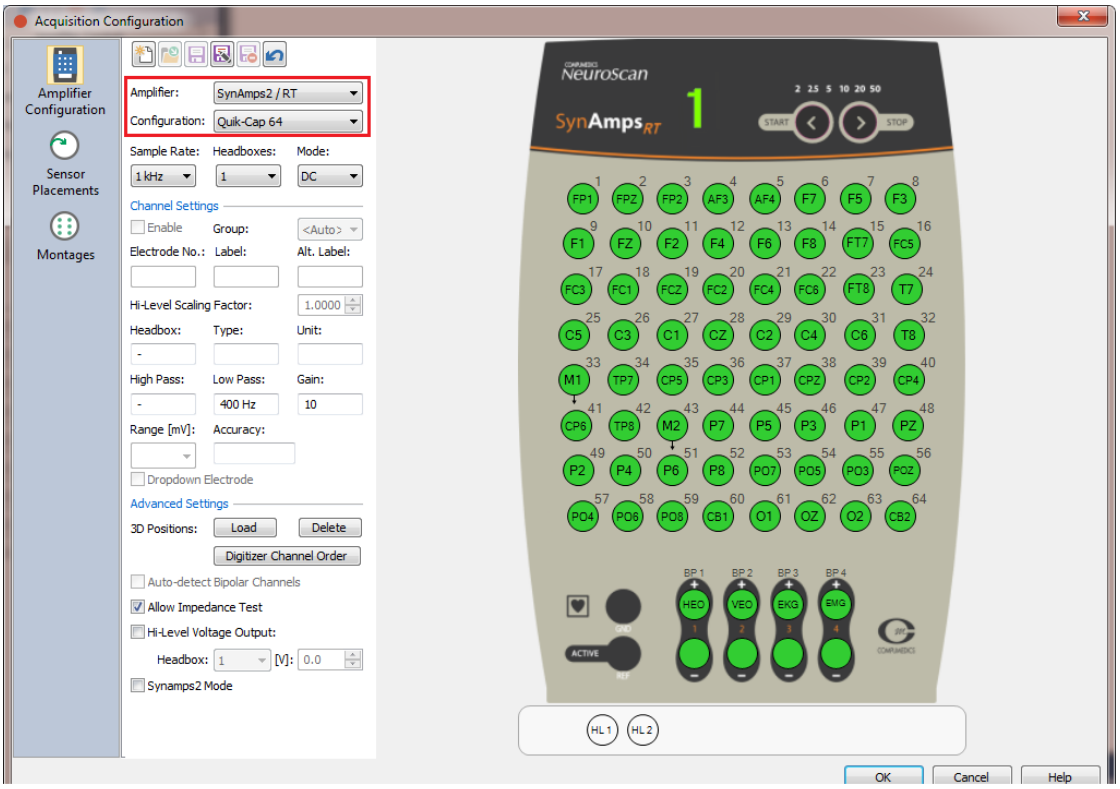
1. For simplicity sake, we will not create a Database in this example. Select Start an Acquisition from the **Workflow** list, or click the **New** icon on the Toolbar. An **Unfiled Study** is seen below whatever Database you may have opened.



2. The **Acquisition** parameter panels will appear.

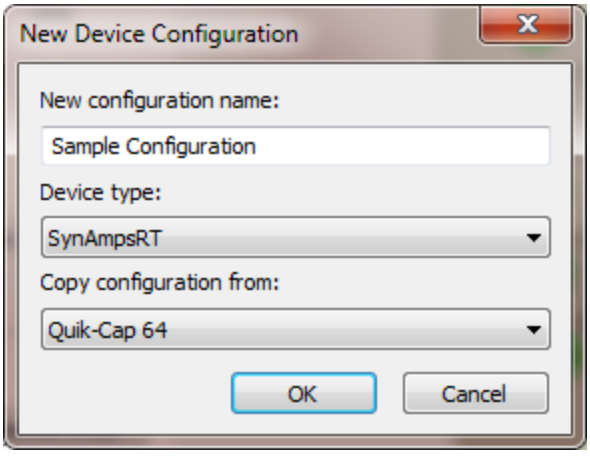


3. Select Create Amplifier Configurations from the **Workflow**, or click the **Acquisition Configuration** icon. This is where the basic configuration of the amplifiers is contained. For **Amplifier**, select the **SynAmps2 / RT**. If you have another type of amplifier, the steps will be very similar. For **Configuration**, select *Quik-Cap 64*. This is one of the actual configuration files (with the .xml extension, described above).



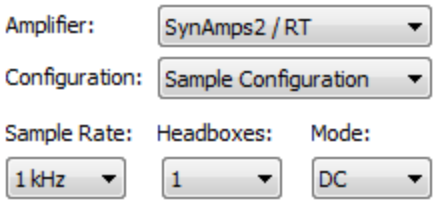
For SCAN users, the **Electrode** number is the same as the **Physical Channel** number as seen in the **Channel Assignment Table**. If you are starting with an .ast setup file from Acquire, use the Channel Assignment Table to make sure the electrodes are in the proper order, modifying them as needed.

4. Click the **New File** icon to create a new Configuration file. If you are going to make modifications to a supplied configuration file, you must save the changes to a new configuration file. Clicking the icon displays the dialog seen below. Enter a new file name, select the amplifier you are using, and indicate the file that you wish to copy the existing configuration information from, then click **OK**. In this case, we will be creating a new configuration file from the existing file shown.

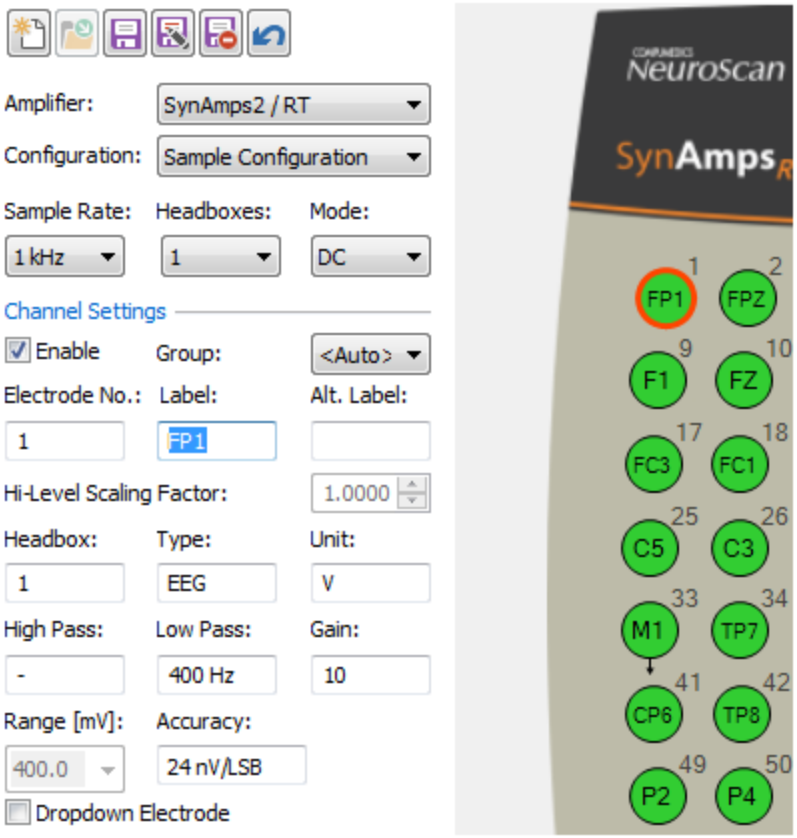


Select the **Sample Rate** that you wish to use (from 100 to 20kHz with the SynAmps RT amplifier). Assume there is only the single headbox with 64 channels. Select **DC** or **AC Mode**.

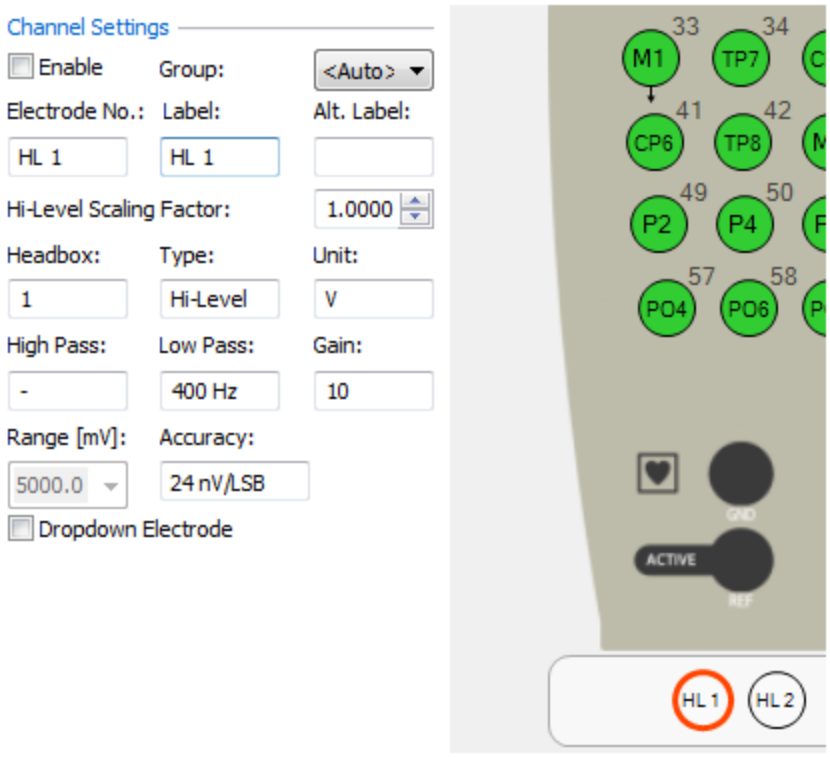
DC Mode records the data with no High Pass filtering. AC Mode applies a 0.15 Hz High Pass filter, which is applied as a secondary step. DC Mode is used when you are 1) recording DC potentials, 2) recording in the Magnet, 3) recording SEPs or other evoked responses where there is a large stimulus artifact (including TMS), or 4) whenever you want to acquire the data without any High Pass filtering (which can always be applied offline). We generally recommend recording in DC Mode all of the time unless you are certain you will never be interested in the slow potentials - if filtered during acquisition, the slow activity cannot be restored. Also, with no high pass filtering, there is no ringing of the filters and therefore any sharp transients will resolve much faster.



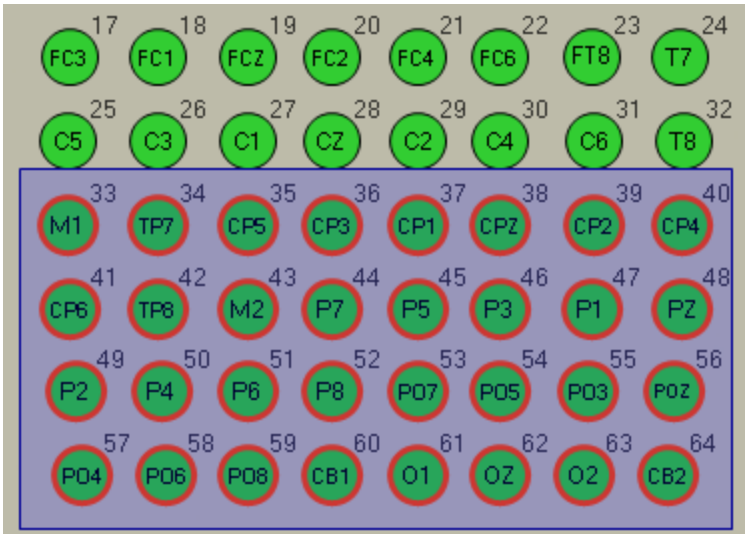
Click on one of the electrodes (such as FP1). The **Channel Settings** fields show that this is amplifier number 1, from headbox 1. **Range [mV]** is the dynamic range of the amplifier, the maximum voltage that can be acquired without saturation. In the figure, the amplifiers were set to DC Mode, giving a Range of at least +/-200mV. In AC Mode, the Range is at least +/-0.95mV. **Accuracy** is the resolution in the amplitude domain. In DC Mode, with a SynAmps RT, this is approximately 24nV (in reality, this number will be slightly larger). Amplitude is measured to the nearest 24nV. In AC Mode, the Accuracy is approximately 3nV (for a SynAmps RT). This will vary by amplifier. **Channel Type** can be EEG, Bipolar, High Level Input, etc. (seen when you click on an electrode). **Units** are in V in nearly all cases. There is no **High Pass** filter in this case, since we had selected **DC Mode**. The Low Pass filter will vary with the AD Rate (the Low Pass filter is typically 2/5 of the sampling rate).



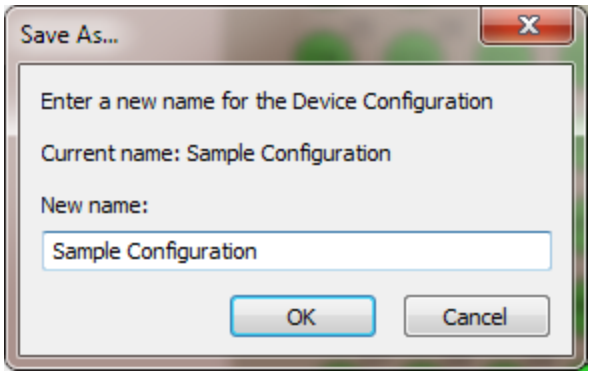
5. Click on an **HL1** channel. This is a High Level Input channel used, for example, for recording EKG from a pulse oximeter (or pulseometer, for MicroMagLink recordings). The range for the HLI channels is +/-5V.



If you want to add this, or any other, channel, just *double-click* on it. To remove a channel, *double-click* on it so it is not green, or click once on the channel and disable the ☐ Enable option. Signals from disabled channels will not be recorded. To disable (or enable) a block of channels, drag a box around them, then disable (or enable) them using the ☐ Enable option.



6. Save the Configuration File by clicking the **Save** button. This will save the changes to the "Sample Configuration" we created. You could also click the **Save As** button to save the file using a different name.

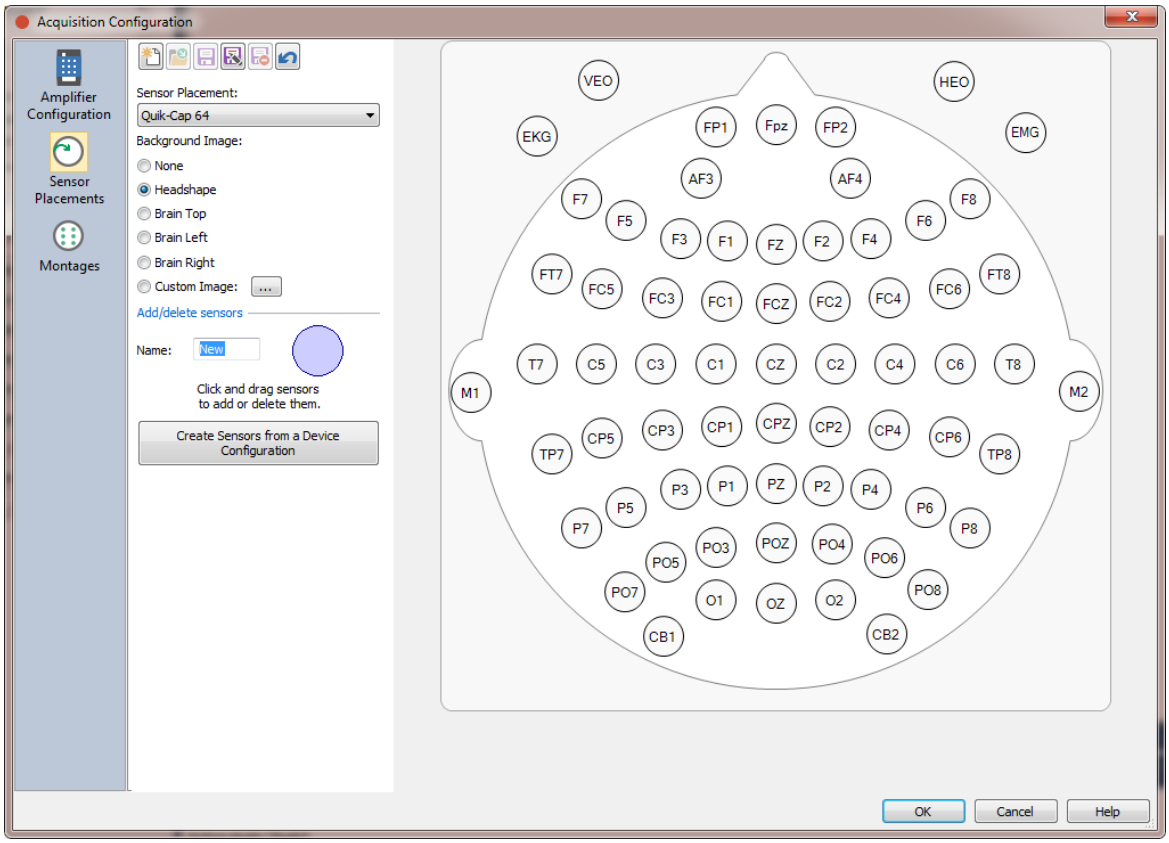


To delete the current configuration file, click the **Delete** button. A dialog will ask if you really want to delete the file (do not delete it).

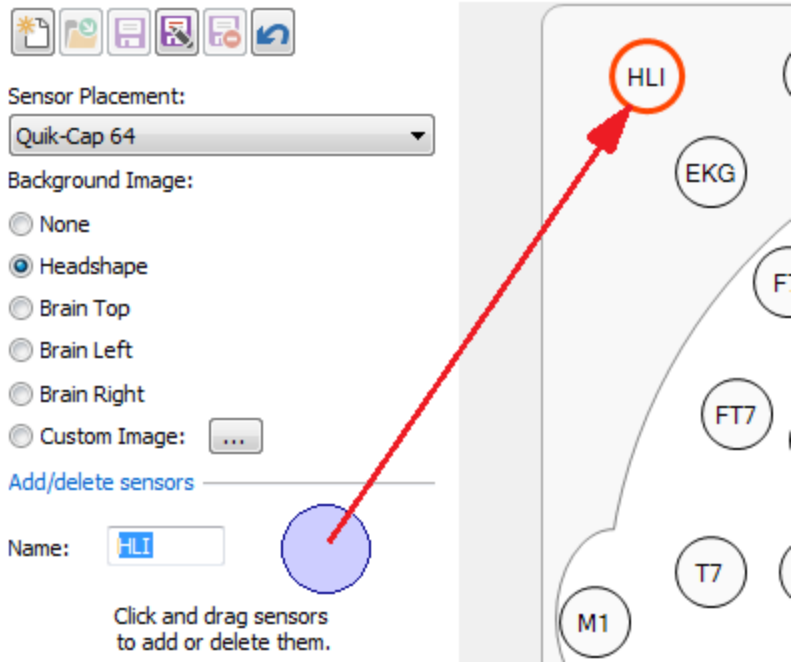
The **Undo** button is used to all operations since the file was last saved.

7. We will create a new configuration file including the HLI channel. Click the **Sensor Placements** button

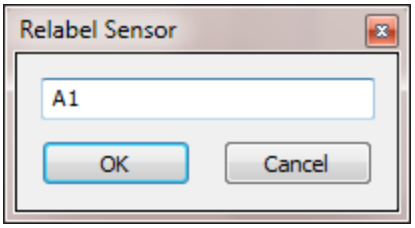
(on the left side of the display). In the **Sensor Placement** list, select *Quik-Cap 64*.This displays the electrode positions that correspond to the cap. We will make changes to this file and then save the new file with a different name (you cannot overwrite the supplied sensor placement files).



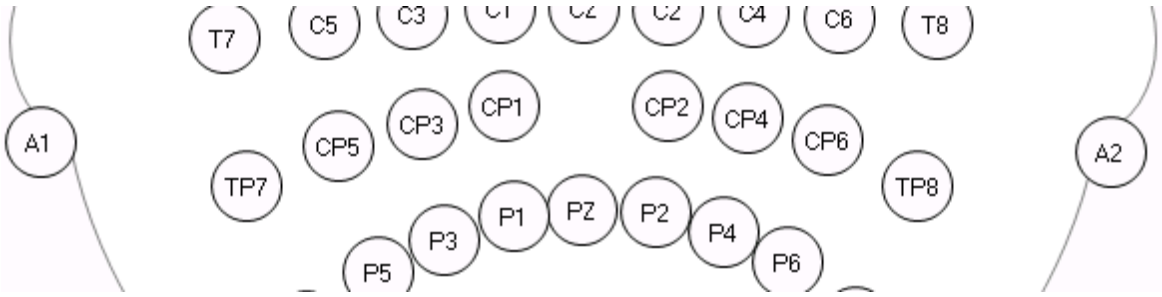
Now we will add the **HLI** channel. Type **HLI** in the **New name** field, then drag the shaded circle to the desired position and drop it. Note that you can grab and drag any of the electrodes into new positions. If you do not see the electrode names, enlarge the display.



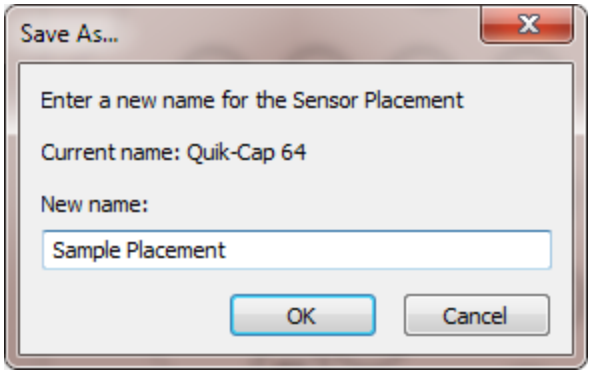
Say you are recording A1 and A2 instead of M1 and M2. To rename a channel, *right click* on the electrode select **Relabel Sensor**. Enter the new name and click **OK**. Repeat for A2.



M1 and M2 are now A1 and A2. Drag them to a more representative position.



Save the Sensor Placement file by clicking the **Save As** button. Enter a new file name (*Sample Placement*) and click **OK**.

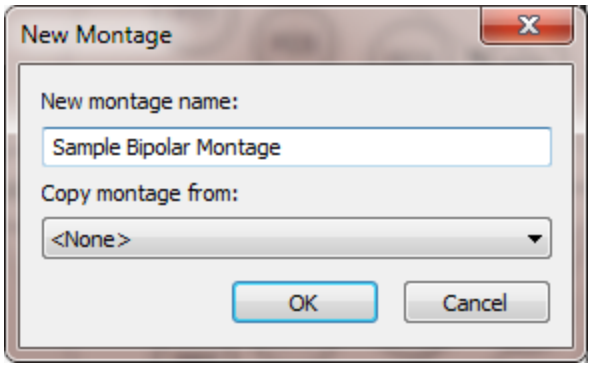


8. The final step is to create any montages that are desired. Montages in this sense are not just bipolar or referential montages, but also montages that reorder the channels, or contain only a subset of channels that can be used for display purposes.

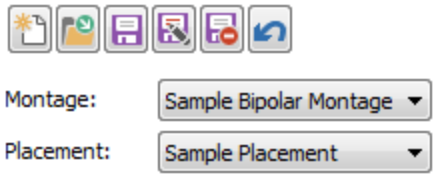
Click the **Montages**

button.

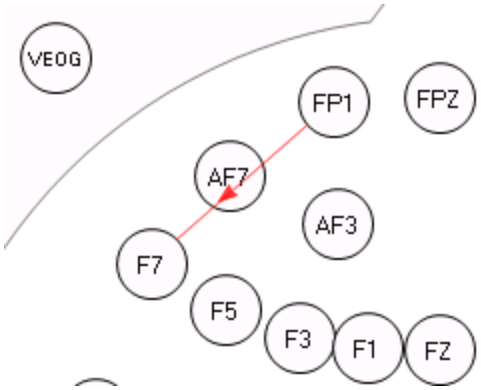
First we will create a bipolar montage. Start by clicking the **New File** icon to create a new Montage file. Name it *Sample Bipolar Montage*. We will create the file from scratch rather than copy it from an existing montage file.



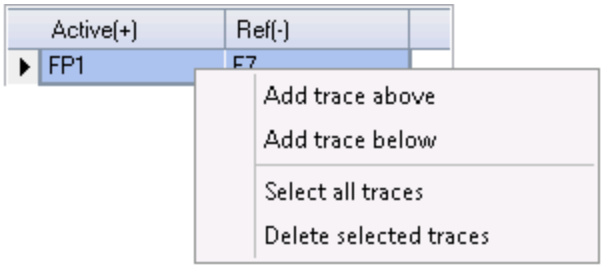
Select the **Sample Placement** file for **Placement**.



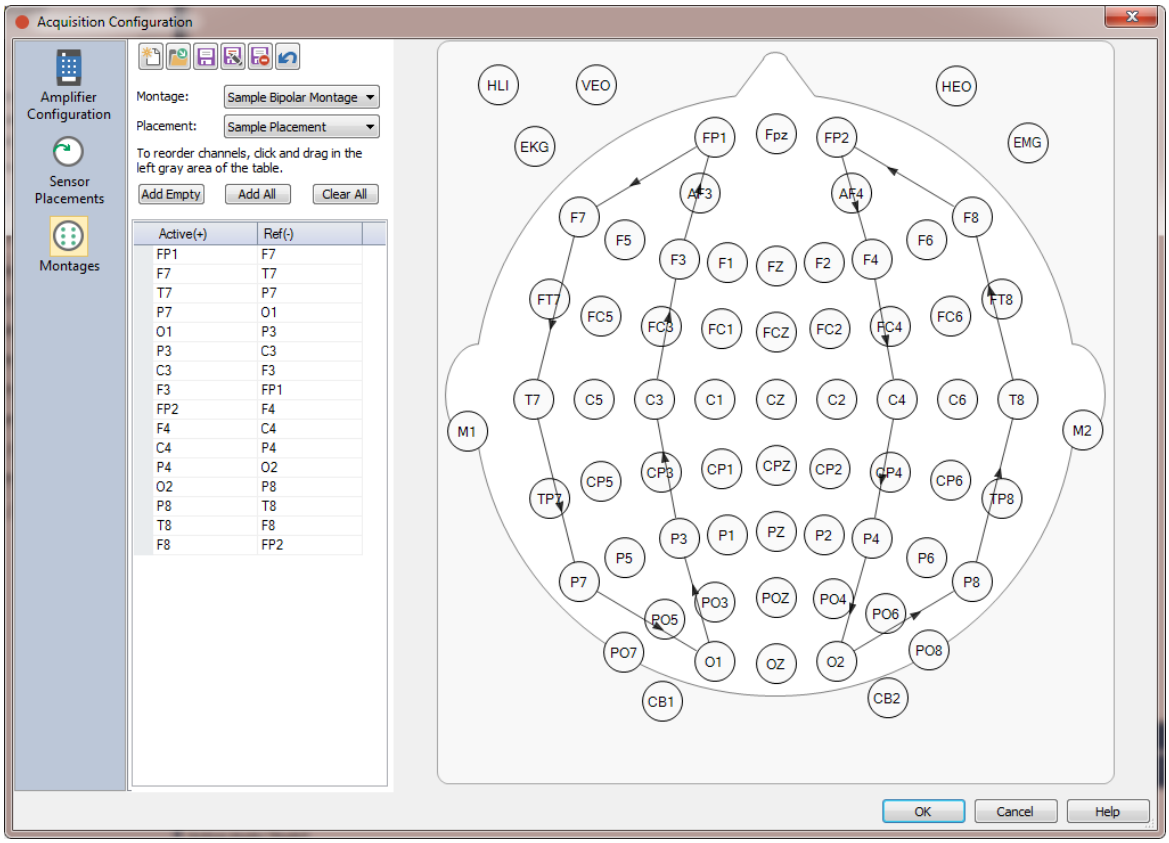
The next step is to create the bipolar channels. If the first desired bipolar channel is FP1-F7, just drag an arrow from the first to the second electrode.



After releasing the line, the arrow will remain and you will see the bipolar channel in the list. *Right click* on the row to see additional options.

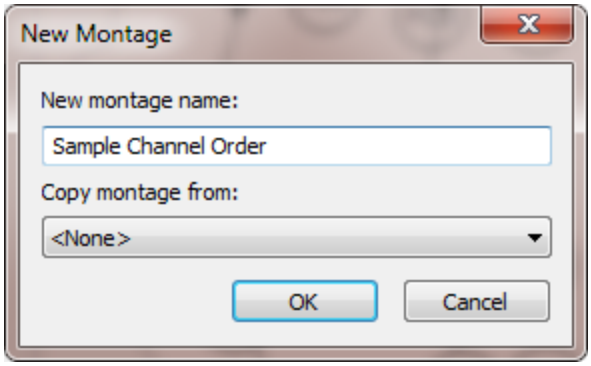


Continue in this manner to create a bipolar montage. If you make a mistake, highlight the bad row by clicking to the left of the label and click the *Del* button on the keyboard.

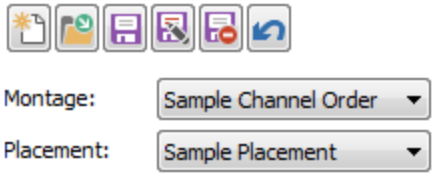


Click the **Save** button to save the montage file.

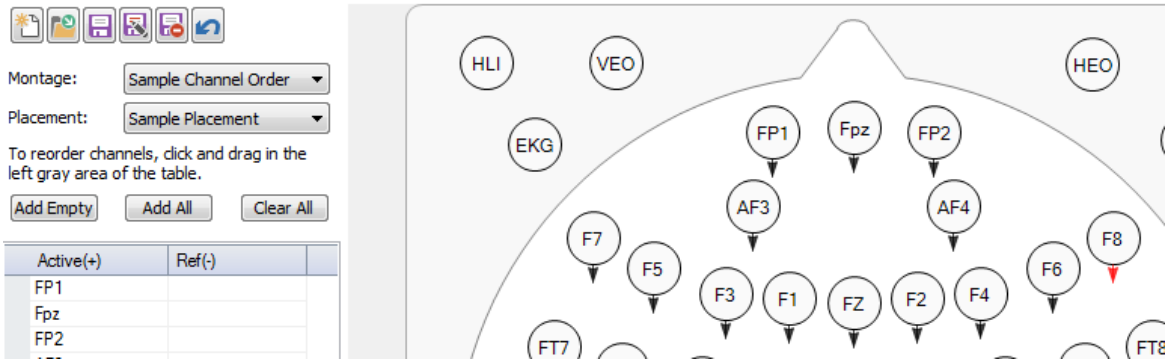
9. To reorder the channels, start by clicking the **New File** icon to create a new Montage file. Enter a file name for the new channel order.



Select **Sample Placement** for **Placement**.



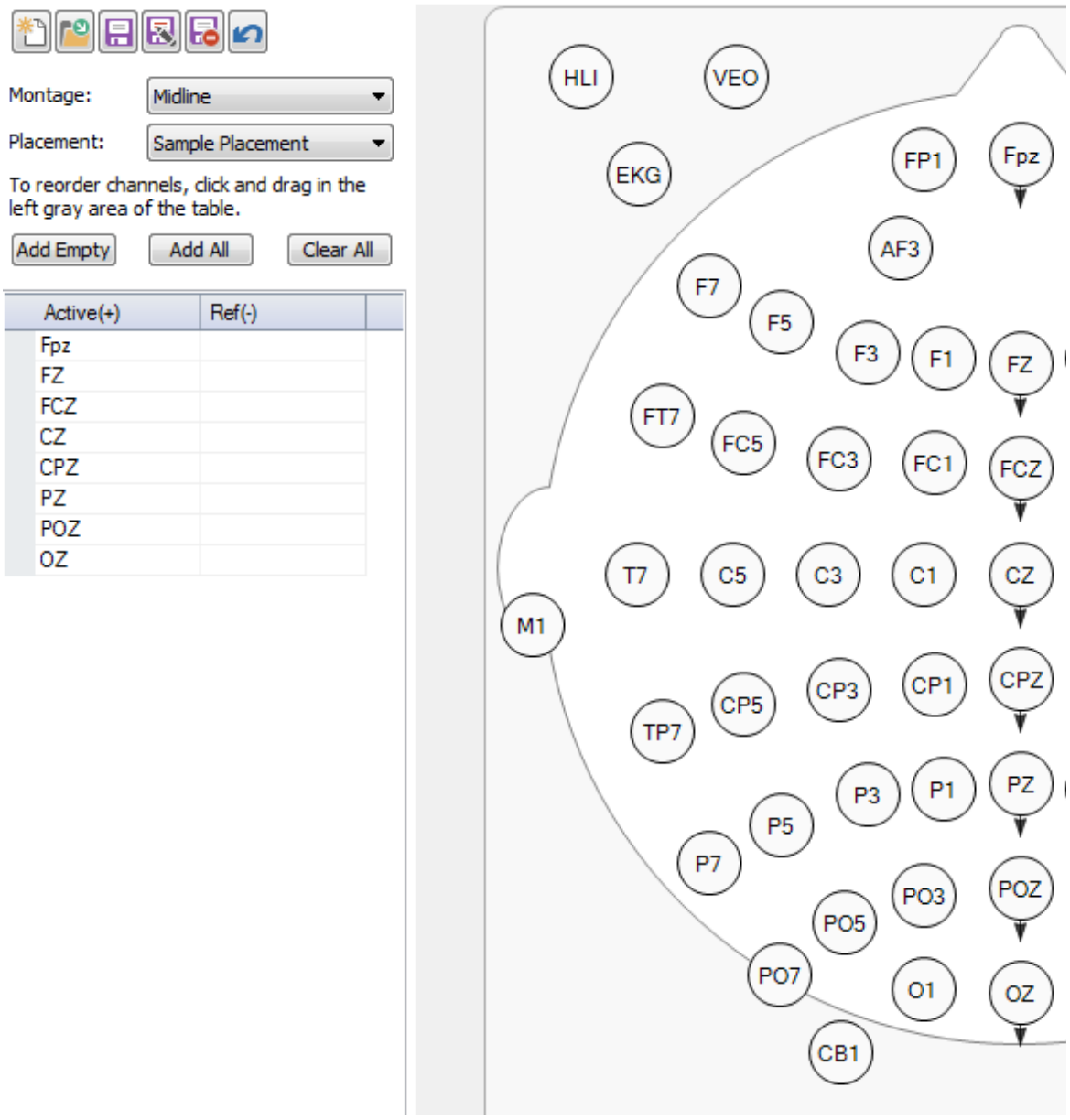
There are two ways to create a new channel order. You can click the Add All button, and all channels will be added to the list. Then you can drag-and-drop the channels to get the desired order. Or, simply *double-click* the electrodes in the order you wish them to appear. An unattached arrowhead will be seen below each one, and the channels will appear in the list. Continue until all desired channels have been selected.



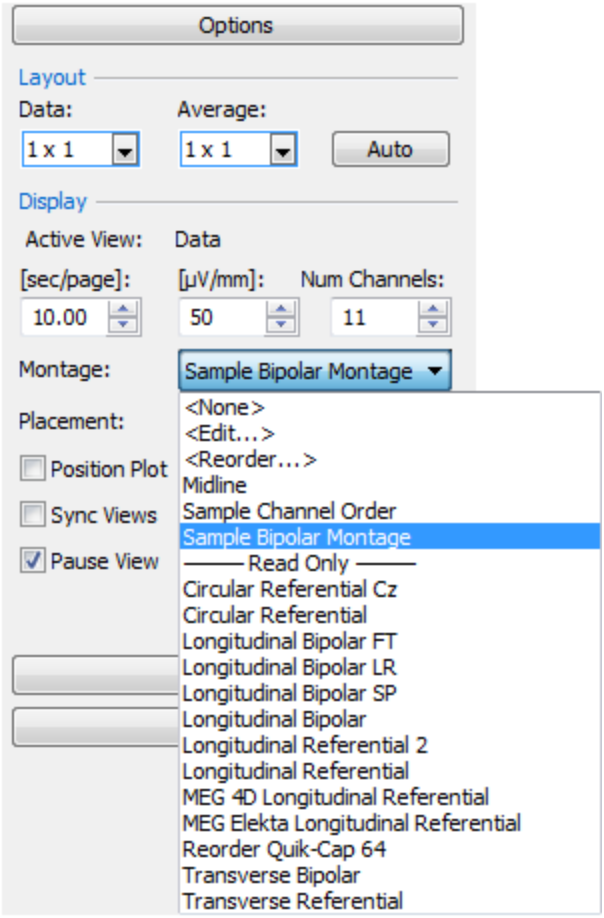
After creating the new order, click the **Save** button to save the montage file.

Lastly, if you are familiar with the Scan software, there were "Display Pages" you could create that would display only a selected subset of electrodes. These are especially useful when you have more channels than can be seen easily in the data display. In CURRY, you can create multiple "display pages" by creating a "reorder" montage that has a subset of channels. The process is the same as in the previous steps.

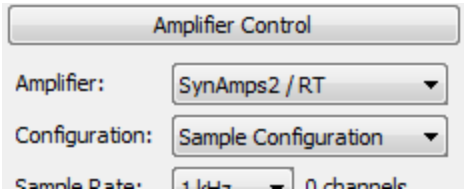
Create a new montage, select the desired channels, and save the file. In the example below, only the midline electrodes were selected.



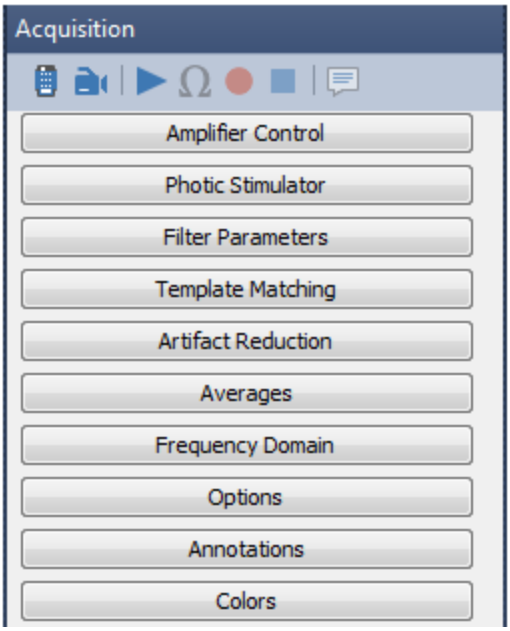
During acquisition, you can select any of the montages you have created by going to Options and selecting the file from the **Montage** drop-down list.



Everything that has been done so far has been saved in the Configuration File or in the Montage file(s). You can select these from the Configuration field in the Amplifier Control panel. You can have multiple configuration files for multiple acquisition paradigms. CURRY will "remember" the last file you used, and that will appear by default when you next open the program.



So far, we have described the functionality accessed from the **Acquisition Configuration** icon . The changes you make and the files you create will all be saved as configuration files. Additional parameter settings are found in the **Acquisition** parameter panels.

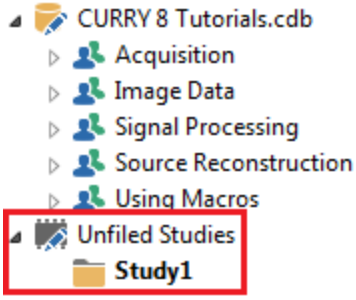


These will be discussed in the subsequent tutorials. The important thing to understand at this point is that these parameter settings can be saved as **Study Parameters**. They are not saved in the configuration files. Study Parameters can be loaded into a Study when you are preparing to acquire data, and therefore you will not need to enter all of the information each time.

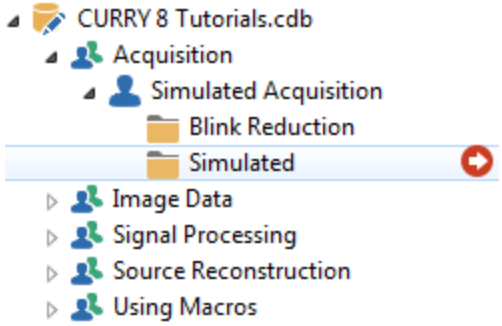
2.2.2 Simulated Acquisition

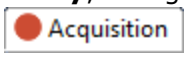
Before you connect to a live subject, you should spend some time becoming acquainted with the acquisition functionality. You can do this most easily by placing the system in **Simulator** mode. In this Tutorial, we will examine the common options that are used during acquisition. We will demonstrate them by replaying an existing data file. In the process, we will be making selections from the Acquire parameter panels. The following tutorial touches on some of the more commonly used options; see the remaining Tutorials - online and offline - for a wider sampling of options.

1. To place the system in acquisition mode, select Start an Acquisition from the **Workflow** list, or click the **New** icon on the Toolbar. This method is used primarily when you want to do a quick acquisition. An Unfiled Study is created below the Database you have opened. Close the Study to exit acquisition.



If you are planning on recording multiple data files, it is a good idea to use the Database structure. In that case, you can create an "empty" Study, that is, a Study with no Functional or Image data files in it, or, you can create a more formal Database for organizing all of the subject data you will be recording. The *CURRY 8 Tutorials* Database has an empty Study, shown below. When we make a recording, the file will be inserted into this folder.

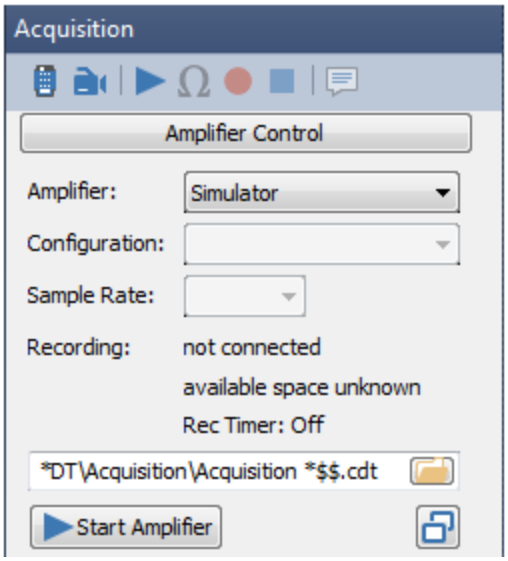


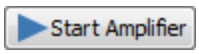
2. Open the Simulated Study (*double-click* on it, *right click* and select **Open Study**, or highlight the Study and click the icon). You will see the 

display, with nothing in it (other than the Not connected message).

3. The **Acquisition** parameter panel will appear, with the

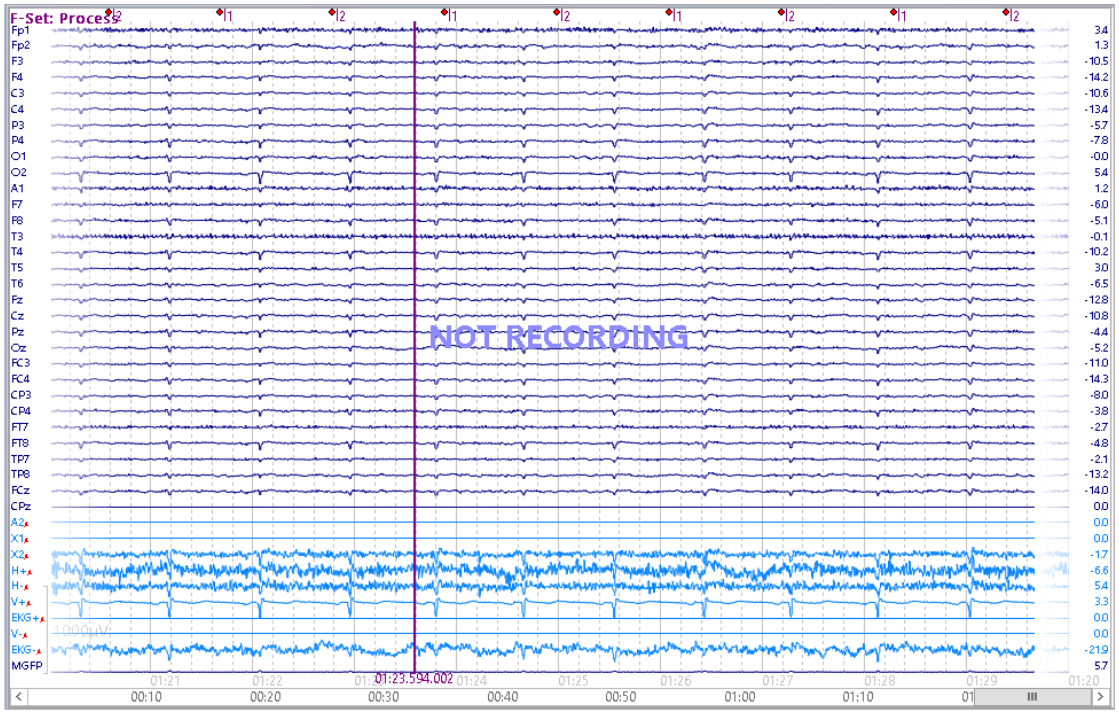
panel expanded (or expand it as needed). Select **Simulator** from the **Amplifier** drop-down list. (To learn more about the paths and substitutions for the files to be saved, please see the **Substitutions for Paths** tutorial).



Click the 

button. You will see an open file dialog. Go to the *C:\CURRY 8 Tutorials\Acquisition\Simulation* folder and select the *Tone Pictures with EKG Artifact.cnt* file. This is a file in which alternating tones (Type 1s) and pictures (Type 2s) were presented to the subject. The file was recorded intentionally with large pulse artifact, and there are occasional blinks in it. After selecting the file,

you will see it being replayed. Use the *mouse wheel* to control the display scale (click in the display if needed to change the scale).



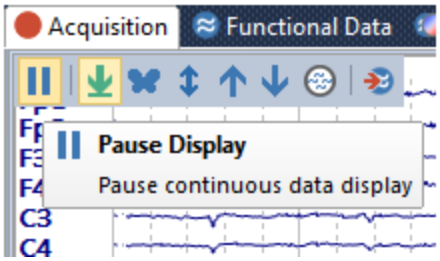
Note the 1's and 2's at the top, indicating the latencies of the tone and picture stimuli. Click in the data display. The voltages on the far right correspond to the placement of the vertical line.

4. There are several channels at the bottom in a different color. These are "Other" channels, and they include some channels that were not connected, and others that were artifact channels. "Other" channels will be excluded from certain analyses, such as PCA/ICA, MGFP, etc., where their presence would distort the results. The red A indicates that these channels are Autoscaled.

To hide the flat line channels, *right click* on each of their labels and select **Hide Channel**.

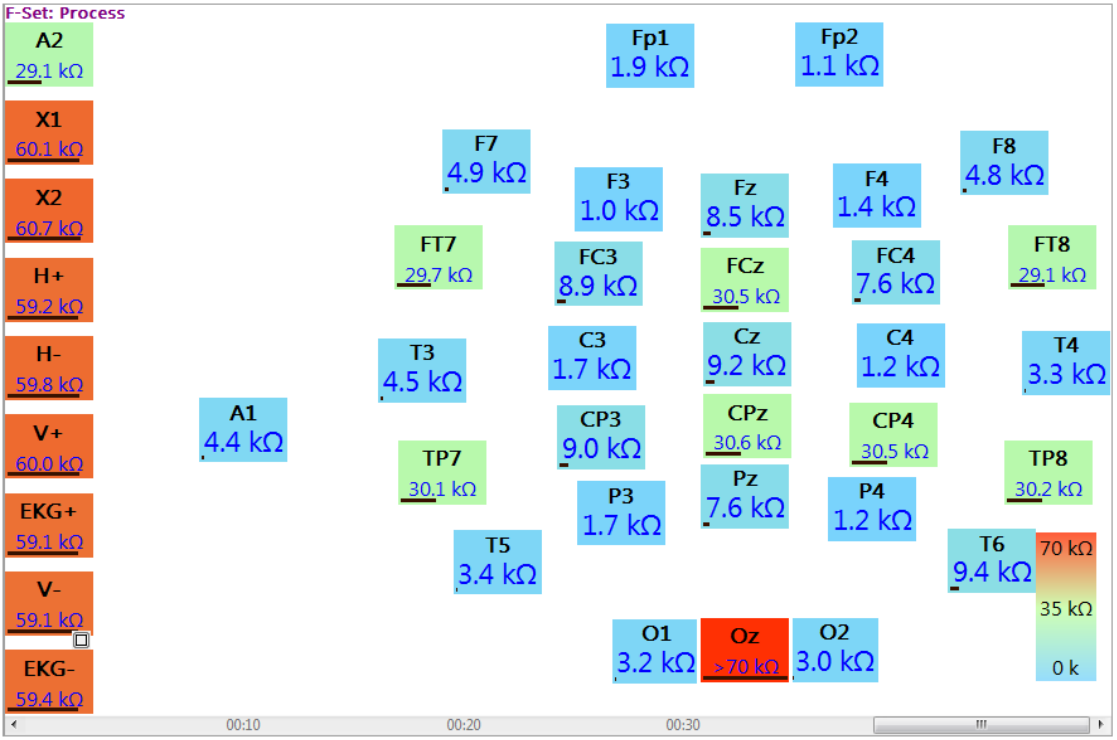
5. Note the sliding bar at the bottom of the display. The longer the replay runs, the shorter the bar becomes.

Grab the bar and drag it to the left. The scrolling display stops. Data are still being replayed, but the screen has been paused. Drag the bar forward and backward to see any part of the file that has been displayed. To restore scrolling, move the slider all the way to the right. You can also click the Pause button on the Acquisition Toolbar to pause or restart the display.



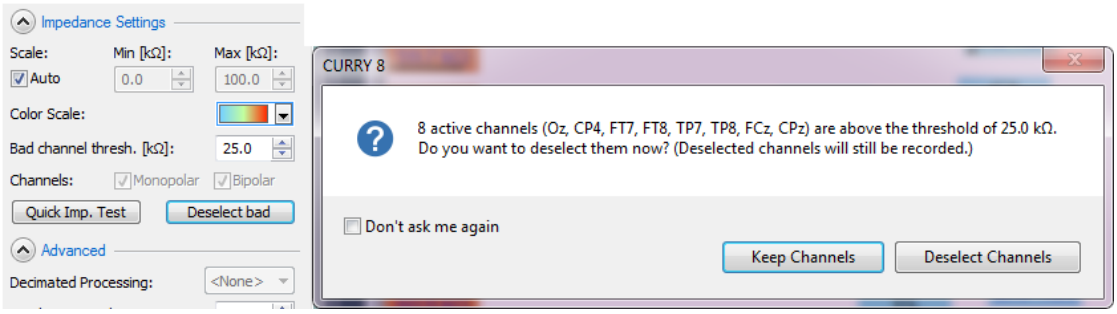
At times you may need to select a Timerange (such as, when using Template Matching or source reconstruction). With the display paused, click once before the area of interest. Use *Shift+left mouse* to set a second cursor at the end of the section.

6. Obviously, with no amplifiers connected and no real subject you cannot do an Impedance test, but you can do a simulated one. With the replay running, click the button. What you are seeing are simulated impedance values, where one EEG channel is intentionally bad as well as the artifact channels.

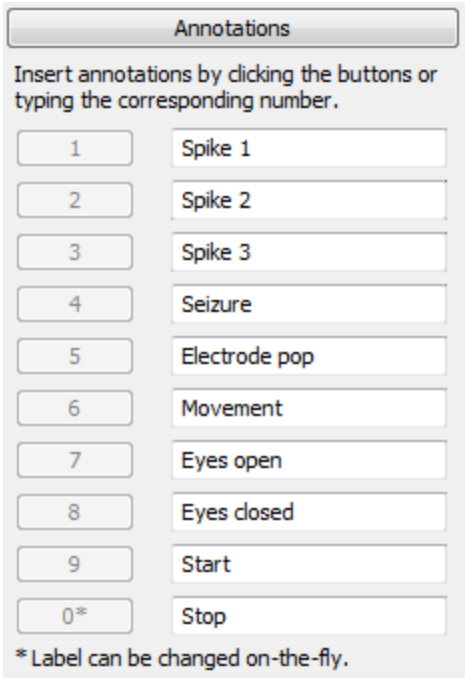


Experiment with the Impedance Settings to see what each does. Change the **Min** and **Max** values, try a different **Color Scale**, and select a different **Bad channel threshold**. For example, set the threshold to **25** kOhms, and then click the

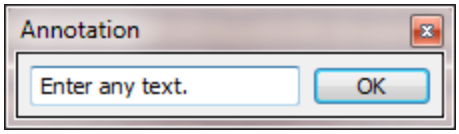
button. A message will appear listing all of the "bad" channels, and asking if you wish to Keep them or Deselect them. Click Deselect. Click the Impedance button again to return to the data display, and you will see the deselected channels have been grayed out (but would still be recorded).



7. Expand the Annotations panel. Click on one of the buttons from 1 through 0* (or the *1-0* number keys) to add that text to the continuous data file. You can change any of the text fields, and the new text will be added when you click the button. You can add the text when the data are scrolling, or after pausing the display and clicking where you want the text to appear. You may save the changes you make as Study Parameters (or Global or Last Used Parameters).

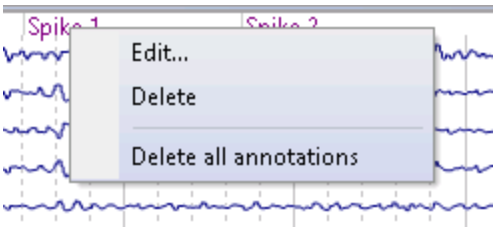


The 0* field has a slightly different function. If you click the 0* button, or the *0* key on the keyboard, while the continuous display has the focus, you will see the following dialog appear. You can enter any text at this point, and the annotation event will be added to the file *at the point where you clicked the button or key*. This lets you click a point in the recording as it happens, and then decide what text you want to enter. In all other cases, 1-9, the text has been entered already.



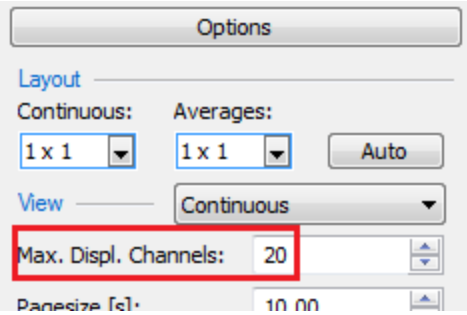
The annotations appear at the top of the data display.

Right click on an annotation to see the following options. If you have the display paused, you may grab-and-drag the annotation to a different location.

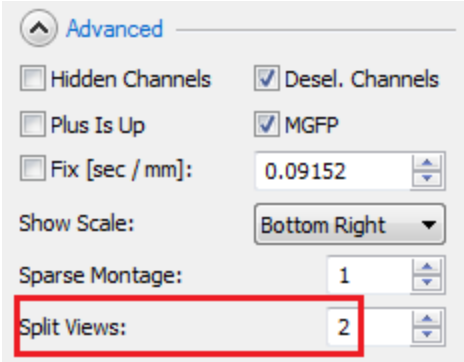


The annotations will be saved in the data file, and will appear as m1, m2, m3 ...m0 in the **Event List**, with the Annotation displayed. These events are treated as any other events (you may create epochs about them).

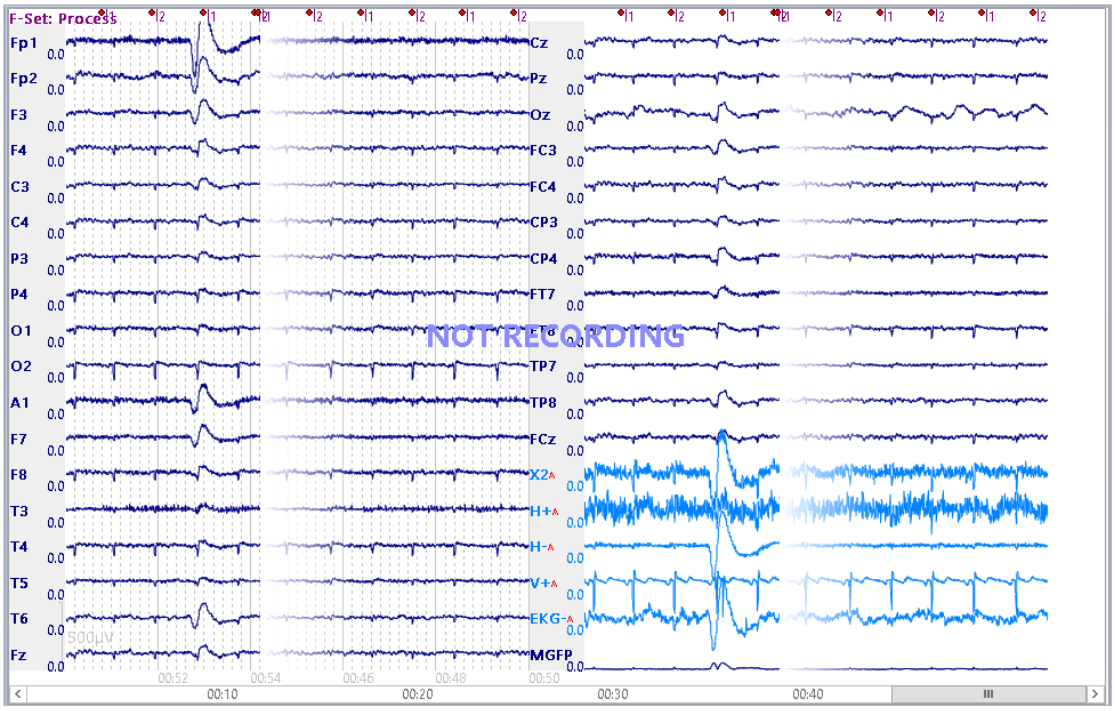
8. Expand the Options panel. Decrease **Max. Displ. Channels** to **20**. Now only about half of the channels are displayed at a time. Use the scrolling bar on the far right to scroll down to see the other channels.



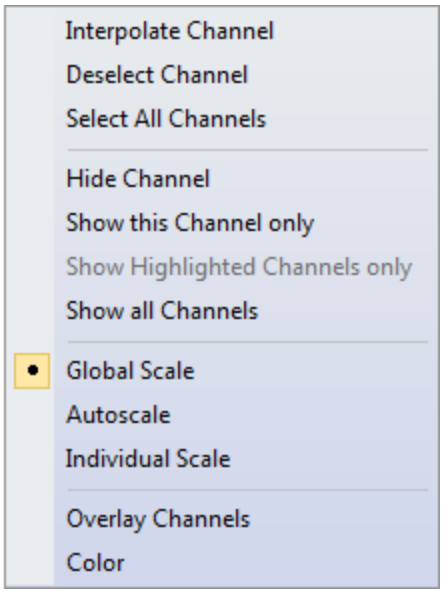
Return **Max. Displ Channels** to **36**. In the **Advanced** section under **Options**, change **Split Views** to **2**.



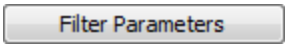
Now half of the channels are on the left and half on the right. Set Split Views back to 1.



9. *Right click* on an electrode label to see the following context menu. The options are fairly self-explanatory; context menu options are found throughout CURRY.



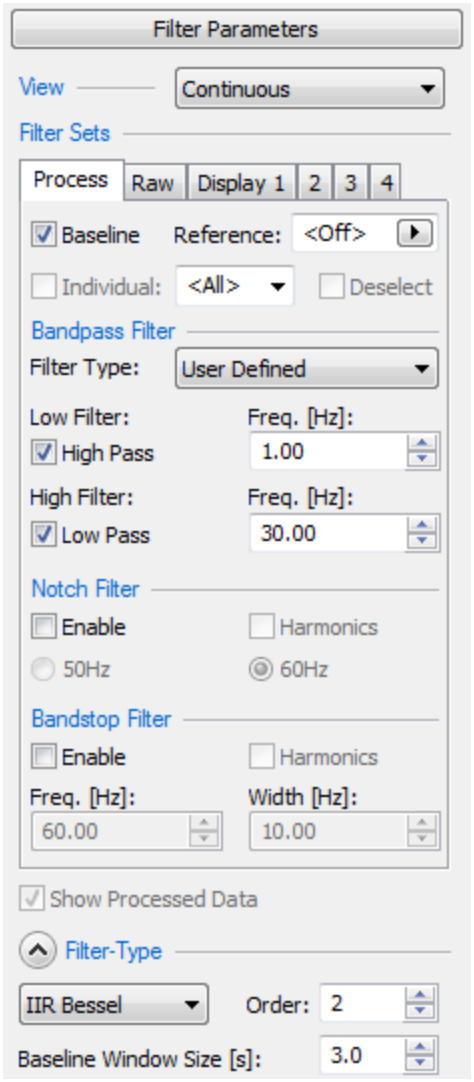
Interpolate Channel allows you to replace the existing, usually bad, channel with one that is the average of neighboring channels. **Global Scaling** means that the *mouse wheel* will rescale all channels, unless they have been designated otherwise. **Autoscale** scales the selected channel automatically, and it will not be affected by the *mouse wheel.* **Individual Scaling** lets you rescale the selected channel as desired. **Overlay Channels** lets you overlay additional channels on the selected one.

10. Expand the 

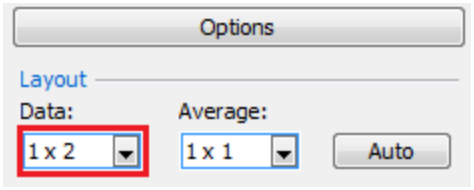
panel. Most of the options are fairly obvious, but we will point out a couple of things. There are up to 6 Filter Sets: Process, Raw, and Display 1 through 4. The parameters can be set individually for each filter set, and those filter sets can be applied to the screen that has the focus by selecting the desired tab. The "Process" option is a special case. The parameters here affect the data that are fed into the Artifact Reduction procedures. A **Baseline** correction is applied per default with the process filter set. The other sets are for display only. In all cases, the raw continuous data are stored, and the online averages are stored with the processing you see.

Note also that Baseline Correction and Re-referencing are included within the Filter Sets. All of the parameters can be applied to selected channels or all channels.

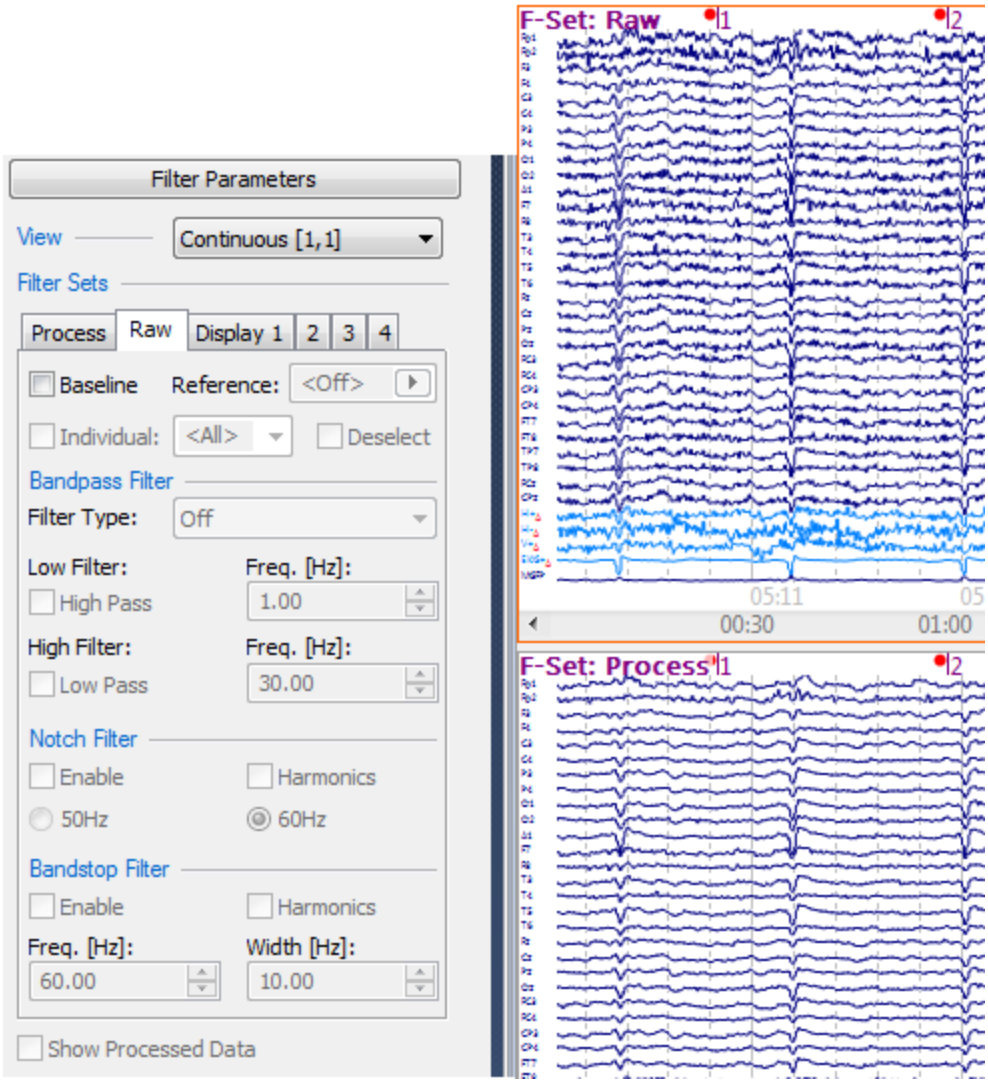
There are three filter types: Bandpass Filter (attenuates frequencies below the Low Filter, or High Pass filter, and above the High Filter, or Low Pass filter), a sharp 50 or 60 Hz Notch Filter to attenuate line noise, and a Bandstop Filter (attenuates frequencies above the Low Filter, or High Pass filter, and below the High Filter, or Low Pass filter). A Bandstop Filter is like a Notch Filter where the cutoff frequencies can be set to other frequencies.



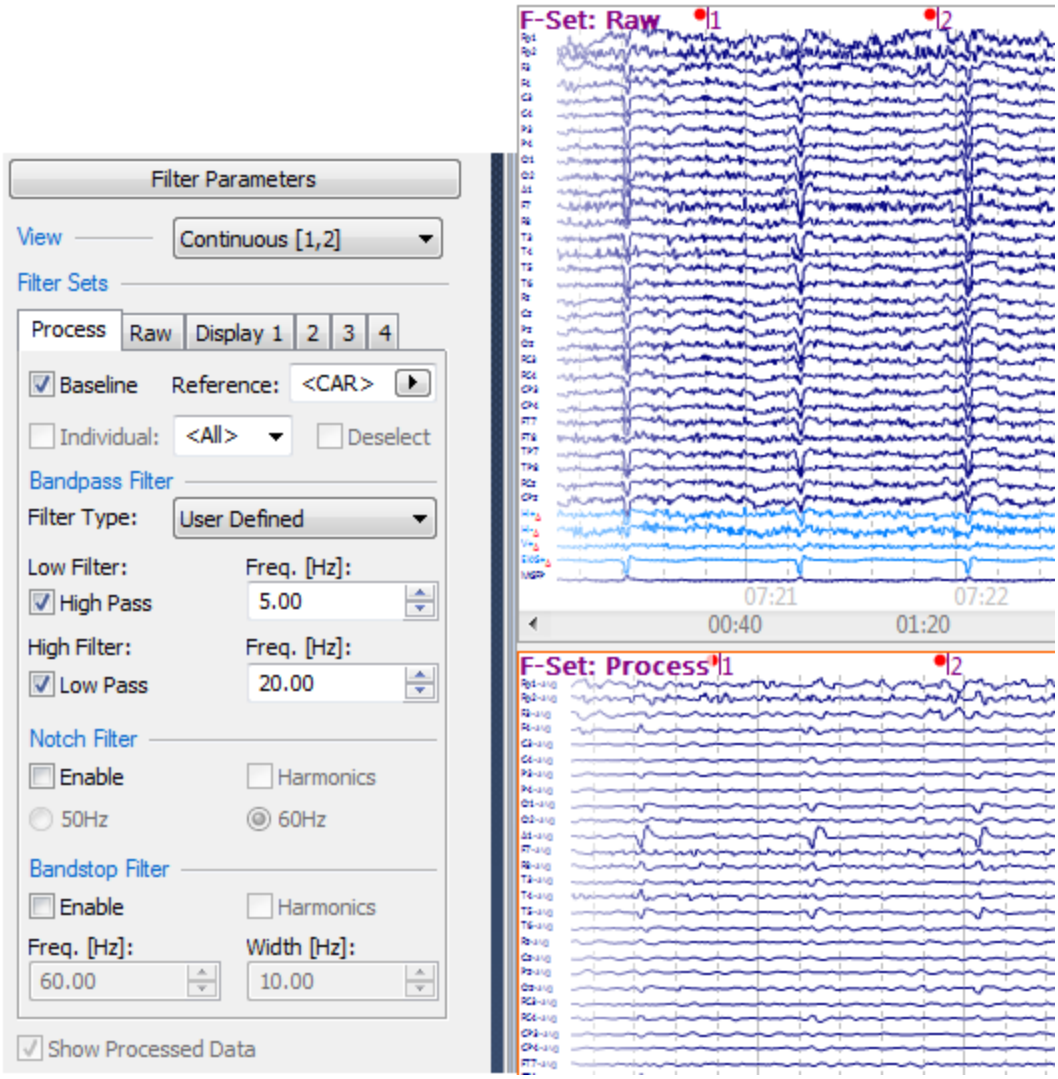
To illustrate Filter Sets, go to **Options** and set the **Data** layout to **1x2**. You will then see two identical continuous displays. We want to show the raw data in the first one, and filtered data in the second one.



Click in the upper display in order to give it the "focus". Then return to the panel and select the **Raw** tab. The only option is whether to apply a Baseline Correction, which is not needed in this file.

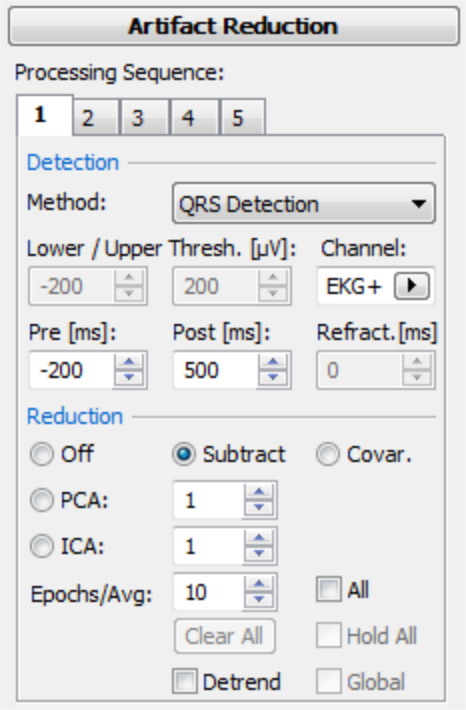


Click in the lower data display, and then select the "Process" tab (if needed). All of the options are active. In this case, we enabled the **Baseline** correction, selected the **CAR** reference, and applied a 5-20 Hz Bandpass filter (to make the effect easier to see). The effects are seen in the lower data display only. Remove the CAR when finished (**<Off>**). Set the **High Pass** filter to **1.0 Hz**.

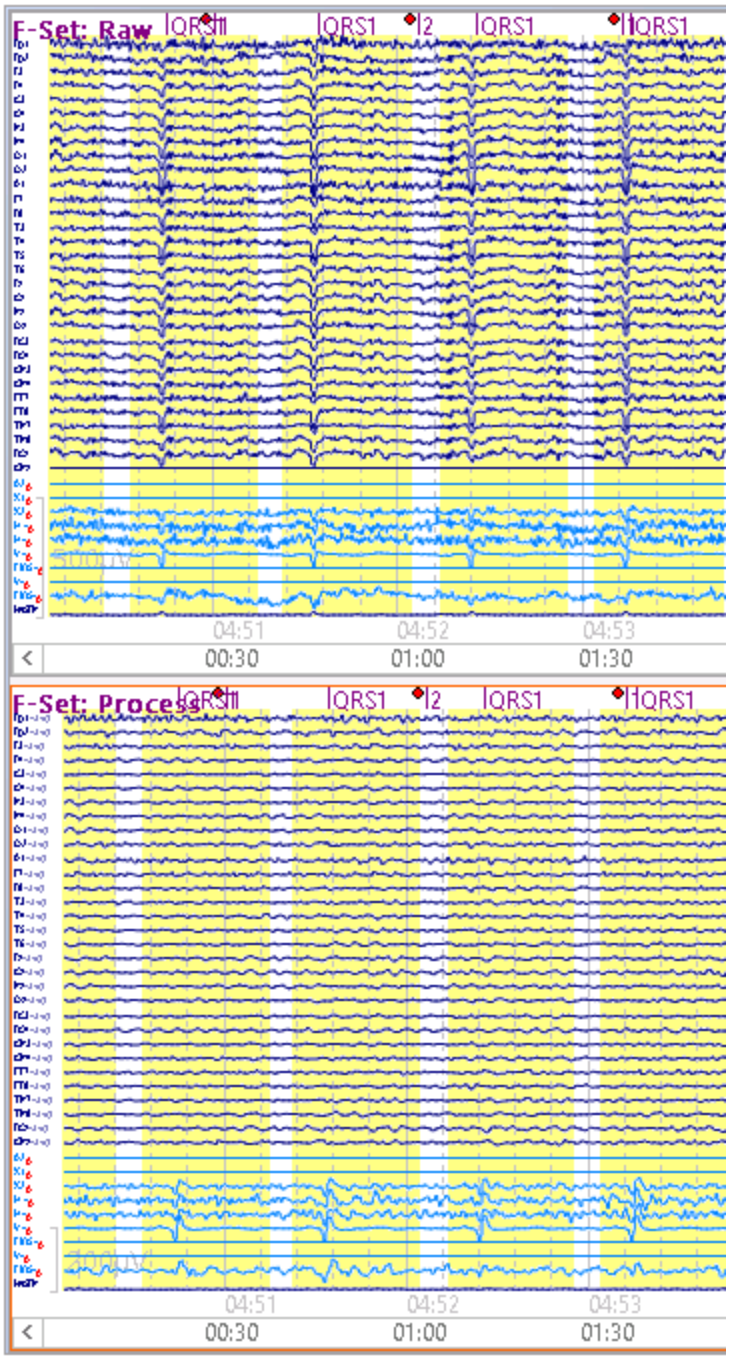


11. In this file there is a prominent pulse artifact as well as occasional blinking. We will reduce both of them. Expand the Artifact Reduction panel (Artifact Reduction from the Workflow). Recall that it is the "Processed" data that will be fed into artifact reduction.

We will first use the QRS detection method with the EKG+ channel to reduce the pulse artifact. Make sure the first tab is selected for the Processing Sequence, then select the **QRS Detection** method. Select the **EKG+** channel. Set the **Pre** and **Post** times to **-200** to **500 ms**. Select the **Subtract** reduction method, with at least **10** for **Epochs/Avg**.

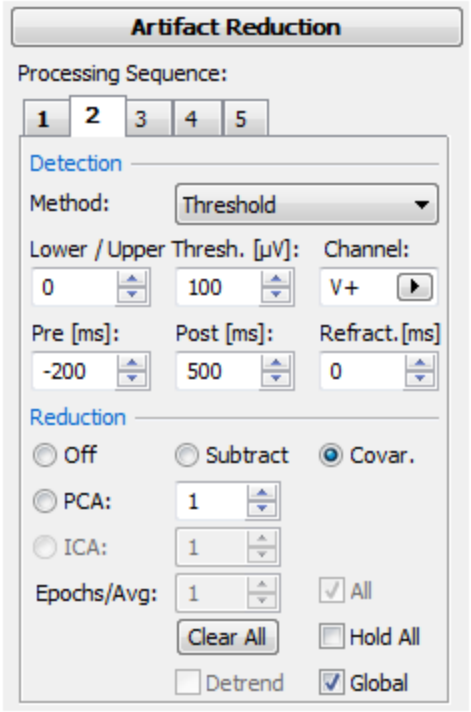


After a few seconds, you will see the pulse artifact being reduced in the lower display.

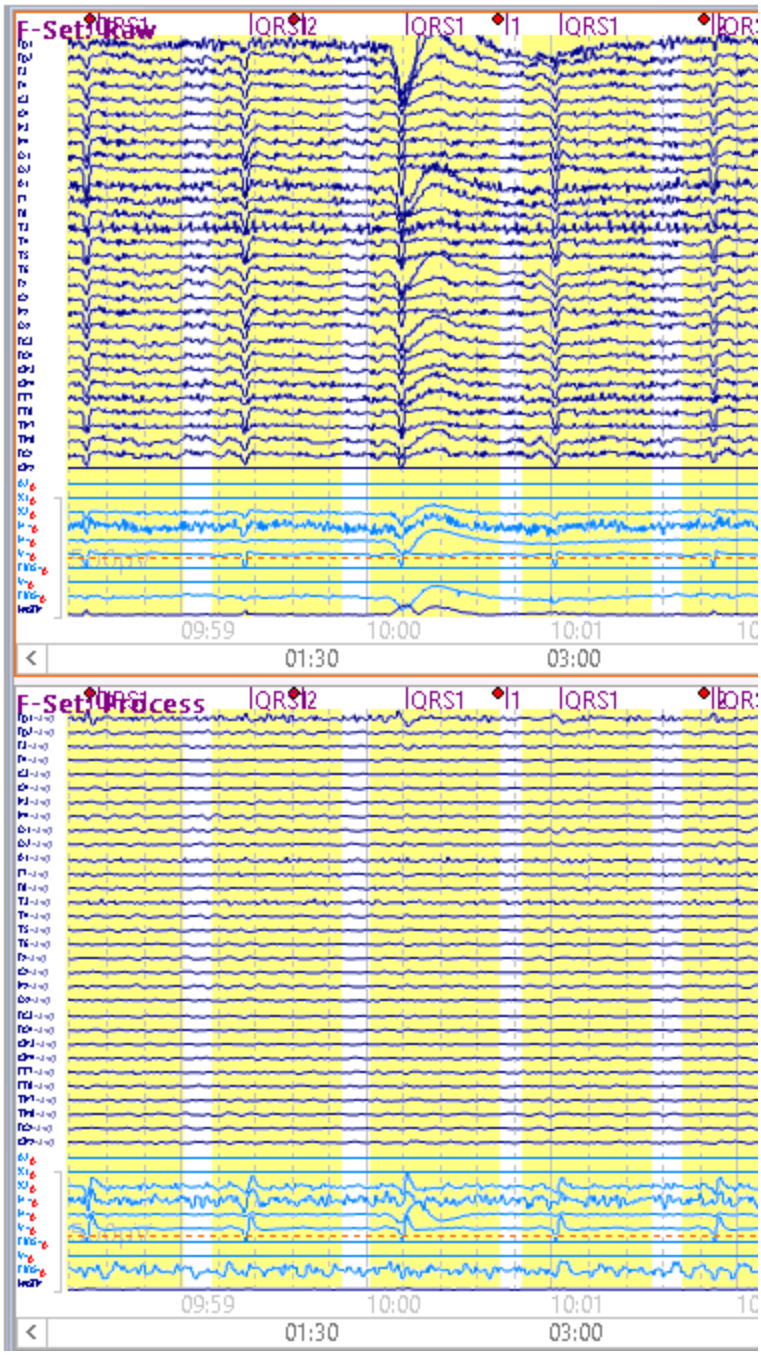


To reduce the blink artifact, first measure a few blinks (pause the display and go back in the file to a blink, then click on it and read the voltage on the far right) to determine what a reliable voltage threshold should be, such as 200μV. Select the second tab for the Processing Sequence and enter the following parameters. The **Lower Threshold** of **0** disables it, meaning that we are only using the **Upper Threshold** of **100μV**. We will use the **Covariance** method to reduce the blinks. Enable the **All** option.

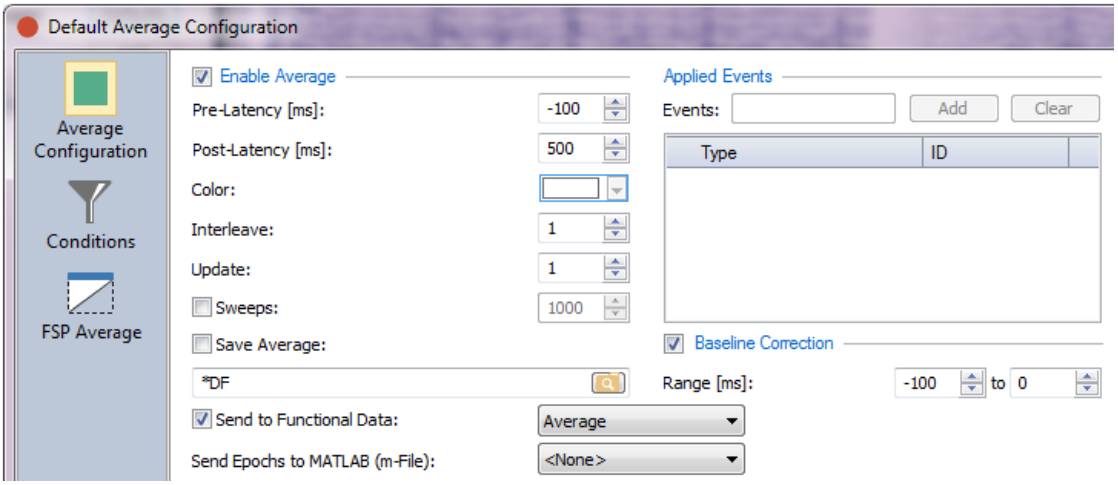
We'll digress for a moment to explain the other options: **Epochs/Avg**, **Hold All**, **Clear All**, and **Global**. If **All** were disabled, you would then use the **Epochs/Avg** field. The artifact average is then created in a rolling fashion, using the N most recent blinks (which should be at least 5-10 or more for the online correction). The **All** option means that all detected artifacts will be used to create the artifact average. The counter shows how many artifacts have been detected thus far. If you enable **Hold All**, there will be no more artifacts added to the average artifact, and the counter will no longer increment. This means that you should not enable Hold All until you have enough blinks, in this case, to get a stable average (if no artifacts have been detected when you select Hold All, there will be no correction). **Clear All** resets the artifact average and zeroes the counter. When **Global** is selected, the correction will be applied to all data points in the file from that point onward, as opposed to just those points in the artifact interval. Global is used to avoid the abrupt voltage steps that can occur at the start and end of the artifact interval.



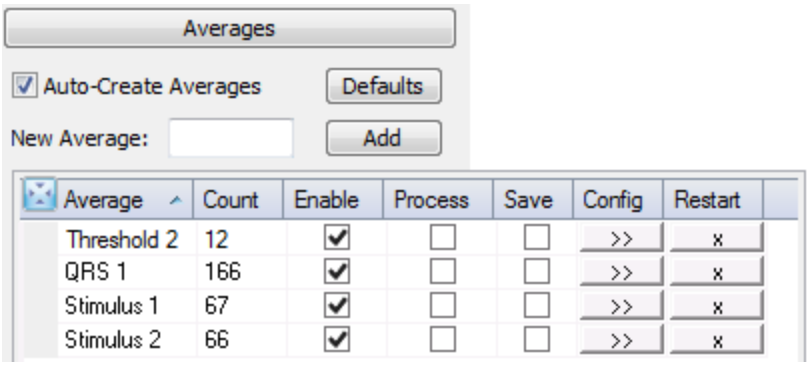
Now both the pulse and blink artifact will be reduced. The artifact is not corrected in the V+ channel (the selected channel) when you use Covariance.



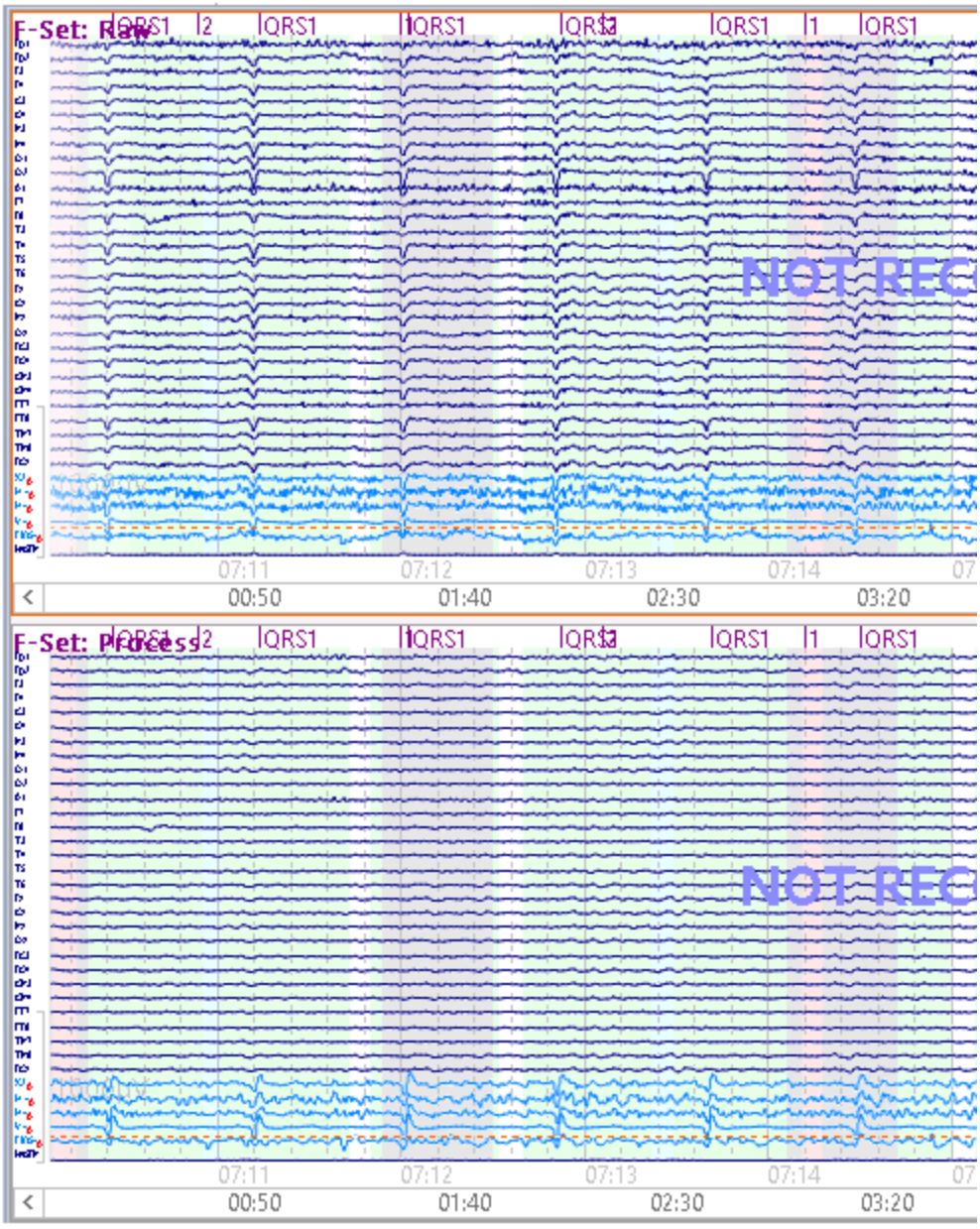
12. Expand the Averages panel (Online Averaging from the Workflow). For this example, we will do nothing more than create the online averages. More complex possibilities are seen in the online **Averaging** tutorial below. Click the Defaults button and enter **-100** and **500**ms for the **Pre-** and **Post-Latencies**. Note that the **Baseline Correction Range** also is now set to **-100** and **0**ms. Click **OK**.



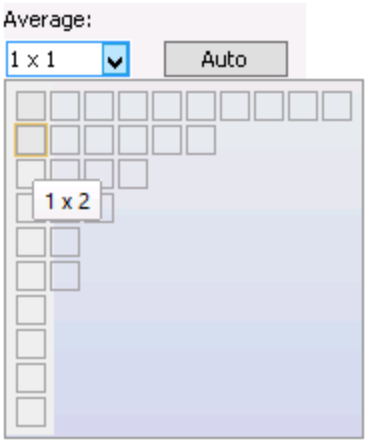
Then enable the **Auto-Create Averages** option. Averages will be created for each event, including the QRS 1 and Threshold 2 (blinks) events. We could have excluded the QRS and blink events by not using Auto-Create Averages, and instead just entering 1 and 2 for the New Averages. Exclude them now by clicking just to the left of the QRS 1 and Threshold 2 labels to highlight the line, and pressing the *Del* key.



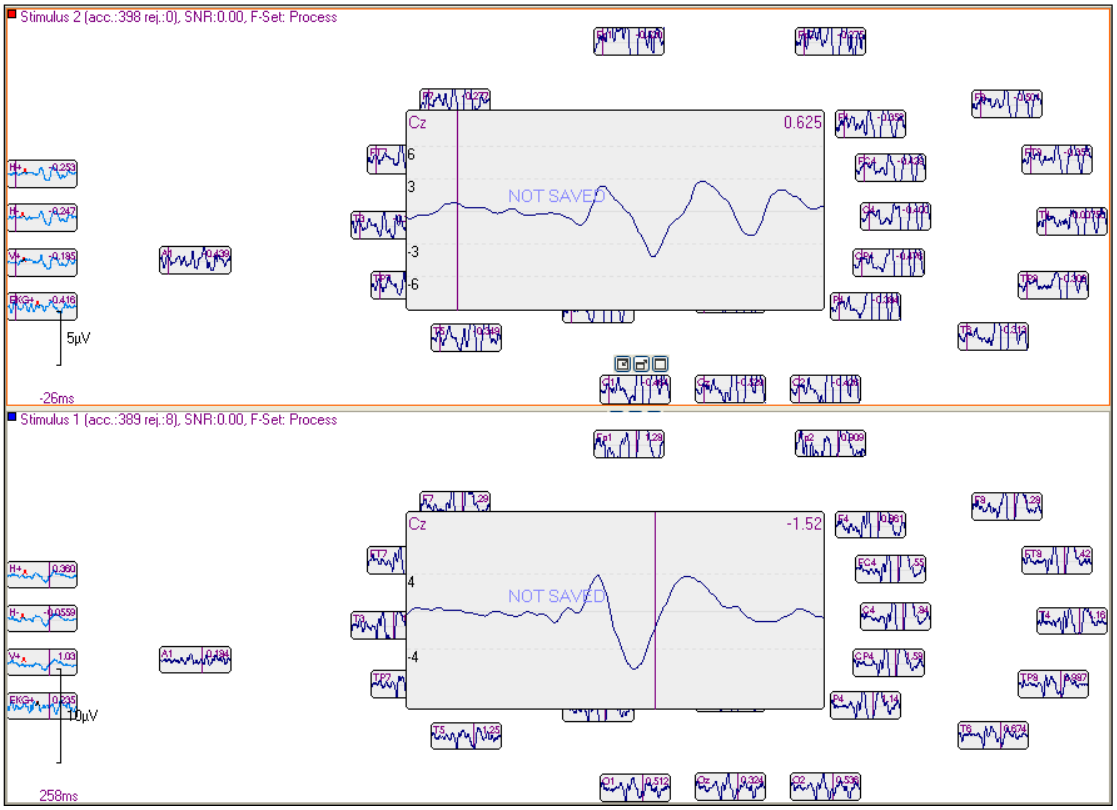
The Continuous data display becomes multi-colored, as each event type has a different color, and there will be overlapping events.



To see the averages, click the Averages tab below the data display. In the Layout field (**Options**), select the 1x2 display (for Average). You can also use the **Auto** button (in the **Options** panel) to create as many windows as needed to display all existing averages.



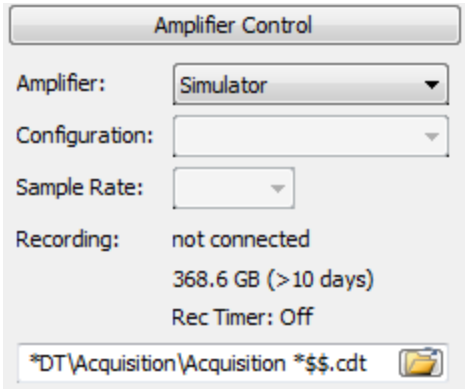
The two averages are displayed. To see the waveforms in more realistic positions, *right click* in each display and select **Position Plot**. Expand a window and scale as desired. You mayscale/move *all* channels at the same time by pressing *Alt* while scaling/moving one window.



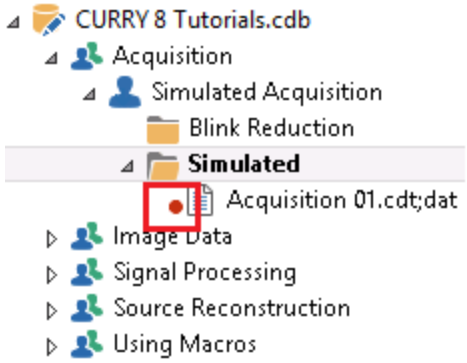
Stop the replay by clicking the disconnect button .

13. So far, we have been replaying an existing data file only. In practice, you will be recording the continuous and/or average data. To record the continuous data, first expand the Amplifier Control panel. Note the information in the **Recording** field: *DT\Acquisition\Acquisition *$$.dat. (This field will be inactive

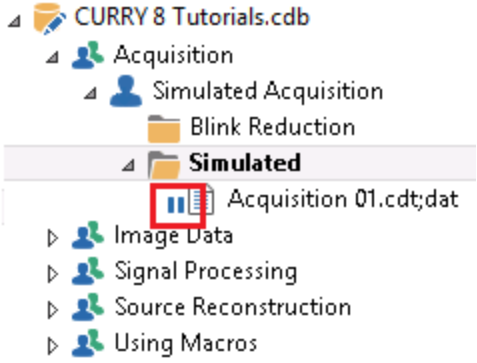
while you are recording the data - you must set the information before connecting to the amplifier, or simulator). If we were to record a data file, it would be stored on the Desktop (*DT), in a folder called Acquisition, and be named *Acquisition 01.dat* (or whatever the next available number is). See the **Substitutions for Paths** tutorial for more information. You can of course just click on the **Browse** button and save the file in the conventional method.



Click the arrow again and reselect the same data file (you may need to select the Continuous display, and set it for a single display of the raw data). Click the **Record** button to start recording the data. You will see the file being recorded in the Database. (Only the raw data are saved).



After a few seconds, click the button again, or the Stop button , to pause the recording. You will see the pause symbol appear.

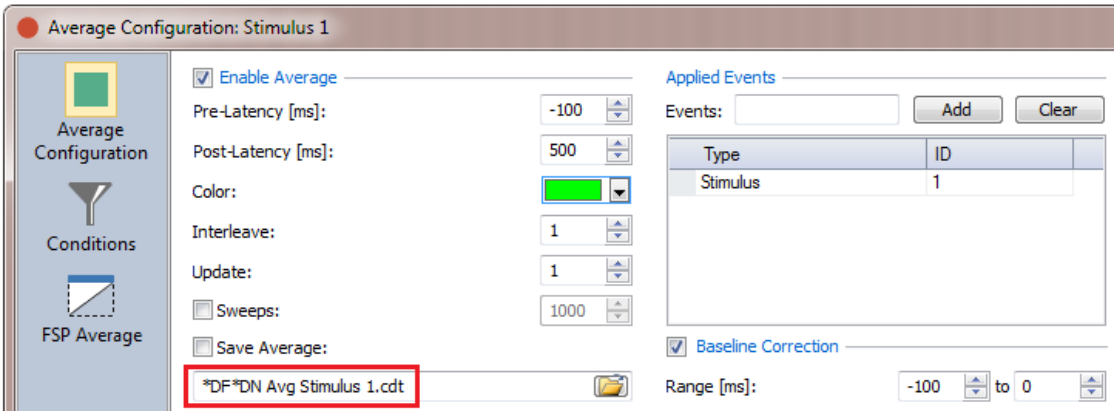


Click the button again to resume recording to the same file. Click **Pause** (on the Acquisition Toolbar) to pause the display. Click it again to resume. Click the button to stop the recording, and then click it again to disconnect from the amplifier (or Simulator).

14. If you look where the files were stored, you will see that three files have been created. The actual data file is the .cdt file. The .ceo file (CURRY Events Original) contains the events that occurred during the acquisition (this has the same format as .cef files; .ceo files are never overwritten by Functional Data operations offline). The .dpa file is the CURRY Parameter File. This are needed when you open the file offline so you can bypass the Functional Data Import Wizard. (Whenever you move the data files, be sure to move all of the files along with them). [Note that the .cdt file replaces the prior .dat file from CURRY 7 and earlier versions, and that the .dpa file replaces the earlier .dap and .rs3 parameter files].

Acquisition 01.cdt	3/31/2015 7:09 PM	CDT File	3,382 KB
Acquisition 01.cdt.ceo	3/31/2015 7:09 PM	CEO File	11 KB
Acquisition 01.cdt.dpa	3/31/2015 7:09 PM	DPA File	5 KB

Saving the averaged data files is similar. From the Averages panel, in the **Config** section, you will see the default path (same as above) and a default file name. You can alter the path using Substitutions, or you can click on the Browse button and select the folder and file name manually in the conventional way. See the **Substitutions for Paths** tutorial for more information.



In this Tutorial we have demonstrated some of the basic operations you will be performing during acquisition. Additional functionality is contained in the **Online Options** tutorials below.

2.2.3 Digitization of Sensor and Landmark Positions

Please refer to the *CURRY 8 User Guide* for installation directions for the digitizer before proceeding with digitization. See the *User Guide* also for information and procedure for using the Krios digitizer.

Using the Digitizer
The information below pertains primarily to the Fastrak digitizer.

Prior to starting the digitization process, you should have the subject sit on a comfortable chair in an upright position. The chair should have good back support, but should not have any head support to obstruct access to the back of the head. You should be able to move easily around the subject so that all electrodes are easily accessible with the digitizing stylus.

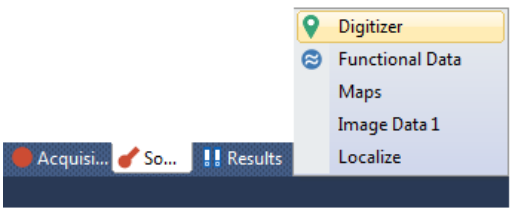
Avoid having any sources of metal in the immediate area. Use a wooden or plastic table and chair. Distortions in the digitized positions can results from metal in the recording area.

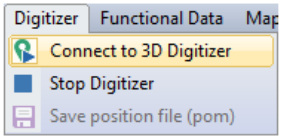
Position the magnetic transmitter less than 30cm from the subject's face. Be sure that the orientation of the transmitter is such that the positive X axis is in line of site with the subject's face, and with the power cord to the transmitter going away from the subject.

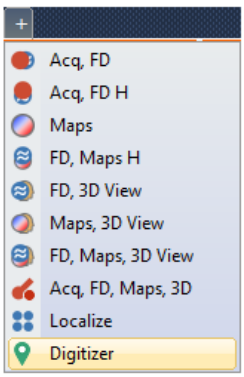
Position the three receivers on the subject's head, forming a triangular plane. One receiver should be placed at each temple and the third may be placed near the nasion (or inion). If an electrode cap is used the receivers can be attached with a Velcro strip sewn into the cap. If it is not possible to use the electrode cap, you can affix the receivers to a sturdy eye glasses frame, taking care not to move the glasses during digitization (measuring the nasion can be difficult, but possible). It is not necessary to have the head in a fixed location, although the subject should be instructed to keep his head still. The important point is to have the receivers form a triangular plane around the head; measurements are made at the point of the stylus, in relation to the plane.

Please follow these steps for using the digitizer. It is recommended that you practice the procedure with a plastic head or other object prior to using a real subject.

The **Digitizer** section is a stand-alone module, requiring a D license, that is accessed by selecting Digitizer from the options under **Acquisition**, or by selecting **Connect to 3D Digitizer** from the **Digitizer** option on the Main Menu bar, or by selecting **Digitizer** from the display options.

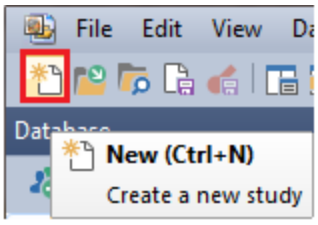




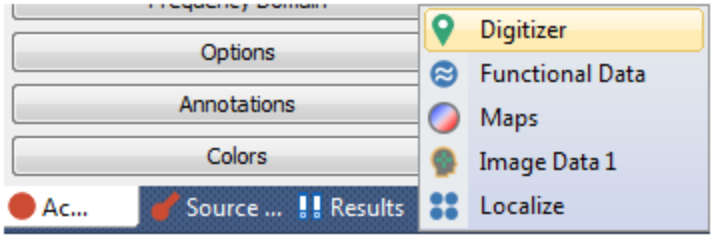


For more information regarding the digitizers and digitization, please refer to the *CURRY 8 User Guide*. For this tutorial we will use the Simulator option, which will orient you with the functioning of the program. This will give you sufficient preparation for using a live subject.

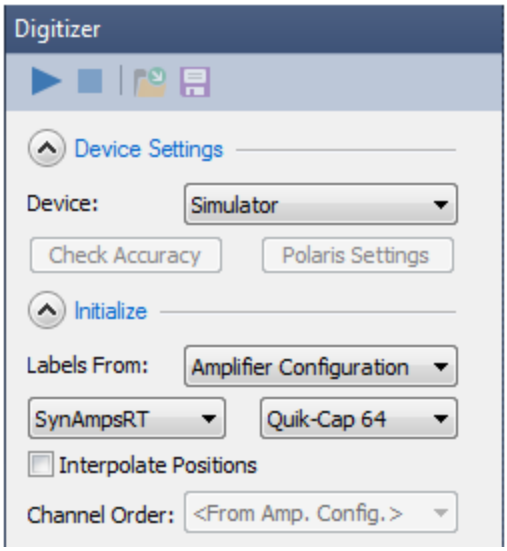
1. Click on the **New** icon on the Standard Toolbar to initiate acquisition.



2. If the Digitizer option is not seen at the bottom of the Acquisition parameter panel, select it from the list.



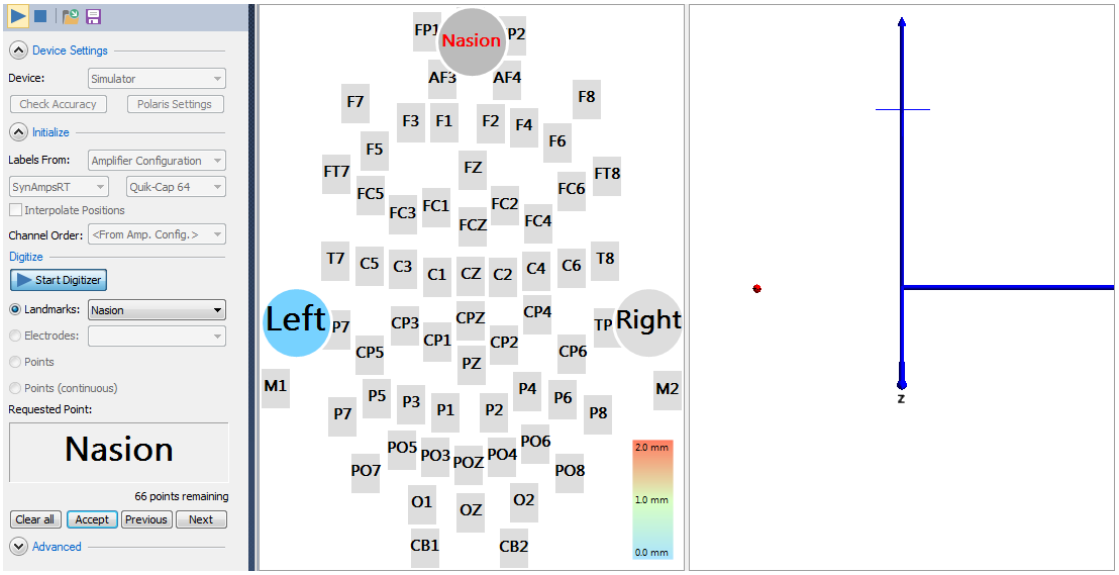
3. You can initialize the Digitizer using different sources. For this example we will use the common one - the Configuration file that will be the same as that selected under Amplifier Control. We will simulate what is seen with the SynAmpsRT amplifiers and the Quik-Cap 64 configuration file. Details for the other options are found in the *User Guide*.



4. Now click the **Connect to 3D Digitizer** button Start Digitizer. The **Landmarks** are digitized first. Note that the Left ear has been selected automatically in the

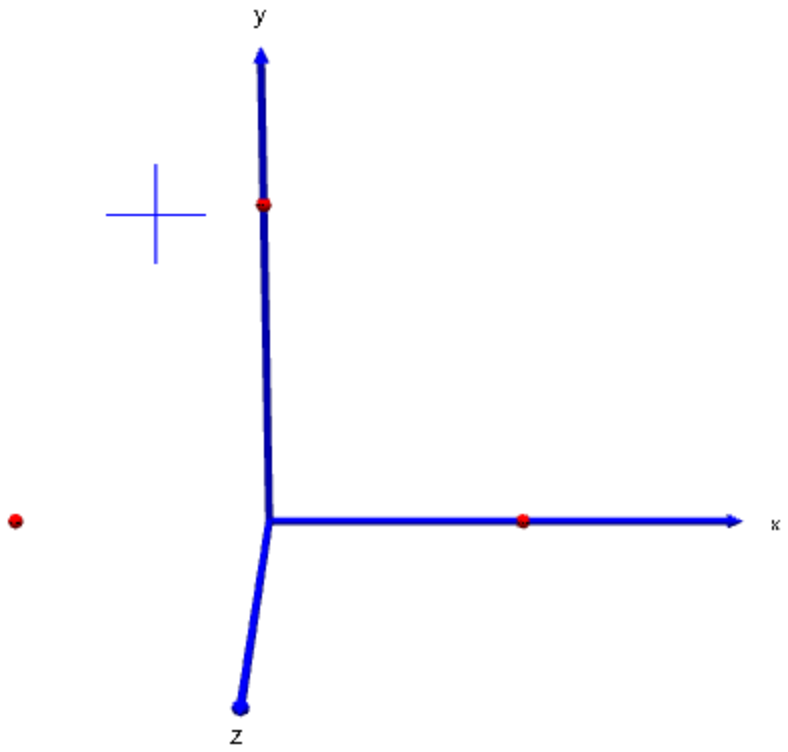
Digitizer panel, in the position plot display (Left is in red), and you see the simulated digitizer tip position in the 3D View (blue plus). In reality, you would position the stylus at the left preauricular point and click it to measure the XYZ coordinates of the position. For the Simulator, just click the **Accept** button

. The program will advance to the next landmark, the Nasion.

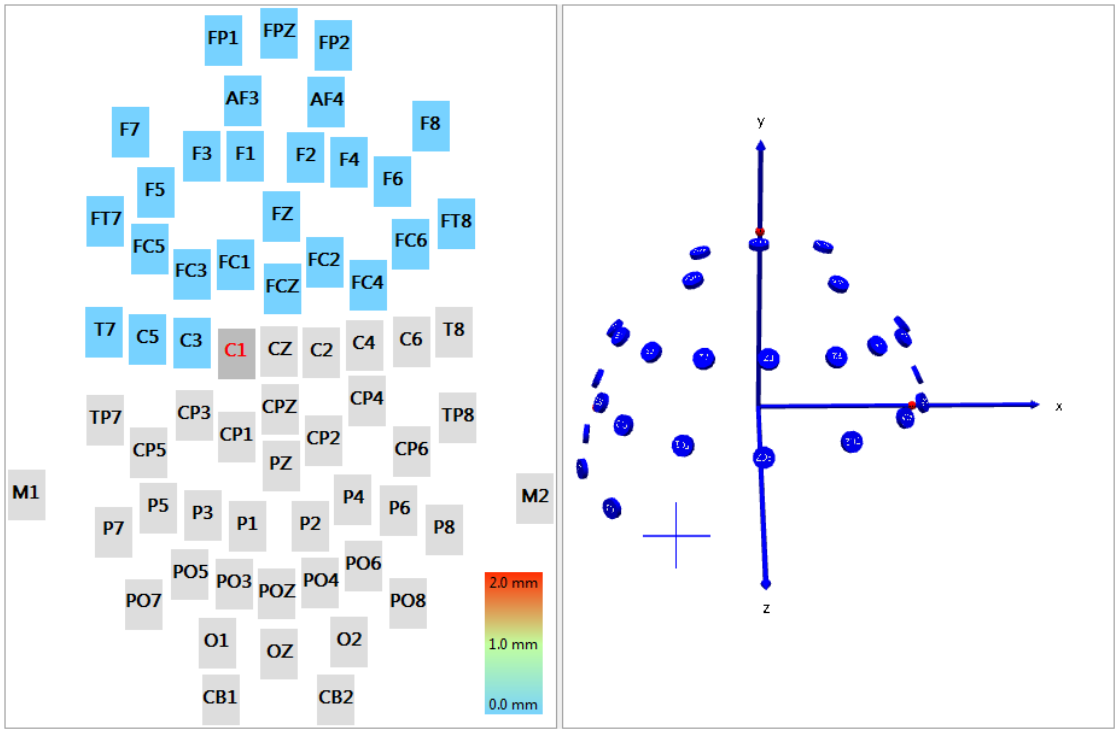


When the measurement has been taken, the "Left" symbol will turn a color. The color corresponds to the color scale on the screen. A series of points is collected and the standard deviation is computed, letting you know how stable you were holding the stylus point. You will hear a beep as well as a voice that says "Left" when the measurement has been made (hold the button down for half a second to a second; less than that could result in reduced accuracy).

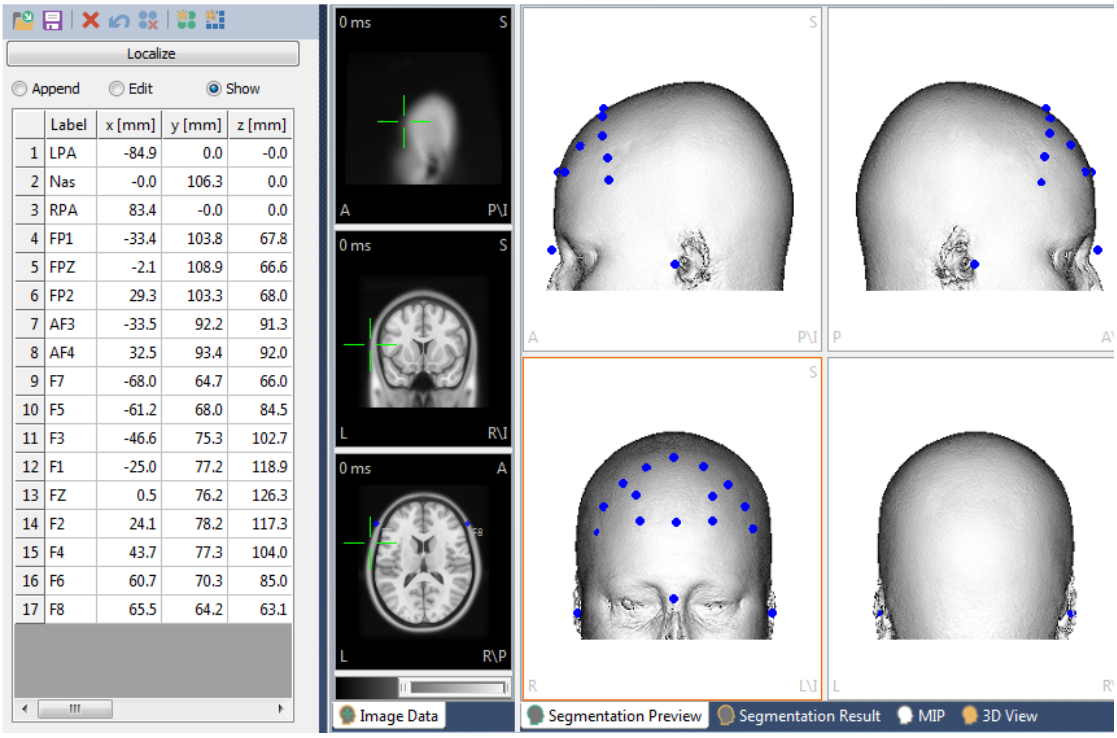
After measuring the three landmarks, you will see the positions in the 3D View as red dots. The next electrode - FP1 in this case - will be flashing red.



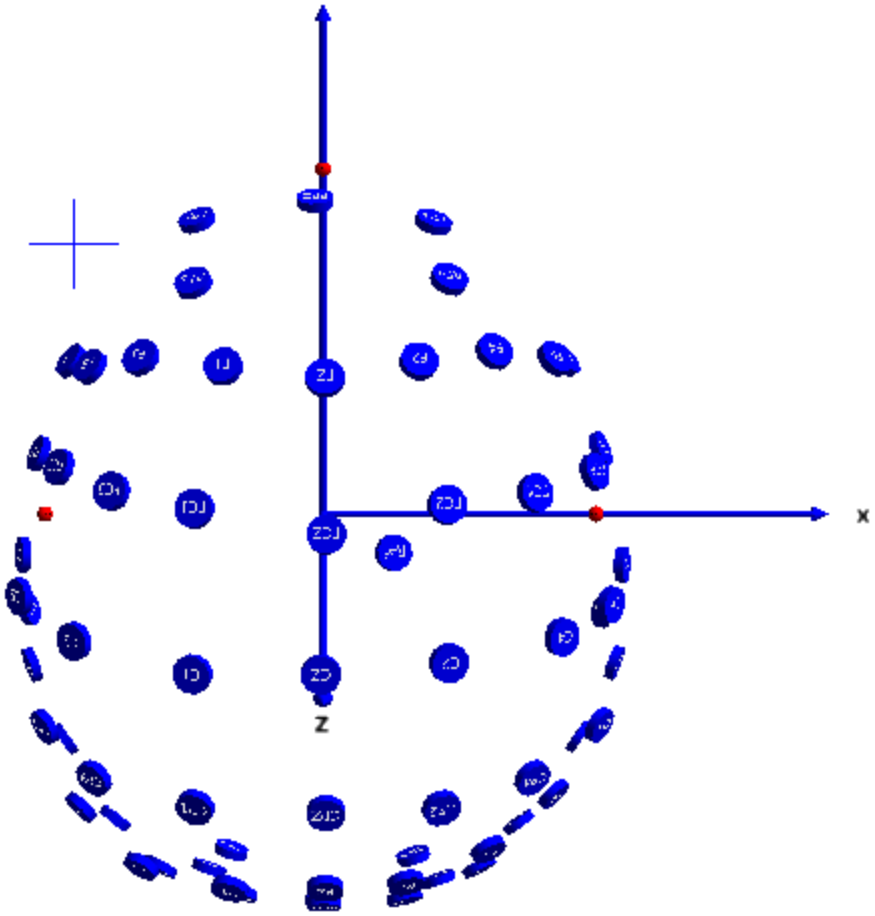
5. You will see the electrodes appear as they are "digitized", again color coded to let you know how stable the measurement was.



If you select the Localize display, you can see the electrodes on a head shape, as well as see the XYZ coordinates.



6. At the end you will see all the electrodes in position. You can grab and rotate the 3D View display to get different perspectives.

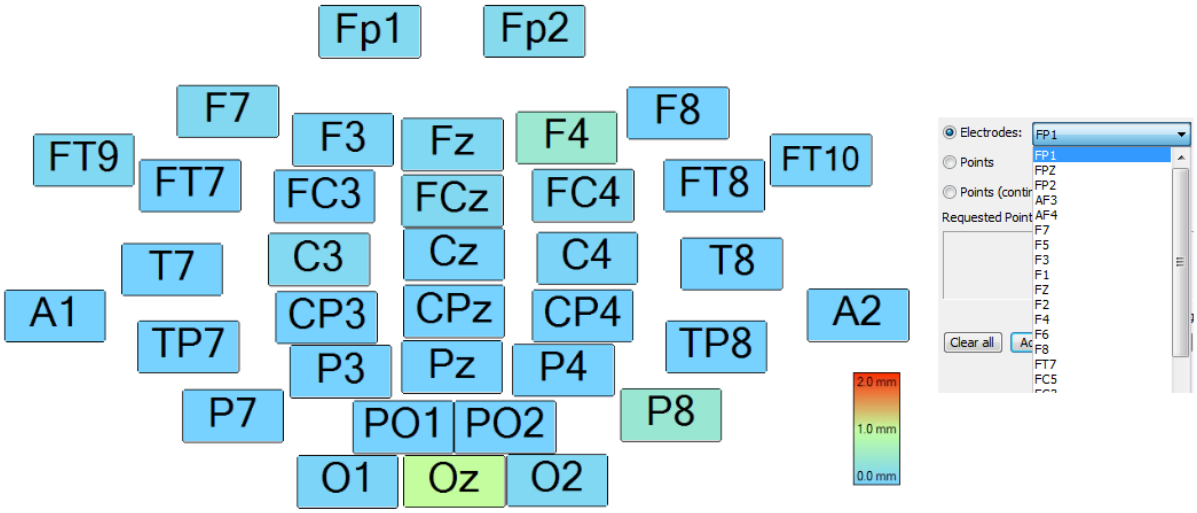


7. If you have an acquisition running, it is not necessary to save the position information explicitly. The digitized electrode positions are automatically stored with the recording you acquire (in the parameter file).

You can, however, save the positions as a .pom file from **Localize** using the **Save** icon at the top of the **Digitizer** panel. There are times when you may wish to do this. If you close and reopen CURRY, the electrode position information will not be retained. Therefore, if you will be recording subsequent files from the same subject, you should save the .pom file, and then select it either in the Database (**Insert Digitizer File**), or in the Functional Data Import Wizard. When you digitize points other than the electrodes (by using "Points" or "Points (continuous)" as a mode), you will have to save these positions to a .pom file explicitly. "Points" and "Points (continuous)" are not currently written to the .dpa files.

8. Click the **Stop Digitizer** icon when you are finished.

Additional Information
If you need to remeasure an electrode, such as OZ, you can select it from the Electrodes list and redigitize it, or *double-click* on the electrode in the Digitizer view.



If you make a mistake, such as, moving the stylus while digitizing, you will hear a different sound and the electrode will appear in red, rather than blue. The program has already moved ahead to the next electrode (F4).

In that case, you can click the Previous button, or you can select the electrode from the **Electrodes** list. Alternatively, you can move the digitizer away from the head at least 30cm and then press the button. This will automatically move back to the previous electrode. You must have **Stylus Gestures** enabled to use this option.

The last electrode in the list will be the **Reference** electrode, which is optional (and not available for NuAmps). If you digitize its position, it will not appear in the Digitizer display, but it will appear in the Functional Data display and the 3D View. It will be seen as a flat line unless you create a Common Average Reference (CAR). This will in effect give you an extra channel.

If you want to measure extra points, you can use the **Points** option. 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 (such as, for calibration purposes). If you wish to digitize the head shape, you can use the **Points (continuous)** option.

When you open the data file off line, for signal processing, the electrode positions will be present in the .dpa file. If you load image data that has properly identified landmarks, coregistration between the functional data and image data will occur automatically.

Using the NDI Polaris digitizer

Most of the information above will apply to the NDI Polaris digitizer also. If you have not followed the installation procedures already, please refer to the *NDI Polaris User Guide*. See also the Digitizer section of the *CURRY 8 User Guide* for a description of the specific options.

Generally, you need to be careful to make sure that the stylus and reference are facing the cameras at all times, and that you do not block the camera's view of either.

Since the stylus has no button, you can use either the user selected keys on the keyboard, or the voice recognition commands.

Below is a sample placement of the reference tool.

2.2.4 Online Options

There are a number of operations that may be performed online during acquisition as well as offline during the analysis. These include sorted averages, spectral analysis, artifact reduction, source reconstruction, etc. You can record the raw data and perform all of the analyses offline; however, it is useful to know that you are obtaining valid data before the subject leaves. This is especially true when recording data in the

magnet during episequencing. The artifact will be so large that you will not know if you are recording valid data unless you use the online MRI Gradient and Ballistocardiogram Reduction features.

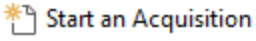
Online Data Processing Sequence
A simplified online data processing sequence uses the following order:

- 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

2.2.4.1 Averaging

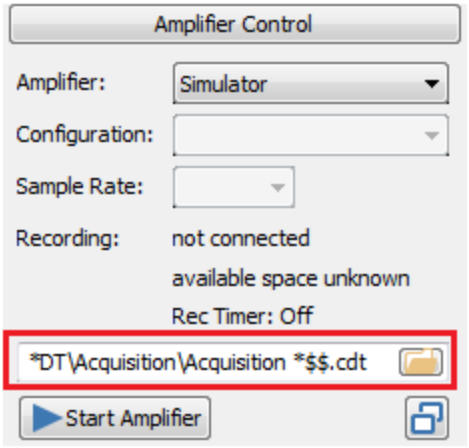
Online averaging of events is one of the most commonly used online options. While it is often the case that offline "cleaning" of the data is more effective than online (and the offline filters have no latency effects), the online averages let you know that you are acquiring good data. Some of the basic operations that involve online averages are described in the **Simulated Acquisition** tutorial above.

As usual, the initial decision is whether to record the files so they will appear in a Database, or record them in a temporary Unfiled Study. In this case, this will be a one-time set of recordings, so we decide not to use the Database, other than the Unfiled Study that will be created automatically at the bottom of whatever Database you have open.

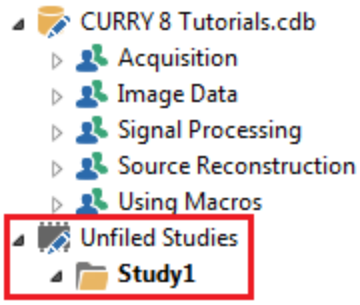
1. Click the 

option from the Workflow (or Toolbar icon) to access acquisition, and select the **Simulator**.

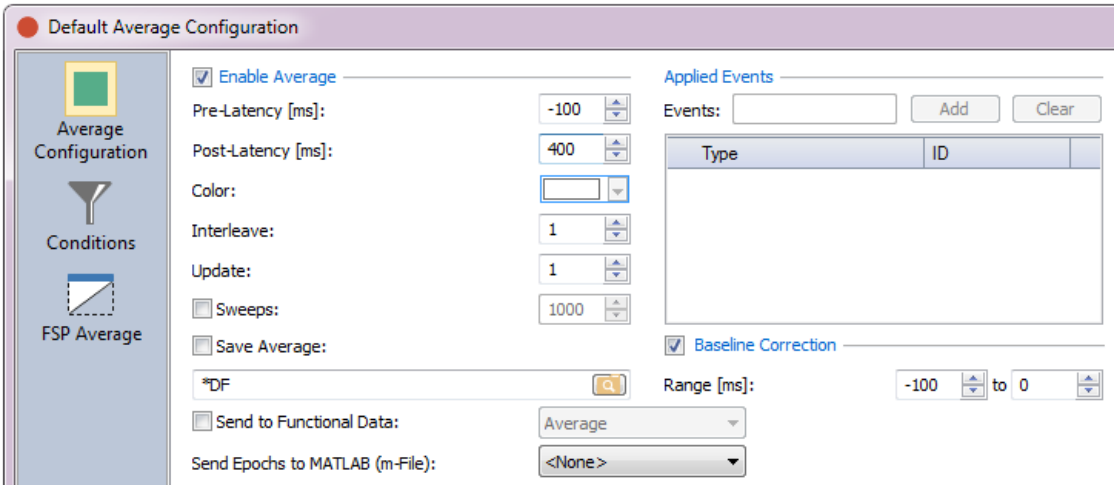
Note that a default file name and path appears in the Recording field (see also the **Substitutions for Paths** tutorial). ***DT** is a substitute for the regular path to the desktop (a Tooltip will appear showing the full path as well as what the other recognized substitutions are). **Acquisition** just after it creates/selects a folder on the Desktop called Acquisition. This is where the continuous data file will be stored. *Acquisition *$$.cdt* is the file name. *$$ is a numbering convention, meaning that files will start with 01 (or whatever the next available number is); subsequent files will be incremented automatically. The file name in this case will be *Acquisition 01.cdt*. Rather than change the path or file name, we will use the default ones.



Notice also that an Unfiled Study has been created in the Database (currently empty).

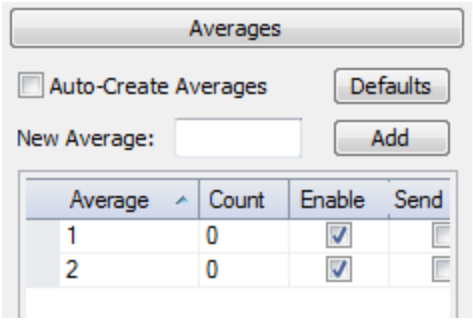


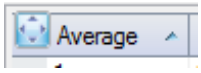
2. Expand the Averages panel and click the **Defaults** button. Set the **Pre-** and **Post-Latency** fields to **-100** and **400**ms. **Baseline Correction** is enabled using the pre-stimulus interval. As these are the default settings, all averages will use these parameters (they can be changed for individual averages later, if desired).



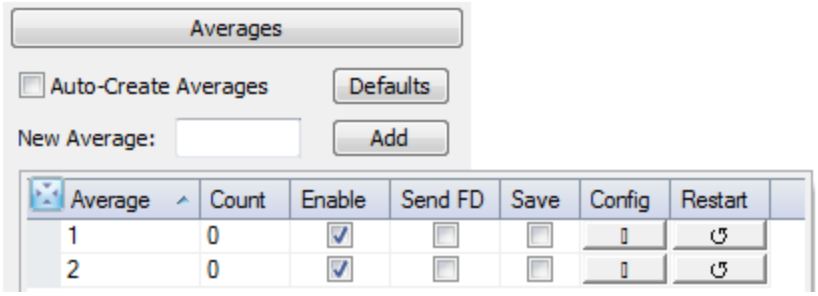
Click **OK**.

3. Generally, you will know in advance what the event codes are for the averages you want to create. In this case, there are 1's and 2's. In the Averages panel, enter **1** for **New Average** and click Add, then click **2** for **New Average** and click Add again. (We could have used **Auto-Create Averages** instead, but we want to go to the Configuration part first before doing the actual acquisition). If you want to have multiple events included in the same average, you may specify them in the field, such as, **1,2** or **1-10, 15, 20-25**. For Responses, you must use, for example, **r1**. For multiple responses, use, for example, **r1-3**.



Position the mouse to the left of "Average" to see the enlarge/reduce button 

. Clicking this displays the entire table (this is the case with all similar tables).

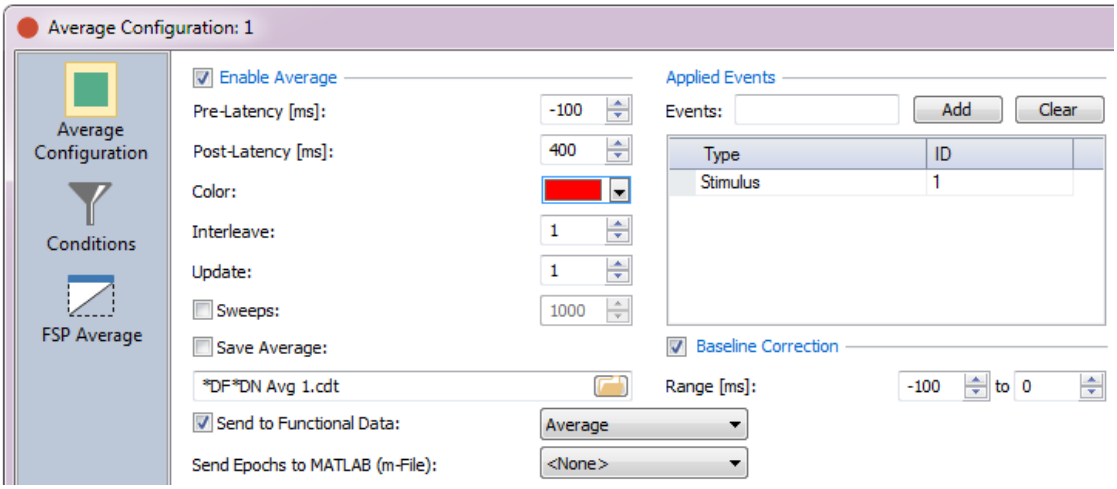


From the **Config** button (or by *double-clicking* to the left of one of the average lines), we can access all of the screens to configure the individual averages. These are also accessible from Defaults. **Defaults** will set the values for all averages; the **Config** button accesses the same screens to set the parameters for each average individually. Once you set the individual parameters, you cannot go back and change the defaults.

Click the **Config** button for Stimulus **1**. The following dialog will appear. Note that here you may change the epoch interval, the color of the shaded region, etc. **Interleave** defines how often the display updates, how often the average gets "processed", and how often it gets saved. It is used to reduce the online CPU consumption when events come in very fast; all of the epochs will be added to the average. The online average will continue to build until it reaches the number of **Sweeps** you enter.

Enable **Save Average**. Note that the file name **DF*DN Avg1.cdt* has been created by default. ***DF** is the data folder that has been specified for the continuous data file we noted above, which was *DTAcquisition - a folder on the Desktop called Acquisition. *DN is the data file name for the continuous data file - *Acquisition 01*. To that is added *Avg 1.cdt*. So the file name will be *Acquisition 01 Avg 1.cdt*, where the 01 will incremented as needed. You can select a different folder and file name by using the **Browse** button, as desired.

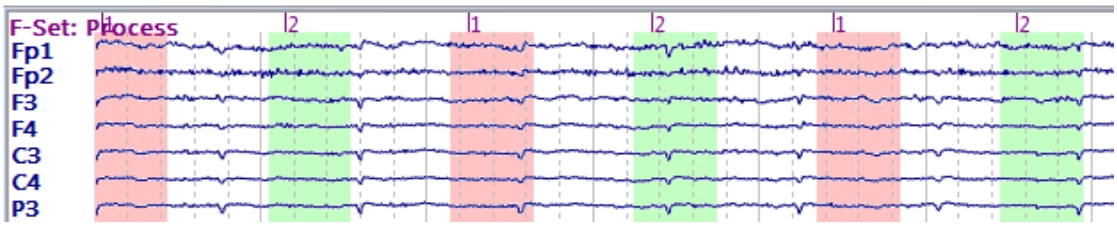
Send to Functional Data is enabled if you want to transfer the average (or single epochs) to the offline parts of CURRY during acquisition, including, for example, source reconstruction (enable it). You can also do this "on the fly". **Applied Events** shows you what events are being included. You can add more events by entering them in the **Events** field and then clicking Add. **Baseline Correction** can be enabled for the online average. Click **OK**.



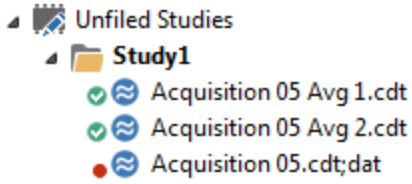
Click the **Config** button for Stimulus **2**, and note the same settings are there, except the **Color** is different and the file name will be *Acquisition 01 Avg 2.cdt*. Be sure to click the **Save Average** option. Click **OK**.

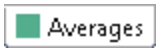
4. Click the Start Amplifier button, or the **Connect** arrow on the Toolbar, go to *C:\CURRY 8 Tutorials\Acquisition\Simulation* folder, and select the *Tone Pictures with EKG Artifact.cnt* file.

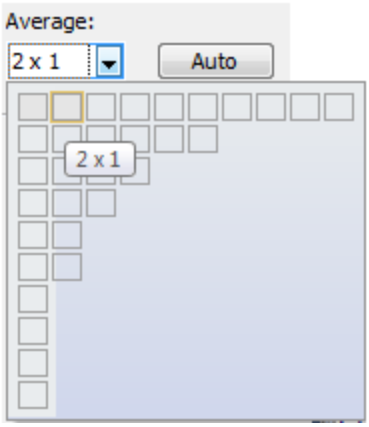
You will see the events being detected in the data display. Each will have a different color (as selected above), and the width of the color fields denotes the epoch intervals.



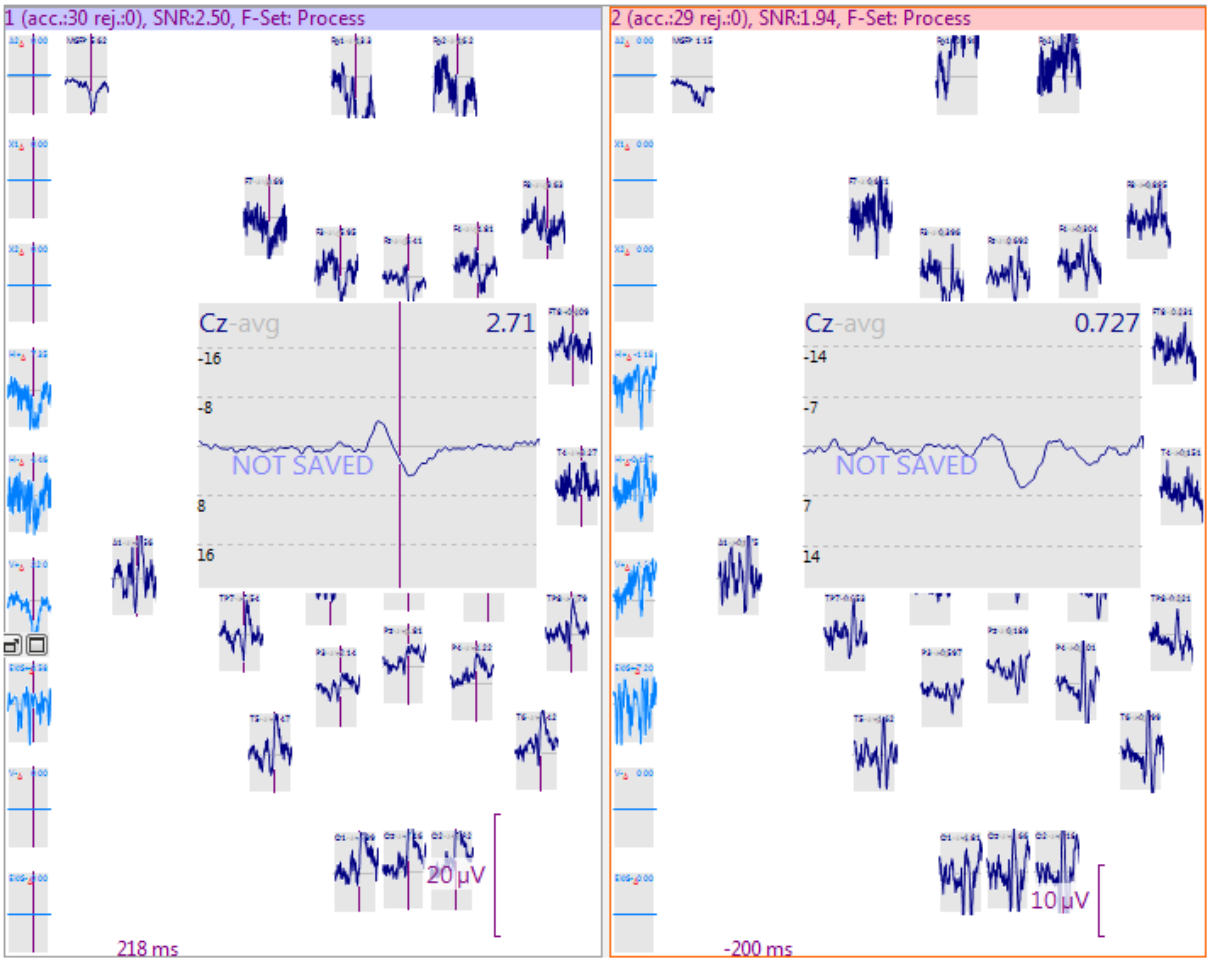
5. Click the Record icon to start saving the continuous data and the online averages. You will see them in the Unfiled Study in the Database.



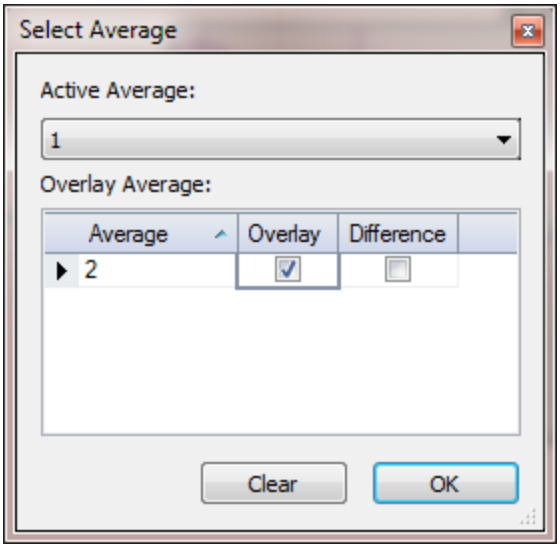
6. Click the  tab to see the averages. If you see only one, select the **2x1** layout display (under **Options**, **Average**). This will position the two averages side by side.



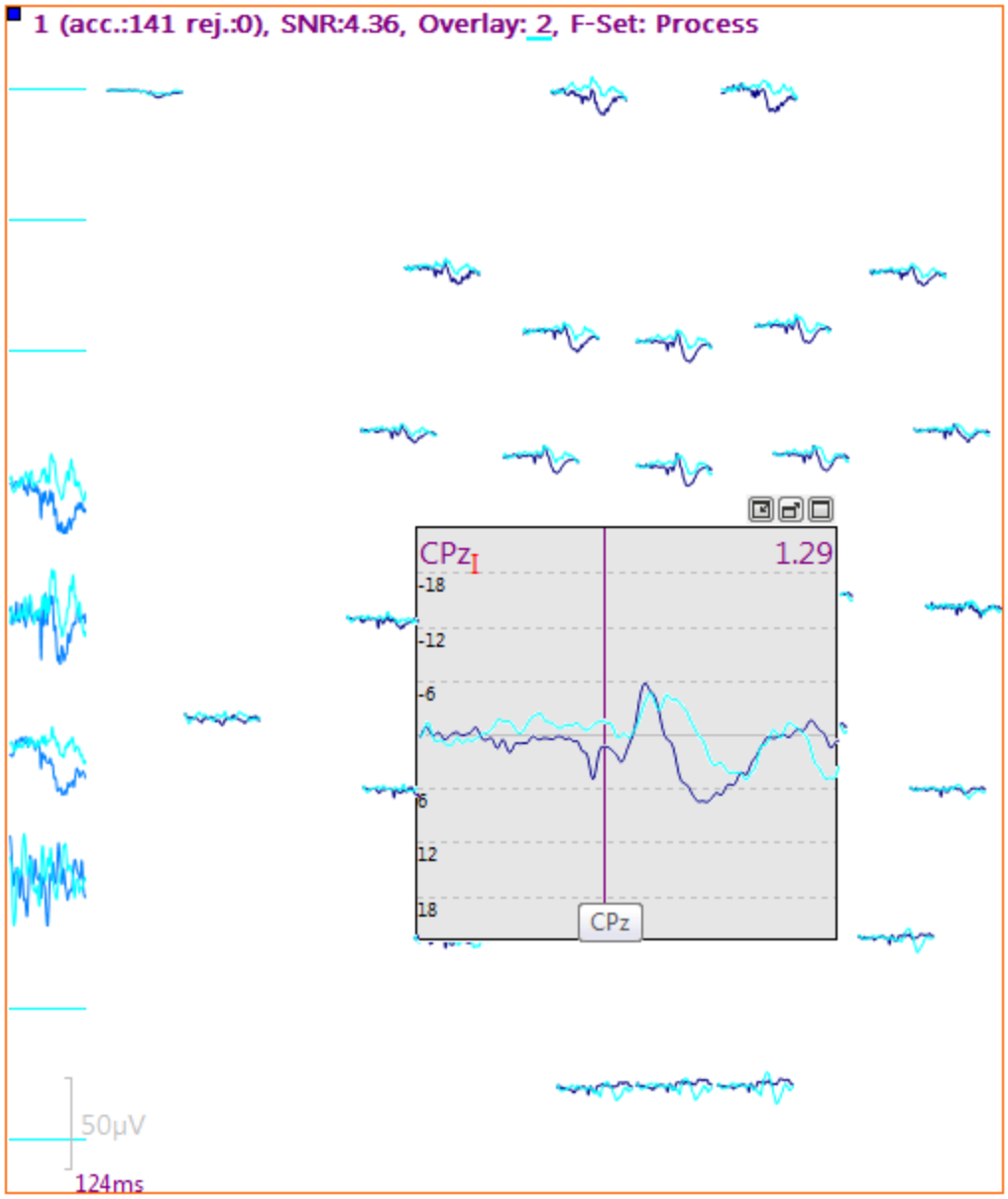
In both cases, the **Position Plot** option was selected (from the context menu). The channel labels that were not recognized, and were therefore designated as "Other" channels, are displayed on the left side (there is no position information for them). A single channel was selected and enlarged, and both displays were rescaled.



Right click in the Stimulus 1 display and select **Select Average**, or click the button from the Functional Data toolbar. Enable **Overlay** and click **OK**.

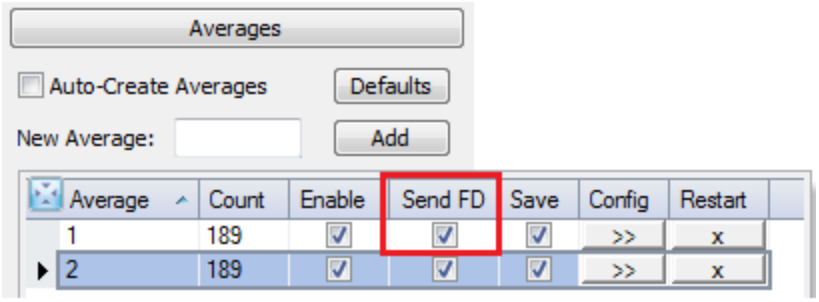


You will then see the two files together.

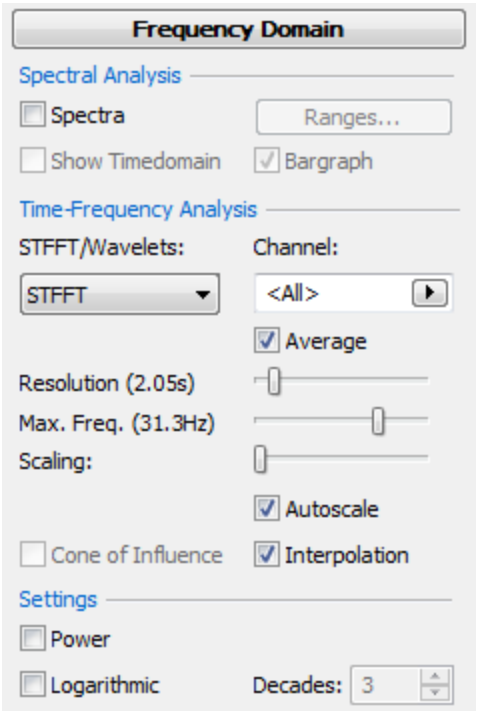


Right click again and select **Select Average**. Deselect **Overlay** to remove the compared file. *Right click* and select **Reset Layout** to restore the original layout, if needed.

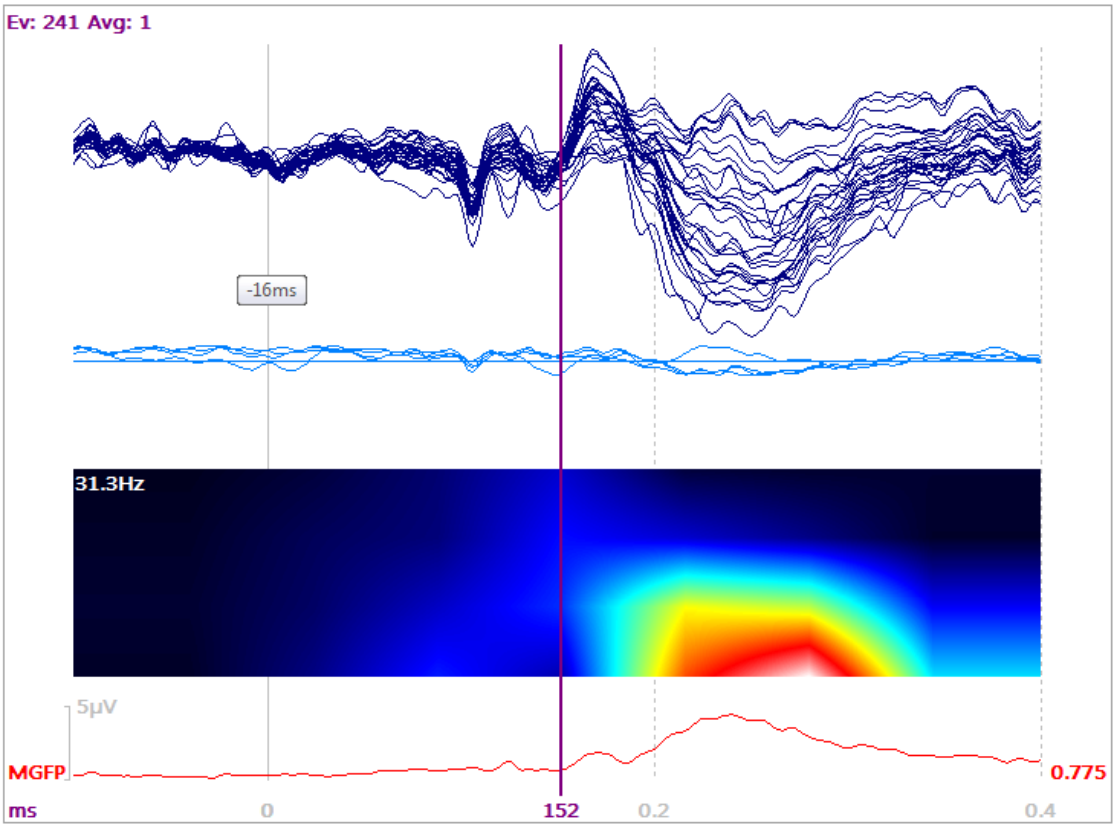
7. You have access to much of the offline functionality with the online averages. Go back to the **Averages** panel and enable **Send FD** for Stimulus 1, if you have not already done so.



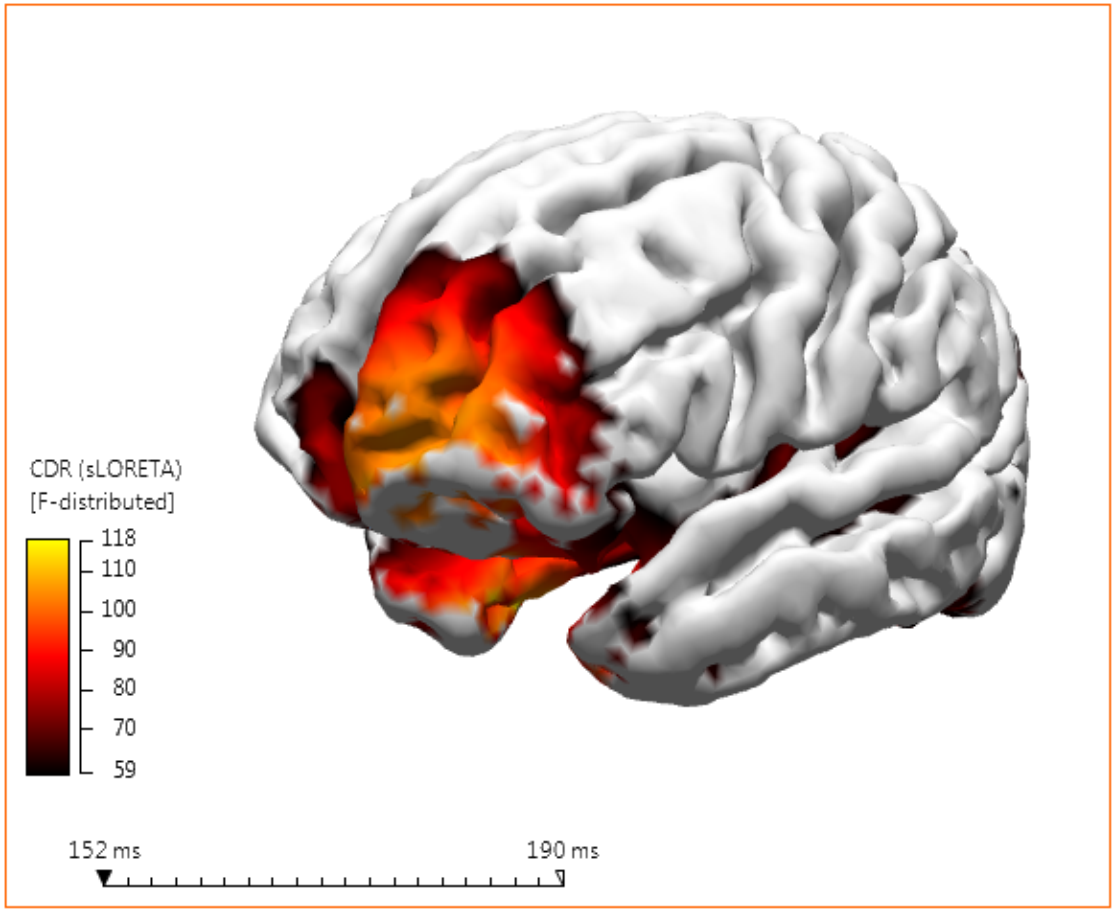
Click in the Stimulus 1 average data display to give it the focus, and click the Functional Data display. Now you are seeing the average continue to build, while having access to the offline functionality. For example, expand the **Frequency Domain** panel and select the **STFFT** option (Short Time FFT).



You will see the STFFT for the average (this cannot be done with continuous data, unless you send just the page to Functional Data).



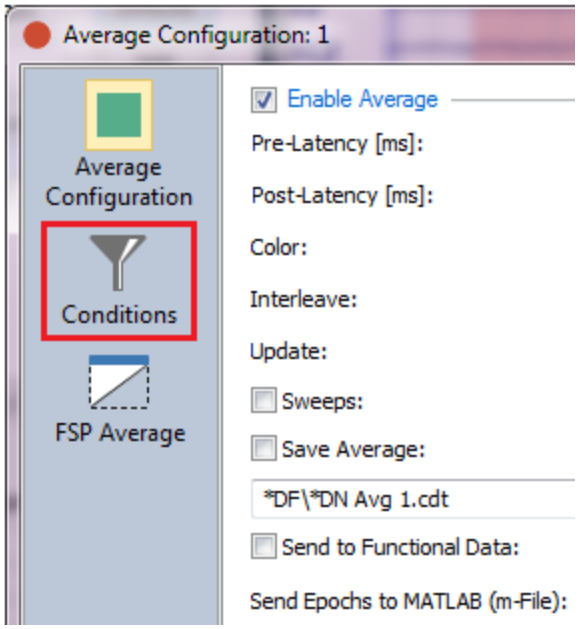
You can perform all of the steps needed to obtain, for example, a CDR source analysis.



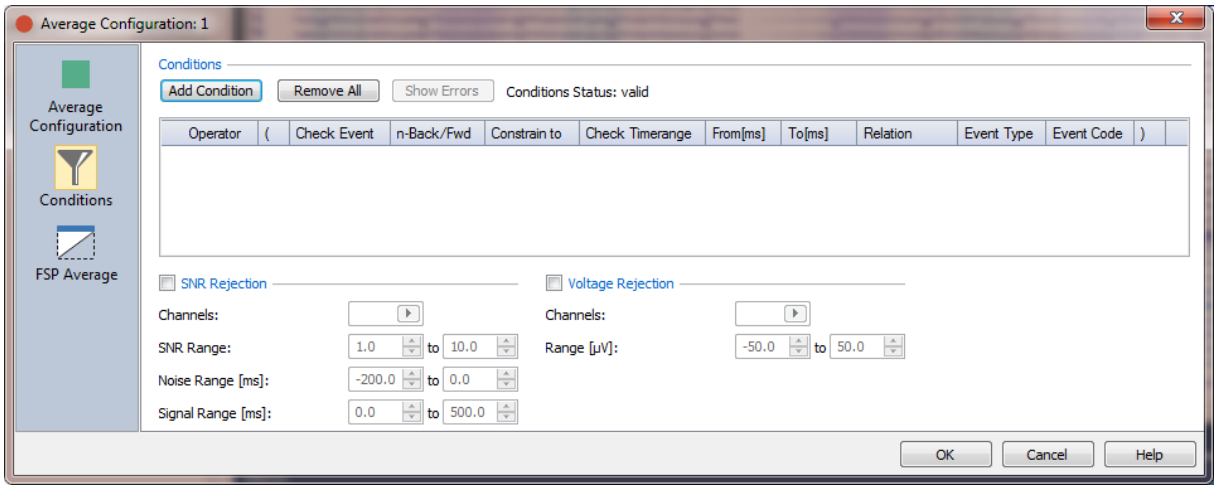
8. Click the button to disconnect from the Simulator.

9. At this point we still have the data files in the Unfiled Study. You can drag-and-drop **Study1** to a point in the displayed Database. Or, if you want to see the files offline, either open them one at a time, or create a small Database where you insert the files you want to look at. If you record to a previously created Study, the averages will be in their own subfolder called "Averages".

Another feature of online averaging is the ability to impose conditions on which epochs are included in the averages. These can be set individually for each average. From the **Average Configuration** dialog, described above, click the **Conditions** button.



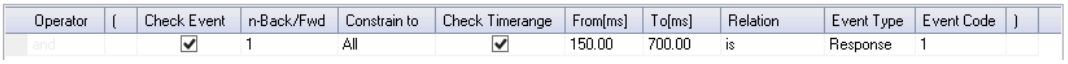
The **Conditions** screen is used to set up conditions for epoch selection. These include conditions related to the events themselves, as well as SNR and/or voltage levels for each epoch that is encountered.



Example 1
For example, you are recording a basic P300 paradigm, where the frequently occurring stimuli are event type 1's, and the "oddballs" are event type 2's. The subject makes a response (type r1 in the continuous data file) to the "oddballs", and you impose the constraint that valid responses can only be between 150 ms and 700 ms.

For the type 1 events, there are no conditions in this example, so the Conditions section is not used. It is used for the type 2 events (be sure to select the **Config** button in the type 2 line). In this example, we want to include only the epochs where the response occurs after the type 2 stimuli, between 150 and 700 ms. Click Add Condition and enter/select the values

shown. This literally says: If the next event is a Response Type 1, occurring from 150-700 ms after the stimulus, then include the stimulus event in the average.



Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	Event Code	)
and		☑	1	All	☑	150.00	700.00	is	Response	1	

If this is the only change you want to make in the screens, click **OK**. Start acquisition and only the epochs that meet the conditions will be added to the online average.

Constrain to requires some extra explanation. In this example, the options for **Constrain to** are **All** and **Responses**. **All** is the default setting, and it will be appropriate in most circumstances. A couple of examples may help clarify the difference. In a real-life recording, some subjects may fail to respond when they are supposed to, or they may make two or more responses to the correct stimulus. While one may be tempted to conclude that setting **Constrain to** to **Responses** is appropriate, since the presence and position of the responses determines the acceptance or rejection of the epoch, that is not the case.

If the subject does not respond to the first s2, the event table will look like:

```
s2  s2  r1 ...
```

CURRY is "considering" the first s2. When set to **All**, the next event is not an r1, so the epoch is rejected. If we had selected **Responses** for **Constrain to**, the next response would have been the r1, which is paired with the second s2, not the first one. We would have to make sure that the s2's are more than 700 ms apart so that no response is wrongly assigned. The **Responses** option is not needed in this case, and it could even be problematic.

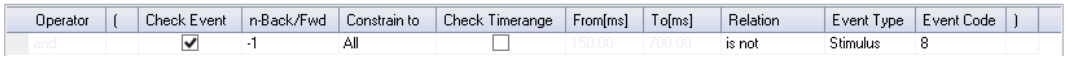
If the subject responds twice to the first stimulus, the event table will look like:

```
s2  r1  r1  s2 ...
```

CURRY is "considering" the first s2. The next event is an r1. If this r1 is within the Timerange, the epoch is accepted. The second r2 is not considered. Setting **Responses** for **Constrain to** would have no effect. It would not do any harm - the result would be the same. It is not needed, so use **All** instead. Basically, use **All** unless you are certain you need to use **Responses** (see the next example).

Example 2
Let's take a more complicated example. Let's say you have stimuli from 1 through 10 that are presented randomly. You want to average them separately, but you only want to average the type 3's when they do not follow a type 8, and, you only want to average the type 5's when the stimulus that follows the type 5 is either a type 7 or a type 9.

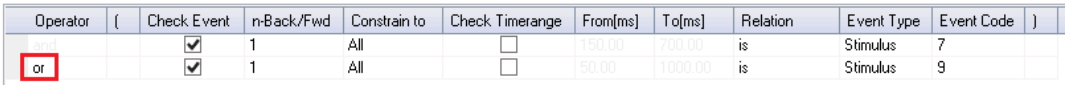
First, there are no conditions imposed on the type 1, 2, 4, 5, 6, 8, 9, or 10 stimuli, so Conditions can be ignored for them. When you select the **Config** button for the type 3's and the type 8's, you will need the Conditional statements. For type 3's, the line would be as follows:



Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	Event Code	)
and		☑	-1	All	☐	150.00	200.00	is not	Stimulus	8	

Type 3 epochs are averaged only if the previous event is not a stimulus type 8.

When you select type 5 to configure, two lines are needed, with an "or" in between:



Operator	(	Check Event	n-Back/Fwd	Constrain to	Check Timerange	From[ms]	To[ms]	Relation	Event Type	Event Code	)
and		☑	1	All	☐	150.00	200.00	is	Stimulus	7	
or		☑	1	All	☐	50.00	1000.00	is	Stimulus	9	

Type 5 epochs are averaged only if the next event is a type 7 or a type 9.

Now, let's say there are responses to some stimuli but not others. For a given event, there could be a response before or after it. We might have a sequence that looks like:

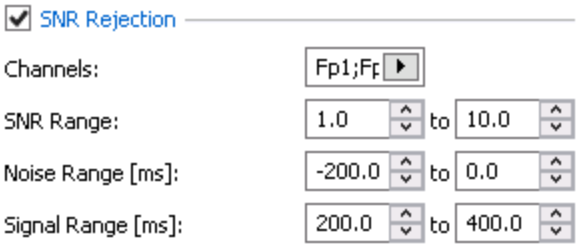
```
s8  r1  s3  s1 ...
```

CURRY is "considering" the s3 event. We said that we only want to include the s3's if the previous event is not an s8. We do not want to look for just any previous event; we want to look for the previous *stimulus* event. So we have to "constrain" the condition to stimulus events only. This is a case where we would select **Stimuli** for **Constrain to**. (Whether you see **Stimuli** or **Responses** as options for **Constrain to** depends on what you selected in the **Event Type** field).

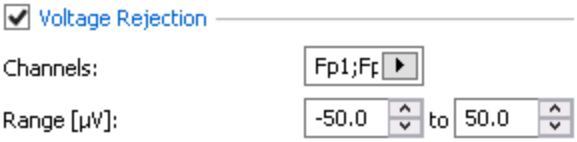
You can see that there is a great deal of flexibility for creating conditional statements, and they can become more complex than these examples (see also the **Conditional Statements** tutorial and the *CURRY 8 User Guide* for more information).

SNR Rejection. When enabled, epochs will be rejected if the SNR (Signal to Noise Ratio), from the channel(s) selected, does not fall within the SNR Range specified. The Noise Range is typically the pre-stimulus interval. Noise, in this case, refers to that part of the epoch interval that does not contain the ERPs. The Signal Timerange is that part of the epoch interval that does contain the ERPs of interest. It is not necessary to define the entire range of the ERPs. The interval where the waveforms have the greatest amplitude will give the largest SNRs. The Signal is divided by the Noise to give the SNR. Generally, SNRs should be greater than 1.0 (there should be more signal than noise). If the SNR is very low, this suggests that either the signal is relatively low, or the noise is relatively high (or both). If the SNR is very high, this may indicate that there is an artifact within the Signal Timerange that is artificially inflating the SNR. (Noise decreases by one divided by the square root of the number of epochs). SNR Rejection provides an alternatively to using voltage thresholds to

accept/reject epochs (or they can be used together). Only epochs that meet the criteria will be included in the online average.



Voltage Rejection. Epochs will be excluded if the voltages from a selected channel(s) exceeds the **Range** that is set.



You may apply **SNR Rejection** and **Voltage Rejection** methods alone or in tandem.

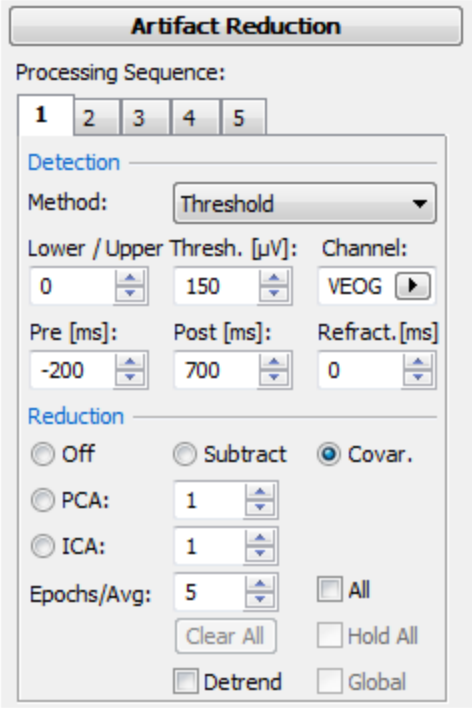
2.2.4.2 Artifact Reduction

In this tutorial we will illustrate how to reduce blink artifact online (there are additional ways to reduce it offline). For this example we will use the Simulator, and replay an existing data file with blinks.

1. Click Start an Acquisition from the Workflow, or click the **New** icon from the Toolbar in order to access acquisition.

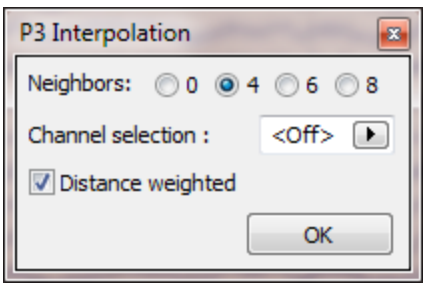
2. Select **Simulator** in the **Amplifier** field in the **Amplifier Control** panel. Click the **Connect** arrow and select the *viscpt.cnt* file from the *C:\CURRY 8 Tutorials\Acquisition\Blink Reduction* folder. The file will begin to replay.

3. In the **Artifact Reduction** panel, set the parameters as shown. Select the first tab in the **Processing Sequence**, with **Threshold** for the **Method** of artifact reduction. Setting **0** for the **Lower Threshold** has the effect of turning it off; **150**µV for the **Upper Threshold** is the only one we will use. Select the **VEOG** channel (consider also using the MGFP channel to detect artifacts). Set the artifact interval to **-200** to **700**ms to capture the full artifact. Select **Covar.** and use **5** for **Epochs/Avg**.

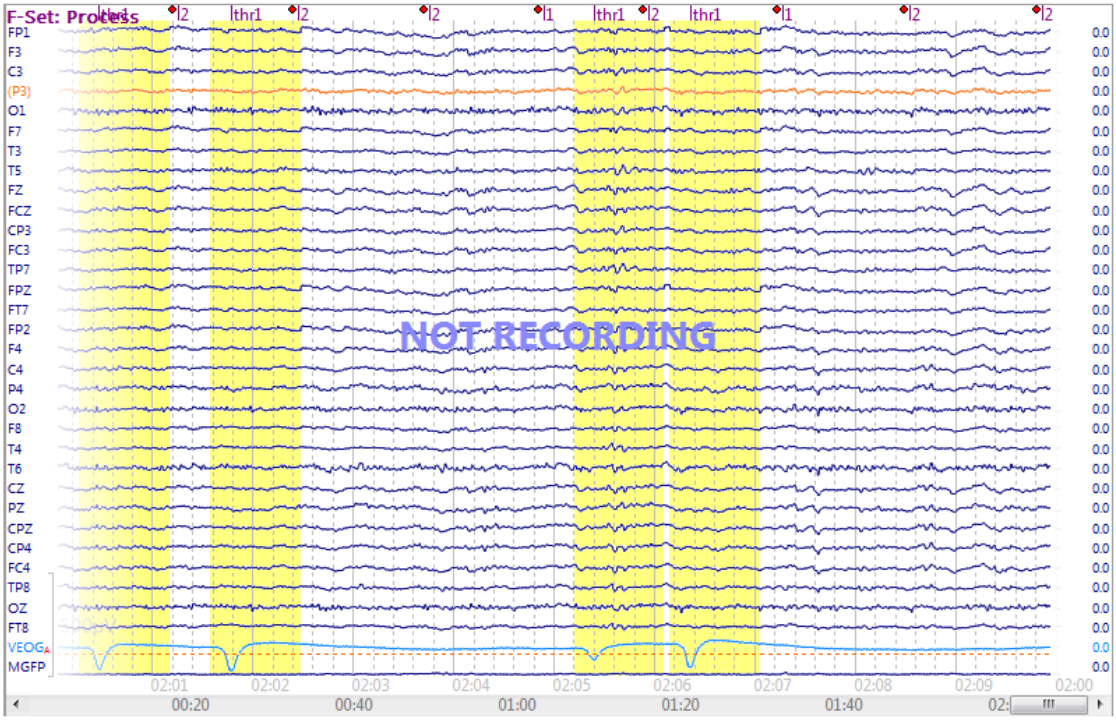


The **VEOG** channel will be monitored, and whenever the voltage exceeds **150**µV, it will be interpreted as a blink. The blinks will be averaged from **-200** to **700**ms from the peak. A **Refractory** period is required to avoid overlapping artifact intervals (a value of **0** will always use the sum of the **Pre** and **Post** times, even if you change them). A rolling average of 5 blinks will be used to create the average artifact, which will be reduced using the covariance method (see the *CURRY User Guide* for details). The purpose of the online artifact reduction is to approximate blink reduction in order to see cleaner data. Generally, you can achieve better reduction offline (and only the raw continuous data are saved). The corrected data are used to create the online averages, however, and the corrected averages will be saved. We could also use the **All** option and **Global** options if desired (refer to the *CURRY User Guide* for more details, or the Artifact Reduction section of the **Simulated Acquisition** tutorial above).

Note that the P3 channel has a recurring artifact, and that blink reduction is affected by that. *Right click* on the P3 label and select **Interpolate Channel**. Set the parameters as shown. The P3 channel, now seen as [P3] and in a different color, will be recomputed as the average of the 4 nearest electrodes, weighted for distance.



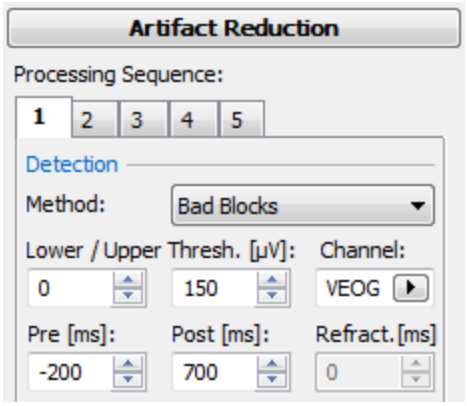
4. As the file replays, you will see blinks highlighted in yellow. The blinks will be reduced in all EEG channels, but not the blink channel (where covariance is 1.0).



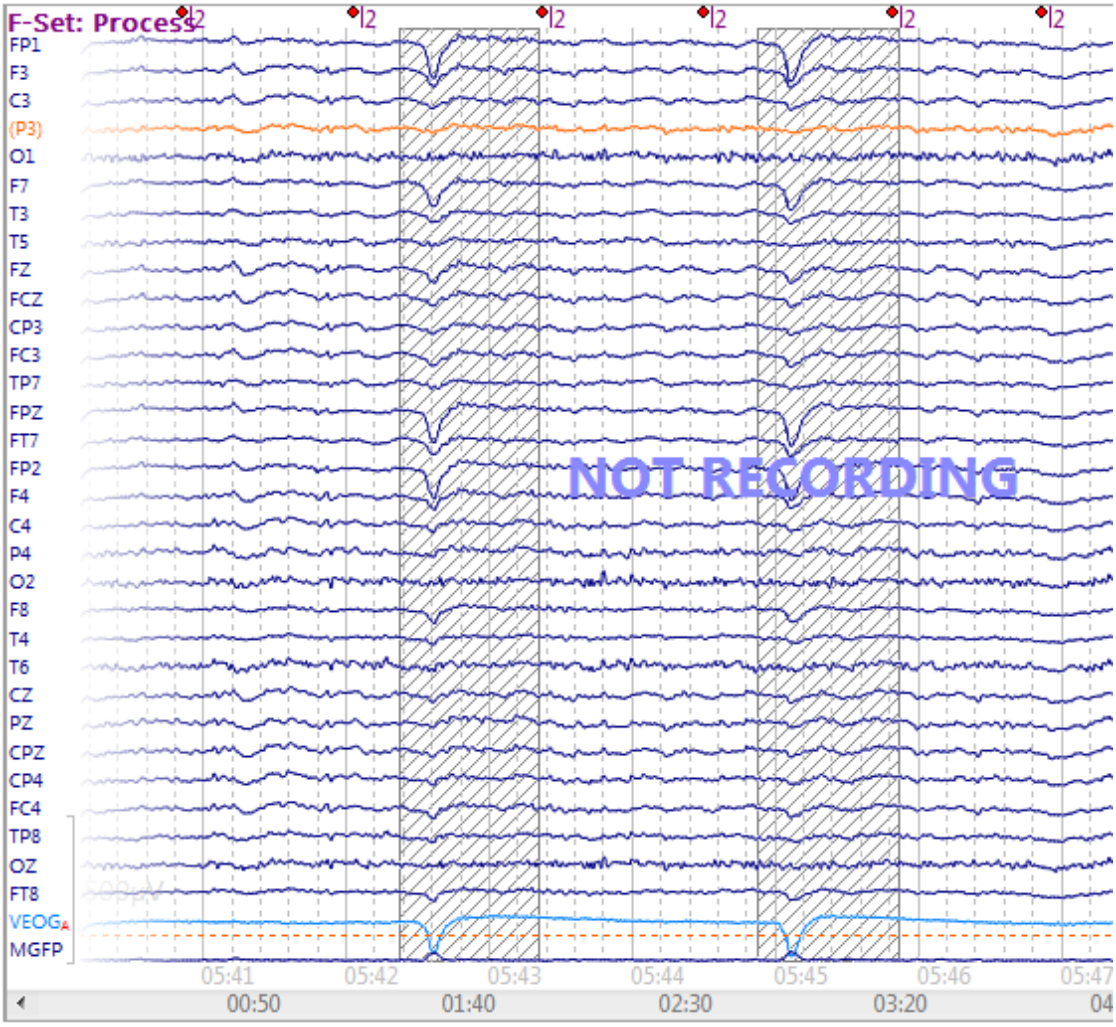
5. While replaying the data file, try switching to the other **Reduction** methods: **Subtraction** and **PCA** (with different numbers of components projected from the data), to see which one is most effective with your data. (You have to wait a few seconds to see the effect of the new method, and that data already on screen will not be affected when you change the reduction method).

6. If you have other types of artifact in the file, use another Processing Sequence to reduce them.

7. In the above example, we *reduced* the artifact using one or another reduction method. It is also possible to *remove* the blinks entirely - at least as many as can be detected with a voltage threshold. Instead of using the **Threshold** method, use **Bad Blocks**. The parameters are shown below.

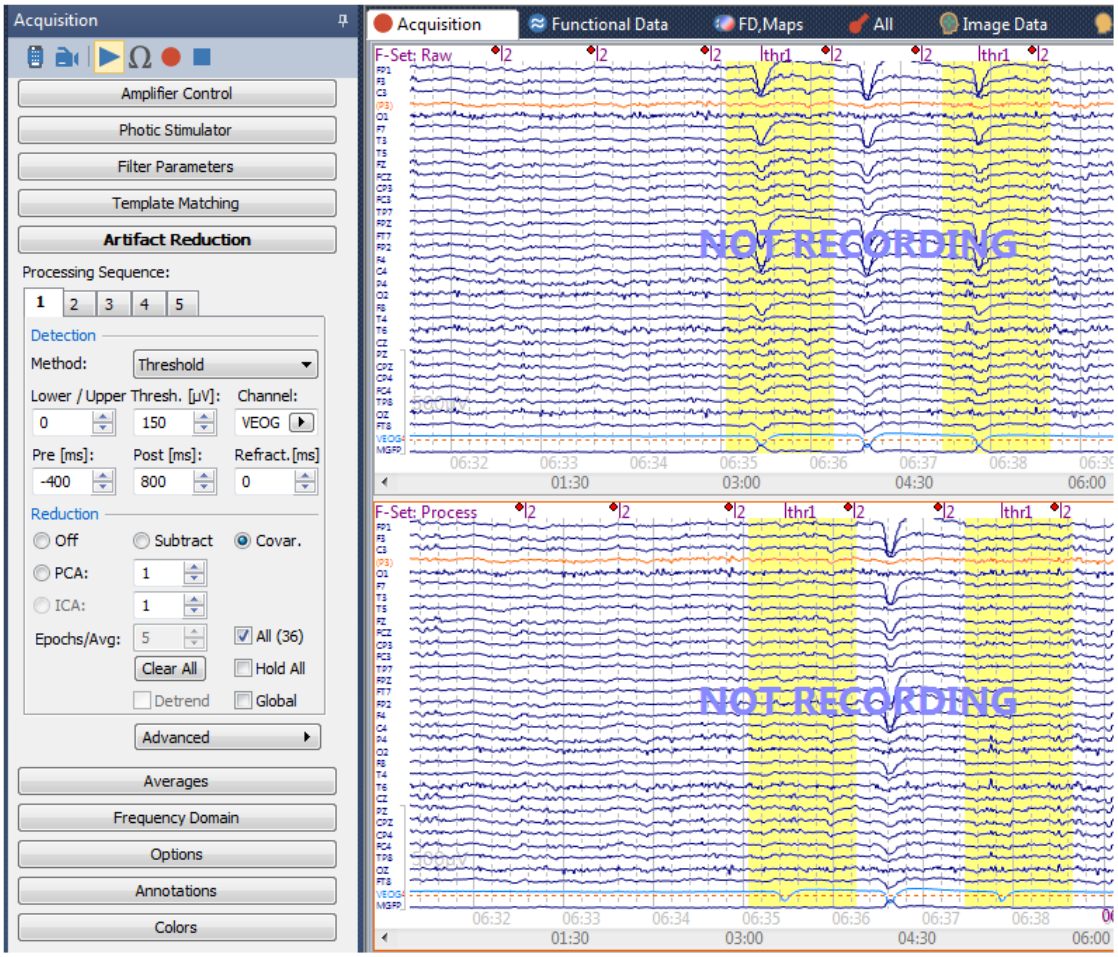


In this case, the blinks are not corrected, but will be converted to Bad Blocks. The program will not include any epochs in the online averages that contain Bad Blocks, so this is one way to exclude blinks from the online averages.



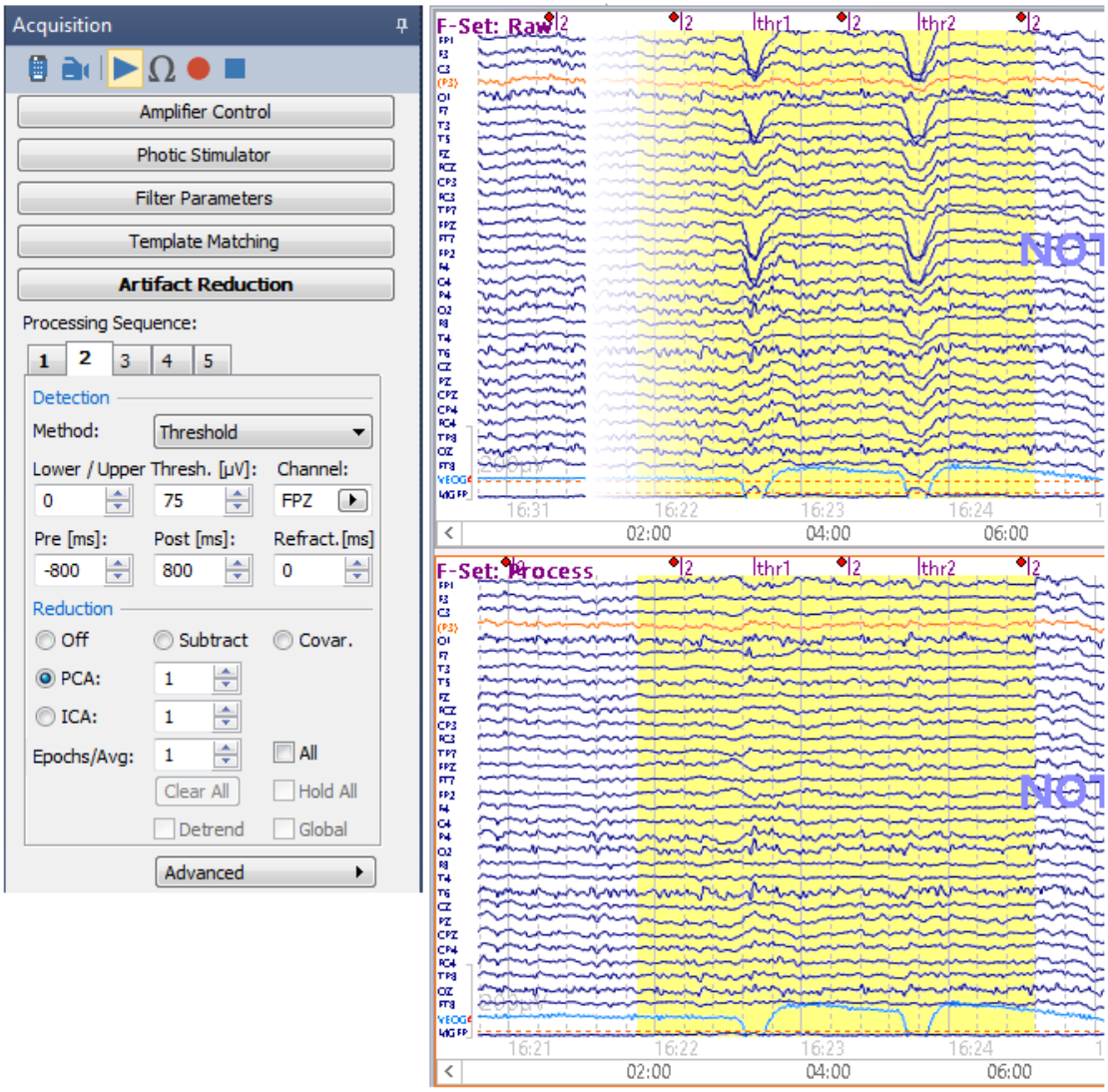
Similarly, in the **Average Configuration** parameters for the online average (**Conditions** section), you can use **Voltage Rejection** to exclude any sweep where the voltage from selected channels exceeds the thresholds you set. Or, use the SNR method to exclude sweeps based on signal-to-noise analyses. In these ways, epochs containing blink other artifact can be excluded from the online averages.

Missed blinks? Artifact intervals cannot overlap. This means that if blinks occur too closely together, not all of them will be corrected. In the figure below, the second blink interval overlaps with the first one, and therefore it was not detected and not corrected. This is the case online as well as offline.



There are different ways to deal with this. One is to use shorter artifact intervals so that they do not overlap. This can be a somewhat time consuming (determining what the interval should be) and not an altogether effective method. You can use the **All** and **Global** options, and all of the data points in the file will be corrected, including the missed blinks.

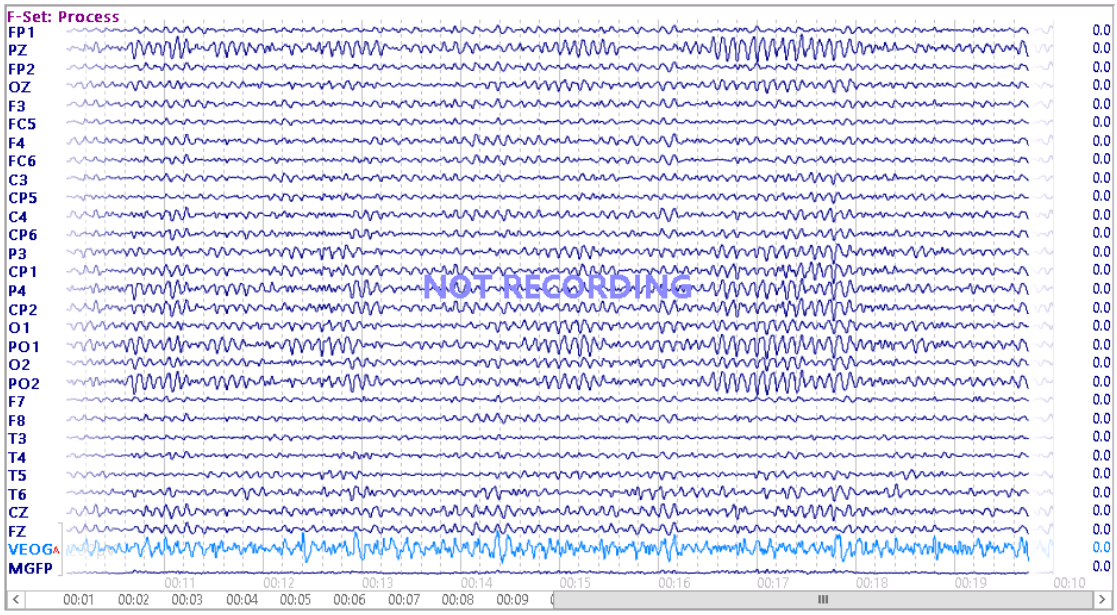
Another option is to use a second Artifact Reduction sequence (online or offline). In this case, you will need to use a different **Channel**, because the VEOG channel is not corrected - the same artifacts will be detected again. Instead, we used FPZ, and lowered the **Threshold** accordingly. Notice that the middle blink now has a "thr2" event. All blinks are now corrected. This will work if you use the PCA correction method. If you use Covariance, the FPZ channel will not be corrected for the "thr2" blinks.



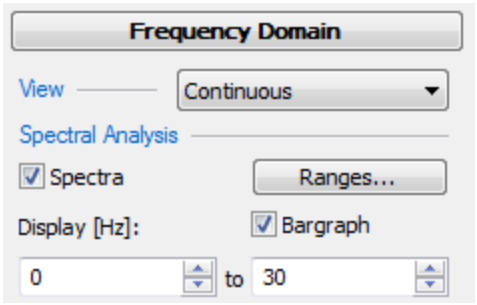
2.2.4.3 Spectral Analysis

This tutorial demonstrates how to perform and map online FFT results. For this example, we will replay a file through the Simulator.

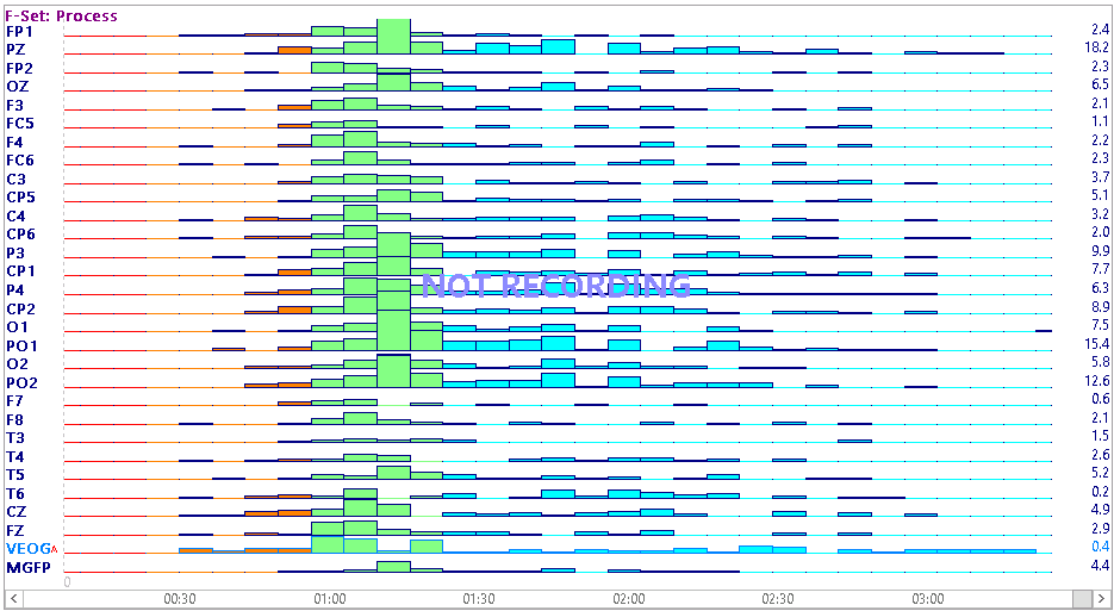
1. Click Start an Acquisition from the Workflow, or the **New** button on the Toolbar to access acquisition. Select **Simulator** in the **Amplifier** field in the **Amplifier Control** panel. Click Start Amplifier and select the *Closed.cnt* file from *C:\CURRY 8 Tutorials\Signal Processing\Spectral Analysis and COH* folder. You will see the eyes closed recording replay. Rescale as desired.



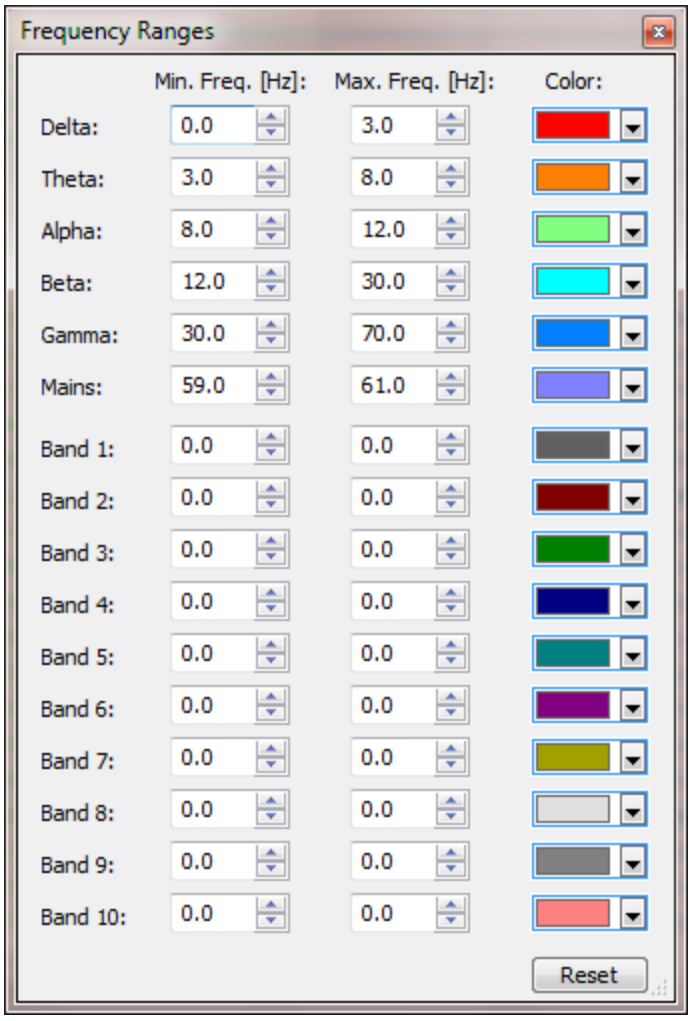
2. Go to the Frequency Domain panel and click **Spectra**. In the **Display [Hz]** fields, enter **0** to **30**Hz to display that range only.



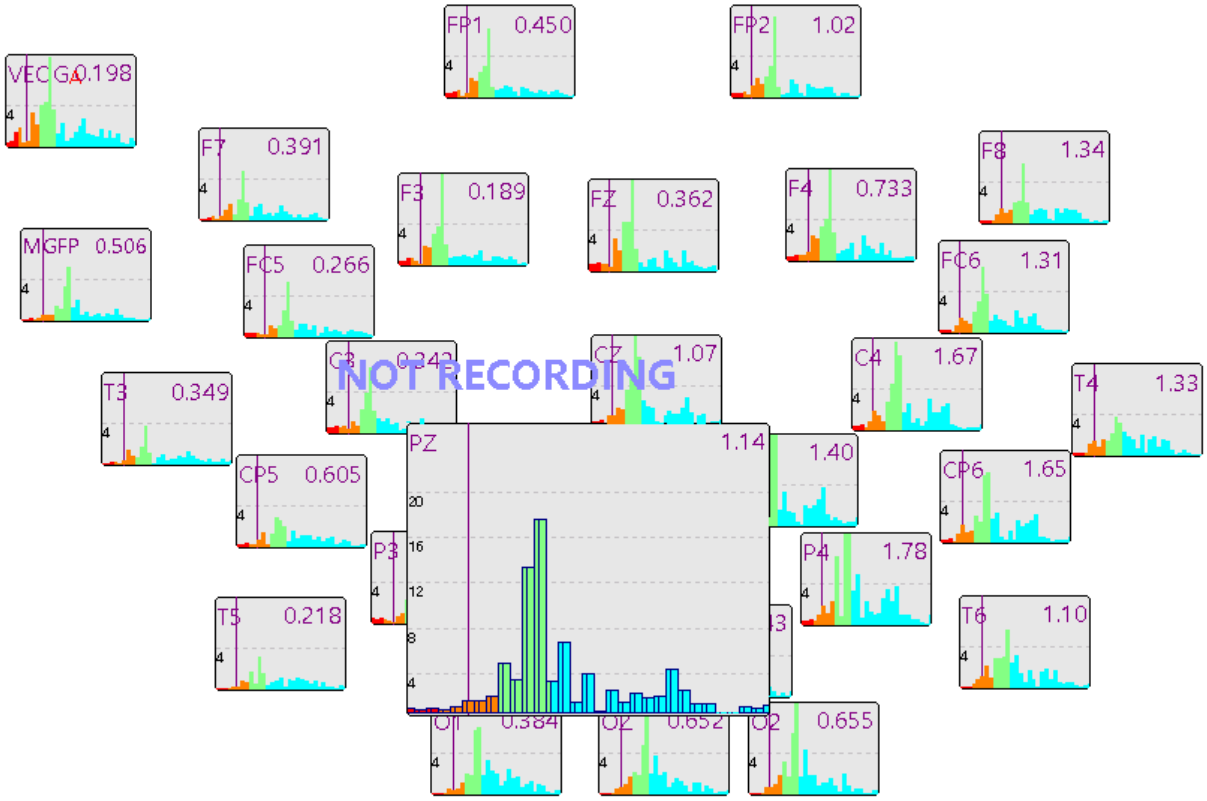
You will see the spectral display similar to that below. The update rate is determined by the number of seconds displayed per page. The spectra are created for the entire display, plus as many samples needed from the previous and next display in order to achieve a number of samples that is a power of 2.



Note that you can display the **Log** of the values, you can display **Power** (microvolts squared) or microvolts (Power disabled). The results can be displayed as a **Bargraph** or in lines. The **Ranges** button lets you redefine the band frequencies and change the colors.



3. *Right click* in the display and select the **Position Plot**. You can now see the spectra in the approximate positions. Additional display options are possible by *right-clicking* and selecting **Send page to Functional Data**. Then you have access to the offline functionality as well, described in the **Spectral and Coherence Analyses** tutorial below.



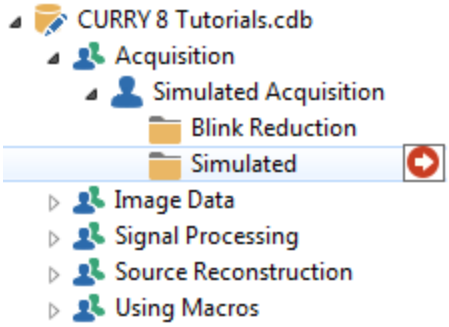
4. Disable **Spectra** and the **Position Plot** to return to the continuous waveforms.

2.2.4.4 Template Matching

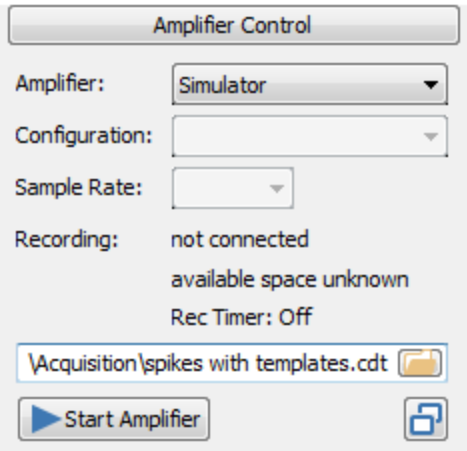
It is possible to use the Template Matching functionality of CURRY online, as well as offline. Online, it can be used to identify, for example, spike activity, and save the detected spike events within the data file. You can average the templates and perform source reconstruction online. It can also 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).

In this tutorial, we will use Template Matching to detect spike activity in the online recording, average them, and save those events for use offline. To do this, we will use the **Simulator** option to replay an existing data file.

Open the Study indicated below in the *CURRY 8 Tutorials.cdb* Database. Open the Study by *double-clicking* Simulated, or by clicking the red arrow.

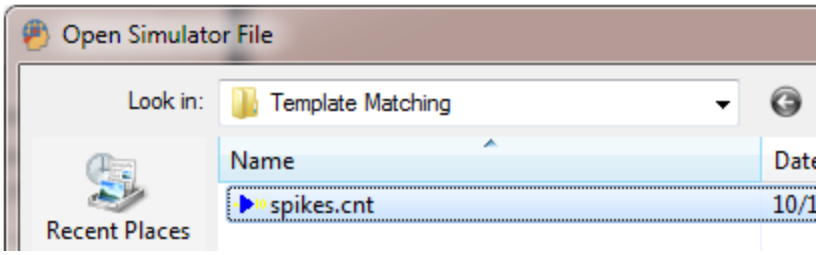


1. The acquisition part of CURRY will be opened. Select **Simulator** for the **Amplifier**. Since we will be saving a file with the detected matches in it, we will first change the file name. (You cannot change the file name once the replay has been started). In the Amplifier Control panel, change the file name to *spikes with templates.cdt*.

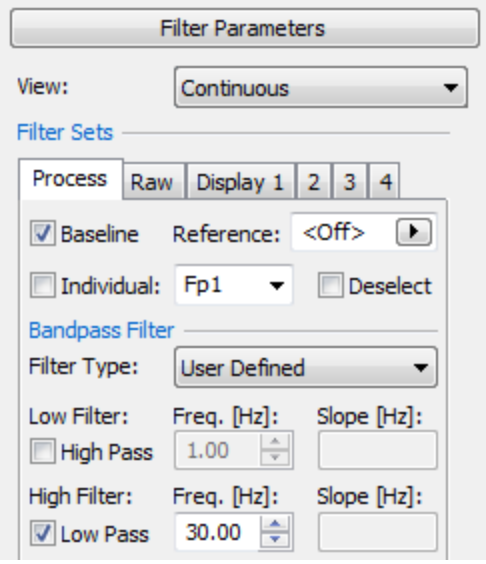


Before going on, let's look at the complete path *DT\Acquisition\spikes with templates.cdt . In this case, **DT* is a substitution for the path to the Desktop. *\Acquisition* will create a folder on the Desktop. When we record a data file, it will be placed in the Acquisition folder on the desktop, using the file name we entered. Additional parameter and event files with the same name (different extensions) will be created automatically and placed in the same folder.

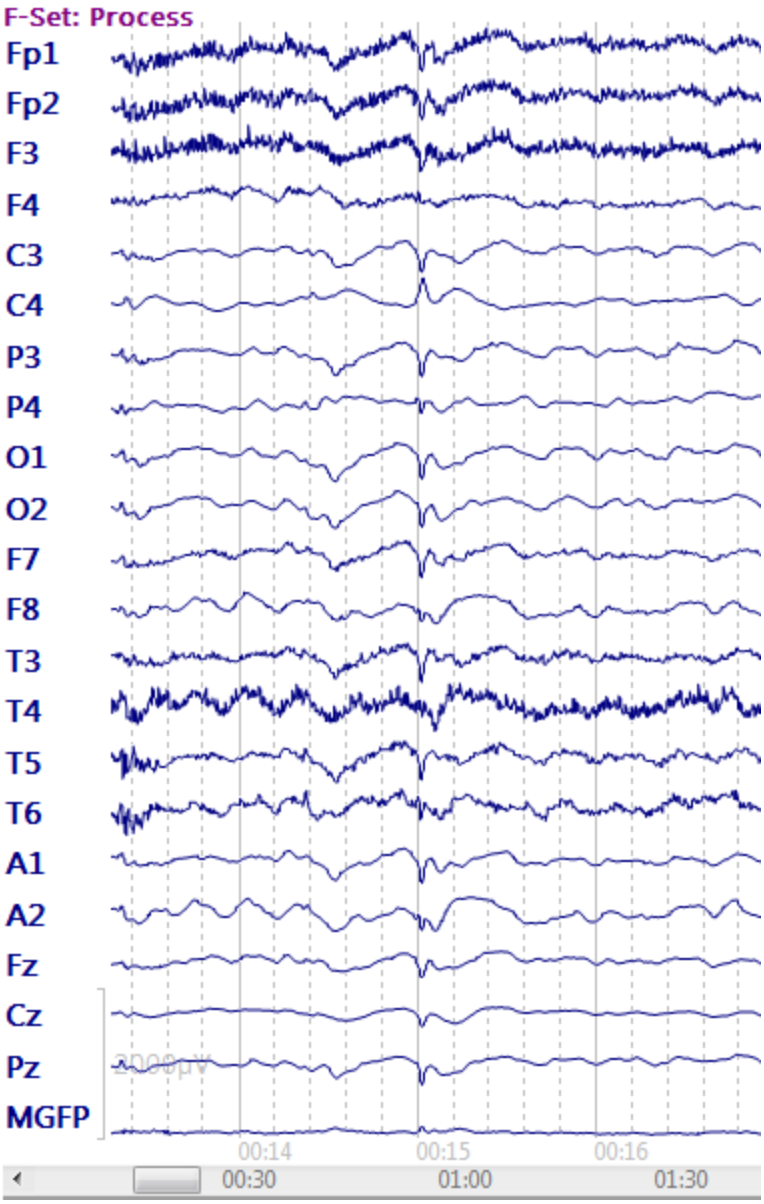
2. Click the Start Amplifier arrow. Navigate to the *C:\CURRY 8 Tutorials\Signal Processing\Template Matching* folder, and select the *spikes.cnt* file.



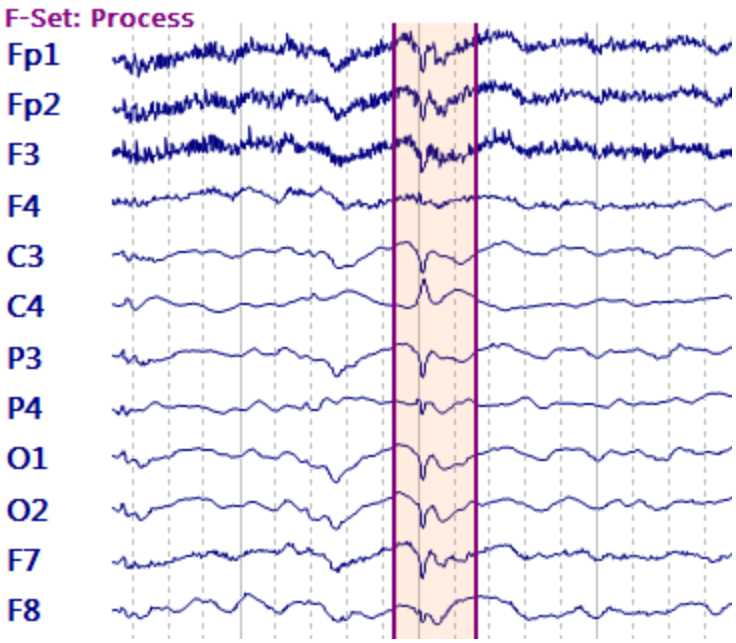
3. There is EMG activity in several channels that we can reduce with Filtering. Expand the **Filter Parameters** panel, select **User Defined** for the **Filter Type**, and select only the **Low Pass** filter, set to **30**Hz.



4. Drag the sliding bar below the data display to the left to pause the display and let you see the data. There is a good spike at about 15 seconds into the file.

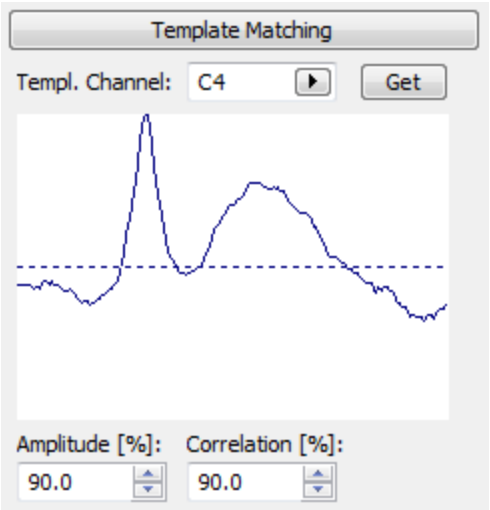


5. With the display paused, we can set the cursors to define a Timerange for the template. We will use C4 as the template channel. Click once to position the cursor at the beginning of the spike. Use *Shift+click* to position a second cursor after the slow wave.



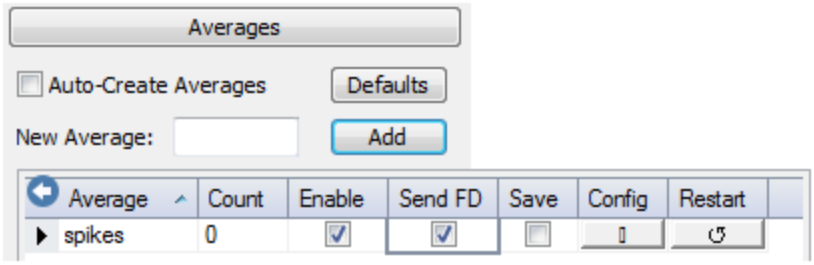
6. Expand the Template Matching panel and select **C4** for the **Template Channel**. Press the Get button to use the cursor positions. The spike and slow wave from C4 will be displayed. Here it is important that there are both positive and negative voltages in the template. All, or nearly all, positive or all negative voltages will adversely affect the template matching algorithm. If you encounter such a situation, either apply a Baseline Correction, a High Pass filter, or alter the Timerange so that there is a mix of valences.

Amplitude and **Correlation** (correlation x 100) criteria are applied to each potential match. If we wanted to see only the best matches, we would use higher values, such as, for example, 90% and 90% as we will use in the example. If we used the lowest values - **30%** and **50%** - all possible matches would be detected. Leave them at 90% for now; we will reduce them shortly.

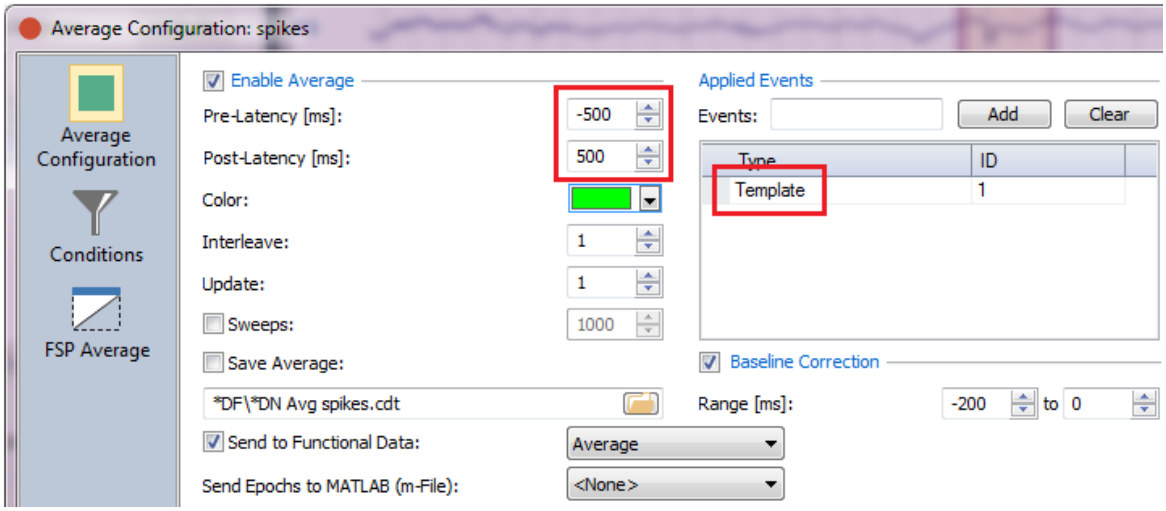


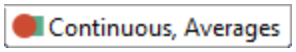
7. Expand the

panel and enter "spikes" in the **New Average** field. Click the **Add** button. In the table, enable **Send FD**. This will let us use the average for additional online operations.

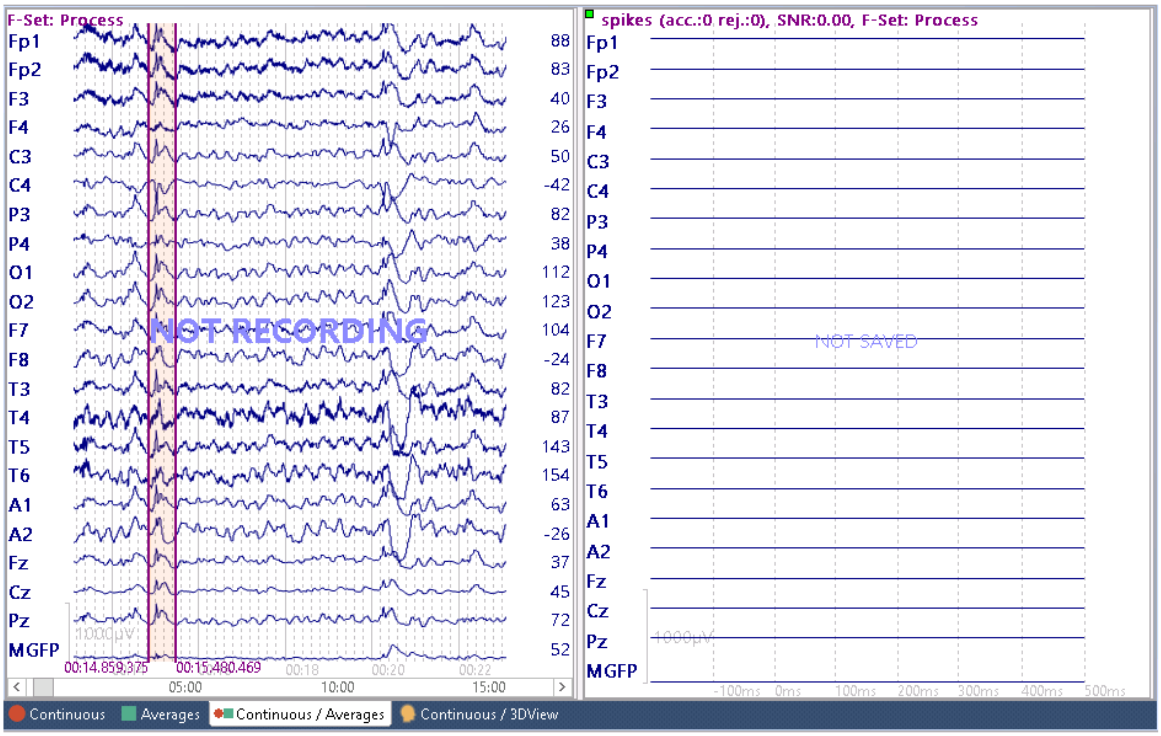


Click the **Config** button to see the **Average Configuration** dialog. Set the **Pre**- and **Post-Latency** fields so they are **-500** to **500 ms**. In the **Applied Events** section, change Stimulus to **Template**. Click **OK**. Now the spikes will be averaged.

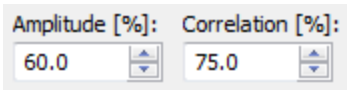


8. Select the 

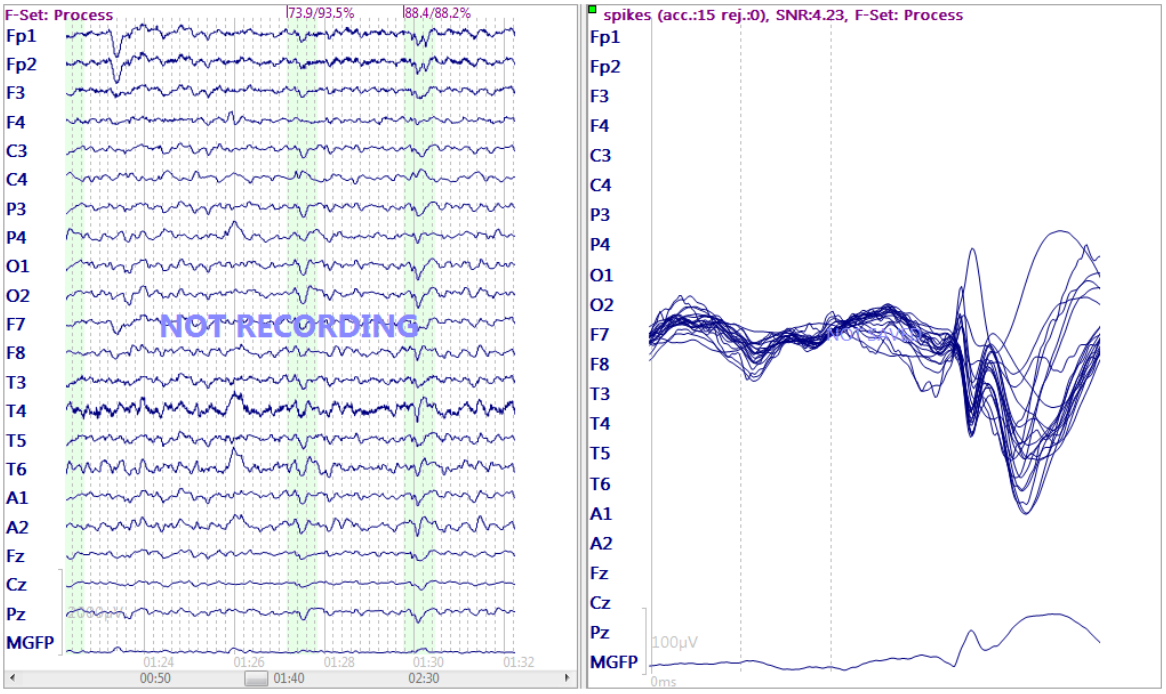
display to see the continuous data and the average of the spikes. If no spikes are being detected, this is typically an indication that the Amplitude and Correlation criteria are set too high.



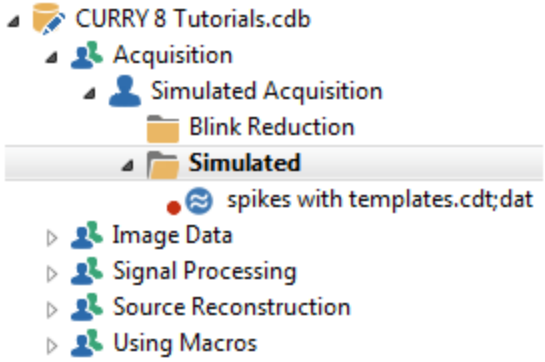
Reduce the criteria to, for example, 60% and 75%. There are sections in the file that have no good matches. The file will replay in a loop, so just let it play for a while until matches are detected. (Drag the slider all the way top the right to restart the scrolling display).



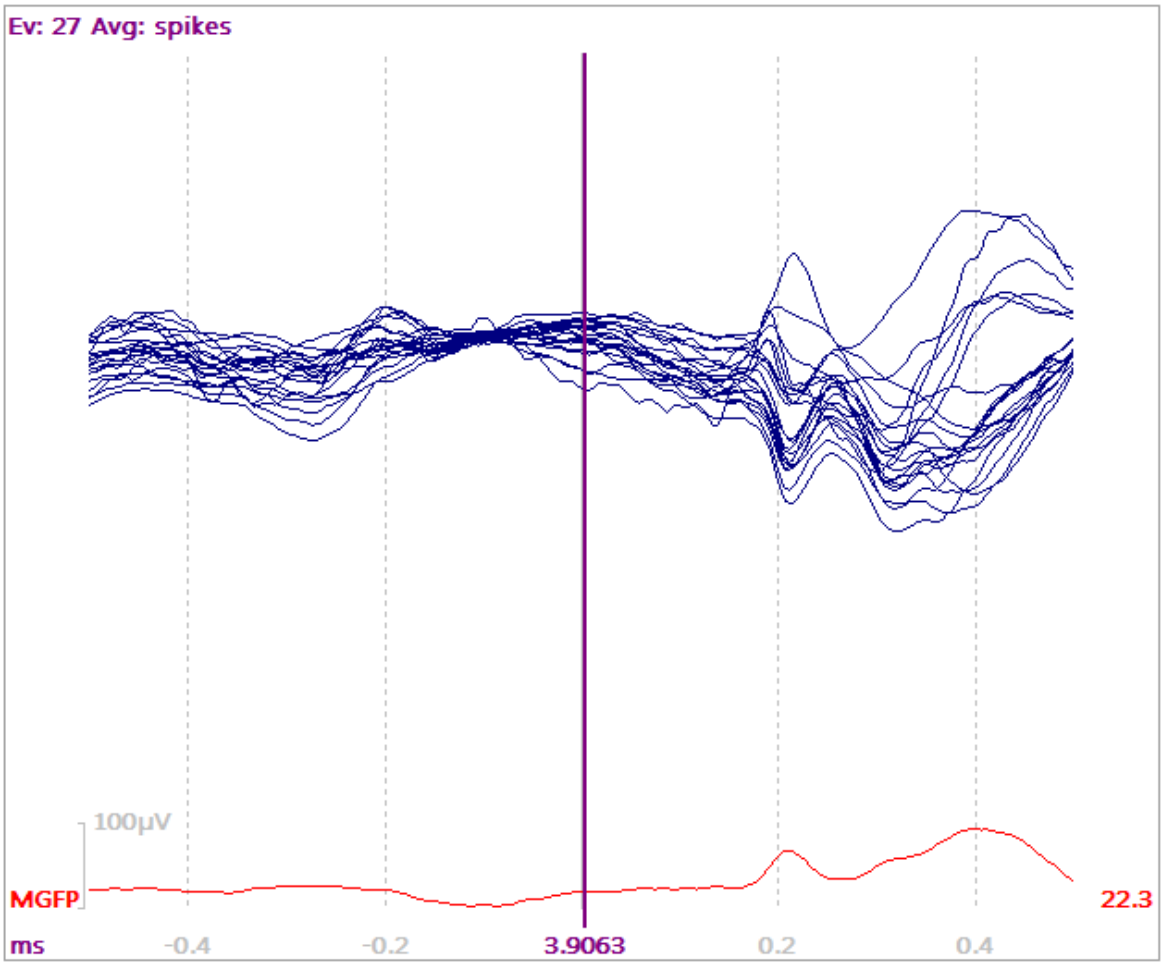
Now we start to see the spikes being detected **(Butterfly Plot**).



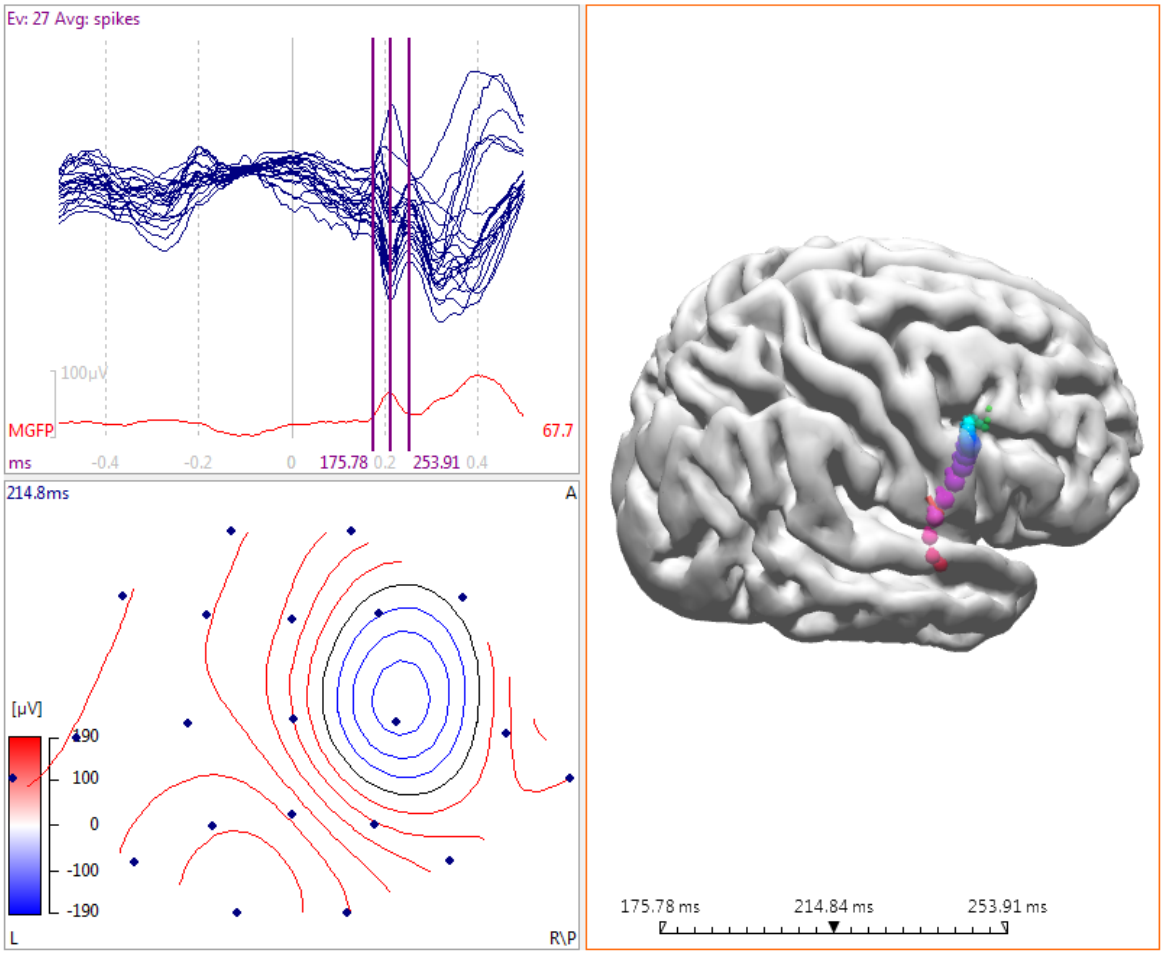
9. Click the Record button to start saving the continuous data file. You will see the file in the Database.



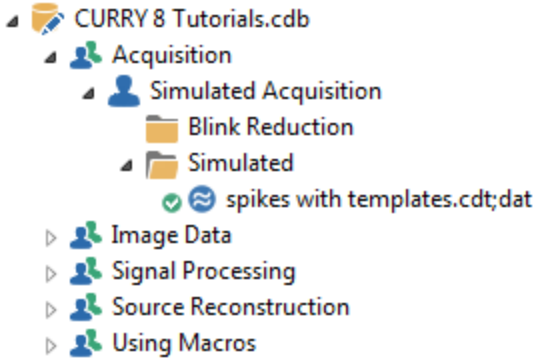
10. Now click the display option. We are seeing the average in the Functional Data part of CURRY 8; the average will continue to be updated.



11. Now we may perform source reconstruction as usual, obtaining a Noise Estimation, setting the Timerange, selecting a Head Model, selecting a Dipole Model, and so forth (see the **Dipole Models** tutorial for details). The results will update with each spike that is detected.



12. Click the icon to disconnect from the Simulator. Close the Acquisition part of the program. Note that the file remains in the Database.



13. Open the **Simulated** study (and select "tmpl" in the **Type** field in the **Event List**). From here you can review the events that were selected, accepting only the best ones, or do source reconstruction without any averaging, etc. See the **Epileptic Spike Detection** tutorial.

2.2.4.5 MRI Gradient and Ballistocardiogram Reduction

EEG recordings obtained inside the magnet, during the actual MRI scans, typically contain two additional classes of artifact: gradient artifact from the scanner itself, and ballistocardiogram (BCG), which is an exaggerated heart beat artifact. Gradient artifact is an exceptionally large amplitude artifact that typically overwhelms and completely obscures the EEG activity. Fortunately, it is generally a very stable artifact, which can be removed by averaging several artifacts together and subtracting the average from individual occurrences. BCG is often far less stable across the recording, so a different method must be used to reduce it. Both types of artifact generally have higher amplitude than the EEG activity that is contained in the same waves.

Note
When configuring your system for recordings in the magnet, you should use the following parameters:

1. Record in DC mode.

2. Use an AD Rate of 1000 Hz or 2000 Hz if you have clock synchronization (*SynAmps RT*). If not, use 10,000 Hz.

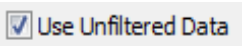
3. Do not enable the 50/60 Hz notch filters for gradient reduction.

It is very important when recording in the magnet to verify that you are getting genuine data, when all you see is the gradient artifact during scans, and mainly BCG in between scans. The online reduction methods may not be quite as accurate as what you can obtain offline (where you can fine-tune the correction); however, they are sufficient to ensure that you are recording genuine data.

There are a few things to keep in mind when setting up Artifact Reduction.

1. As with the offline operations, it is important to set the parameters from top to bottom, that is, Filter Parameters first and Artifact Reduction second, for example.

2. Once you start applying the artifact corrections, you should avoid going back and changing preceding settings.

3. Gradient reduction is most effective using unfiltered data; BCG reduction is better with filtered data. This is controlled by the 

option in the **Advanced** section of **Artifact Reduction**.

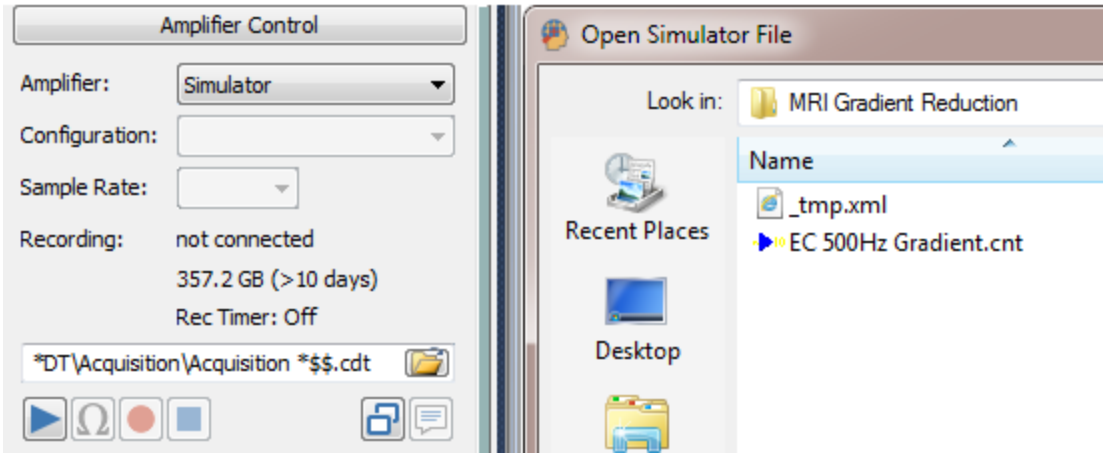
4. Only the raw continuous data are saved. (Averages based on corrected data are saved).

5. The gradient reduction procedure is most effective when the number of slices divides evenly into the Tr Duration.

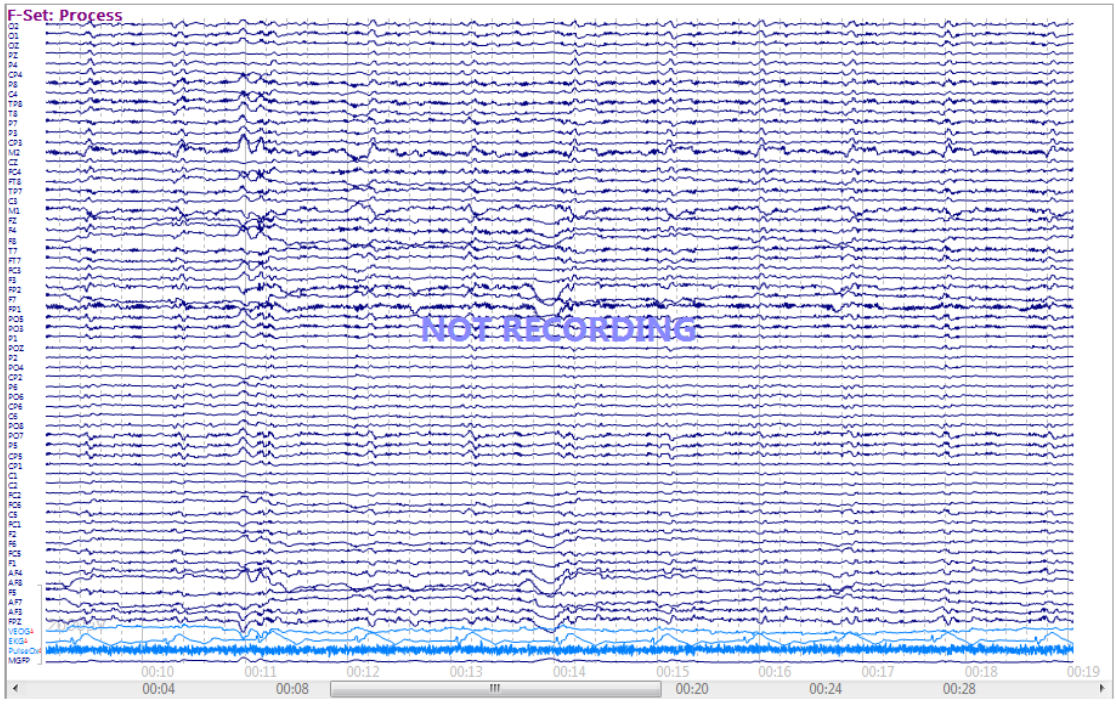
For this demonstration, we will replay a data file using the Simulator.

1. Click the **New** icon to access acquisition.

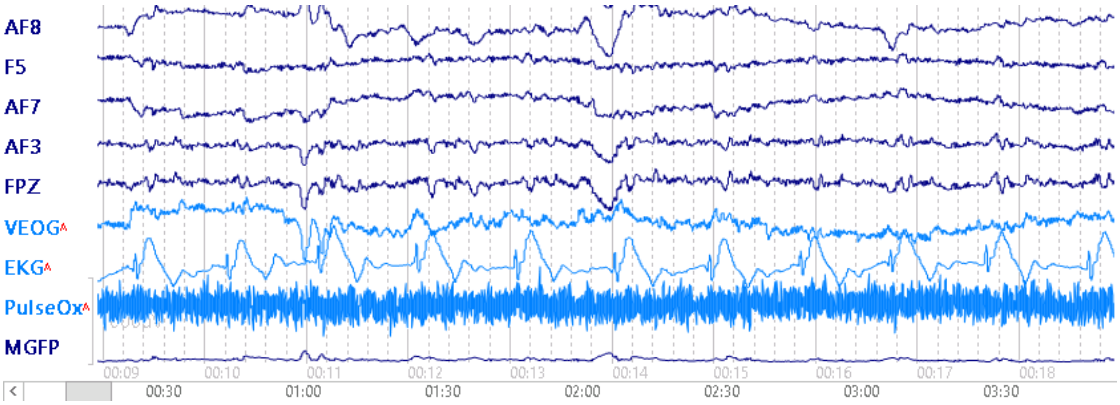
2. Select **Simulator** for **Amplifier**, and click Start Amplifier arrow. Select the *EC 500 Hz Gradient.cnt* file from the *c:\CURRY 8 Tutorials\Signal Processing\MRI Gradient Reduction* folder.



3. Let the file play about 15-20s and then grab the slider and move it backwards a little to pause the display. (The file will continue to replay in a perpetual loop).

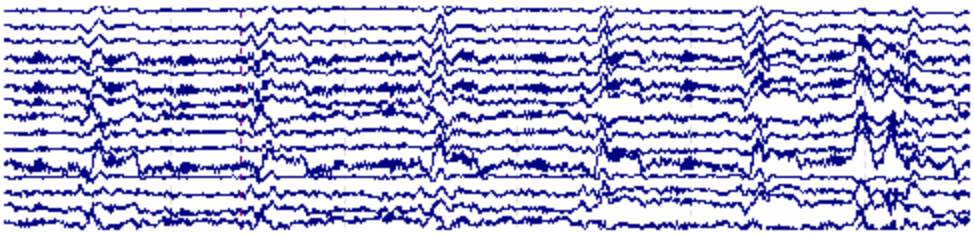


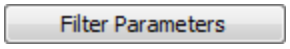
4. Now let's look at the file. Reduce the number of channels to about 20 (under **Options**, or *Shift+mouse wheel*), and scroll down to the lowermost channels.



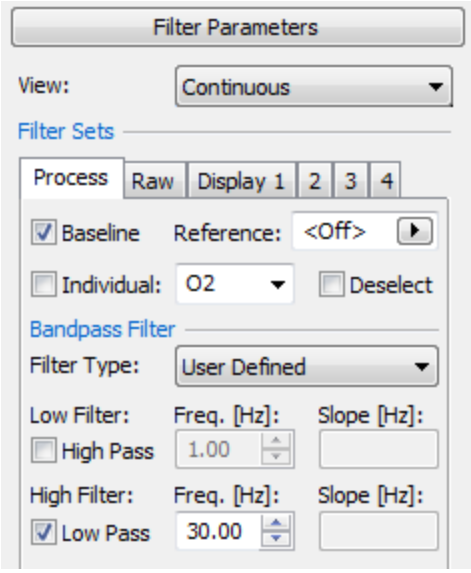
The PulseOx channel is not working, but the EKG is clearly seen in the EKG channel. BCG is seen in the other channels.

If you increase the scaling, you will see periodic bursts of faster activity. This is most likely pump noise artifact. In this case, we will reduce it with the LP Filter (you could also use PCA).

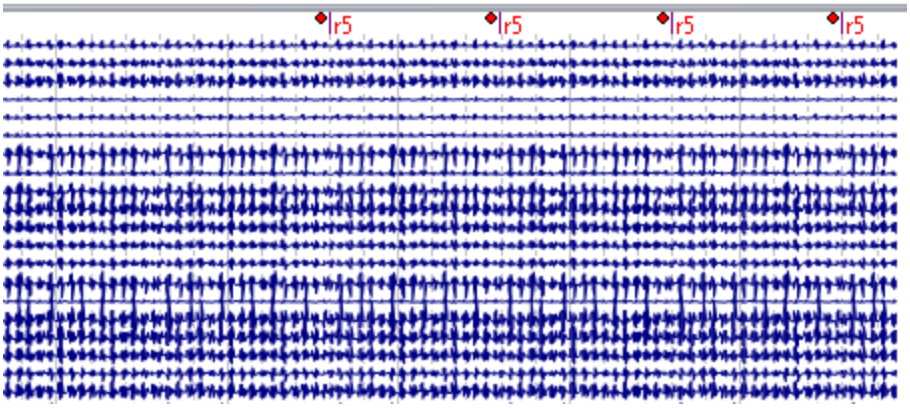


With the replay still Paused, expand the 

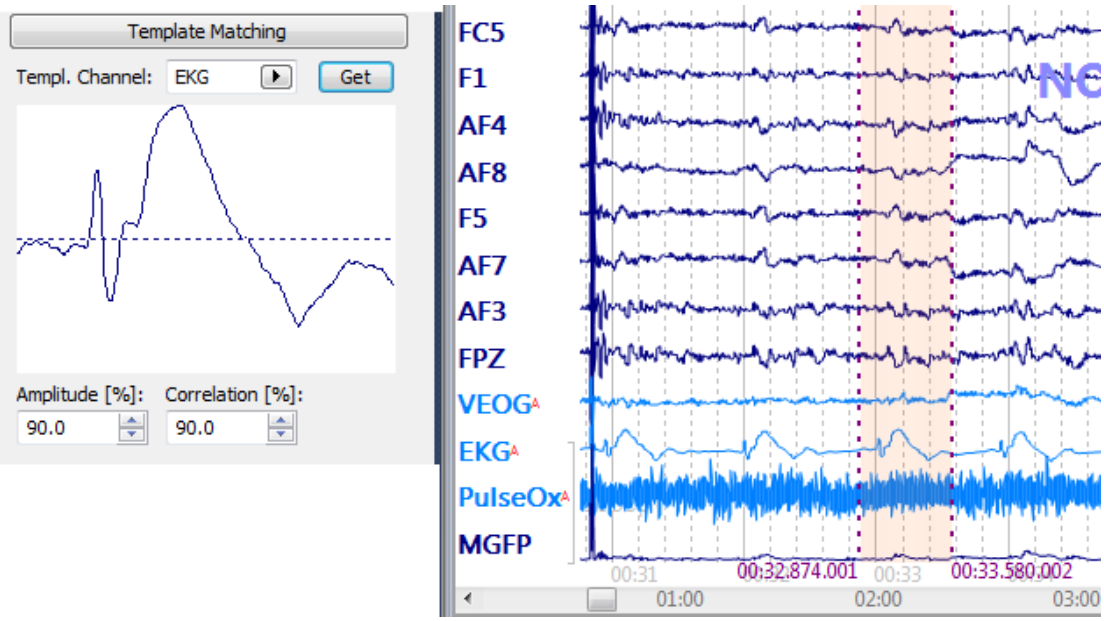
panel and set the **Low Pass** Filter as shown. **Baseline** correction is used to remove the DC offset in the recording. Using a HP Filter will affect the EKG, namely by reducing the amplitude of the pulse we will be using to detect the artifacts, making it harder to detect them reliably. Additionally, the high amplitude gradient artifact make cause the HP filters to ring, creating more artifact. Therefore, the HP Filter is disabled.



5. Scroll further into the file to see the large gradient artifact, starting about 41s into the file, while the event triggers (r5) start a few seconds later. The TR block is 1000 ms (r5's are 1000 ms apart).



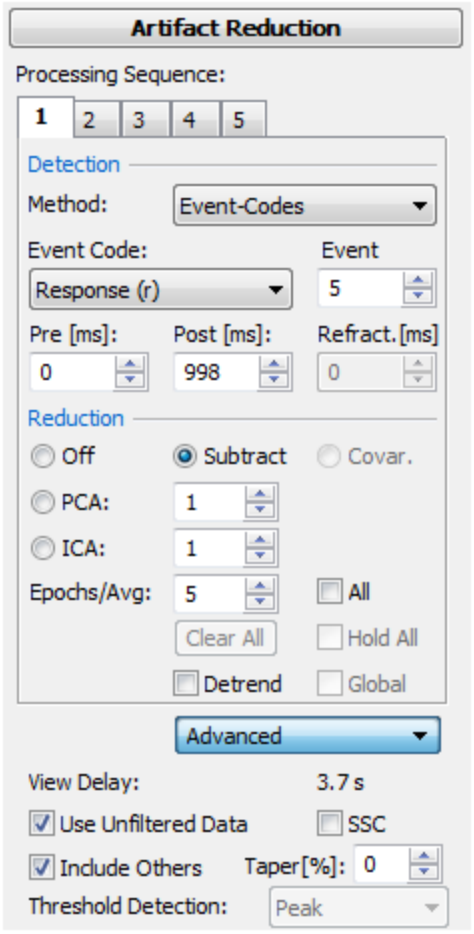
6. Back the file up to where you see a good example of filtered BCG. With the display paused, you can set the two cursors to define a Timerange about the BCG artifact (click to set the first one, *shift+click* to set the second one). Expand the **Template Matching** panel, and select the **EKG** channel. Press the **Get** button to transfer the cursor position latencies. Set the **Amplitude** and **Correlation** criteria to **50**%. This will include most of the matches, even if they are less than ideal. We just want to make sure we are seeing genuine data at this point.



You do not have to use Template Matching to capture the BCG artifact. You could also use the **Threshold** method in **Artifact Reduction**. In some cases, the BCG can drift around, and there can be more than one peak for each BCG artifact, making it difficult for a single voltage threshold to detect the artifacts reliably. Depending on your data, you may find that one way works better than the other.

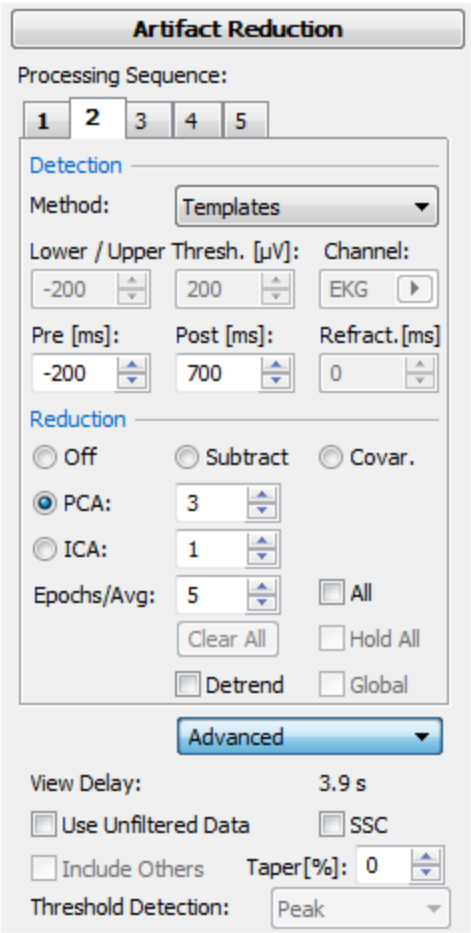
7. Expand the Artifact Reduction panel. We will use **Processing Sequence 1** for the gradient artifact. Event-Codes will use the designated event codes to identify the artifact. Select **Response** and **5**. Note that the **Pre** and **Post [ms]** times are **0** and **998**ms, not 1000 ms. (The AD Rate is 500 Hz). This is a zero-based interval, where the first point is at 0 ms. The next r5 starts at 1000 ms. So the end of the first interval is 998ms. We will **Subtract** the **Average** of **5** artifacts. **Use Unfiltered Data** has been enabled. Otherwise, applying the LP Filter will affect the gradient artifact, making the reduction of it less precise. The data you see in the display are filtered; the average of the gradient artifact is not. (You must enable **Use Unfiltered Data** for the BCG artifact to be detected during corrected gradient sections of the recording).

SubSample 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. **Detrend** is a rarely needed option for reducing gradient artifact in certain data files (online only). In these files, 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** should be an even number.



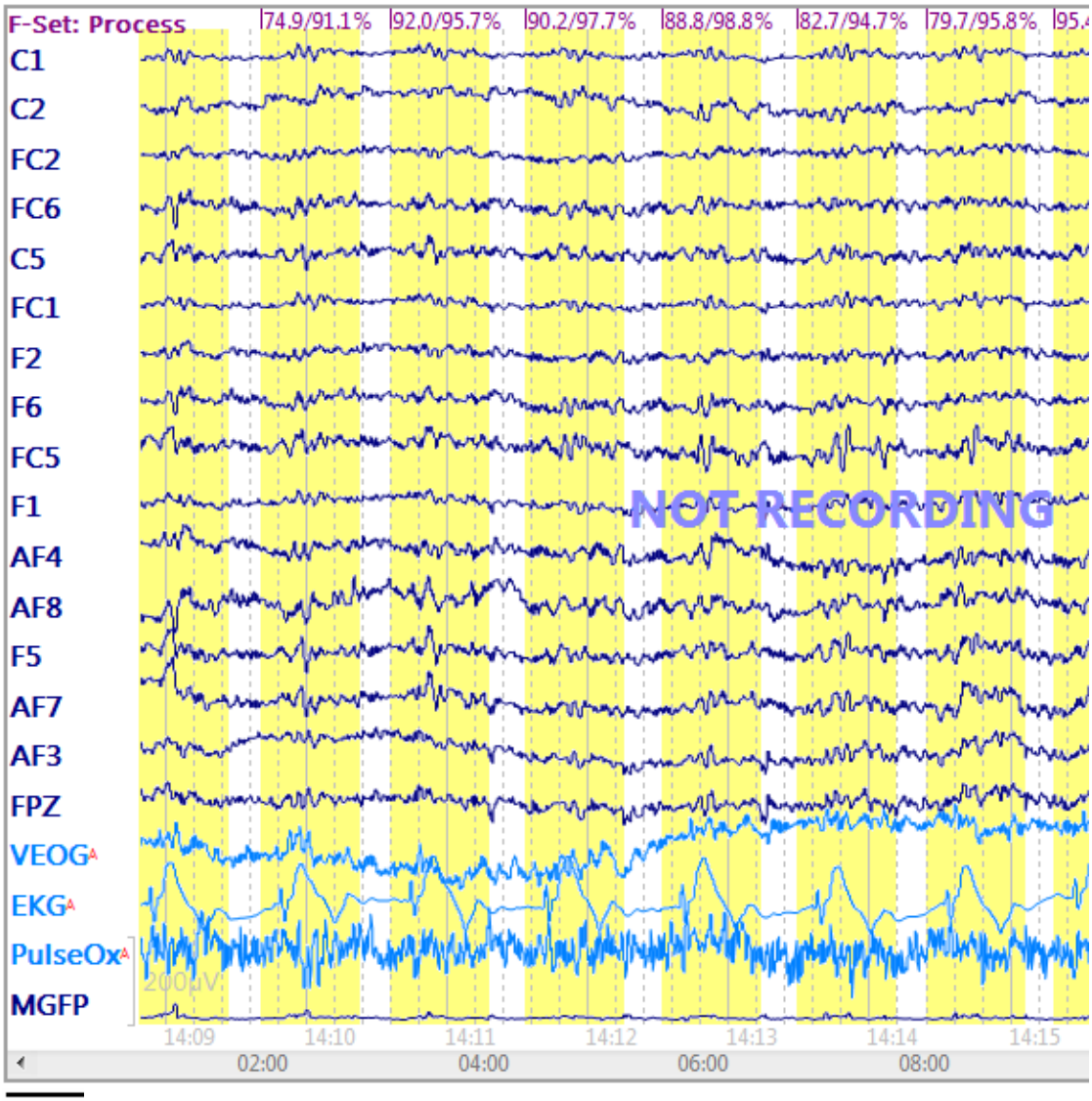
8. Select **Processing Sequence 2**. This will be used to reduce the BCG. The **Templates Method** is selected. **Pre** and **Post [ms]** (**-200** and **700** from the peak) define the artifact interval.

PCA was chosen for the **Reduction** method, with **3** components (which may be changed "on the fly"), and based on the **Average** of the preceding **5** BCG artifacts. **Use Unfiltered Data** has been disabled, since reducing the fast activity will help with the BCG reduction and clean up the data in general. The **All** and **Global** options may be helpful, depending on the data file.



If we were going to use these same settings for additional recordings, we would save the Study Parameters (click the **Save Study Parameters** icon and enter a file name). Use this file for subsequent recordings.

9. Stop Pausing the replay and see the corrections being applied. Let it run until you see the gradient artifacts being corrected (the r5's). The file has been corrected for both types of artifact.



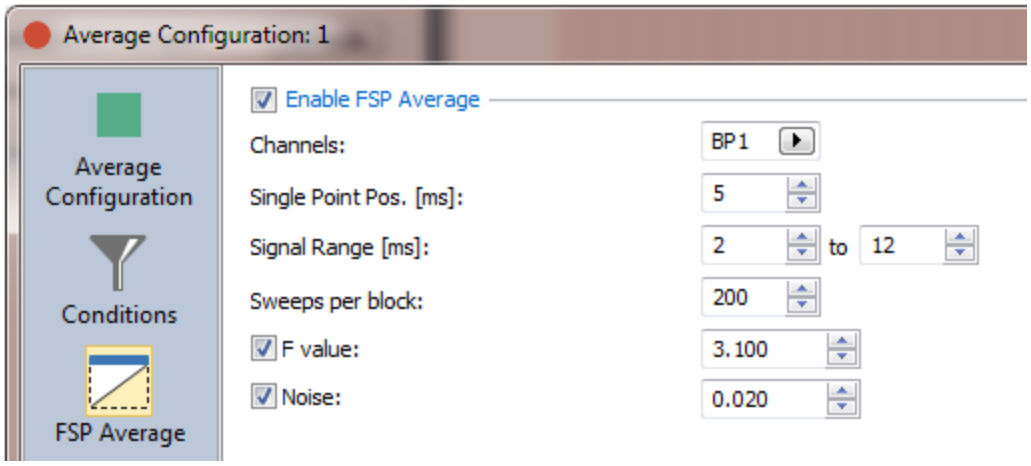
As mentioned above, these corrections affect the display of the data only - the raw uncorrected data are saved. Offline, the corrections will be similar, and often more precise because you have more time to tweak parameters. The purpose for applying the corrections online is to let you verify that you are getting genuine data - while the subject is still connected.

2.2.4.6 Fsp Averaging

If the brain potential you are interested in has a particularly low signal-to-noise ratio (SNR), 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 are constructed from differing numbers of sweeps — will have about the same quality of SNR.

In practice, you can use Fsp online to acquire data until you have reached a statistical criterion.



Enable FSP Average. Enables the Fsp Average capability.

Channels. Select the channel(s) that you wish to include in the analyses.

Single Point Pos. [ms]. This is the latency of the single point. It is a point within the Signal Range, such as **5**ms. You can also use a range, such as 4-6ms.

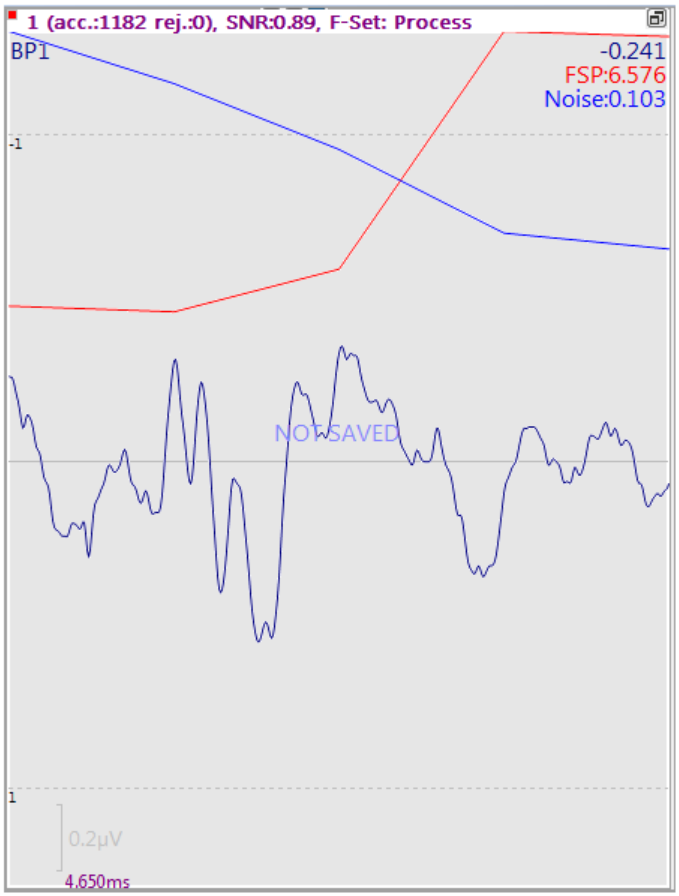
Signal Range [ms]. This is the range that encompasses the signal of interest. For ABRs, this is typically about **2-12**ms. The complete ABR interval is typically **-2** to **15**ms. This is set in the **Average Configuration** fields.

Sweeps per block. Analyses are done in blocks, and blocks are defined by the number of sweeps they contain. For ABRs, where there are typically a few thousands sweeps, the number of sweeps per block **100-200**.

F value. Acquisition will continue until the selected F value is reached. An F of 3.1 is the 95% level.

Noise. Acquisition will continue until the noise level is less than the entered value (typically **0.02** or lower).

To see the F and Noise lines, select the **Position Plot**.



When both F value and Noise are selected, acquisition will continue until both criteria are met.

Please see the offline **Fsp Averaging** tutorial for more details. The online steps and results are very similar.

2.2.4.7 Source Reconstruction

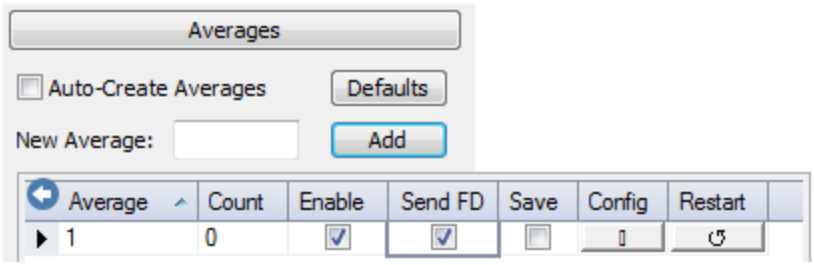
Many of the transforms that you apply offline may be applied online as well. The offline options are described in the **Source Reconstruction** tutorials, but the following steps illustrate how they work online.

We will be using an existing data file played back through the Simulator. The steps for actual online application are essentially the same.

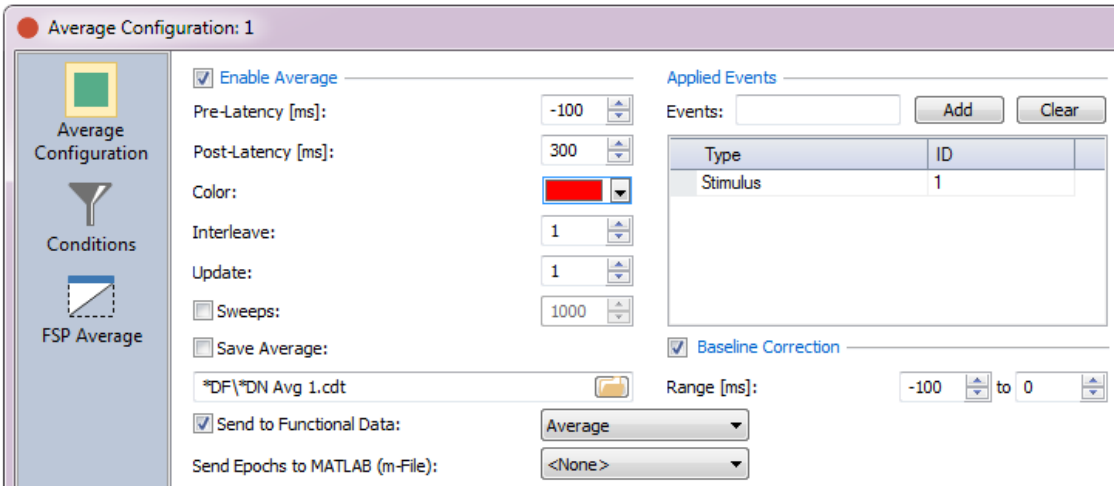
The file that we will be replaying contains Type 1 events for VEP Pattern Reversal stimuli. We will create an online average of the events, and perform dipole source reconstruction while the average is accruing. The source solution will be updated with each new event that is received.

1. Go to the acquisition part of the program by clicking the **New** icon .

2. Expand the Averages panel. The stimuli are just less than 500 ms apart. As we will be looking primarily at the P100 component, we will create an online average from -100 to 300ms. Enter a **1** in the **New Average** field and click the Add button. In the line that is created, enable the **Send FD** field. It is this option that will make the data available for the additional functionality, such as, source reconstruction.

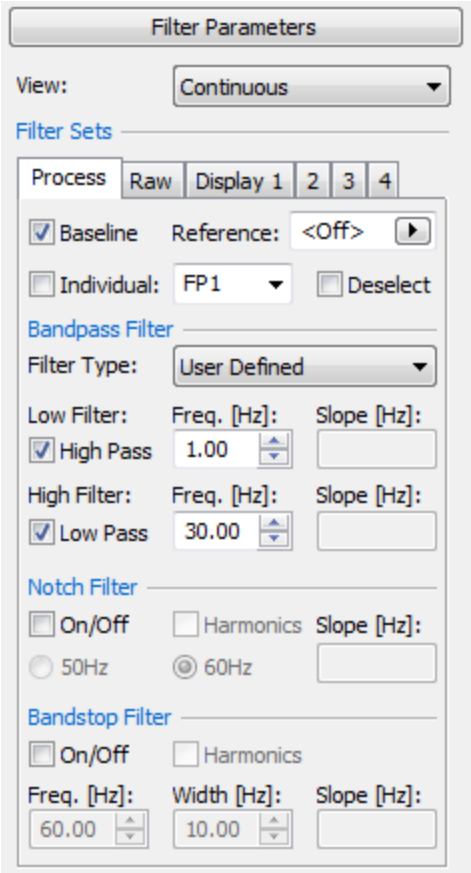


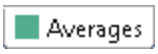
3. Click the **Config** button. Enter -**100** and **300**ms for the **Pre-** and **Post-Latencies**. This defines the start and stop times of the epochs we will be including in the average. Enabling **Process** in the step above also enables the **Send to Functional Data** option in the figure below. Click **OK**.



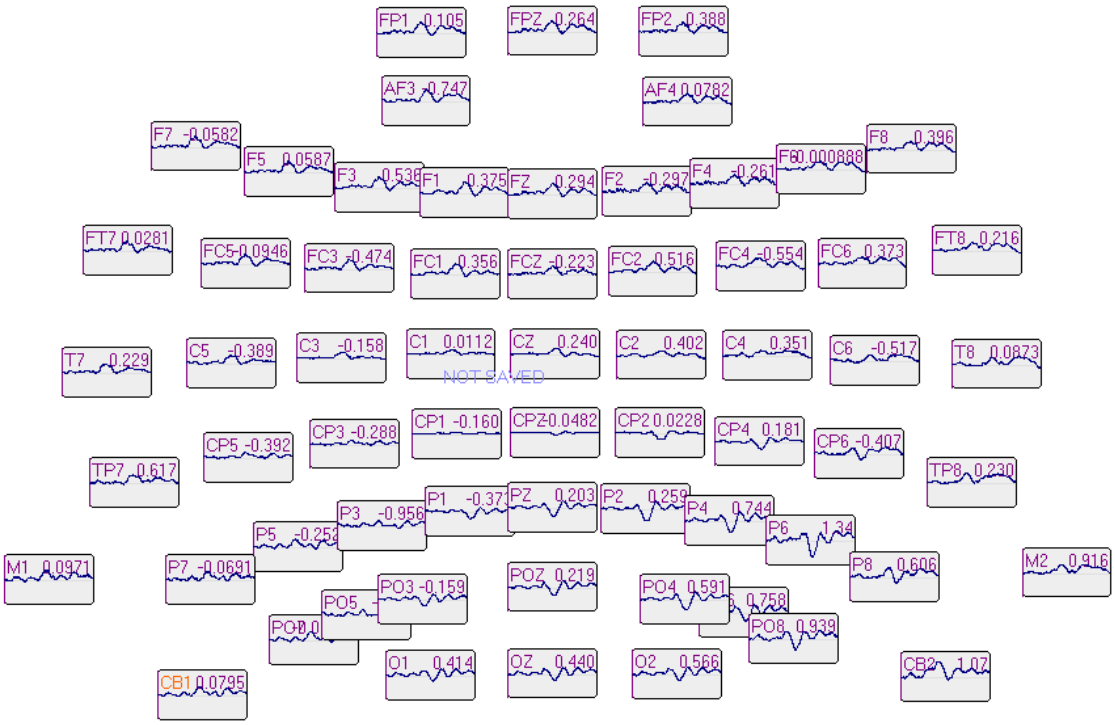
4. Expand the Amplifier Control panel, and select **Simulator**. Click Start Amplifier and select the *VEP DC-200.cnt* file from the *C:\CURRY 8 Tutorials\Signal Processing\Evoked Response Analysis* folder.

5. The file was recorded with a bandwidth from DC to 200 Hz, so we will first filter the data. Expand the **Filter Parameters** panel, and enter the parameters shown below.

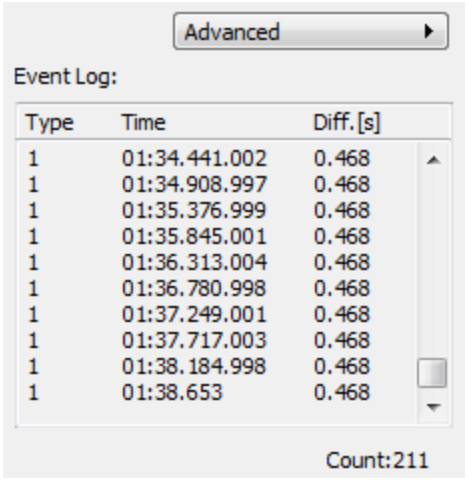


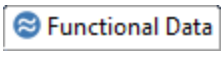
6. Select the 

button to see the online average being created. *Right click* in the average window and select **Position Plot** to see the channels in their approximate positions.

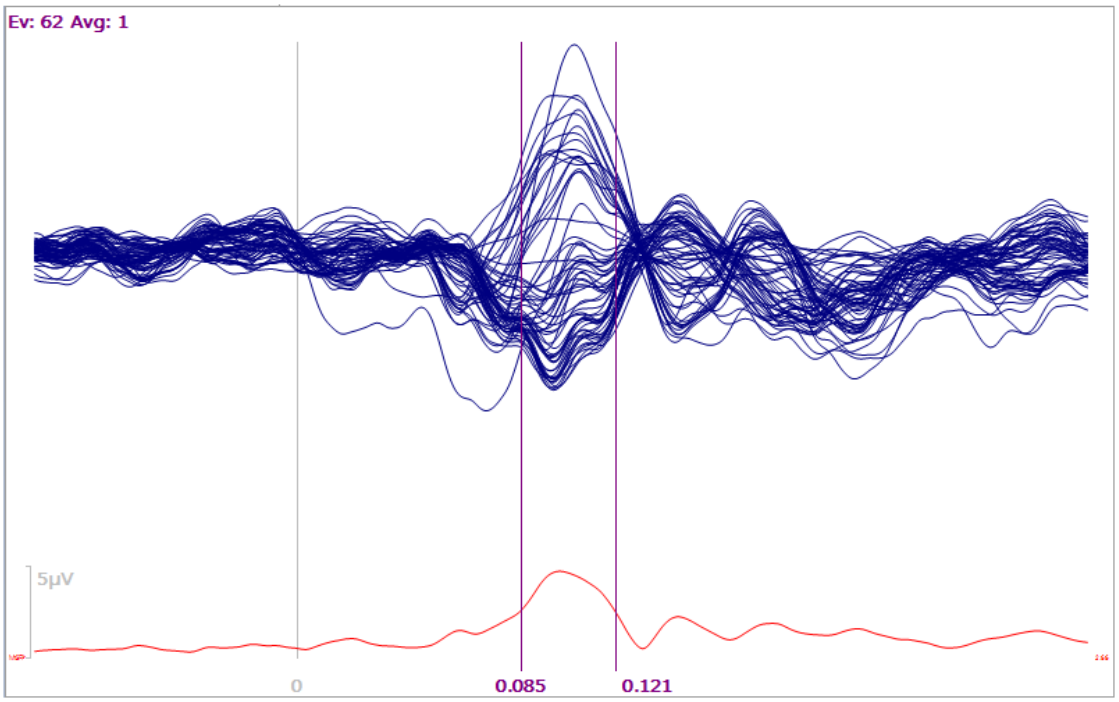


It is often very useful to expand the Advanced section under Averages, and examine the Event Log. This shows the events that are being registered and the times between them.

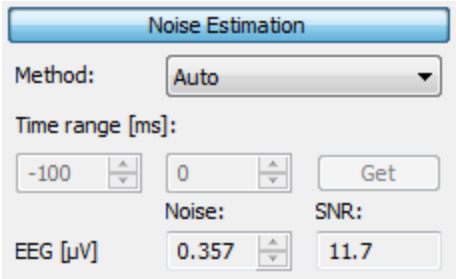


7. Select the 

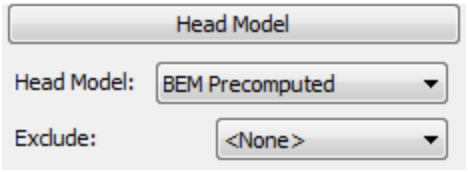
display tab. Rescale as needed (*mouse wheel*). The **Butterfly Plot** was selected, and the polarity inverted . Select a Timerange to encompass the P100 component.



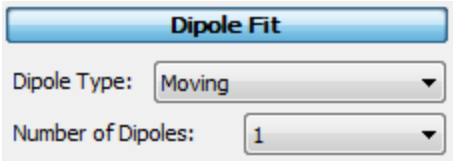
8. The rest of the operations are the same as offline, except you will see the data being updated with each new sweep. As usual, a noise estimation is needed. Expand the Noise Estimation panel and select **Auto** (this applies the **Pretrigger Interval** option with averaged files that have a pretrigger interval). If Auto is the default option, you need not do anything.



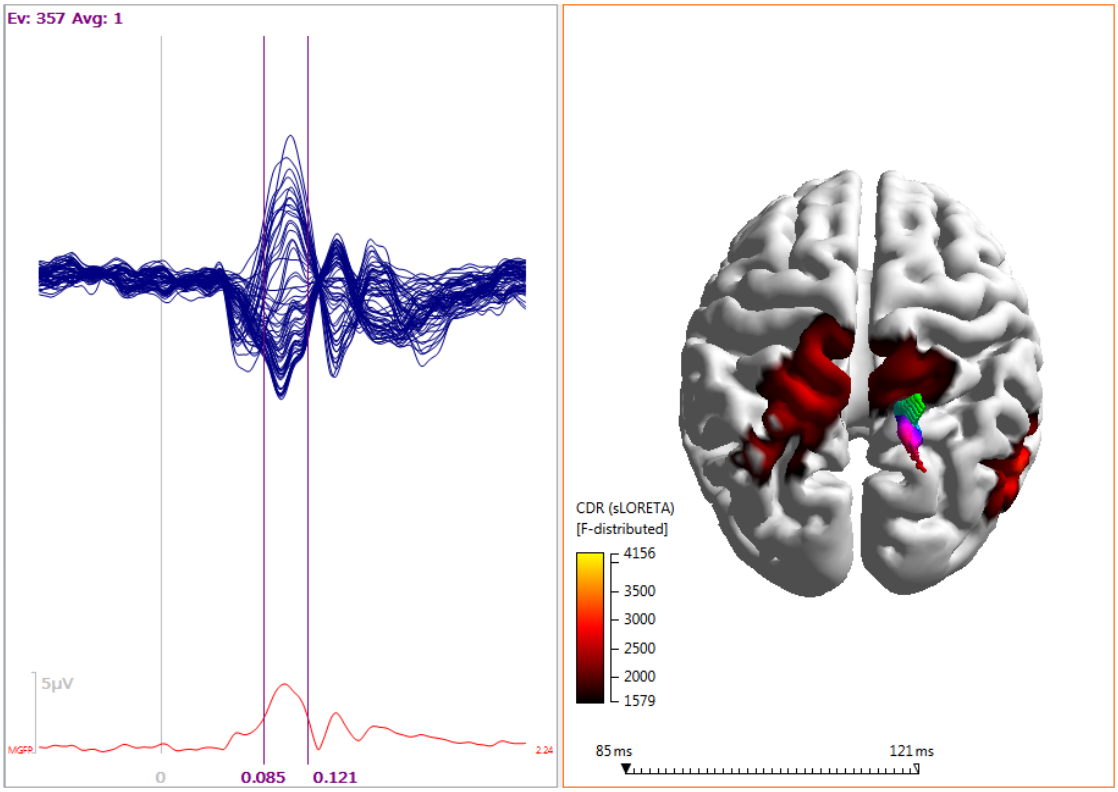
9. Expand the **Head Model** panel (under **Source Reconstruction**), and select the **BEM Precomputed** head model.



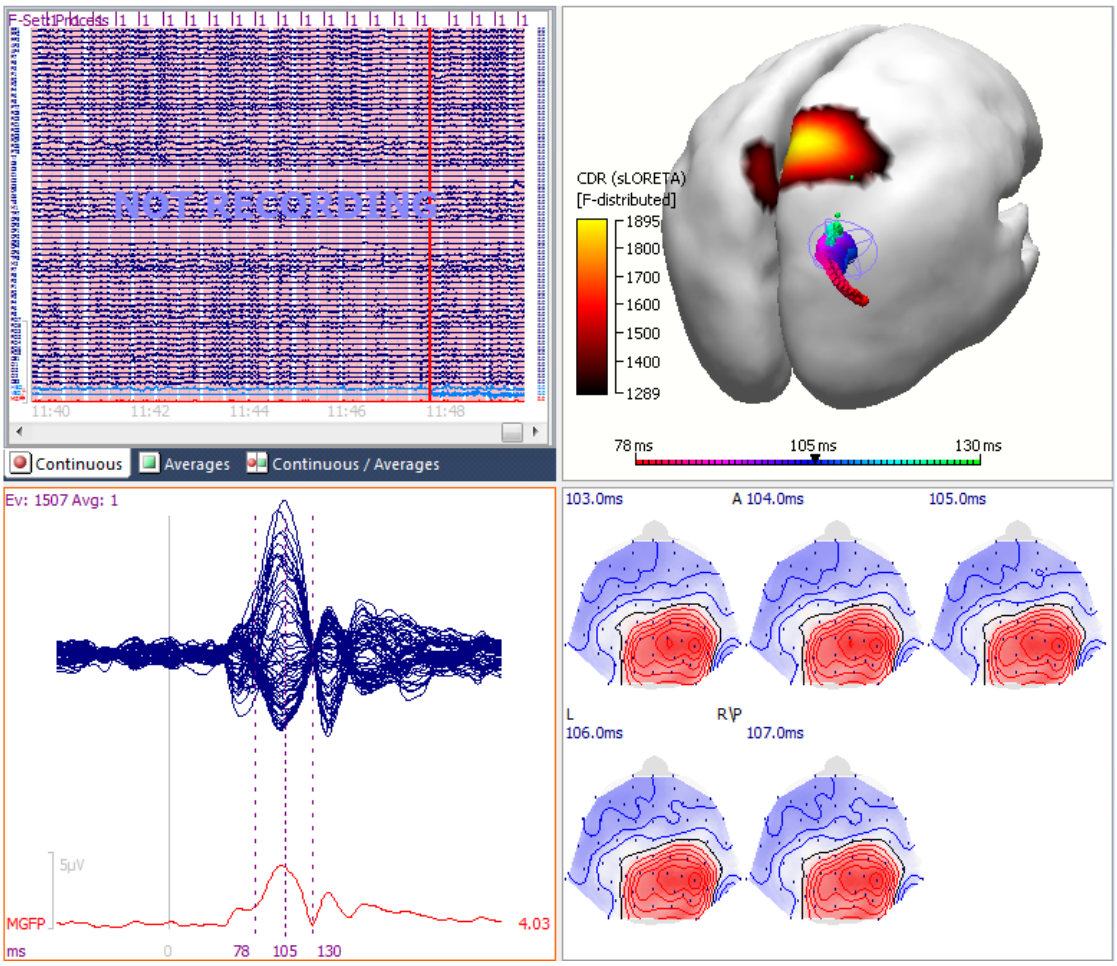
10. Expand the Dipole Fit panel, and select a **Moving** dipole.



11. Select the FD, 3D View display tab. The moving dipole results will appear and update with each new sweep. Expand the **Current Density** panel and select **sLORETA** for the **CDR Type**. For **Source Locations**, select **Standard Cortex**. Now both analyses will update with each epoch. (This puts a load on the CPU, so you may not be able to perform all of these operations; you will see an error message if that happens).



12. To return to the incoming data, click the Acquisition tab, or select Acq, FD, Maps, 3D to see acquisition, the average, the Maps display, and the 3D View simultaneously (**Standard Brain** was selected).



Once you get to the Functional Data step, you will have access to many of the same options that are available offline.

Click the button to disconnect from the Simulator when finished, and click the **X** to exit acquisition.

2.2.4.8 Video

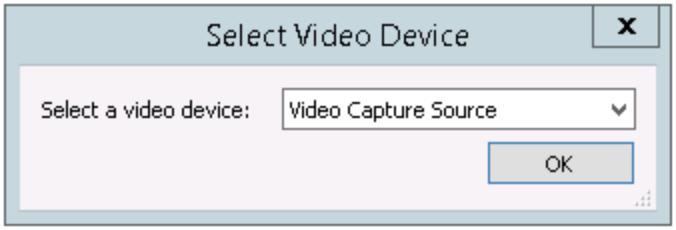
Using Digital Video

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** section in the *CURRY 8 User Guide*). The "V" license is not needed to replay previously recorded video files.

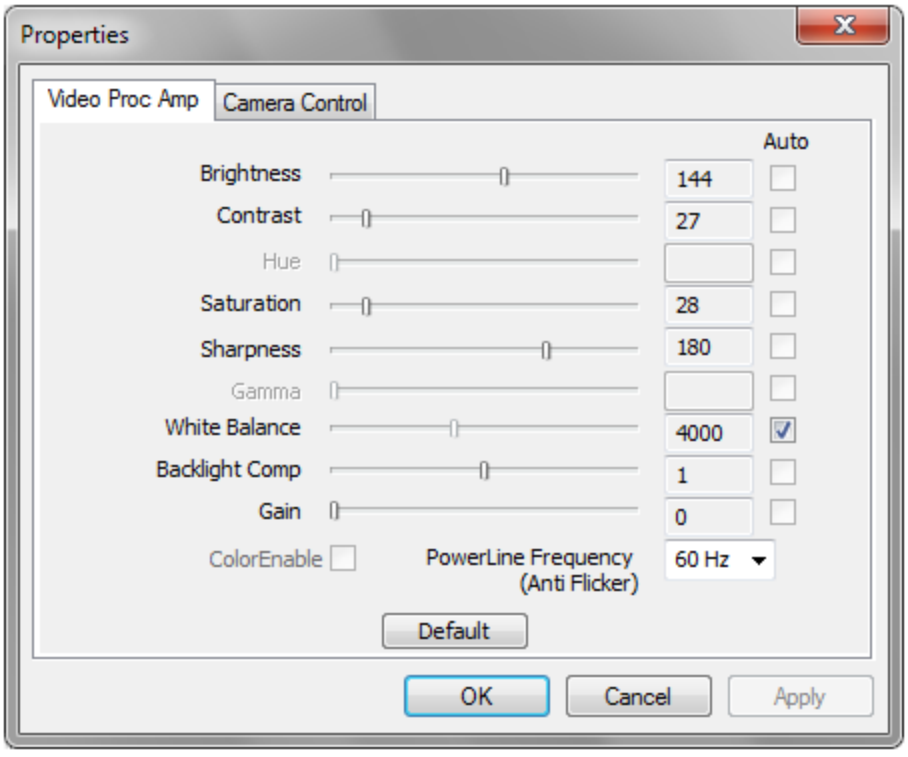
With the CURRY 8 software closed, install the software for your digital camera, and verify that it is working. Then close the camera's software.

For this example, all that is needed is any continuous file that can be replayed in the Simulator. Click the **New** acquisition icon .

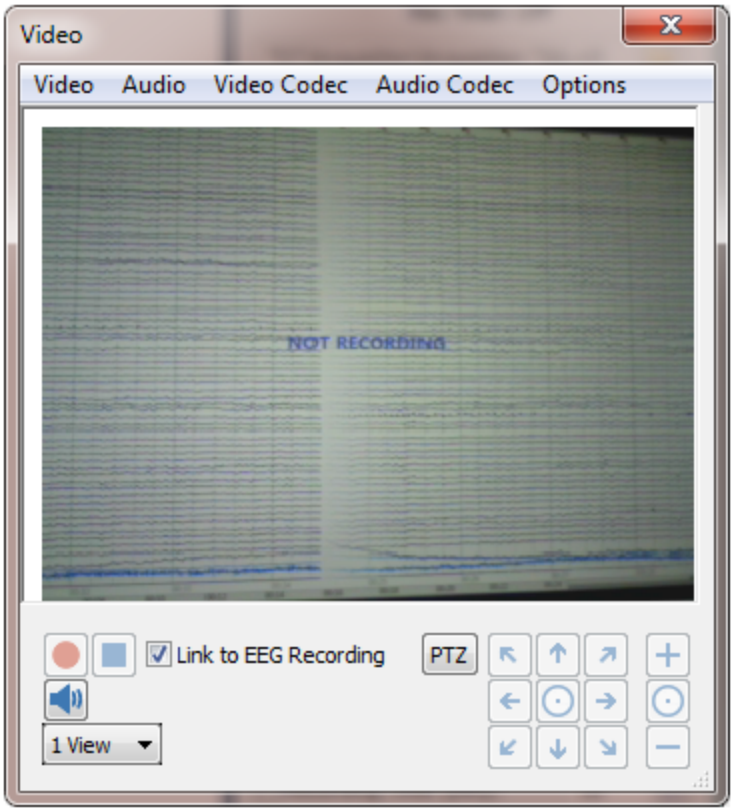
1. Set the **Amplifier** to **Simulator** in the **Amplifier Control** panel. Enter or at least note the target folder for the file to be recorded. Select a continuous file after clicking the button. Enable the **Video** option from the icon on the Toolbar. If this is the first time you have clicked the Video icon, you will see the Select Video Device window. It may have one or several items, depending on what has been installed on your computer. Select the digital camera that you are using.



After clicking **OK**, you will see the **Properties** window (the contents will vary from camera to camera). Make changes as desired and click **OK**. You will not see these windows again after the first installation. See the **Video** section in the *CURRY 8 User Guide* for more details. (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**).



The **Video** window should then display the camera view.



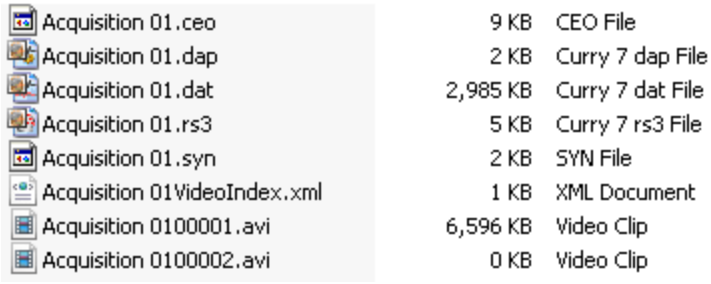
Position the cursor in the display and use the *mouse wheel* to zoom in or out. Drag the displayed as desired. *Right click* and select **Reset View** to restore the original view (or double-click in the display).

2. The **Video** and **Audio** lists let you select whatever devices are detected. Codecs are programs that encode a data stream or signal for transmission, storage or encryption, or decode it for playback or editing. CURRY will select the **x264vfw** video codec and the **MPEG Layer-3** audio codec automatically.

The **Options** list contains the standard Audio and Video Filter settings (brightness, contrast, treble, bass, etc.). The **Video Settings** option contains settings for the Stream Format, including Color Space / Compression and Output Size. Vary these to find the best resolution (and test it while saving the EEG data; you may have to use a lesser resolution when saving as opposed to just viewing). Enable **Stay On Top** if you want the dialog to remain visible (this is the default setting but it may need to be forced with this option).

3. When you start recording the EEG file, the video file will be saved at the same time. In practice, the video will be slightly behind the EEG display. It is a good idea to have the subject blink a few times at the beginning of the recording, or touch an electrode so you see the artifact in the recording. You can use this offline to adjust the playback so that the EEG and video are synchronized (the delay will vary from camera to camera). The video will stop recording when you stop saving the EEG file.

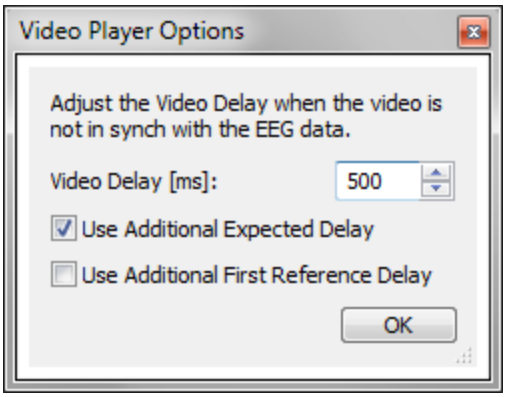
4. If you look in the folder where you saved the EEG data, you will also see files related to the video. The number of .avi files depends on several points. The video files cannot be much larger than 200 MB (for crash safety). Video files are split when you pause and resume a recording. Video files are split when the software detects a synchronization error in the "video rendering and encoding pipeline". The .syn file contains the synchronization information; the "VideoIndex.xml" 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.



5. 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.

As you move through the file, the video will be synchronized, although 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.

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).

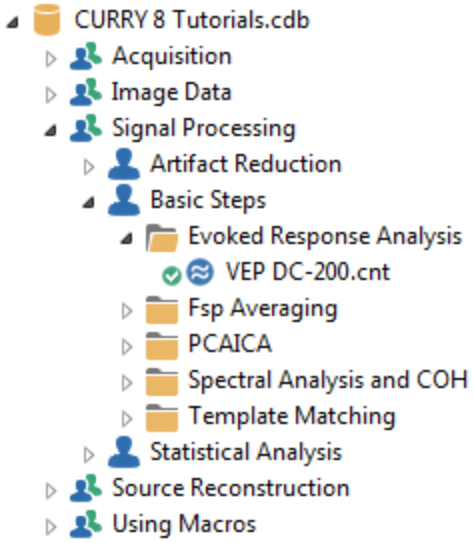
2.3 Importing Data Files

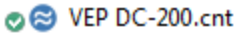
All types of files that you will be using are imported when you open a Study. The two main file types - functional data and image data files - each have their own "wizard" to facilitate file import. A third "wizard" will be accessed when importing digitizer files that are not recognized. Tutorials for the first two wizards are presented next; for information about the Digitizer File Wizard, please see the *User Guide*.

2.3.1 Functional Data Import Wizard

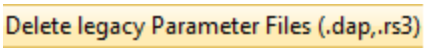
The Functional Data Import Wizard is a function of CURRY that will autodetect parameters in your data file the first time you load it. It creates a parameter file (.dpa extension) that is read when you subsequently use the same data file, bypassing the need for the Wizard again. One of the primary purposes of the Wizard is to specify the files or method used to co-register the functional data with the image data. (The .dpa file replaces the .dap and .rs3 files used in prior versions of CURRY).

In this example, we will use the Study shown below.



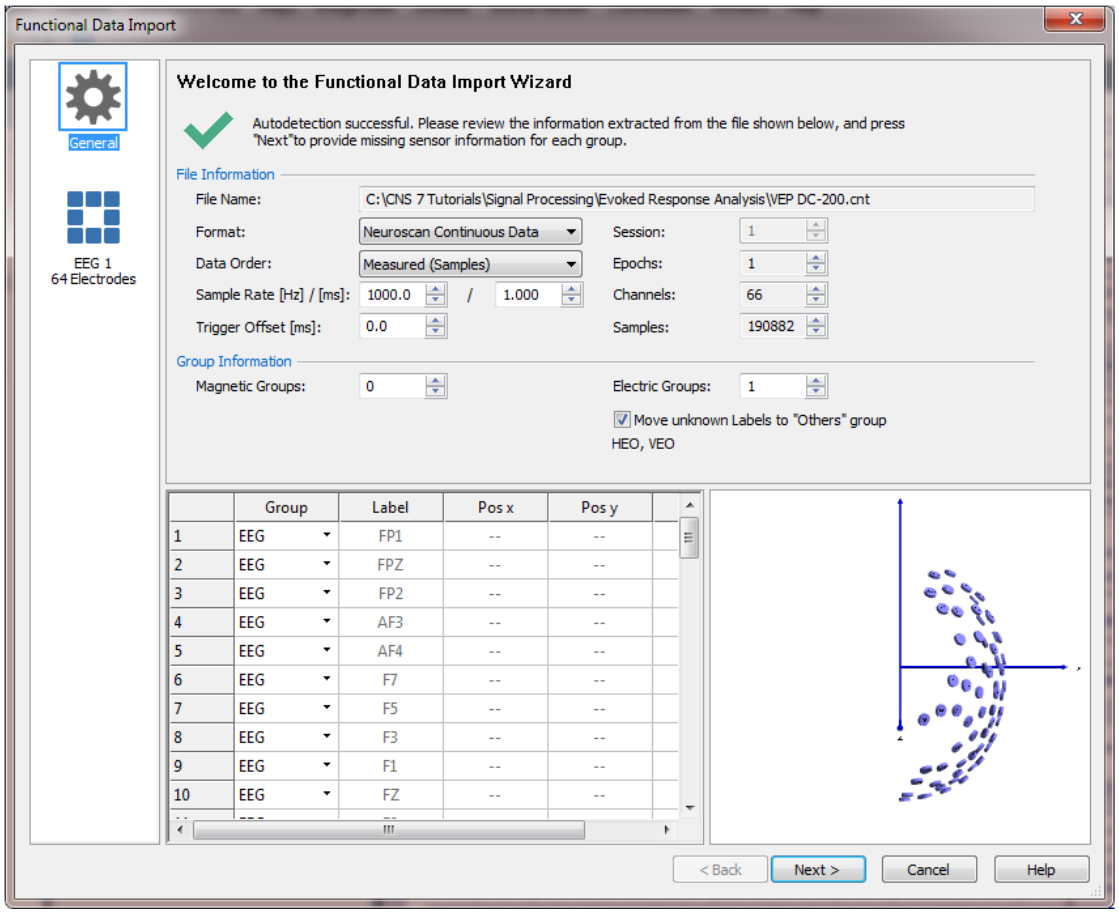
Note the green check mark before the file name 

. The check mark indicates that the file has been loaded before and the parameter file for it has been created already. If we were to open the Study right now, the Wizard would not be seen and the data would appear.

Right click on the data file name and select 

(this file initially has the older .dap and .rs3 files; these will be replaced shortly with the newer .dpa file). The check mark then disappears. The Tutorial is now set to simulate what you will see when you load a functional data file for the first time. If you have recorded the file from CURRY 8 to begin with, the .dpa parameter file is created automatically, the green check mark will be seen, and the Wizard will be by-passed.

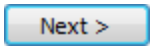
1. *Double-click* on the Study to open it (or click the arrow). The Wizard appears.



2. Note that Autodetection was successful - CURRY recognized the file type. Data Order refers to the order in which the data are organized in the data file (by samples or by channels). There is 1 Epoch, since this is a continuous data fie. The AD Rate is 1000 Hz, giving a data point every 1.0 ms. There are 66 Channels. There is no Trigger Offset (no prestimulus interval). One Electric Group was detected.

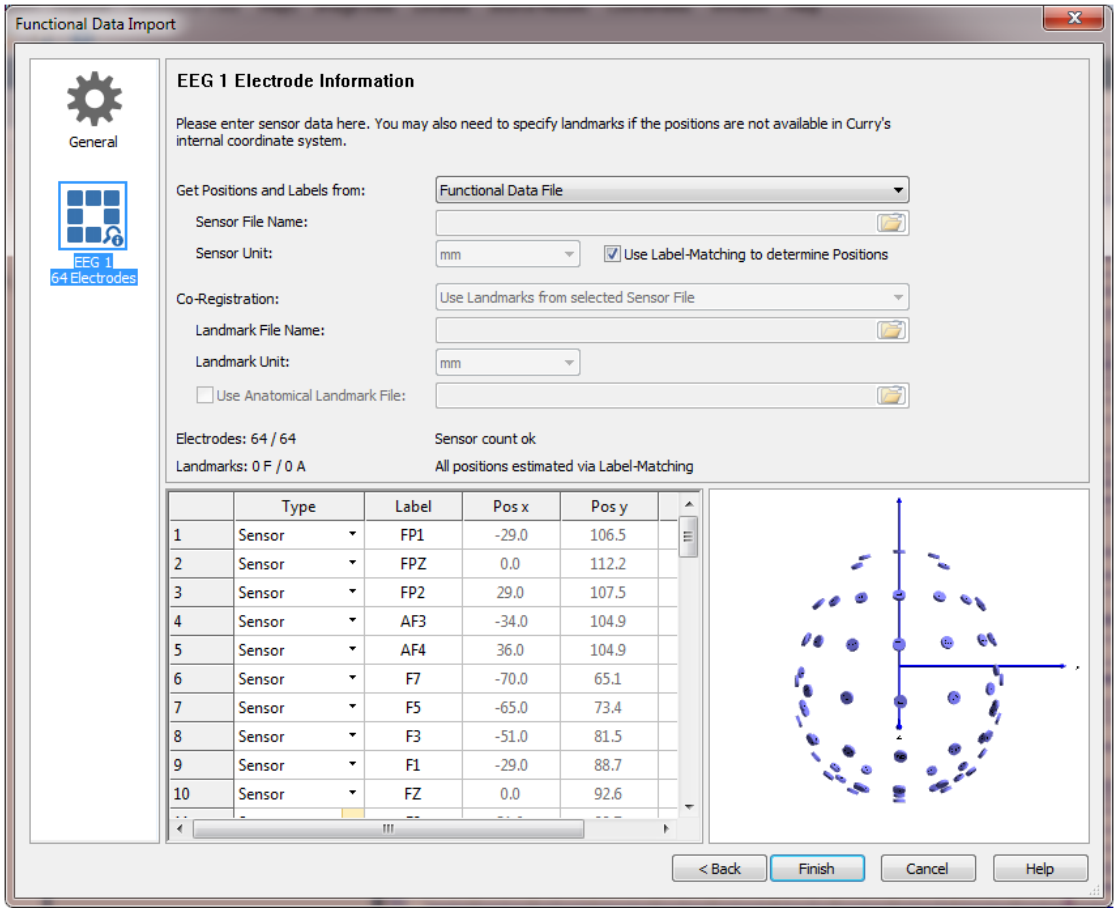
Enable **Move unknown Labels to "Others" group** (if needed). HEO and VEO are shown as being "Other" channels. While CURRY recognizes HEOG and VEOG, it will not recognize HEO and VEO. These are example of unknown labels. Use the scrollbar to go to the bottom of the list, and see that the last two labels are HEO and VEO, and they are designated as **Other** channels. "Other" channels will be excluded from operations where their inclusion would distort the results.

No electrode positions were supplied, and so the XYZ columns are empty. The display of the electrode positions (based on default settings) is clearly incorrect.

Click 

or the button.

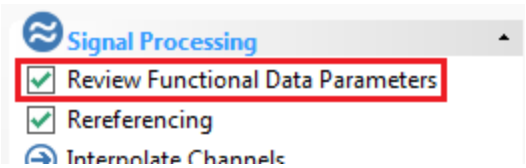
3. In the final screen of the Wizard, enable **Use Label-Matching to determine Positions**. (It is always preferable to use the real 3D positions, where available). You will then see realistic positions in the lower right part of the display, and the electrodes will have estimated position information.



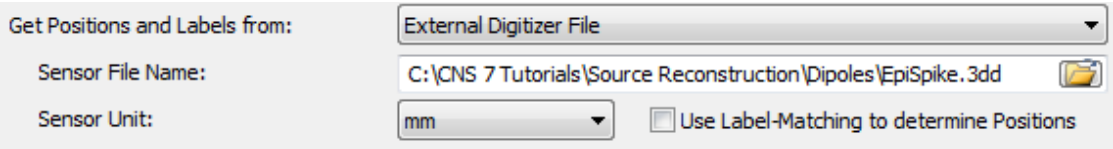
Click the Finish button to complete the data file import. The parameter files will be created automatically, and the data file will be displayed. The green check mark appears again before the file name VEP DC-200.cnt .

The next time we open the Study with this data file, the parameters will be read and the file will open correctly.

4. If you want to review the functional data parameters, sensor positions, or functional landmarks, you may click the desired option from the **Workflow** window, or just click the icon from the Standard Toolbar.



If you have a 3D Digitizer file, or other file that contains the electrode position information (usually with the anatomical landmarks positions, e.g., Nasion and left and right preauriculars), you can provide the accurate position information. There are two ways to do this. You can insert the digitizer file into the Database by *right-clicking* on the Study and selecting **Insert Digitizer File**, or you can select the digitizer file from the second page of the Functional Data Import Wizard, as shown.



In this tutorial you have seen how to use the Functional Data Parameters Wizard. When you load magnetic data, the procedures will be analogous. When you load an individual's image data, there is a different procedure, which is the subject of the next Tutorial (**Image Data Wizard**).

If you are using a digitizer file (a file that contains anatomical landmarks and/or electrode positions), and the digitizer file format is not recognized, you will see the Digitizer File Import Wizard. This is described in the *CURRY 8 User Guide*.

2.3.2 Image Data Parameters Windows

This chapter will provide an overview of the initial steps that are required before a new MR data set can be analyzed for the first time. In order to access the data, a Database is created first. Then, an image data set is accessed using the **Image Data Parameters** windows.

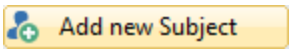
Note
The *CURRY 8 User Guide* provides background information on the import of image data, functional data, and sensor locations, together with detailed descriptions of the file formats supported and their individual treatment.

Image data can be stored in a single file (such as the .dat file we will use below), there may be a collection of individual files stored in a single folder, or as in most cases, there may be multiple subfolders with various files for each of the sequences that was recorded. In those cases, CURRY will select the folder with the most files, anticipating that is the one you will want. You can select other ones as desired.

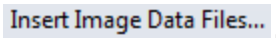
The examples that are shown in this chapter do not yield any results that are worth saving. In order to keep them apart from the somewhat more valuable results that are created in the other chapters, they will be placed in a new Database.

Image Data Parameters Windows

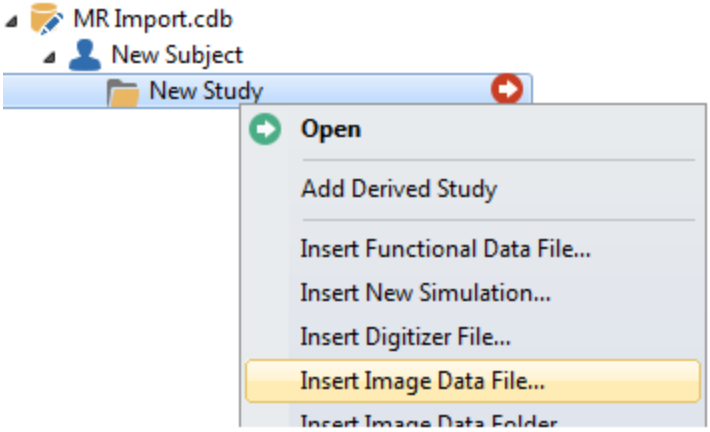
1. Create a new empty Database: **Database** → **New**, and enter a file name in the Create New Database window (such as, *MR Import.cdb*).

2. *Right click* on the Database name line, and select 

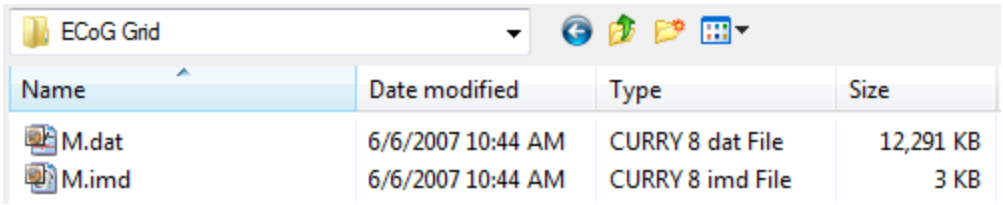
, or click the indicated icon (we will not use Groups in this example).

3. *Right click* on the **New Study** folder, and select 

. When importing your own data, you may have a folder with separate files for the slices in it. In that case, you would select Insert **Image Data Folder**, and then select that folder.



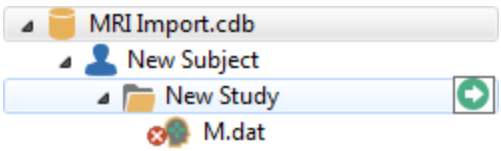
In the Open dialog, navigate to the *C:\CURRY 8 Tutorials\Image Data\ECoG Grid* folder.



In this folder are the *M.imd* and large *M.dat* file (containing the MR slice data). The .imd file is a parameter file created by CURRY. If you were loading data for the first time, you would see the *M.dat* file only. (Other MR data sets may have individual files for each slice rather than a single .dat file). When you attempt to view the MR data, you would instead see the parameter screens below. The .imd file will be created at the end of the process.

To simulate loading MR data for the first time, *right click* on the *M.imd* file (in the Open File window), and **Rename** it (this will allow you to return to the original parameter file if needed). Then select the *M.dat* file to load it in the **Image Data** folder.

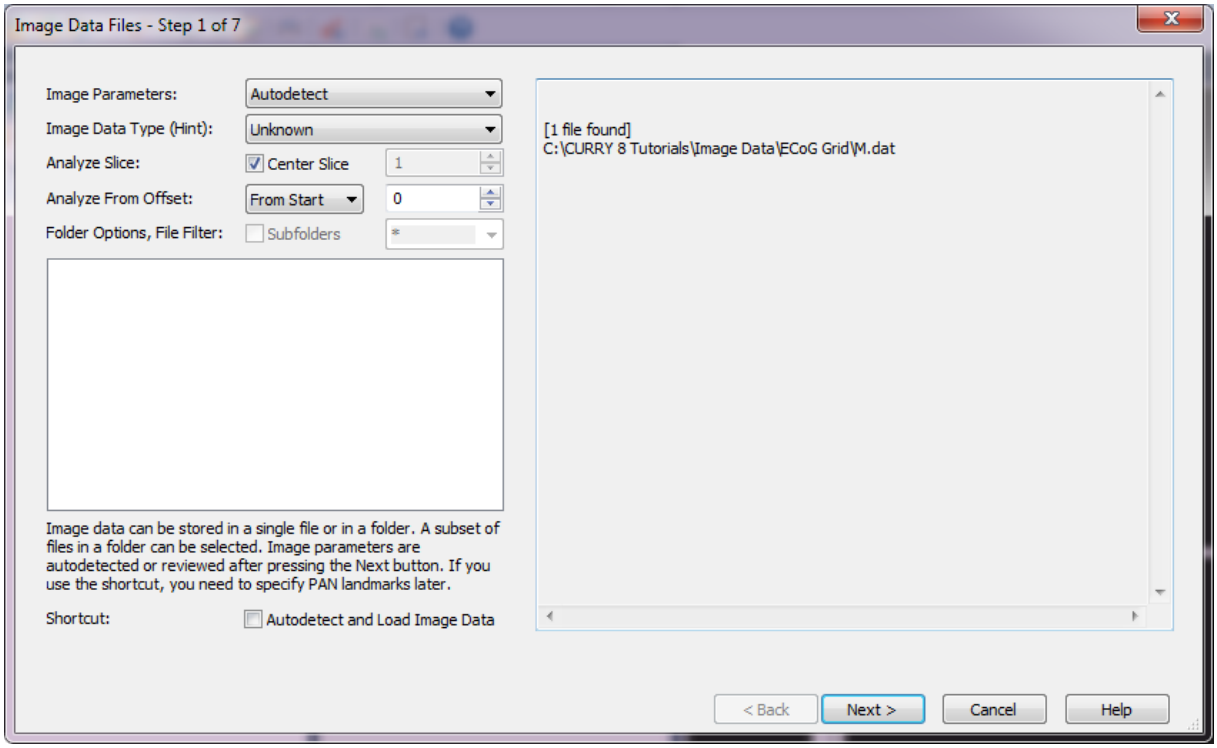
4. Click the green arrow that will appear for the New Study line to open the Study. The red X indicates that no parameter file was found.



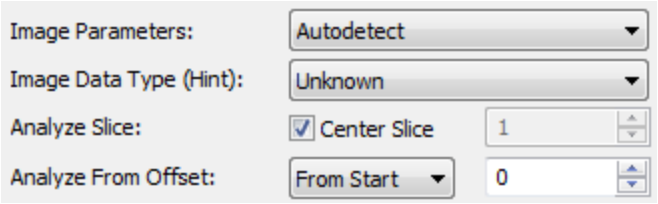
The **Image Data Files - Step 1 of 7** screen is displayed (you will not see this if you leave the .imd file in place). This is the initial screen for the **Image Data Parameters** windows. The list of files that were found is shown below (one in this case - the *M.dat* file). In many instances, you will have multiple image data sets in the same folder. CURRY will autoselect the one with the greatest number of files, which is typically the greatest number of slices, as that will give the best results.

Note
Details pertaining to the function of all of the settings in all of the following screens are described in the *CURRY 8 User Guide.*

Note
CURRY will autodetect the image data parameters to the extent possible; however, the successful importation of image data requires that you know certain parameters that are not necessarily contained in the image data file(s). Therefore, you should not assume that the settings CURRY displays are all correct - some are default values. Failure to use the correct parameters settings can affect the accuracy of source localization, so be sure that the parameters are correct.



Step 1: Generally, you want to help out the autodetection with as much information as you have. In this case, set **Image Parameters** to **Autodetect**, **Image Data Type** to **Unknown**, if needed. The **Center Slice** and **Analyze From Start** (at **0**) options should be enabled already. Click Next >.



CURRY will analyze a single slice of the image data, and attempt to locate and interpret a file header in ACR-NEMA format. The slice to analyze is always the **First Slice** to be Read, and it is typically analyzed **From Start**.

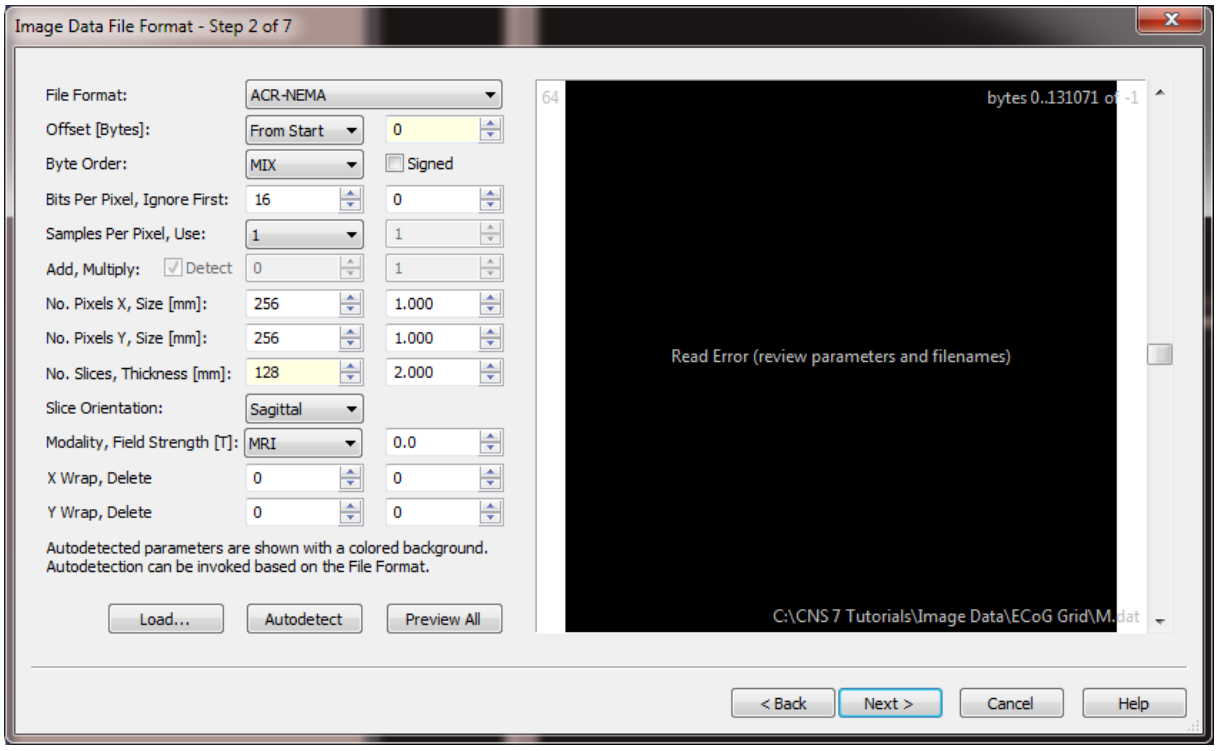
Note

In many if not most cases, you can simply highlight the desired file or folder in the list (if more than one data set is detected), *and then click* ***Autodetect and Load Image Data***. The parameters will be detected automatically, bypassing the remaining steps below. If the image data appear correct in the Image Data display, you are ready to continue. If you need to define the Landmarks (generally the case), you may go to that part of the **Image Data Parameters** windows directly by selecting **Image Data** → **Landmarks**. This will take you to **Step 6** below. If you need to refine the segmentation thresholds, go to **Image Data** → **Segmentation Thresholds**. This will take you to **Step 5** below. If the image data are not displayed correctly, you will need to return to the **Image Data Parameters** windows (**Image Data** → **Image Data Parameters**) and make the necessary corrections.

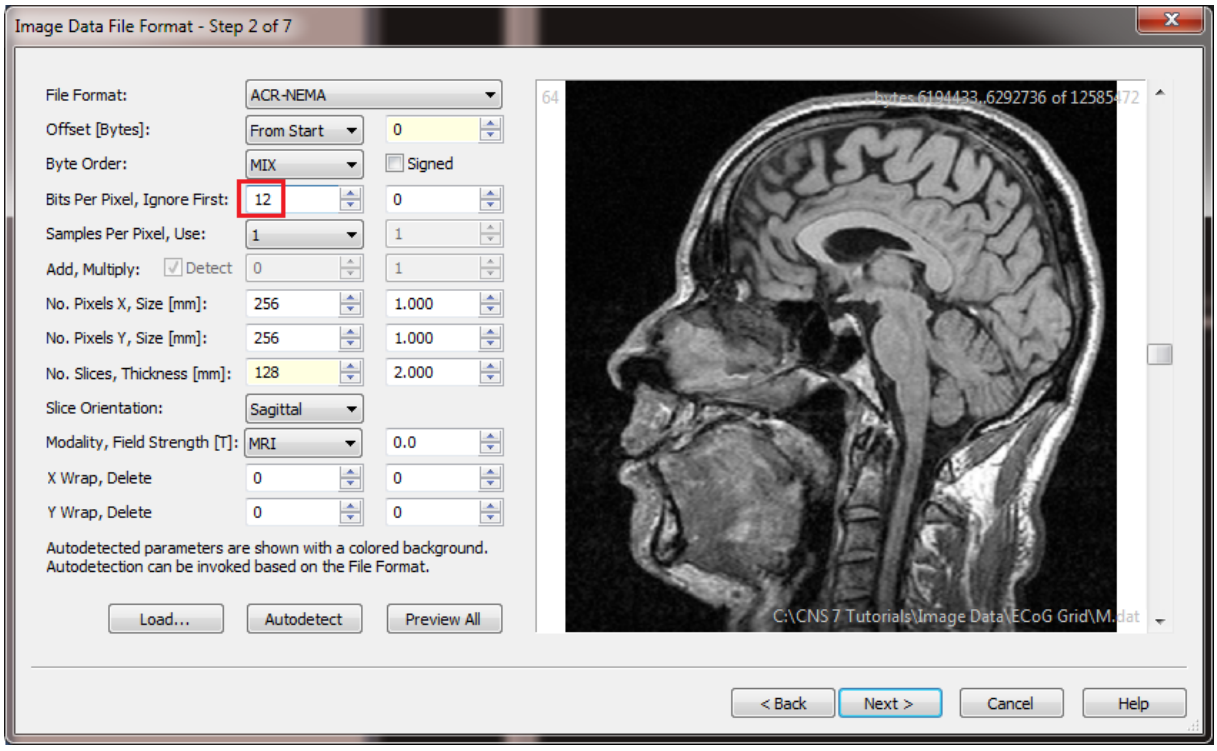
Step 2: The **Image Data File Format** display will appear. These parameters determine the file format for a 2D slice.

Note

The first few slices of this data set 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.



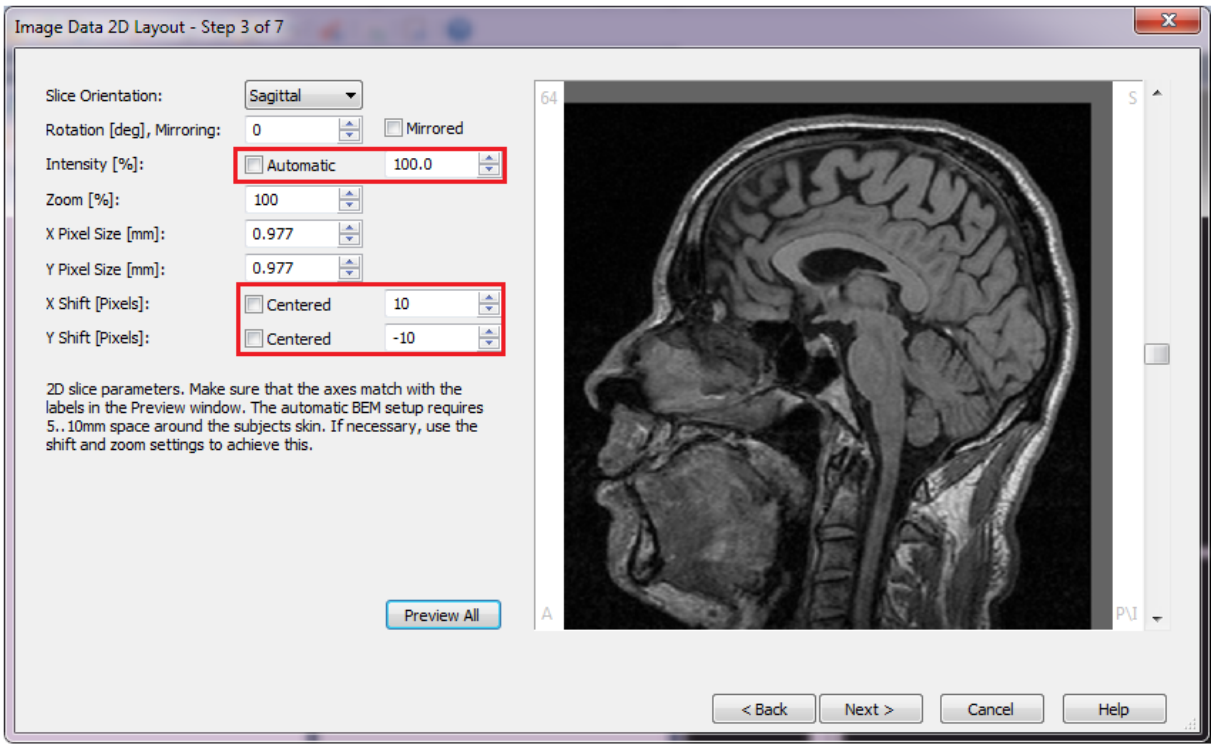
The detected parameters are displayed in yellow. The parameters in white are not autodetected, and must be supplied. Obviously, there is something wrong since the images are not seen at all. We know from the scanner information that these are 12 bits per pixel, not the 16 that appeared by default. Change **Bits Per Pixel** to **12**. Now we see the correct images (click the Autodetect button if the image is not clear).



Enter **0.977** for both the **X** and **Y Pixel Size [mm]**. Change **Thickness [mm]** to **1.8**. We know these values from the scanner protocol; they will vary across scanners and protocols. Click Preview All to scan through the images. In this case the parameters are now all correct. You should verify them when you import your own data files. In general use, clicking the Autodetect button will fill in the fields with whatever parameters are detected (or to restore the autodetected values if you change them). If you already have an .imd file that has the correct parameters, you can apply it using Load....

Click the Next > button to continue.

Step 3: The **Image Data 2D Layout** screen is displayed. In this display you need to make sure that the axes match with the labels in the Preview window (sagittal in this case, where A and P in the Preview window truly are Anterior and Posterior, and S and I are truly Superior and Inferior).



In this example, disable the **Automatic** Intensity option, and enter **100**. Verify that the **X** and **Y Pixel Sizes** are **.997**. The automatic BEM setup requires 5-10mm space around the subject's skin. If necessary, you can use the Shift and Zoom settings to achieve this. Disable **Centered** for **X Shift [pixels]** and enter **10**. Disable **Centered** for **Y Shift [pixels]** and enter **-10**. In some cases, you may not need to make any corrections at all; in others you need to make sure the parameters are correct.

Click the Preview All button to scan through the images. The image intensity, position, size and quality are now acceptable.

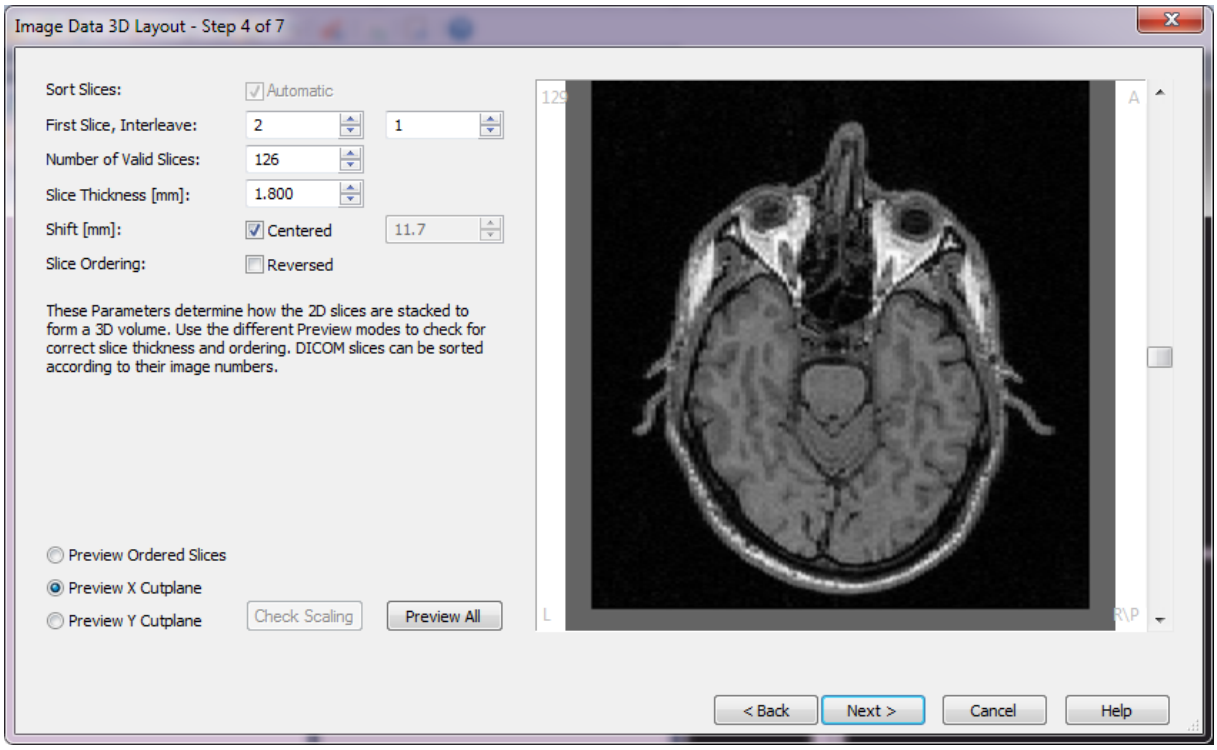
Note
Very often, the **Intensity** must be increased significantly before the images in the preview window become visible. Intensity factors of **1000**% are common.

Click the Next > button to continue.

Step 4: The **Image Data 3D Layout** screen will appear. These parameters determine how the 2D slices are stacked to form a 3D volume.

In this example, increase the **First Slice** to **2**, and enter **126** for the **Number of Valid Slices**. **Slice Thickness** should be **1.8mm**.

Click the Preview All button to scan through the images, using the **Preview Ordered Slices**, **Preview X Cutplane** and **Preview Y Cutplane** buttons to change the orientation.



Care

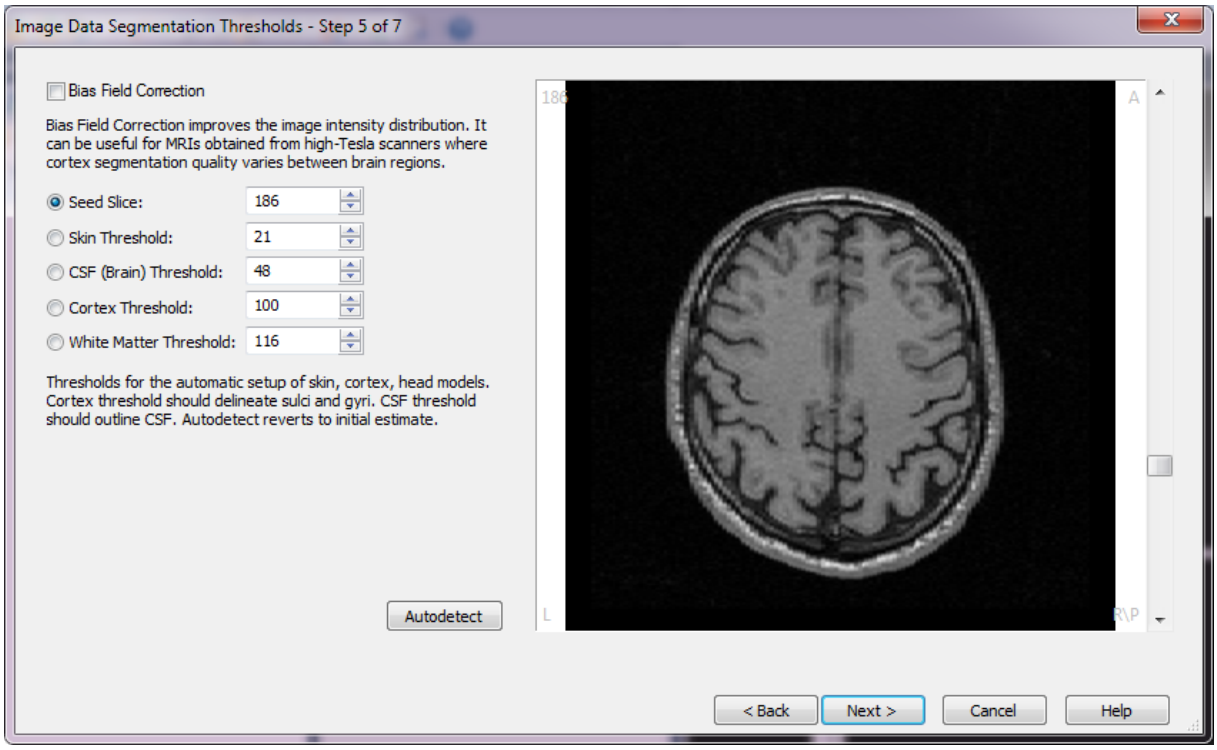
Even if the **Slice Thickness** is automatically detected, its value may be incorrect! This is the most difficult parameter to determine, and it is not always stored correctly in the file headers.

Click the Next > button to continue.

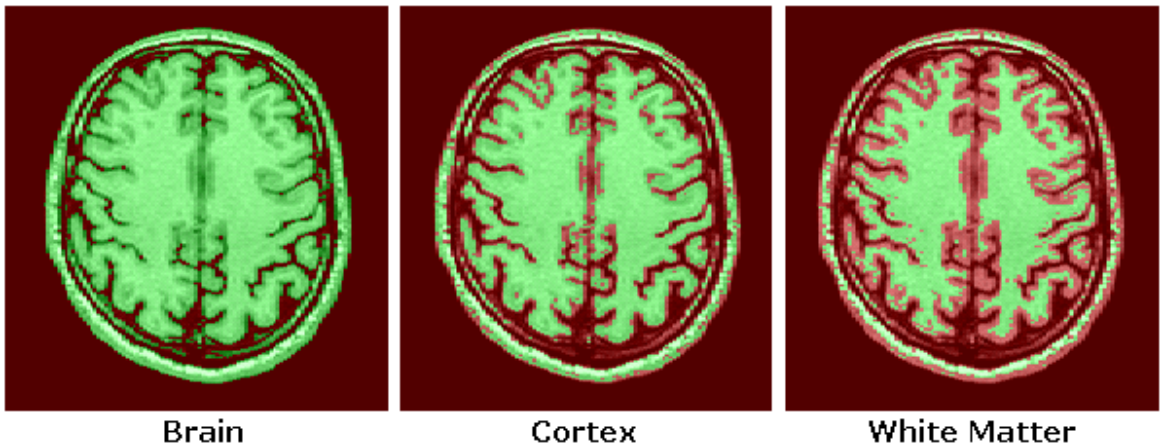
Step 5: The **Image Data Segmentation Thresholds** screen will appear. These are the thresholds used for the automatic setup of the skin, cortex, and BEM/FEM models. The Cortex Threshold is generally the most important one. It is what later determines the shape of the cortex created by BEM/FEM Geometry (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.

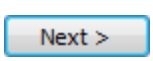
The values shown are the Autodetected thresholds, which are usually good estimates. If the image data has an intensity artifact (which is often the case in MRIs from high-Tesla scanners), the **Bias Field Correction** can be applied. This correction improves the intensity distribution and most of the times the subsequent segmentation result. The **Seed Slice** is shown first. Click **Next**.



You will then see the segmentation results for the **Skin Threshold**. The **Stop Markers** are in red, and the **Pass Markers** are in green. There should be a separation between the skin (pass) and the exterior (stop). Click **Next** again (3 times) to see the **CSF (Brain)**, **Cortex** and **White Matter Thresholds**. You should see the Pass and Stop Markers clearly differentiating the boundaries, with little or no "bleeding".



Brain Cortex White Matter

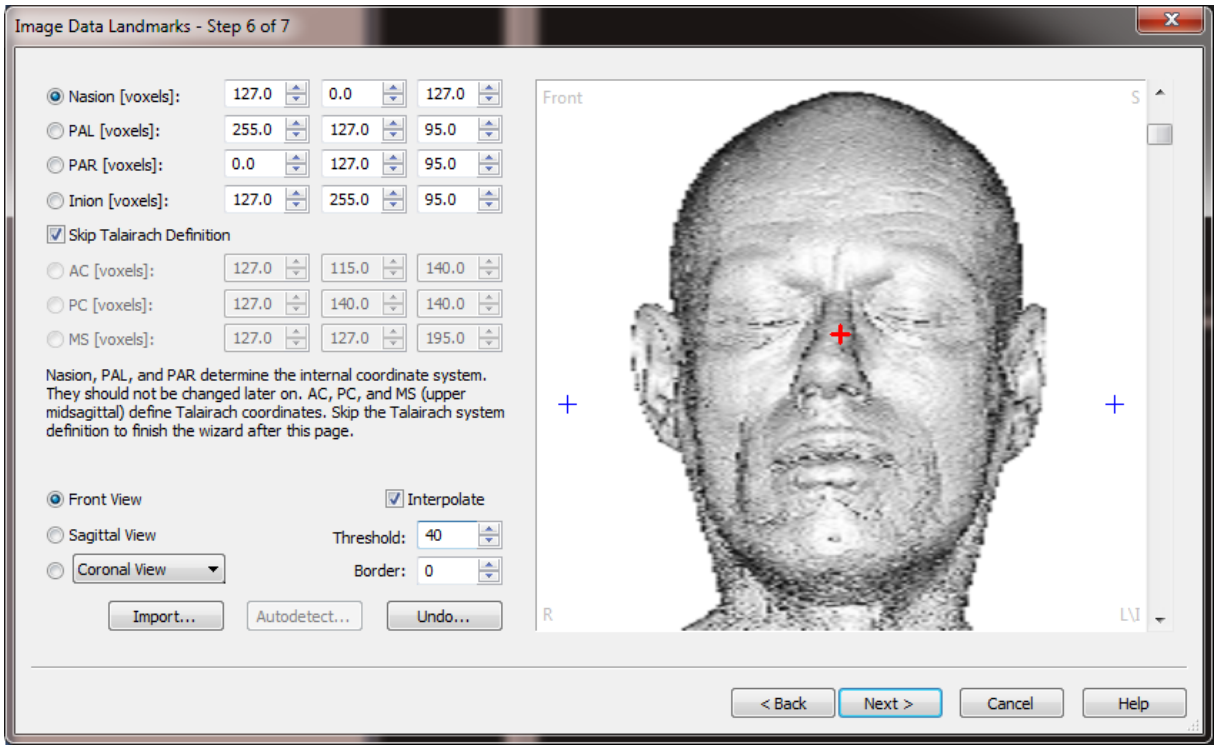
Click the 

button to continue.

Step 6: The next step is to set the **Landmarks**: Nasion, Preauricular left (PAL), Preauricular right (PAR), Inion, Anterior Commissure (AC), Posterior Commissure (PC), and upper Midsagittal (MS). The latter three are used in defining the

Talairach system coordinates. For the data set we are using, we need only the Nasion, PAL, and PAR. For demonstration purposes, we will set all of the landmarks anyway.

Increase the **Threshold** setting to obtain a clearer image (to approximately **40**). **Interpolate** was enabled to achieve a smoother display.

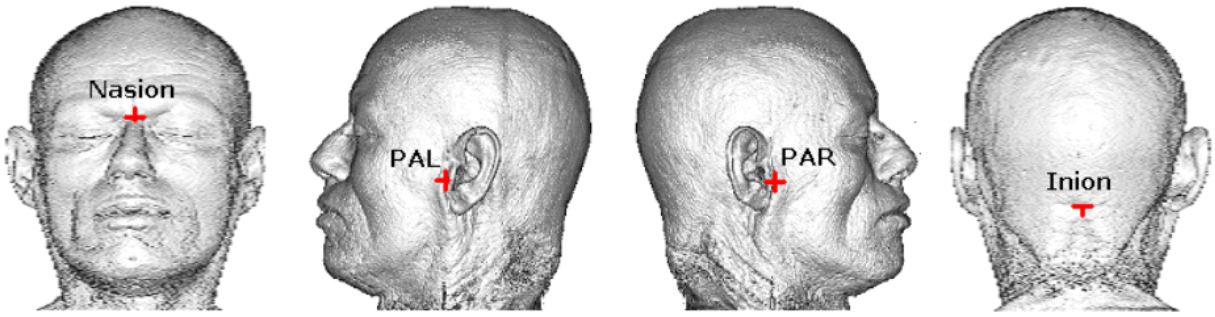


Care

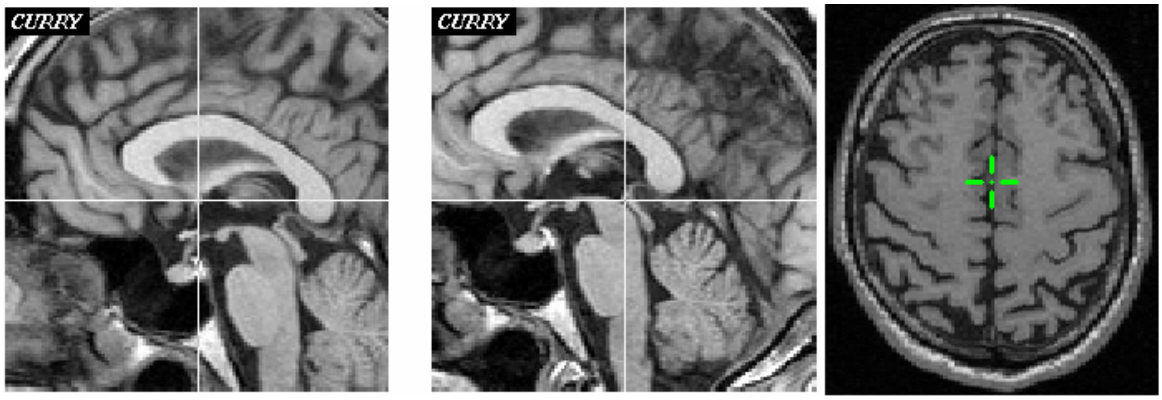
As discussed in the *CURRY 8 User Guide*, the internal landmarks for at least the nasion and the preauricular points should be defined as early as possible. If you will be using the Talairach system, the AC, PC and MS positions should be selected carefully as well.

The markers for the landmarks are seen as a red crosshair; however, the crosshair is in a default position initially (the nasion, for example, is near the tip of the nose). Grab and drag the marker to the correct nasion position; the coordinates in the Nasion fields change accordingly.

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. Grab-and-drag the crosshair to reposition it. The Next > and < Back buttons will step through the landmarks. Set them all in their proper positions. Use the Undo... button if needed to restore the previous positions.

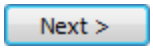


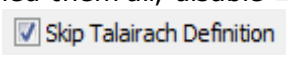
The AC and PC as seen in a midsagittal slice are shown below as well as the MS location.



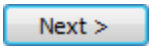
anterior commissure posterior commissure midsagittal

When you have positioned them all, disable

and click the 

button. (If 

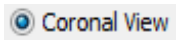
is enabled, you will see the

button instead). Click 

to complete the MR data import. (You can skip the Talairach Definition if you are not going to use the atlas or if you otherwise have no need of the Talairach system.

Step 7: The final step is to define the boundaries of the brain, based on the mm distance from the positions 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.

Note that you can change the view using the **Sagittal**, **Coronal**, and **Axial View** options to help in the placement of the boundaries. For each measurement, one of the three Views is tied to the boundary position. For example, if you select the

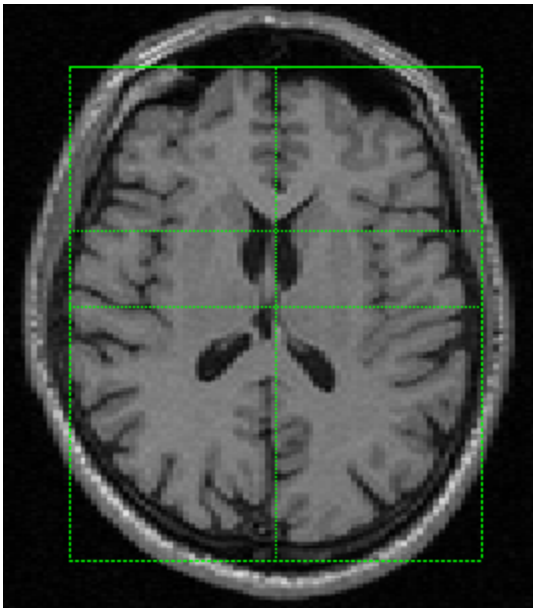
measurement, the 

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 boundary by seeing where the brain no longer appears in the MR images. That position is transferred automatically

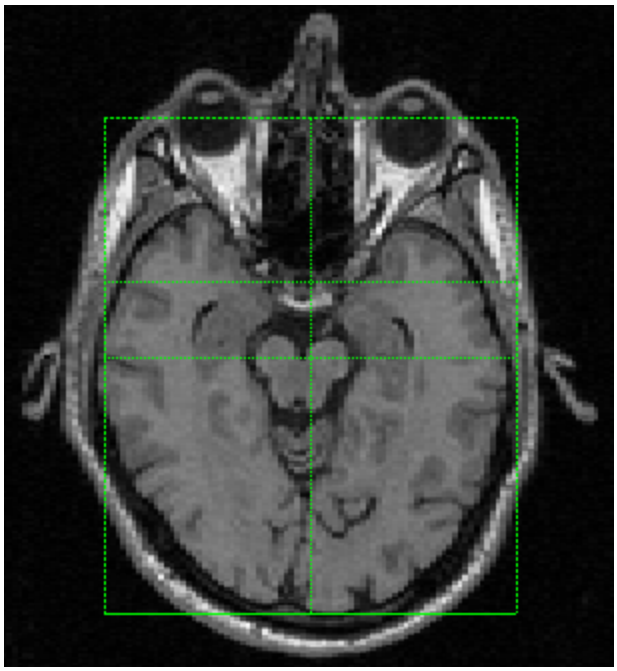
(continuously) to the Anterior-AC measurement

. If you are using the mouse wheel, depressing it while turning it will give finer control.

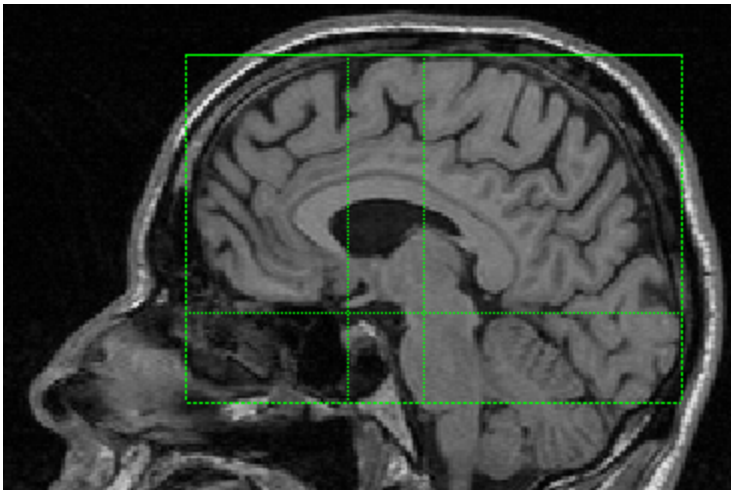
First, set the Anterior-AC boundary. The boundary you are setting will be a solid line, while the others are dotted lines. Drag that line to the proper position. The measurement is made from the anterior commissure (the uppermost horizontal dotted line).



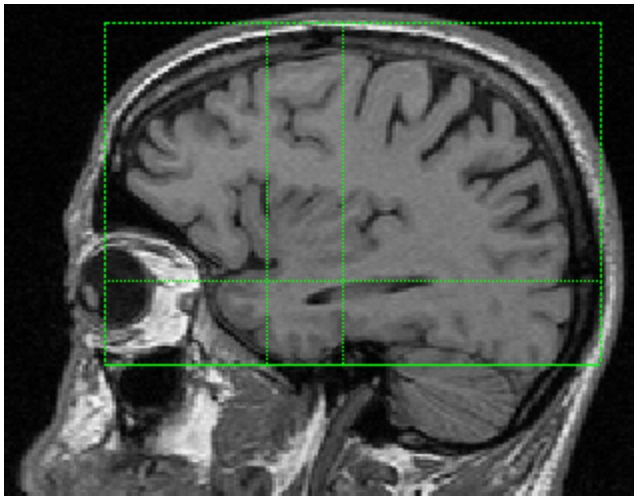
Then set the Posterior-PC boundary. The measurement is made from the posterior commissure (the lowermost horizontal dotted line)



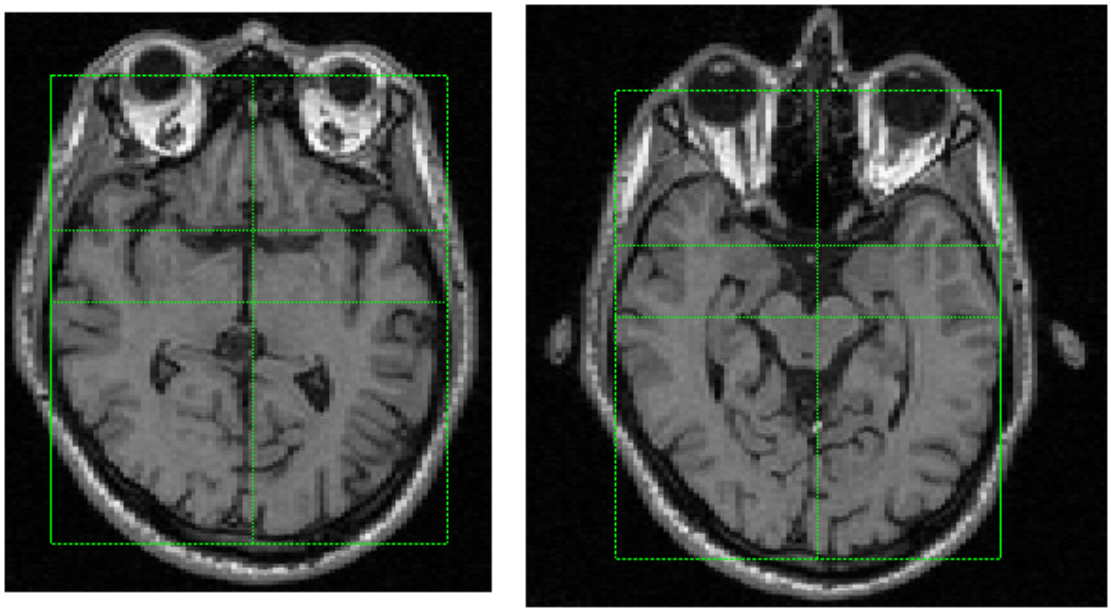
The Superior-AC boundary is the maximum extent of the cortex to the top of the head. Remember to check different slices and orientations to determine the correct position.



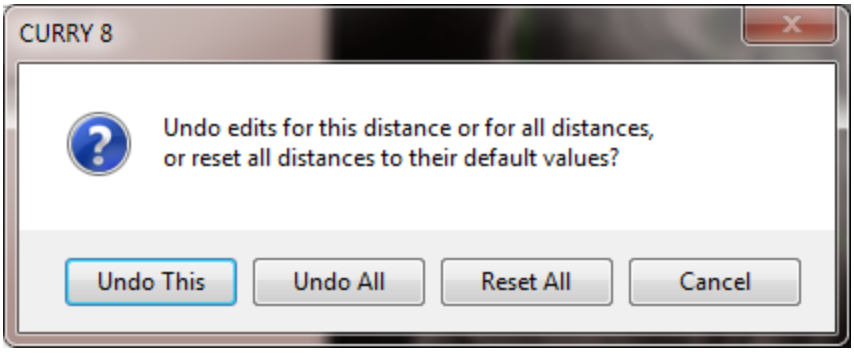
For the Inferior-AC, use the lowest point of the temporal lobe, not the cerebellum. You will nee a more lateral slice to find it.



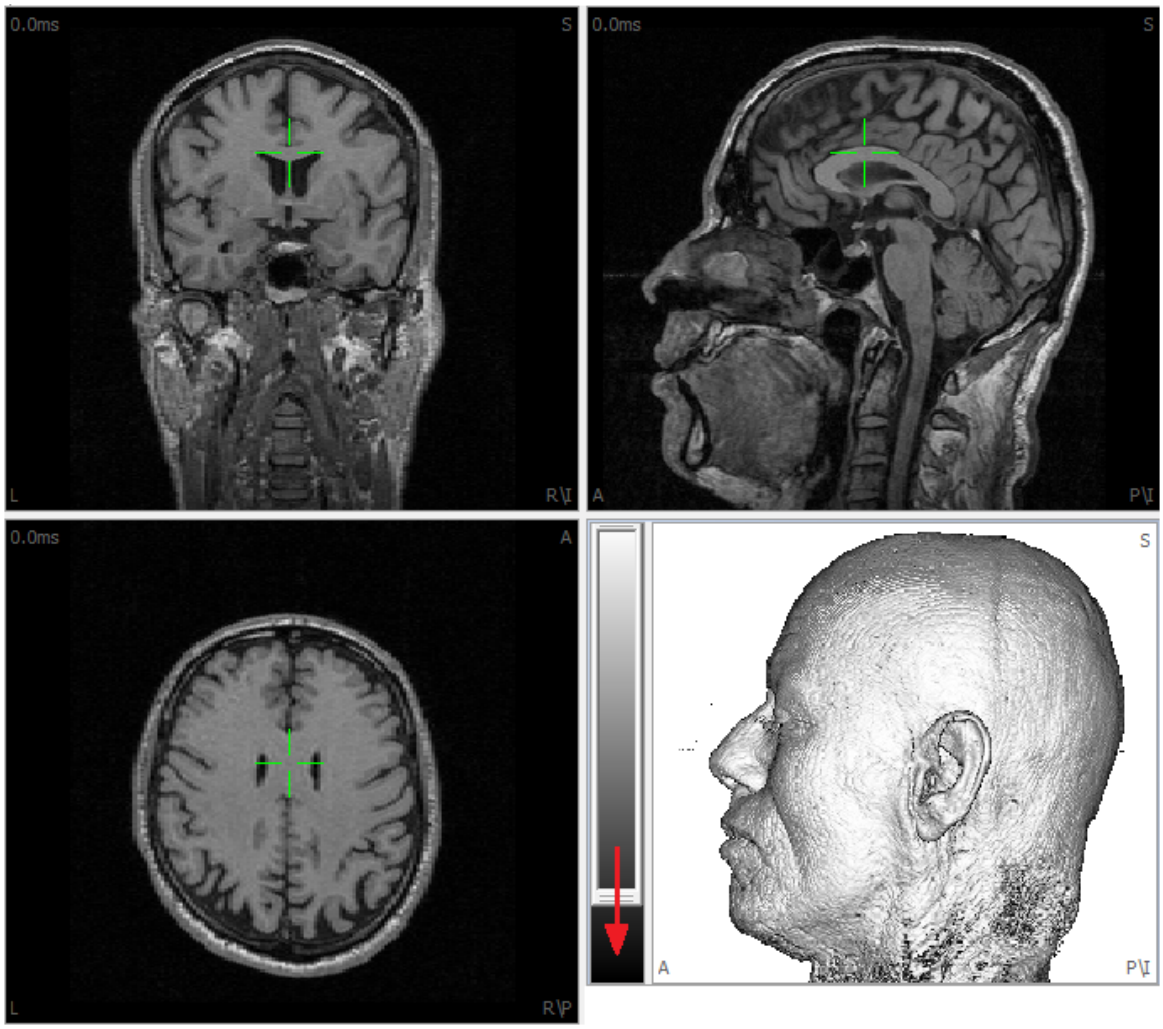
Lastly, set the Left-AC and Right-AC boundaries.



The Undo button [Undo...] 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. Click it to see the image data (the anatomical landmarks are written to the .imd file). Drag the sliding bar (shown below) downward to see a clearer view.



Note

CURRY will use the landmarks you specify for co-registration. The landmarks are saved with the parameters file (.imd), and it is not necessary to redefine them in the Localize display. If desired, you may redefine them and use the .pom file that is created for co-registration (see the *CURRY 8 User Guide* for more information).

Care

The internal landmarks are used to couple the internal coordinate system to the individual anatomy. This makes it possible to compare results between subjects easily. The landmarks must be defined carefully and as early as possible. Changing the nasion or the pre-auricular landmarks at a later time will invalidate the results already obtained.

Note

In practice, you may need to import MRI, CT and other image data sets. It is important that the MRI data are inserted first, above the CT or other data sets. This is necessary for a couple of reasons. The MRI data are imported first, and the

landmarks are measured. Then the CT data are imported, and the landmarks are approximated. Volume-based coregistration is used (via the **Autodetect** button seen in Step 6 above), and the CT data set is in that way fitted to the MRI data set. Therefore, the MRI data need to be loaded first. Also, when verifying that the coregistration has been accomplished accurately (see the **Merging the two image data sets** section in the **MRI and CT Grid Merging** tutorial), you can only import the Image Data 2 results (CT bone segmentation) to Image Data 1 (MRI data) - you cannot do this step in the opposite direction. So again, the MRI data should be inserted into the Study above the CT or other image data.

See the **Averaged MR Data Sets** tutorial for more information.

2.4 Signal Processing

It is not possible to provide a Tutorial that describes every method that is available for analyzing your data. There are, however, some common things to all methods, and some general paths that users tend to follow.

Data Display Options and File Navigation
This Tutorial covers the data display options and methods for navigating through the files.

Creating Montages
This Tutorial describes how to create montages, such as bipolar montages, as well as montages that reorder channels and can be used as display pages.

Filtering
This Tutorial is devoted to Filtering. As you will see, there are quite a few options available for filtering, and it is important for you to be aware of the applications of all of them.

Common Artifact Reduction
This Tutorial illustrates the methods for rejecting bad blocks of data, and for reducing the common artifacts (e.g., blink artifact) that are frequently encountered. You will see that there are several methods for reducing artifact, and it will be useful for you to be acquainted with them. One method may work better in some instances, but not in all of them.

MRI Gradient and Ballistocardiogram Reduction
This Tutorial discusses artifact reduction in the special case where data have been recorded in the magnet. These include MR gradient artifact reduction and ballistocardiogram (BCG) artifact reduction.

Evoked Potential Analyses
This Tutorial demonstrates how to create averages from different event types in the continuous data file, and is perhaps the most common method of analysis. Individual averages are created and saved, and a grand average is then computed. The special case of pulse artifact in the absence of an EKG channel, or EEG channel suited for voltage threshold artifact detection, is included as a separate tutorial. Peak Detection is presented in a separate tutorial.

Spectral and Coherence Analyses
This Tutorial demonstrates basic spectral analysis and coherence analysis. For example, you may continuous EEG data recorded during "resting" and task conditions, where you want to see how the power spectrum changes. You might also wish to investigate changes in coherence.

Template Matching
This Tutorial explains how Template matching works. Template matching is used to identify automatically features in the continuous data, such as epileptic spikes or blink artifacts.

Epileptic Spike Detection
This Tutorial demonstrates how to detect epileptic spikes manually, create an epoched file containing the spikes, and display the source reconstruction results for each spike at the same time, as well as the average of all spikes.

PCA and ICA Analyses
This Tutorial demonstrates the use of PCA and ICA decomposition, and the differences between them.

Group Averaging
The Group Averaging Tutorial illustrates how to create a grand average across Subjects.

Statistical Comparisons - Maps
This Tutorial illustrates some of the statistical options that possible with CURRY when using functional data. Statistics with source reconstruction results is presented in the **Statistical Comparisons - Dipoles, CDRs** tutorial.

There are several general paths that may be taken in your analyses. For example, will you be analyzing results in the time domain (where the x-axis is time, such as with evoked responses), or in the frequency domain (where the x-axis is in Hz, as with spectral FFT analyses)? Different paths are involved.

Another question is: do you have a need to save the epochs (time or frequency domains)? In CURRY 8 you may do the complete analyses without saving an epoched file, or you can save the epochs if you want to.

Also, in most cases you will likely want to reject epochs based on various criteria. In CURRY you can create in-place, or "instant", averages, relying on the Artifact Reduction techniques to exclude bad sections or reduce artifact, or you can reject epochs using voltage, frequency, or an SNR based method. You may do this with or without saving the epochs.

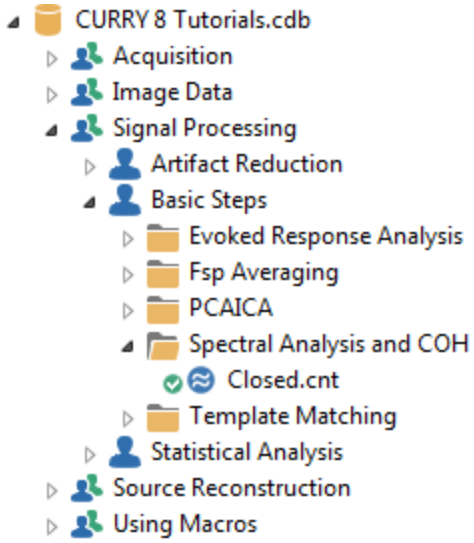
The tutorials above, namely the **Evoked Potential Analyses** (time domain) and the **Spectral and Coherence Analyses** (frequency domain) illustrate the different paths and possibilities.

2.4.1 Data Display Options and File Navigation

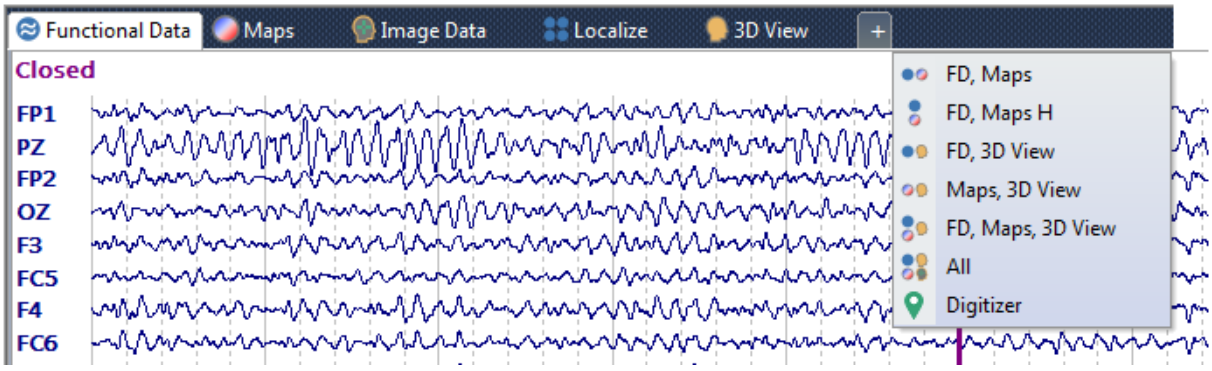
The purpose of this Tutorial is to introduce many of the basic display options as well as the methods for navigating through the data files. It is assumed that you are familiar enough with Databases to open Studies. This Tutorial provides a basic foundation upon which the subsequent Tutorials are built.

Display Options

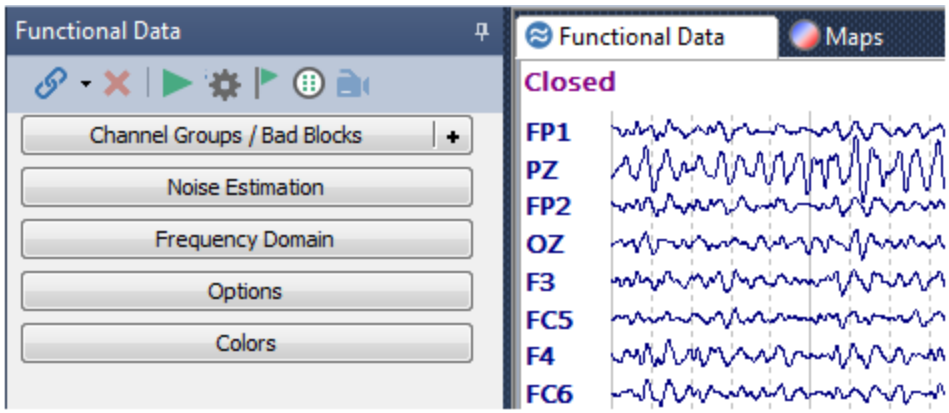
1. For this part, we need any continuous data file; we are using the *closed.cnt* file, which is found in the *Spectral Analysis and COH* Study. Open the Study.



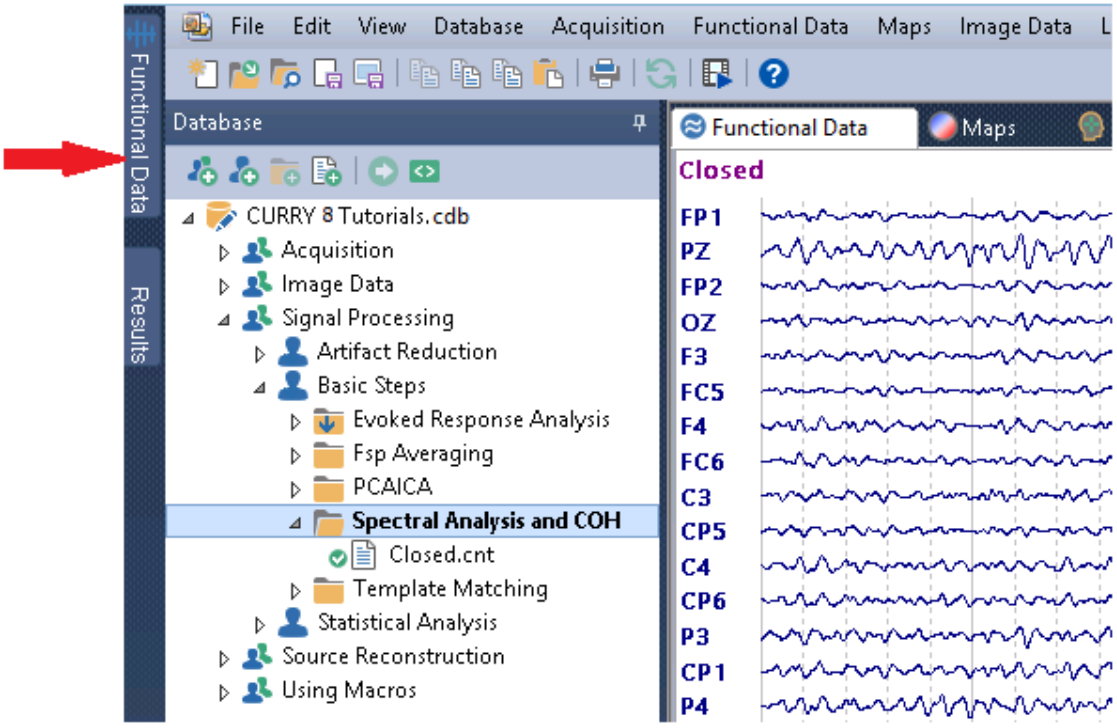
2. Select the Functional Data display tab, if needed (above the data display). The row of tabs above the data display are options for viewing different parts of CURRY. Some are individual display screens, while combination displays may be selected from the + sign list of options.



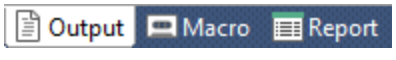
The Functional Data parameter panels are displayed on the left. These contain all of the functionality for basic signal processing of functional data.



Notice the "sticky pin" in the upper right corner of the Functional Data parameters. If you click it, all of the parameter panels will move to the side of the display.

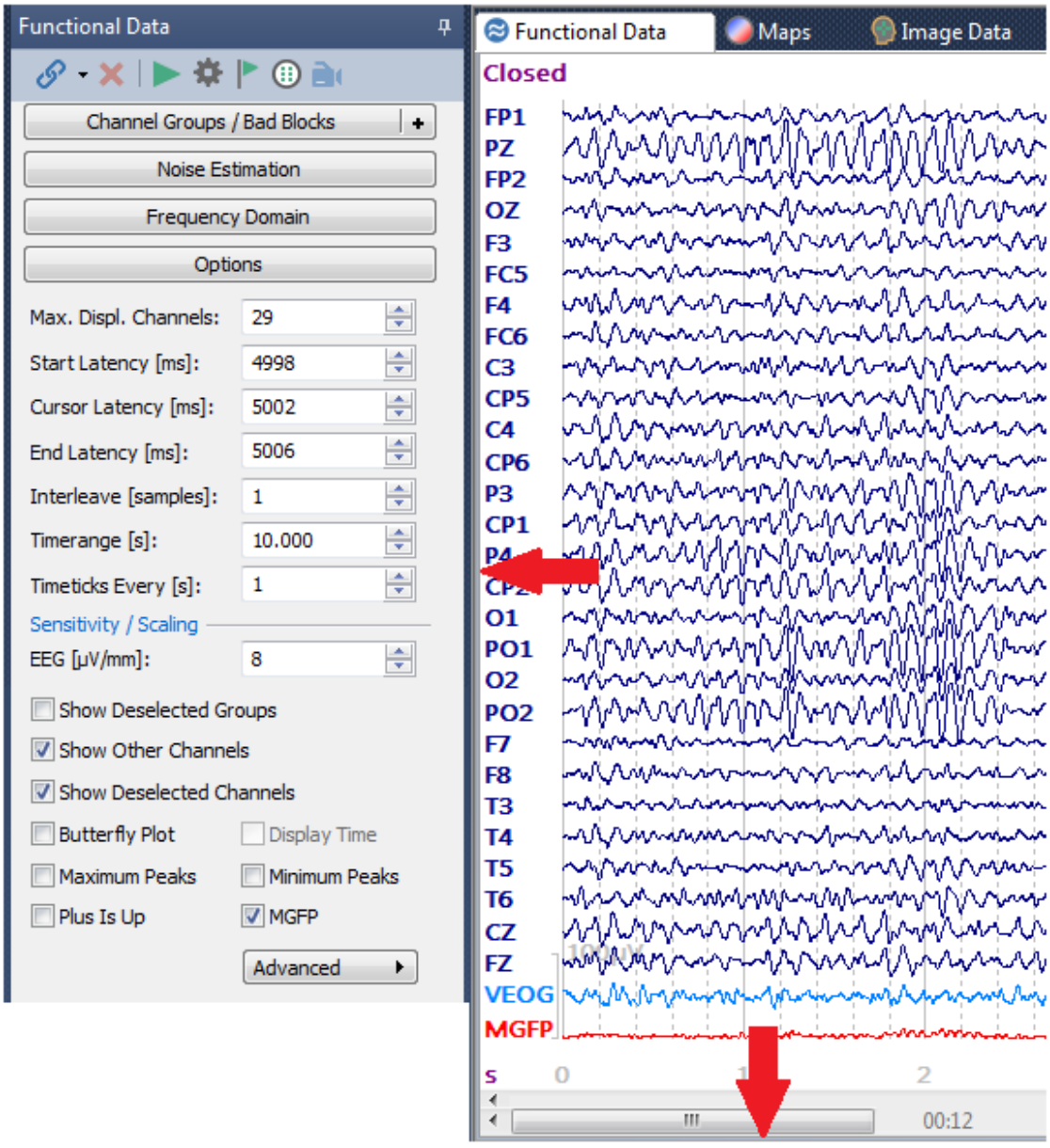


If you move you mouse over the Functional Data tab (or any of them) on the far left of the display, the parameter panels will reappear, as long as you leave the mouse cursor in that display. Sticky pins allow you to free up more of the display area for the data. The various options are seen only when you move the mouse over them. Click on the sticky pin again to stick the display so it will not disappear.

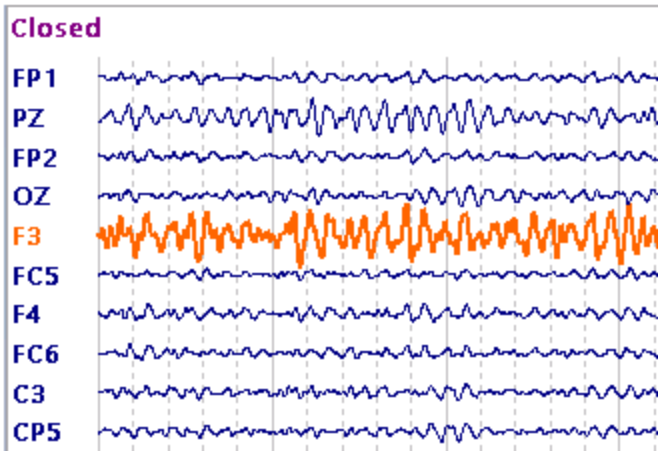
3. Notice at the bottom of the data display is another row of tabs: 

. These display the text output of the various operations that have been performed (**Output**), the options for the Macro Recorder (**Macro**), and the options for creating a laboratory or clinical report (**Report**).

4. The divider bars between the display areas can be repositioned as desired to enlarge or reduce the display regions.

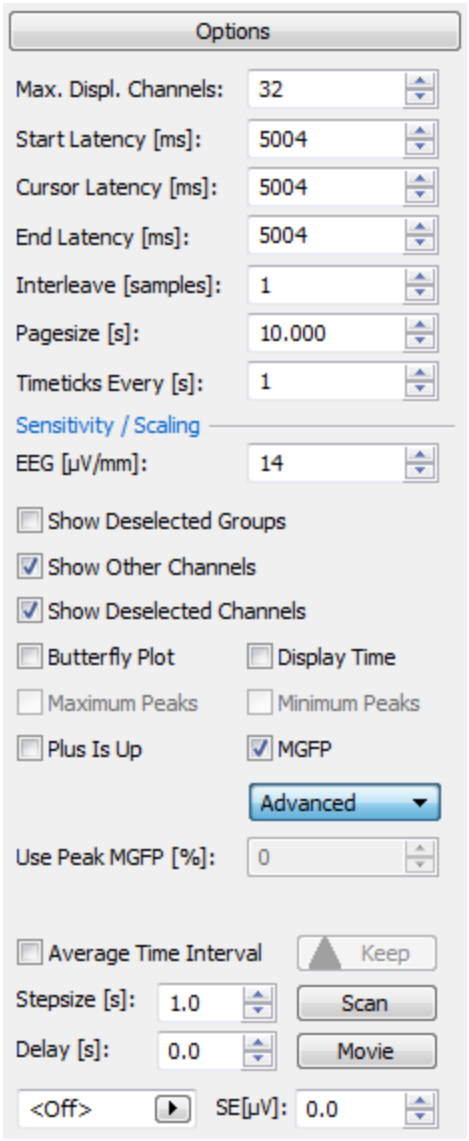


5. The *mouse wheel* has a variety of functions depending on where the mouse cursor is positioned. For example, position the mouse cursor over the data and rotate the *mouse wheel*. The display scale will change accordingly. This does not affect the data, only the display scale. Position the mouse over an electrode label and rotate the *wheel*. The channel will change colors, appear bold, and you can change the scale up or down. When you return the scale to the original position, the boldness will disappear.



If you position the mouse in the data display and use *Shift+mouse wheel*, you can change the number of channels that are displayed. If you use *Ctrl+mouse wheel*, you can change the number of seconds that are displayed.

6. Expand the Options panel under **Functional Data**. We will look at some of the more frequently used Options (described in the *User Guide*). (Some general display and other options are found in **Edit** → **Options**, and these are also described in the *User Guide)*.



7. Click in the **Max. Displ. Channel**. field and rotate the *mouse wheel* to reduce the number of channels displayed (or use the arrows, or enter a smaller value). The number of displayed channels is reduced in the data display. As mentioned above, you can also position the cursor in the data display and use *Shift+mouse wheel* to change the number of channel displayed. Use the sliding bar on the far right to see the additional channels. This option is convenient when viewing files with larger numbers of channels (e.g., 64 or 128).

8. The next three fields show the latencies of the three vertical cursors in the data display (see **Display Cursors and Setting the Timerange** below for more information).

9. **Timerange/Pagesize** displays how many milliseconds are in the current Timerange (epoched or averaged data), or seconds that are shown in the display (continuous data). (As mentioned above, *Ctrl+mouse wheel* will also change the number of seconds that are displayed).

10. **Show Deselected Channels**. If you click on a channel label in the data display, it will change color, meaning that it has been deselected, or removed from inclusion in subsequent analyses. If you disable Show Deselected Channels, the deselected channels will not be seen. Enable it again to see them. Reclick on a channel to reselect it.

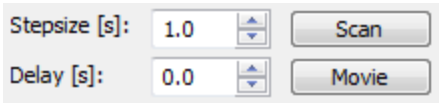
11. **Display Time** toggles the x-axis between time into the file, and the time stamp when the file was recorded (not all files may have this).

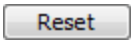
12. **Butterfly Plot**. Enabling this option will superimpose all of the channels. This is useful when looking for potential dipole sources (it is easier to see the positive and negative deflections across channels). The same option can be accessed from the Toolbar , and also from the data display context menu (click the *right mouse* button).

13. **Plus Is Up** toggles the polarity of the data display. When enabled, positives values go up. It can also be accessed from the Toolbar .

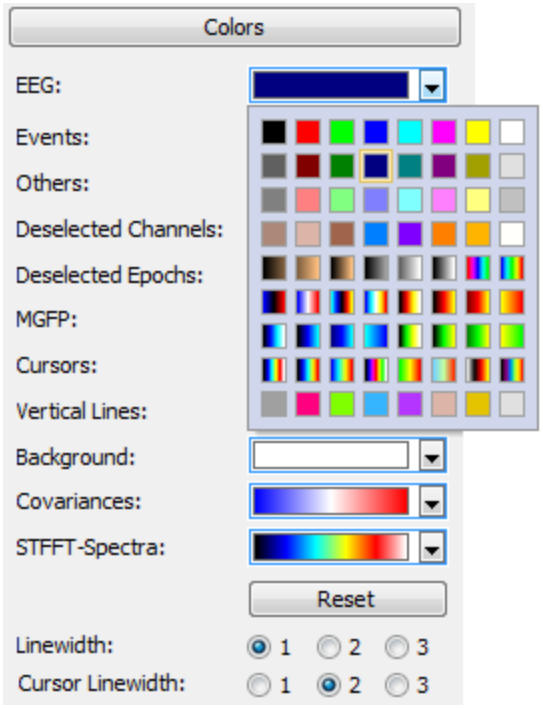
14. **MGFP** toggles the display of the Mean Global Field Power, which is a composite measure of the variability across channels (see the *User Guide* for more details). It is useful in identifying the presence of potential dipoles.

15. The next set of options is used to scroll through the file, and save an .avi movie of the scan. You can scroll continuously by setting the **Stepsize [s]** field to control the speed of the replay, with **Delay [s]** set to **0**. Or, you can set the Stepsize field to the number of seconds you would like displayed at a time, and set Delay to the number of seconds you wish to have to examine each block. Use negative number for Stepsize to scroll backward. To stop the scrolling at any point in the file, press the *Esc* key. Clicking the Movie button will scan the file and give you the option to save it as an .avi file.



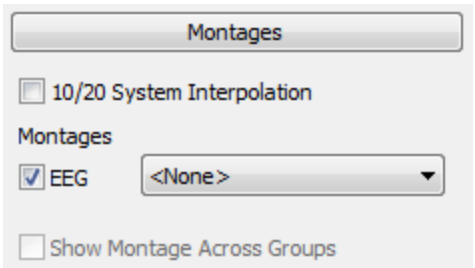
16. Many elements of the various displays in CURRY have user selected **Color** options. Clicking the drop-down list displays the color palette. The 

button will return the colors to the default selections. The width of the waveforms can be selected with the **Linewidth** options. The width of the three vertical cursors can be set with the **Cursor-Linewidth** option.



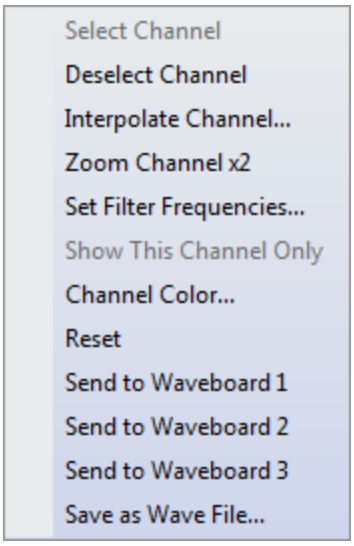
Notice that some of the color options are color scales rather than solid colors . There are places within CURRY where color scales are extremely useful for displaying data, such as, when you are displaying overlapping averaged data files, and you want them to have different colors.

17. Different montages can be selected from the panel.

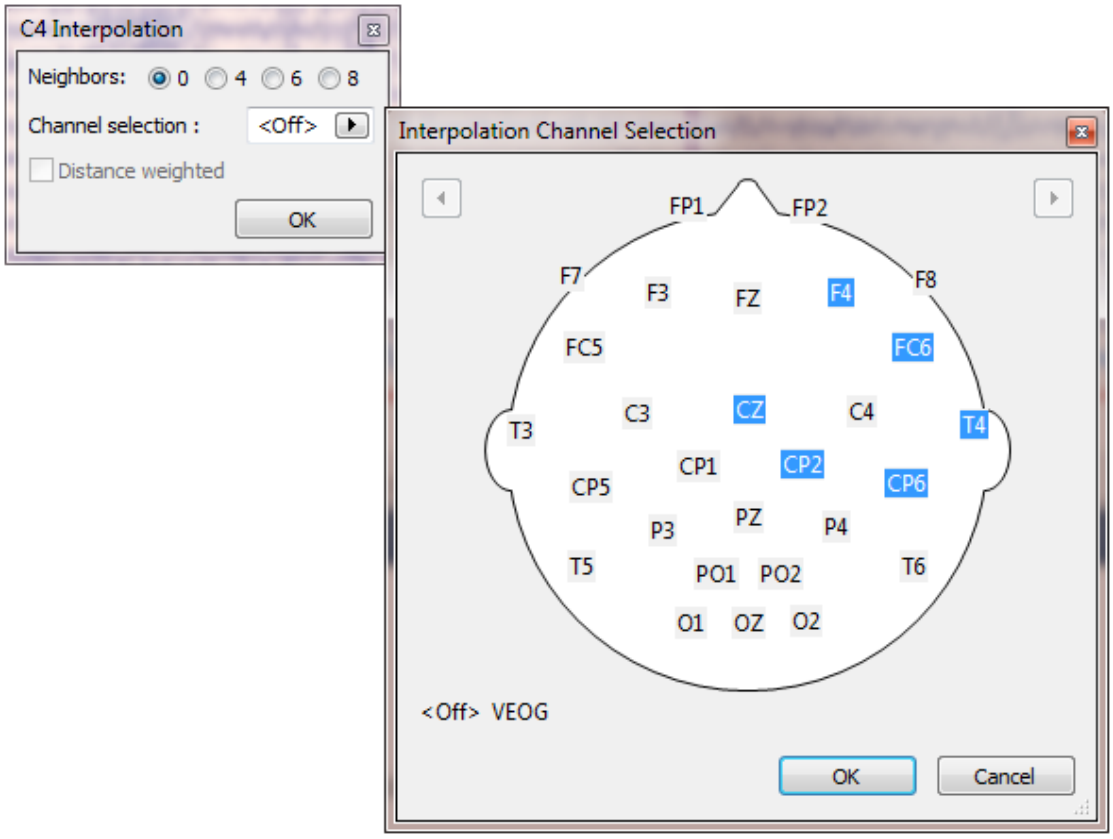


More Display Options

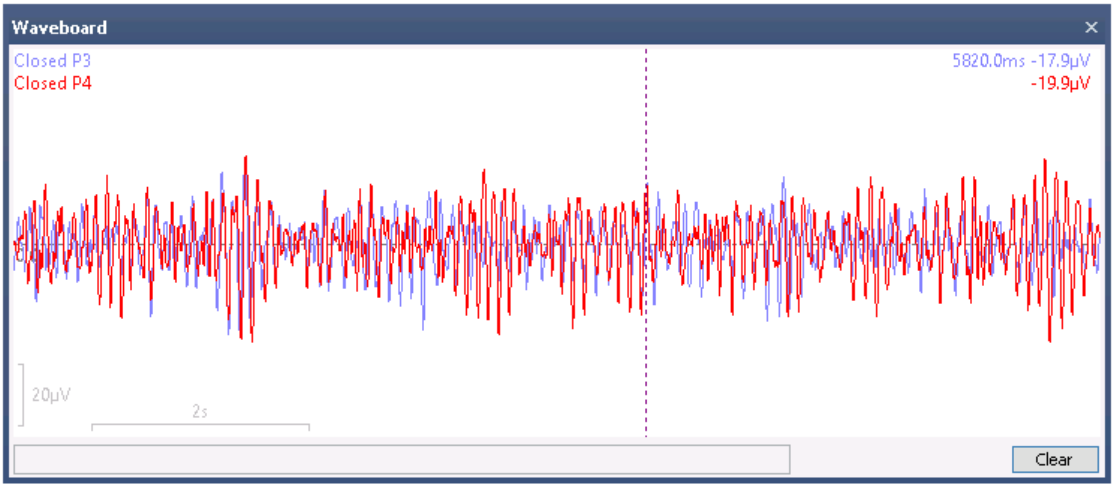
Additional display options are found by *right clicking* on an electrode label. A context menu will appear, allowing you to select/deselect channels, create interpolated channels, zoom in, set filtering and the color for individual channels, display that channel only, and send the channel to one of three Waveboards.



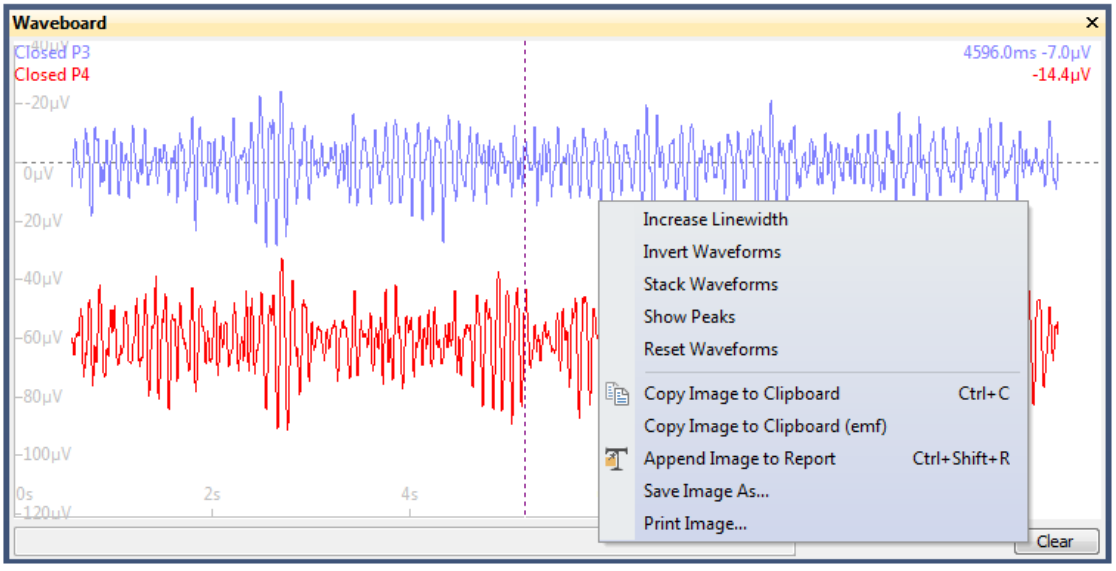
For example, *right click* on a label and select **Interpolate Channel**. Assume this channel was bad (noisy due to poor contact and high impedance). Maybe this is a channel that you really need, and you would rather recreate it as the average of surrounding channels than lose it altogether. You can either select the number of neighbors to be averaged, or else select the channels yourself. The interpolation can take into account the distance from the other electrodes, or not. (*Right click* again and select **Reset** to restore the original data).



Right click on another label and select **Send to Waveboard 1** (there are three independent Waveboards that may be used). Now *right click* on a different electrode and select **Send to Waveboard 1** (*Ctrl+click* will send the current channel selection to Waveboard 1). *Right click* on one of the labels in the Waveboard and select **Color**. This lets you select the desired color for each channel. Amplitude and Latency information is displayed for all channels. (These figures are using a different data file).



Right click within the Waveboard display to see additional options. These are self-explanatory, with the possible exception of Stack Waveforms. Clicking it will create a separation between the waveforms; clicking it again increases the separation. Clicking *Ctrl+mouse wheel* lets you use the wheel to create the separation.

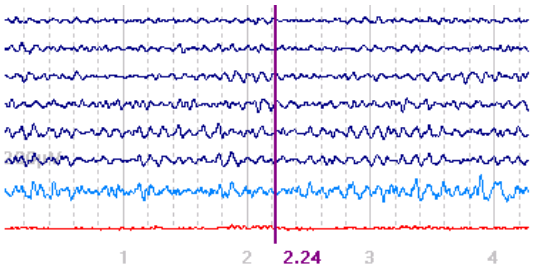


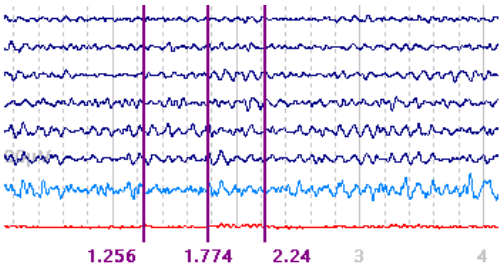
There are additional mouse and combination keystroke commands that can be used.

Mouse wheel - rescales the waveforms
Shift+mouse wheel - expands or constricts the display

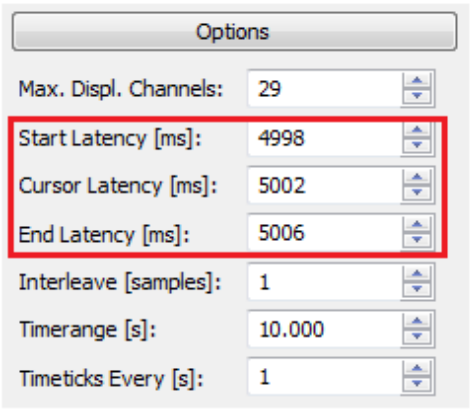
Ctrl+mouse wheel - varies separation among waveforms
Shift+mouse - repositions the contents of the display

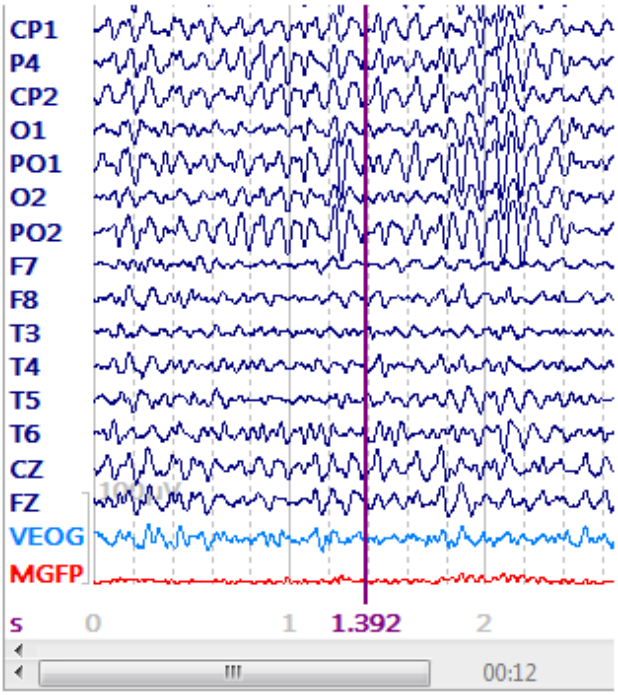
Display Cursors and Setting the Timerange
When you display a data file, you will see either a single cursor, or three cursors that may be moved independently. These were mentioned briefly above.





In fact, what appears to be a single cursor is really the three cursors placed closely together, or directly on top of each other. The three can be seen if you decrease the number of seconds that are displayed. You can see the cursor latencies in the **Options** panel under **Functional Data**. They move as a single unit. This is referred to as *Tracking* mode. Move the cursors as a unit to various points and measure the voltages at the far right of the data display (it is the middle cursor position that is being measured).





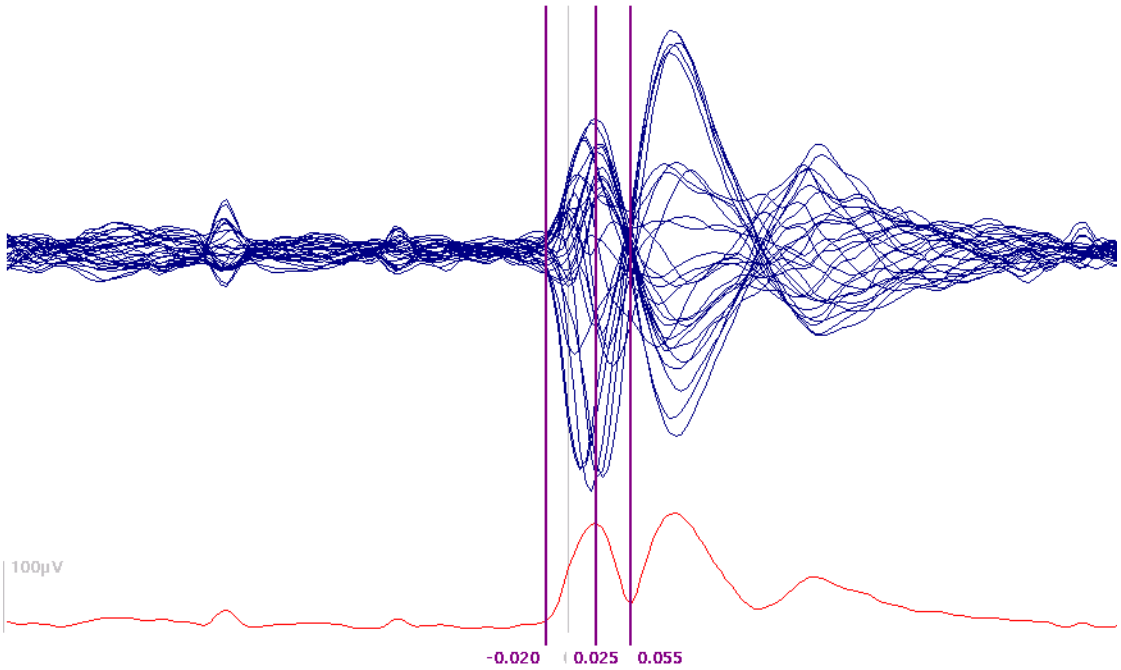
Right click in the data display and deselect **Tracking Mode**. You will then be able to separate the three closely spaced cursors. Hints:

Use *double-click* in the data display to enable **Tracking Mode**.
Use *Shift+left click* to disable **Tracking Mode**.

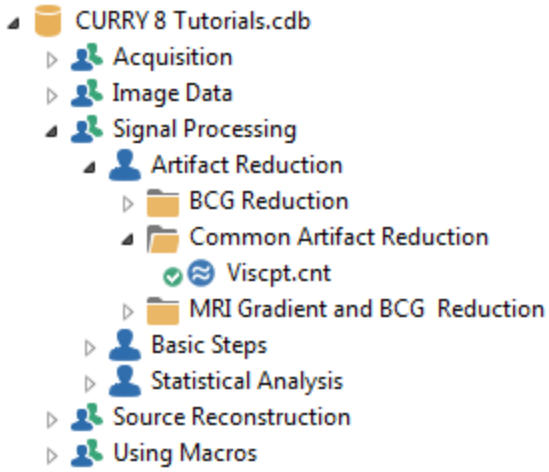
Use *Ctrl+double left click* to spread the outer cursors to the extremes of the display.
Use *Ctrl+drag* to set the outer cursors, with the middle cursor placed halfway between.

The cursors can be grabbed and dragged to a desired position, or, if you know the latencies of the positions, you can enter them in the **Options** fields described just above. You may also use the *mouse wheel* to change the latencies in these fields, or the up and down arrows for each field. You can also move the cursors from the keyboard. The middle cursor is moved by the *left* and *right arrow* keys. *Ctrl+left* and *right arrows* moves the left outer cursor. *Alt+left* and *right arrows* moves the right outer cursor. Or, 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.

There are many places throughout CURRY where you will need to "set the Timerange". The Timerange is simply that interval that will be used in subsequent analyses. This could be a section of continuous data, the entire epoch interval, a section of an averaged data file, etc. *The two outer cursors are used to define a Timerange*. (The middle cursor is used to display the values of the waveforms wherever it is positioned). To set a Timerange, you usually have **Tracking Mode** disabled, so that the cursors can be moved independently. Use any of the methods for moving the outer cursors to define the Timerange. In the figure below, the Timerange was set to define the interval that will be used for source reconstruction.



File Navigation
Close the open Study and select any continuous data file that has events in it (e.g., stimulus events). We are using the *viscpt.cnt* file, which is found in the *Common Artifact Reduction* Study. Open the Study.



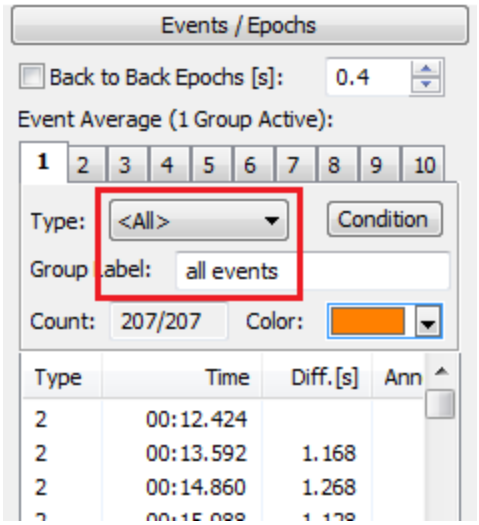
1. There are several ways to move through the continuous data file. You may grab the sliding bar below the data and drag it back and forth to move through the file, or use the **Scan File** option described above. If you have an epoched file instead of a continuous data file, the sliding bar will move across epochs, and the arrows will move from sweep to sweep. You may click on the arrows at the ends to move in about 2.5 sec step increments through the file (10s displayed). Click in the open area on either side of the slider to move one display screen at a time. Use *Ctrl+double click* to go the page/epoch where the mouse is positioned.

Right click in the data display and enable **Use Mousewheel to Scroll** to go through the file half a page at a time using the mouse wheel (continuous and epoched files). Use *Shift + mouse wheel* to scroll through one second 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.

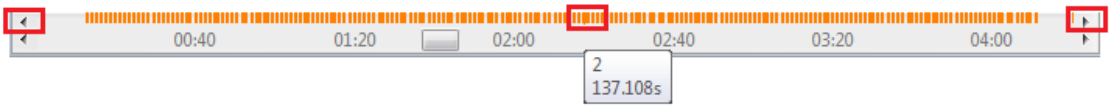
Select

from the lower left area of the CURRY display

. Near the top of the panel, set **Type** to **All**. For **Group Label**, enter "all events".



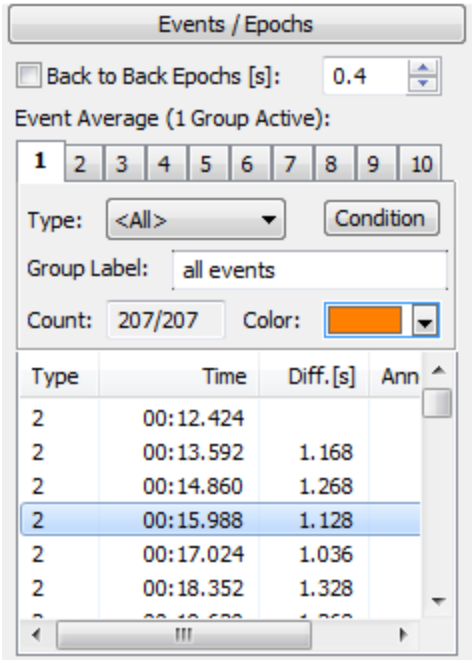
This will display tick marks for all of the events in the file. You can click on a tick mark to go directly to that point in the file. You can click on the smaller arrows, and step from one event to the next.



2. There are Toolbar icons that will move through the file one display screen at a time. The outer icons will move to the beginning or end of the file .

3. If you have events in the file, you can move from event to event using the Toolbar icons . The *Shift+left* or *right arrow* keys have the same effect. The middle button is used to toggle off the event status (no longer an event).

4. You can click on an event in the event list to go directly to that point in the file (which will be centered on the screen).

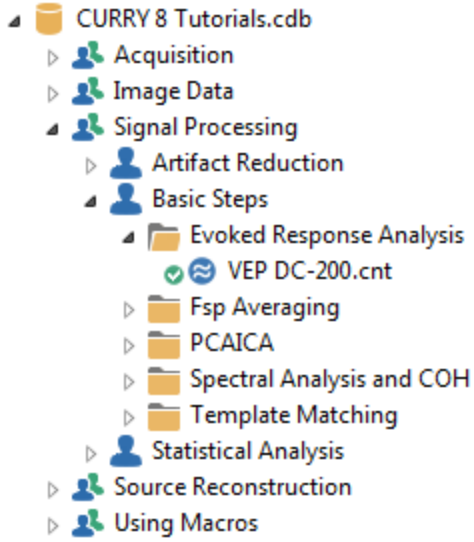


These are all ways to move about in continuous and epoched data files.

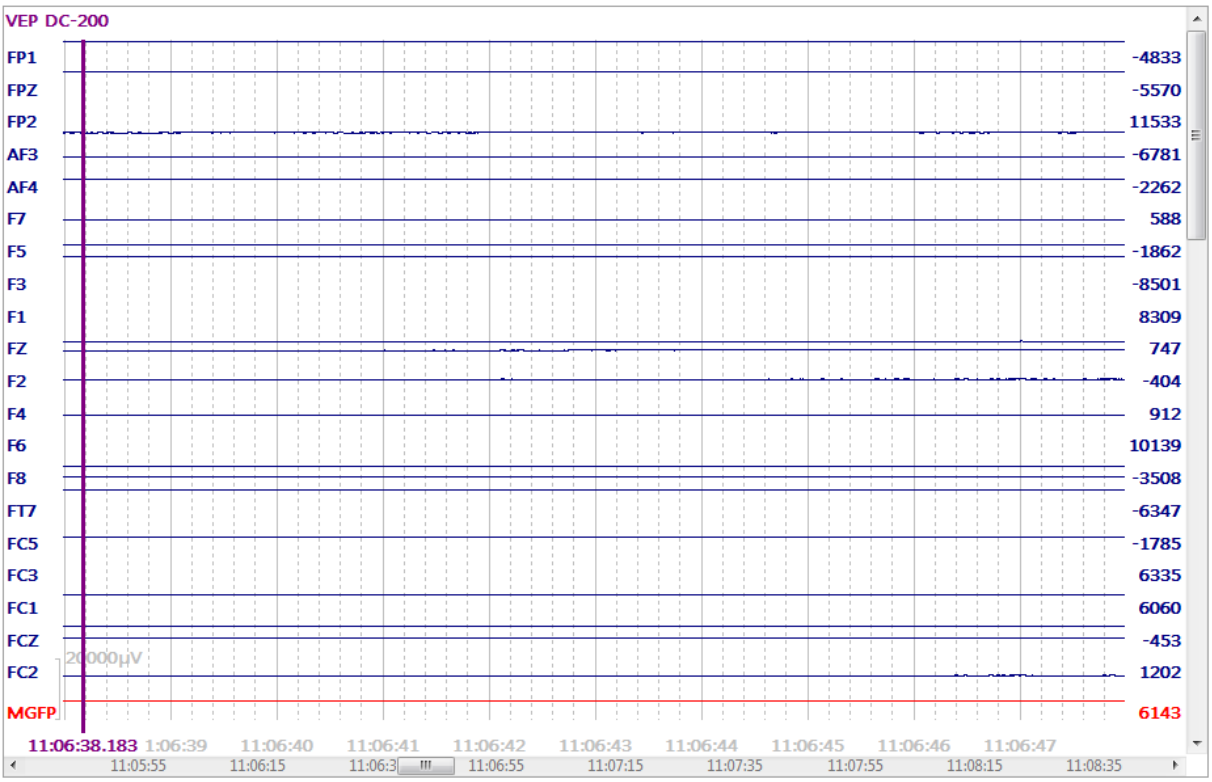
2.4.2 Filtering

In this Tutorial, we will look at some of the common options for Filtering.

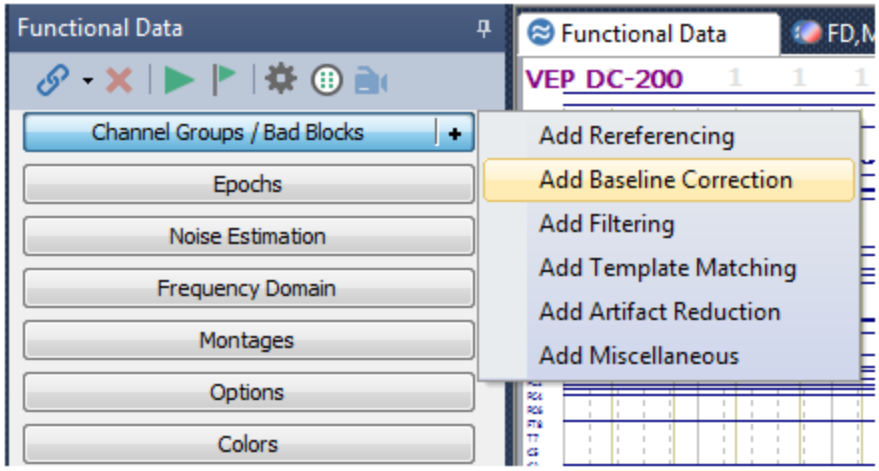
Open the *Evoked Response Analysis* Study. The data file was recorded from DC to 200 Hz with the intention of applying filtering offline.



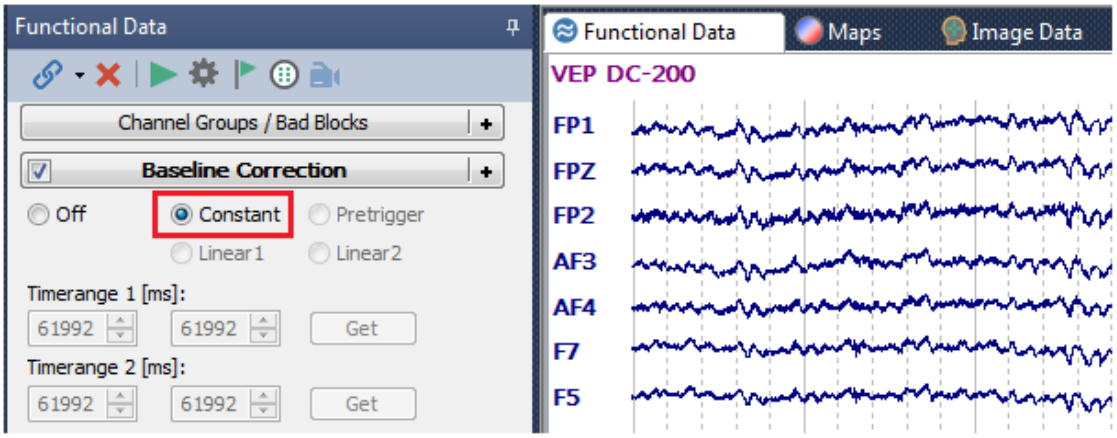
1. To make the traces easier to see, first reduce the number of displayed channels to **20** (**Max. Displ. Chann.** under **Options**). We then moved to a section about midway in the file.



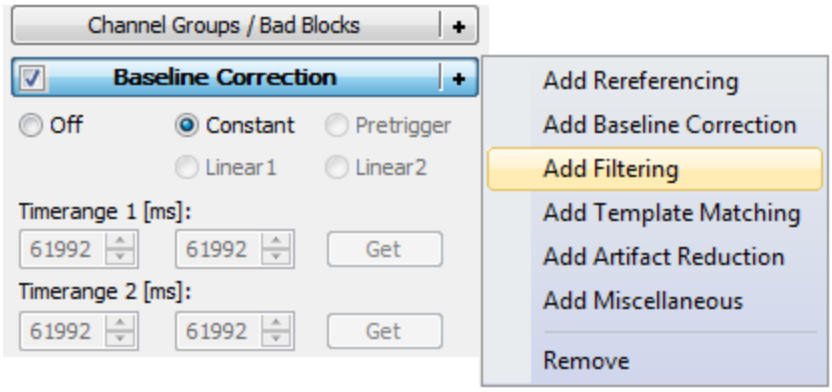
2. Since this file was recorded with no High Pass filtering (DC), it is common to see varying degrees of DC offset, thus the large numbers for the voltages on the far right. In CURRY, the DC offset can also be removed by performing a **Baseline Correction**, with **Constant** for **Type**. Click the **+** sign at the end of the Channel Groups / Bad Blocks + bar and select **Add Baseline Correction**.

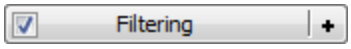


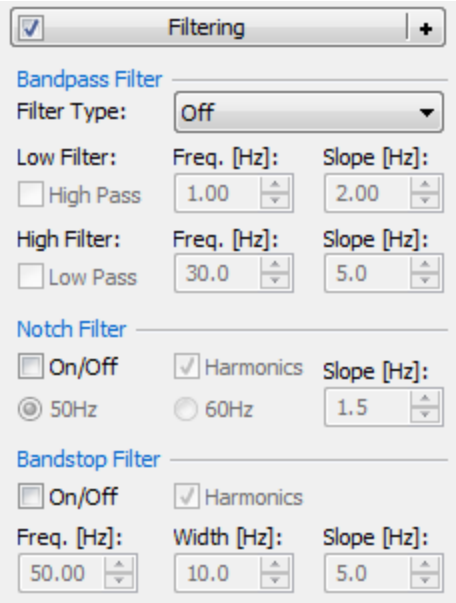
Select the **Constant** option. Use the *mouse wheel* to rescale the data. The traces are centered, but no filtering has been applied.



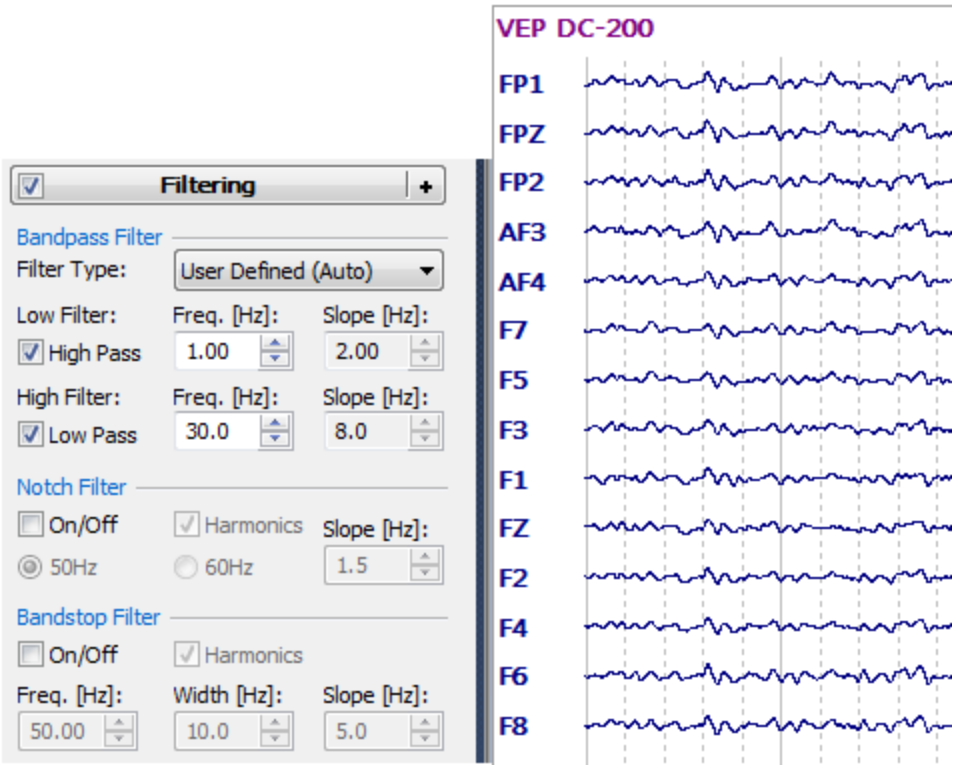
3. Click the + sign at the end of the bar and select **Add Filtering**.



Expand the  panel. We are using the default **Hann** FFT-type filter (in the Advanced section).



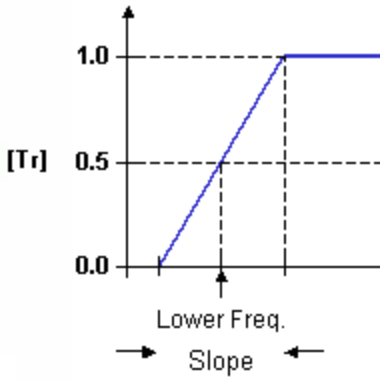
4. The **Bandpass Filter** section is likely the one you will use most often. Select **User Defined (Auto)** for the **Filter Type**, and verify the settings below. **User Defined (Auto)** will set the **Slopes** automatically to avoid having the range of the slope extend below 0 Hz, which should be avoided. You will see the immediate effect on the data.



The other options for Filter Type (Delta-Band, Theta-Band, Alpha-Band, etc.) will selectively filter frequencies other than the band you select.

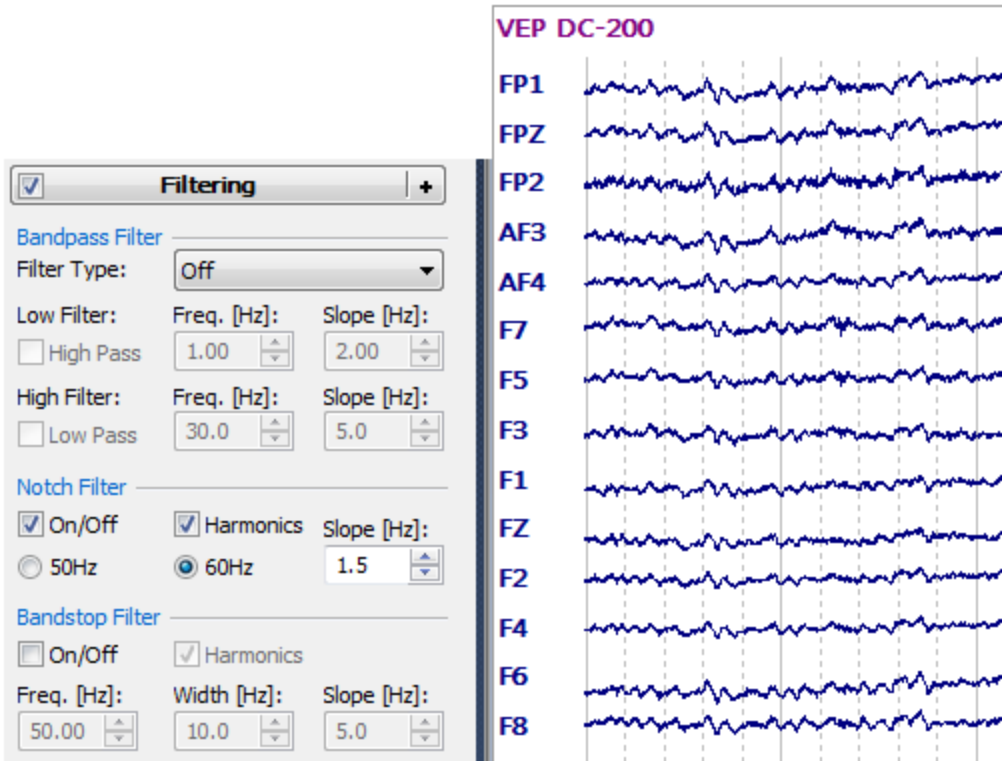
5. Now experiment with the different parameters: enable and disable the Low and High Filters, change the Frequency, change the Slope, etc. The High Pass filter attenuates frequencies below the cutoff frequency; the Low Pass filter attenuates frequencies above the cutoff frequency. The steepness of the filter is determined by the Slope (see the *User Guide* for more details).

As a general rule, you should not select a **Slope** for the **High Pass** filter that would extend below **0 Hz**. For example, the Frequency is the middle of the Slope width. If the Slope is 2Hz, and the Frequency is 1 Hz, then the slope extends from 0 Hz to 2Hz, which is fine. You would not want to use a Slope of 4Hz, since that would extend below 0 Hz. Unpredictable effects could result.

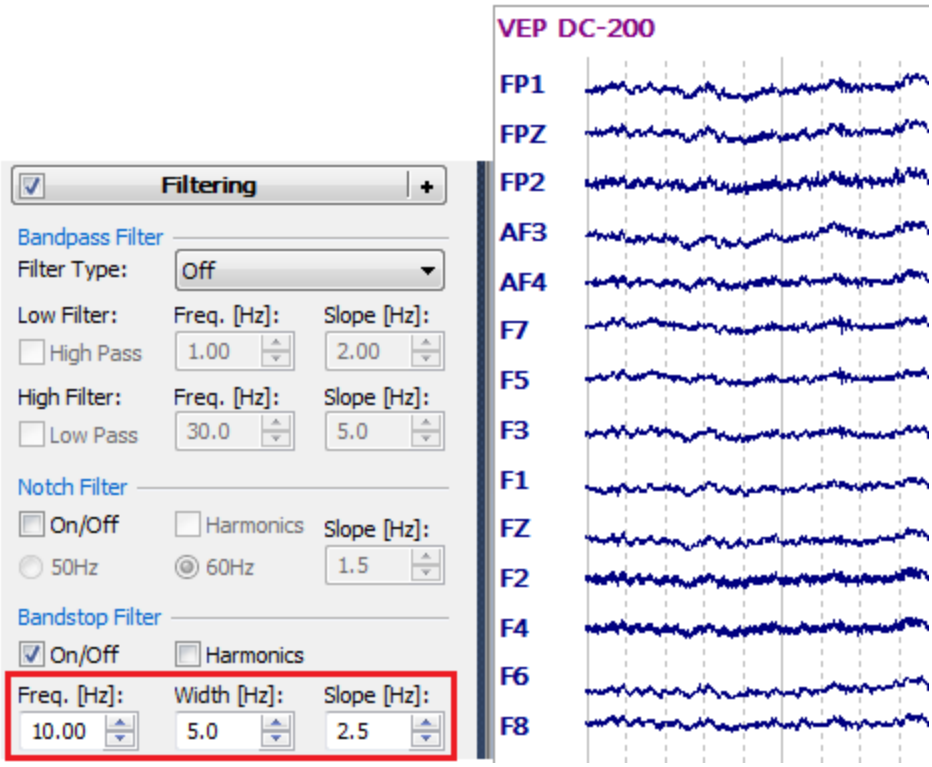


Now set the **Filter Type** back to **Off**.

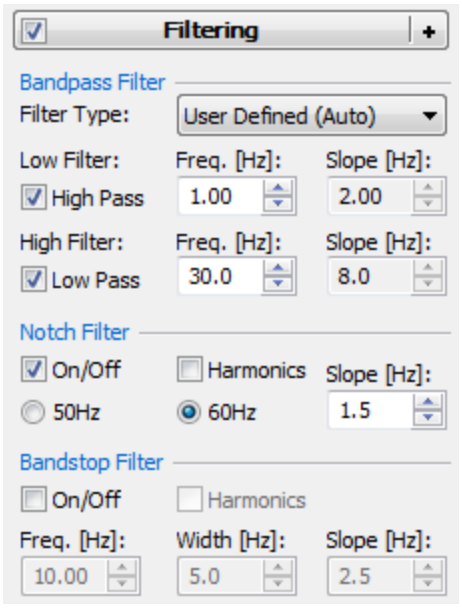
6. Enable the **Notch Filter** and select **60 Hz**. This is a steep filter that will reduce 50 or 60 Hz line noise artifact. Enabling **Harmonics** will have a subtle effect. This attenuates harmonics of 60 Hz, such as 30 Hz and 120 Hz. Disable the Notch Filter when finished.



7. Enable the **Bandstop Filter**. A Bandstop Filter is the opposite of a Bandpass Filter. It attenuates the frequencies about the center Frequency you select. It is more like a notch filter that you can control. The Width determines the interval about the center frequency, and the Slope determines the steepness of the rolloff. For example, set the **Frequency** to **10 Hz**, the **Width** to **5 Hz**, and the **Slope** to **2.5 Hz**. This will selectively filter out any alpha in the recording (turn the filter off and on to see the effect; leave Harmonics deselected).



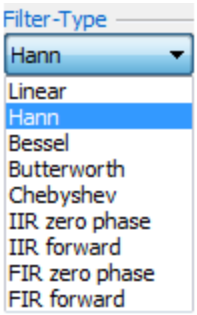
8. You can use the different filters alone or in any combination. Note the parameters in the figure below. The Notch Filter is having no effect, since the Low Pass filter is set at 30 Hz, which is already filtering out any 60 Hz activity. If we enabled the Bandstop filter, the alpha in the recording would be filtered out.



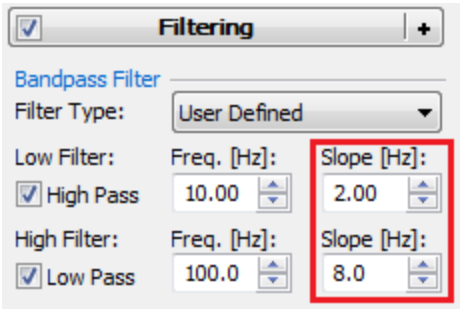
The **Advanced** settings are also described in the *CURRY 8 User Guide*. Unless you have a specific reason to change these, it is recommended that you leave them

with their default settings. If you wish to examine the different filters in more detail, here are some examples that will demonstrate the differences.

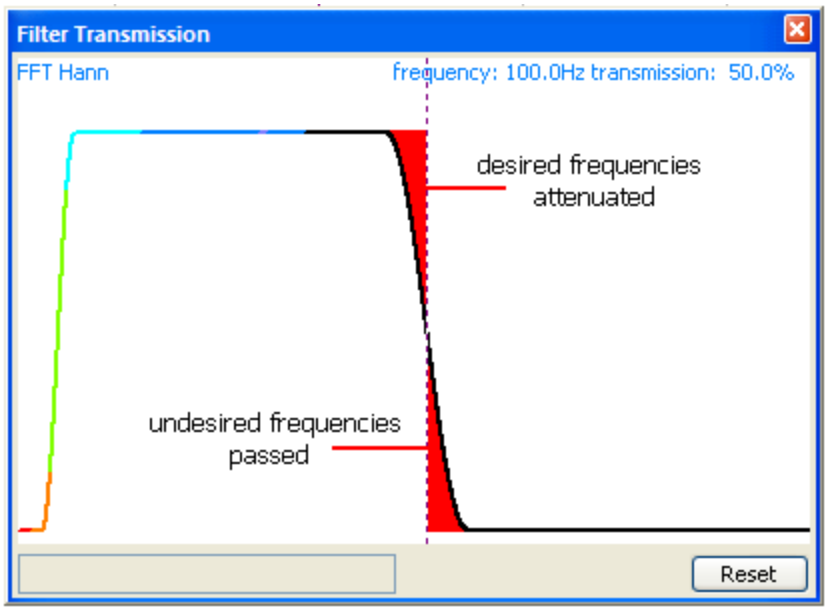
There are 9 filter types. The first 5 are FFT-type filters, and the last 4 are IIR and FIR filters (see also the *User Guide*). Of all of these, the only classes that introduce a phase shift are the **IIR forward** and **FIR forward** types.



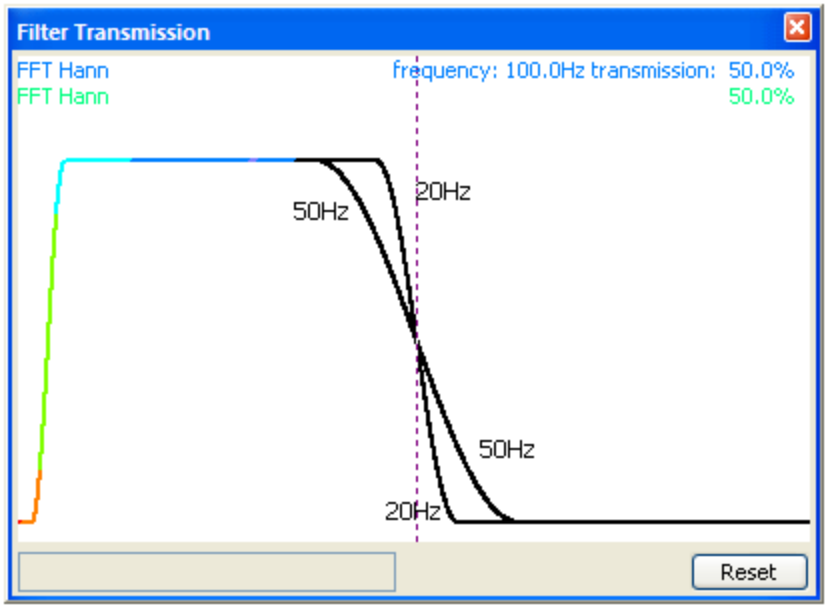
With **Linear** and **Hann** filters, the shape of the roll-off is determined the **Slope** parameters. If you select **User Defined (Auto)**, the Slopes are set for you. If you select **User Defined**, you can adjust the Slopes manually. You should never have a Slope that is more than twice the Frequency (the slope should never extend beyond 0 into negative numbers). Recall from above that a Slope of 10 Hz, for example, means that frequencies will be attenuated starting at 5 Hz before the Frequency, and complete attenuation will occur at 5 Hz after the Frequency.



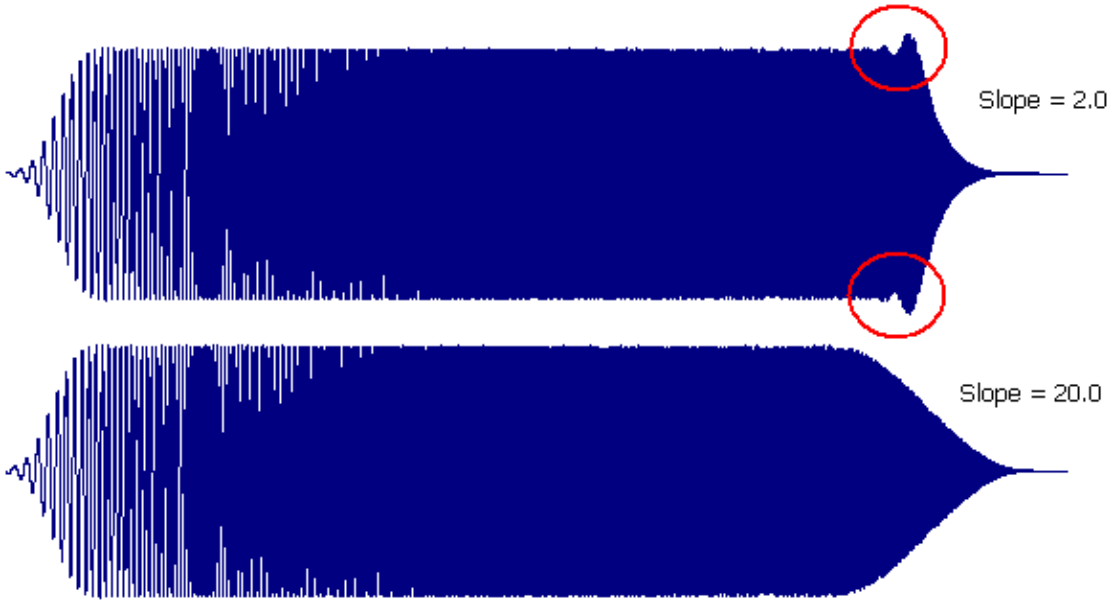
Here is an example of a Hann filter, from **10** to **100**Hz, where the Slopes are **8** and **20**Hz, resp. To see the Filter Transmission function, set the desired parameters and click the View button. Use the *mouse wheel*, *Shift+drag*, and *Shift+mouse wheel* to adjust the display as desired. Looking just at the Low Pass filter, you can see 2 regions: one where the desired frequencies are being attenuated, and one where the undesired frequencies are being passed (albeit attenuated). Ideally, you want these regions to be as small as possible. The same thing happens around the High Pass filter, although it is harder to see.



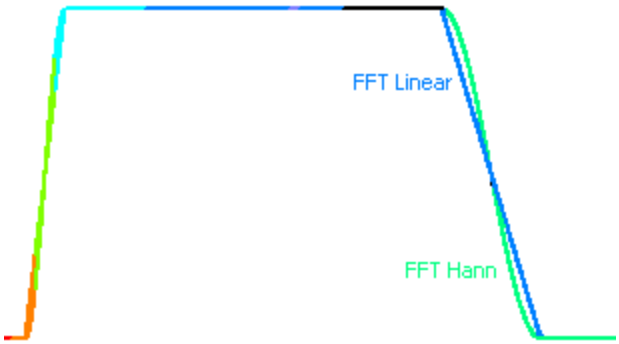
Just to demonstrate, here is the 100 Hz cutoff with Slopes of 20 Hz and 50 Hz.



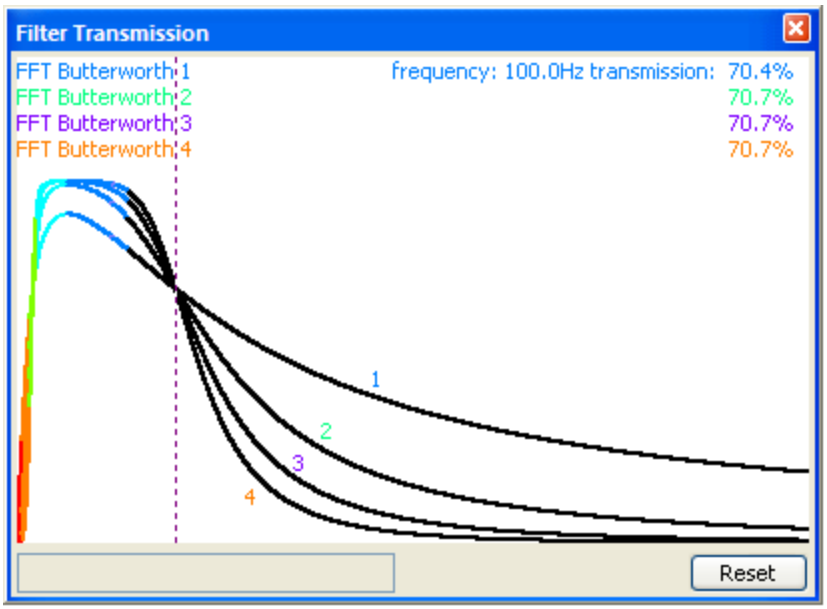
Why not use the least possible Slope all of the time? When the slopes become too steep, you will start seeing a sort of rippling, as shown in this example using a "chirp" file. This is why we recommend using **User Defined (Auto)**, so that the Slopes will be set automatically.



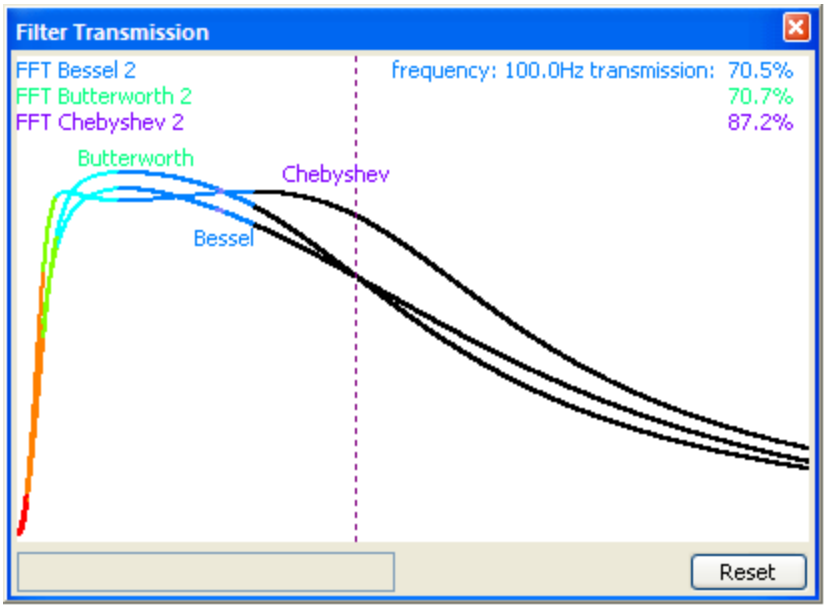
The difference between **Linear** and **Hann** filters is the shape of the roll-off. It is a straight line with Linear, and curvilinear with Hann.



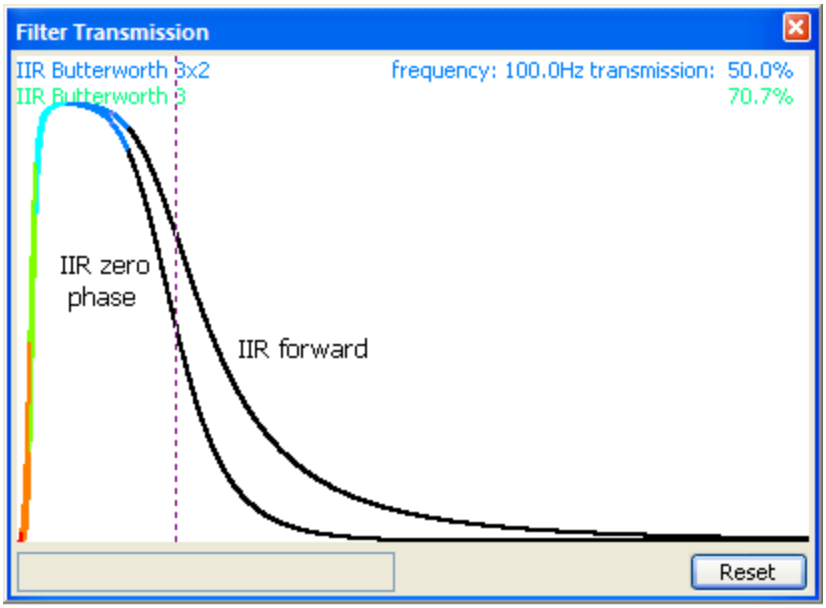
For the next 3 filter types - **Bessel**, **Butterworth**, and **Chebyshev**, the shape of the roll-off is determined by the **Order** (1-4). The larger the Order, the steeper the roll-off. The following shows a Butterworth filter with Orders of 1, 2, 3, and 4. Note how much of the desired frequency band (10-100 Hz) is attenuated with an Order of 1.



The next figure shows the differences between **Bessel**, **Butterworth**, and **Chebyshev**, with an Order of 2.

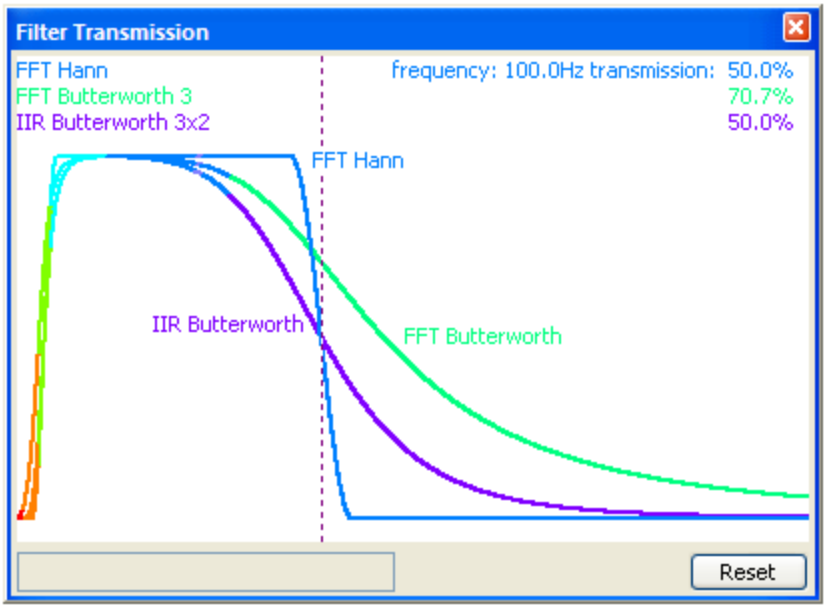


IIR (Infinite Impulse Response) filters can have either zero phase shifts (**IIR zero phase**; filter forward and backward) or can introduce phase shifting (**IIR forward**; filter forward only). With each, you can select **Bessel**, **Butterworth**, or **Chebechev** filtering, and you may select an **Order** from **1-4**. With IIR zero phase, the Order is divided by 2 (data are passed both forward and backward). Below is a comparison between **IIR zero phase** and **IIR forward**, using Butterworth filters and an Order of 3. The **3x2** (IIR zero phase) means that the Order was 3 and the data were passed twice.



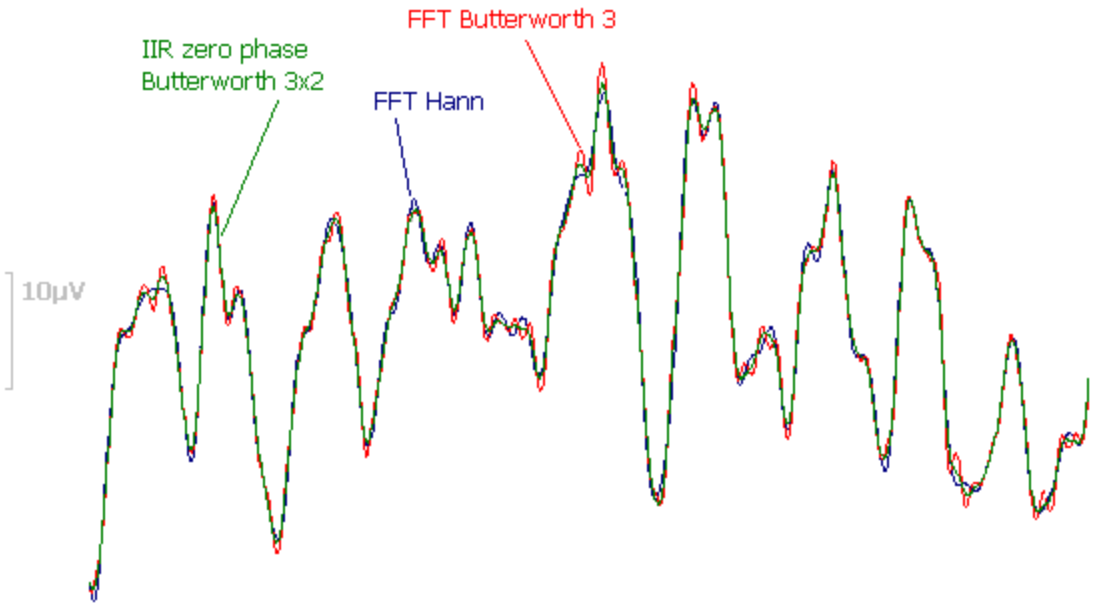
FIR filters (Finite Impulse Response) also can have either zero phase shifts (**FIR zero phase**; filter forward and backward) or can introduce phase shifting (**FIR forward**; filter forward only). FIR filters have an order of 62 and use a Hamming window.

Lastly, we will compare the default **FFT Hann** parameters versus the **FFT Butterworth** filter with an **Order** of **3**, and the **IIR zero phase Butterworth** filter with an **Order** of **3x2**. You can see why we recommend the default Hann parameters.



What differences do the filters make on the waveform data? You have to look closely to find the differences. This is about one second of data, comparing the FFT Hann, FFT Butterworth (3), and the IIR zero phase Butterworth (3x2) filters.

The main difference is that the FFT Butterworth is allowing a little more fast activity, as one would expect from the transmission functions. Even so, the differences are not too dramatic (comparing other filter configurations may show more or less dramatic differences).



CURRY provides many different filtering options, plus the ability to see the effects immediately on your data files. This lets you experiment easily with different settings to find those that are best suited to your data. Once you determine the optimal settings, you will most likely want to use the same settings for all data files in the research study (save the **Study Parameters** and apply them to all subjects).

Note that when you filter the continuous data and then create an average, the Filter settings are then turned off for the averaged file. You have already filtered the data in the continuous data file. If you enable the Filter settings again for the average file, you will be filtering it again.

2.4.3 Creating Montages

Montages have at least three main uses, including creating different derived display montages (such as, bipolar montages), creating displays with fewer channels, and reordering the channels.

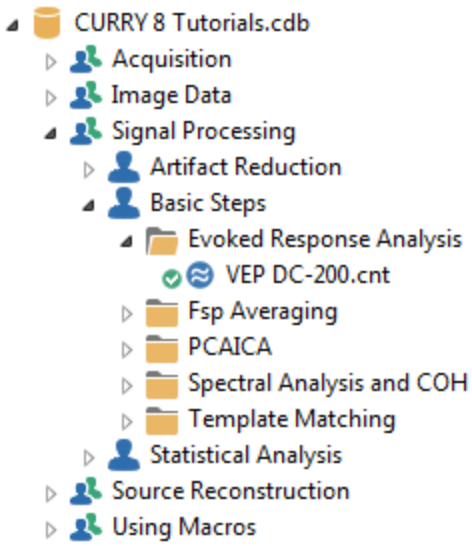
Montage files may be applied one at a time, so if you wish to, for example, create a display page with fewer channels and have them appear in a certain order, you should do that in a single montage file. Re-referencing, such as using an average ear or mastoid reference, should be done in the

panel (see the *CURRY 8 User Guide*).

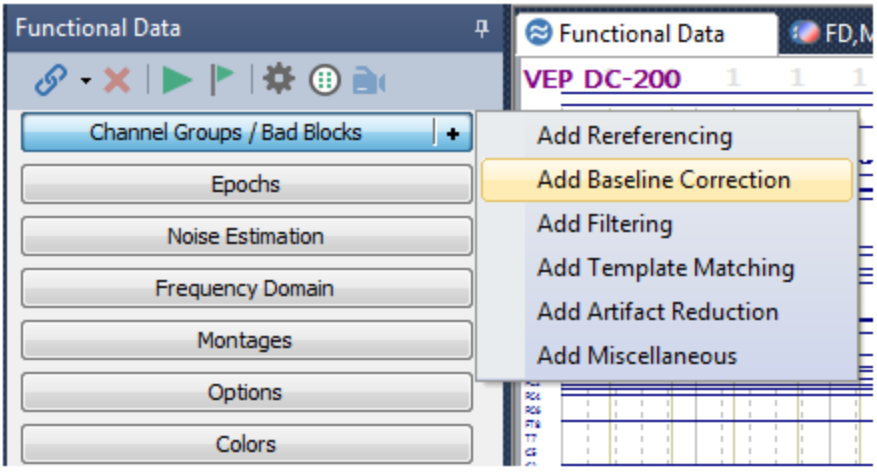
Montage files may be created online or offline. The montage files are *.xml* files, and these are stored one of two folders. Please see the **Target Folders for Windows 7** section for more information.

When you access a list of configuration files in CURRY, you will see both the files that have been supplied as well as those you have created. Those above the horizontal line are ones you have created; those below the line are the ones that have been supplied with the program.

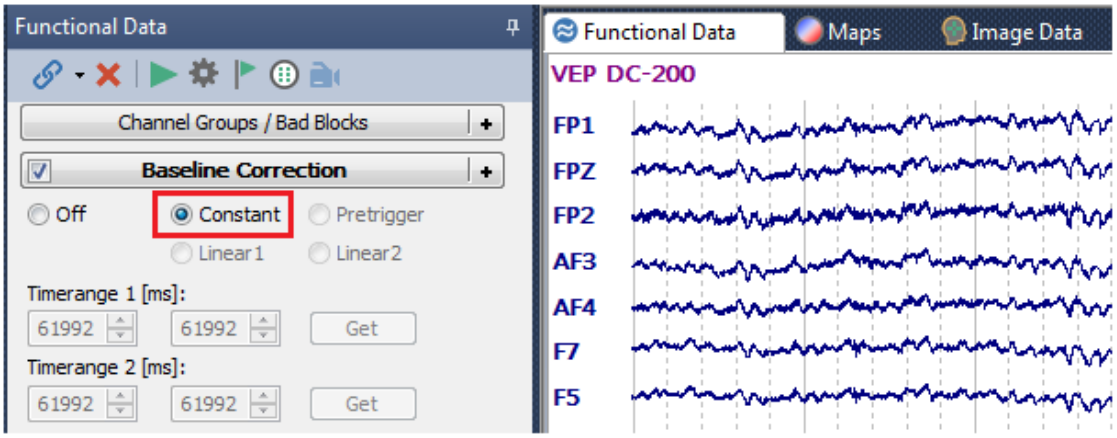
For this tutorial, we will create a bipolar montage, a display montage, and a montage that reorders the channels, using the file in the Study shown below.



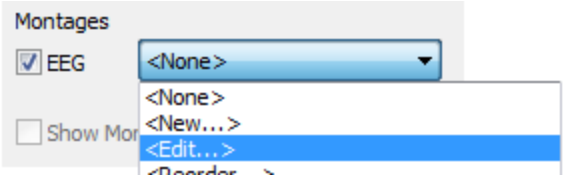
1. Open the Study. Click the + sign at the end of the Channel Groups / Bad Blocks + bar and select **Add Baseline Correction**.



Select the **Constant** option. Use the *mouse wheel* to rescale the data. The traces are centered, but no filtering has been applied.

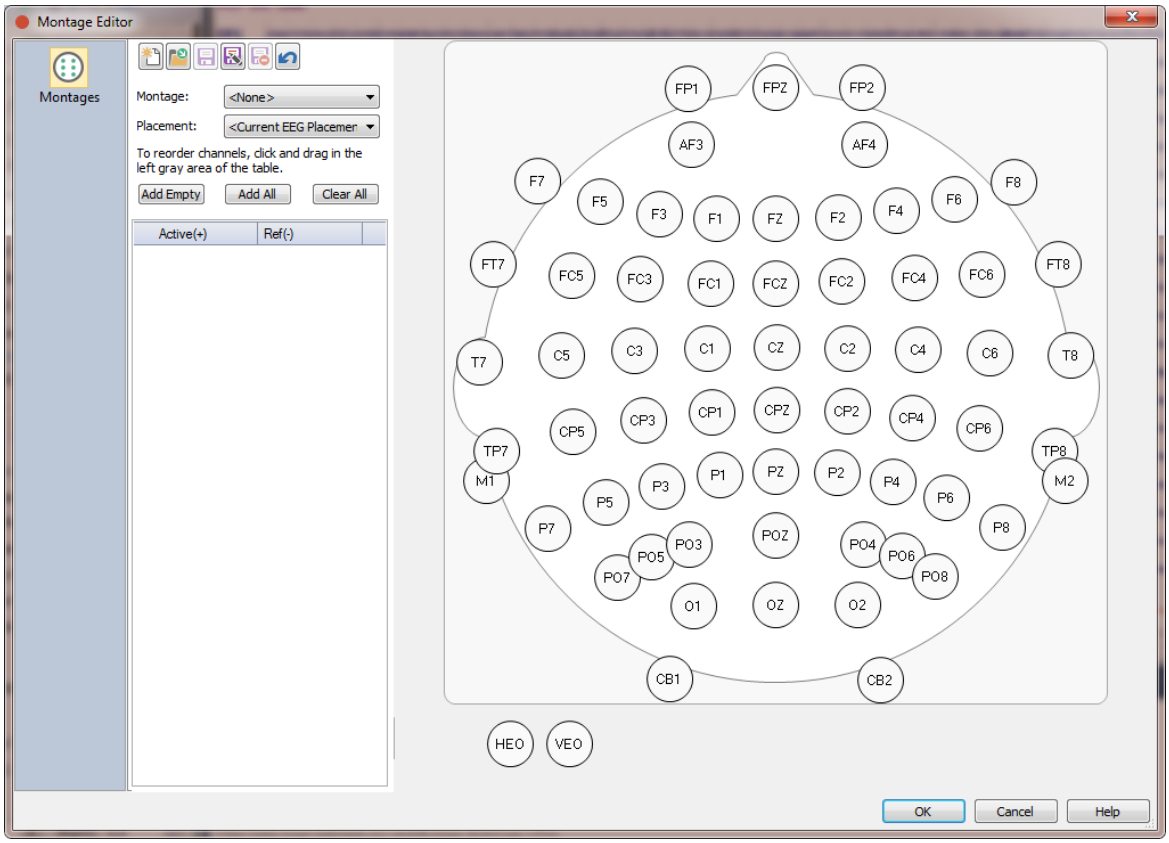


Expand the Montages panel under **Functional Data**. In the **Montages** region, select **<Edit...>** from the drop-down list, or just click the **Montage Editor** icon from the Toolbar.

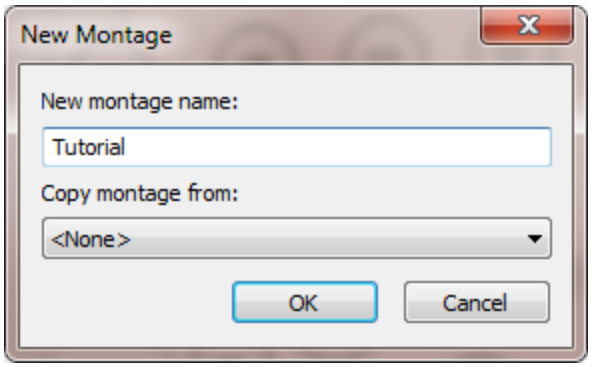


(If you have additional devices, such as MEG recordings, you will see additional fields here). You will see the New Montage dialog, asking if you want to create a new montage. Click **Cancel** for now.

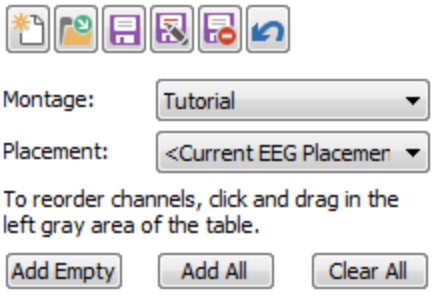
You will see the same Montage Editor that is used in the online part of the program (your display may show a different montage, or none at all).



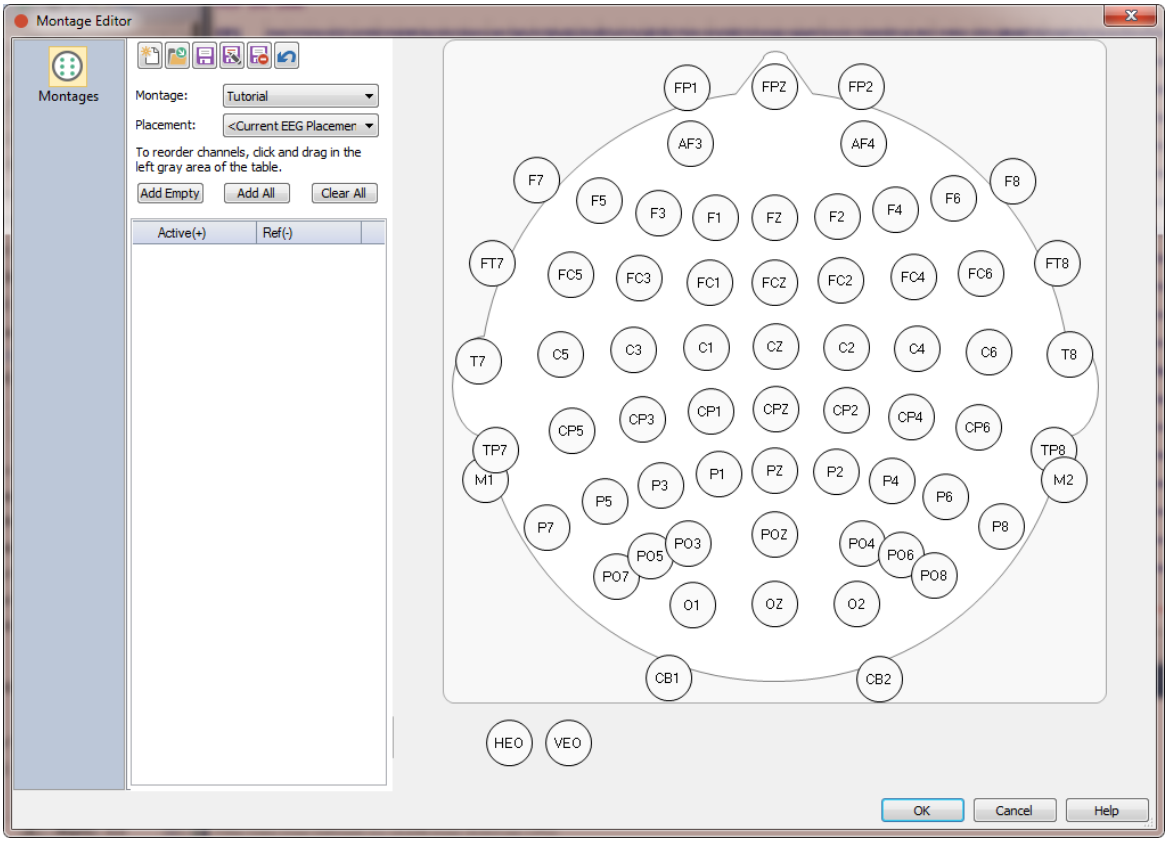
2. First we will create a bipolar montage. Click the **New Montage** icon to see the following dialog. Enter a **New montage name** (Tutorial), and leave the other fields set to <None> (for this example). Click OK.



3. Then, in the **Placement** field, select **<Current EEG Placement>** (if not already selected). This option is useful in files where the electrodes do not completely fit the 10-20 or 10-10 placements.

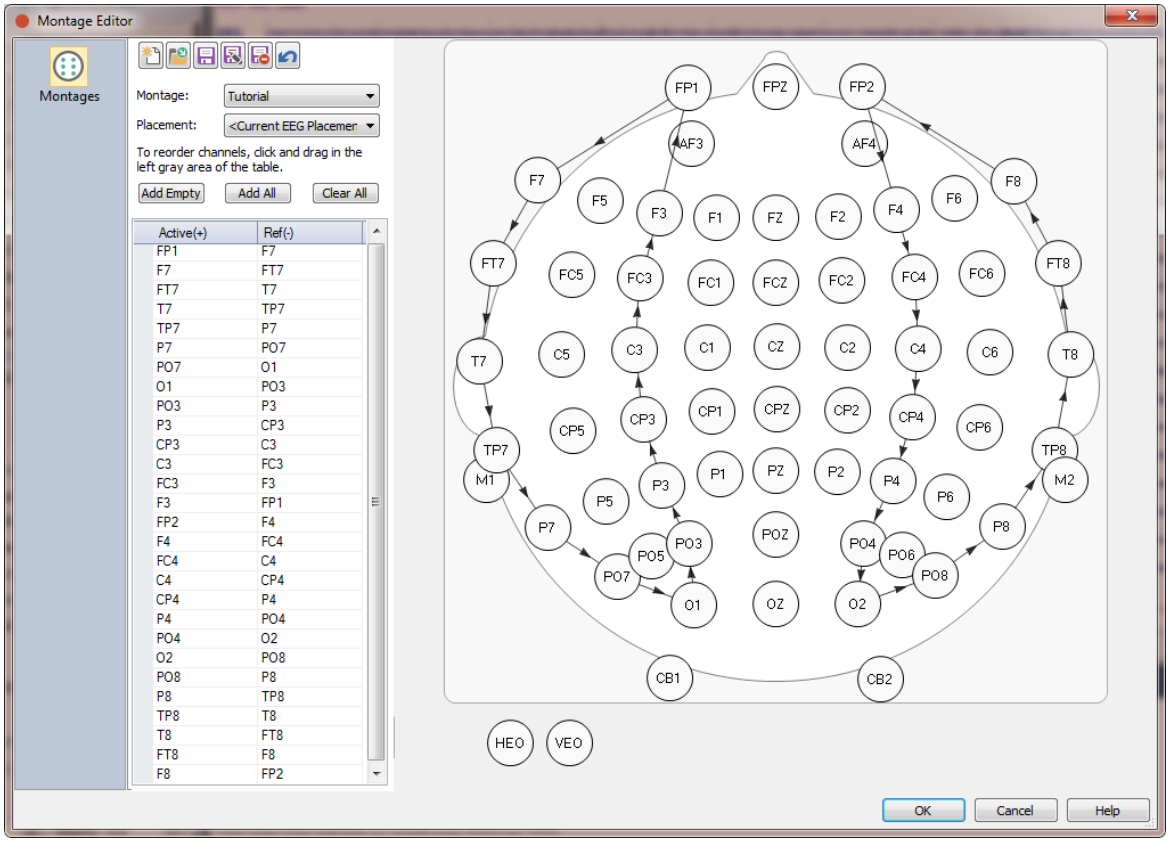


You will then see the following display.



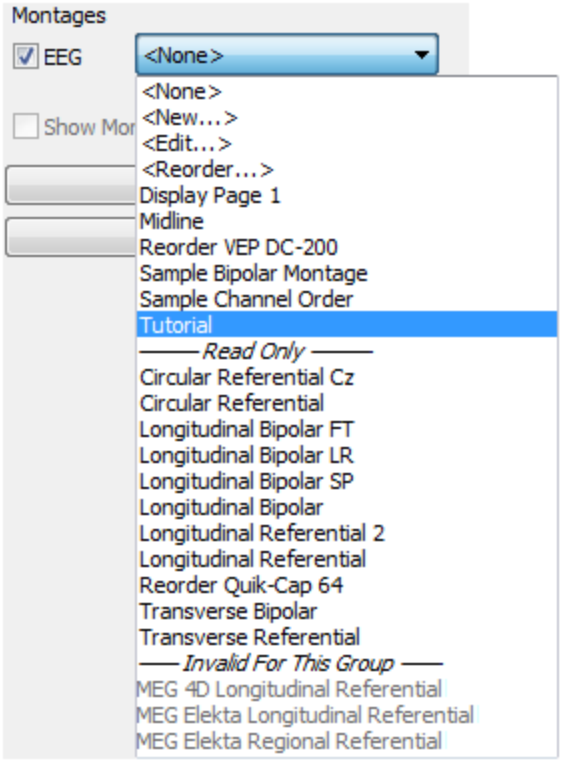
4. To create a bipolar montage, drag an arrow (drag and drop) from **FP1** to **F7**. When you drop it, you will see the **Active** and **Reference** electrode labels in the list.

Repeat the process to create the desired montage. If you make a mistake, highlight the pair in the list and press the *Delete* key on the keyboard (or position the cursor on the arrow to highlight it and click the *Delete* key).



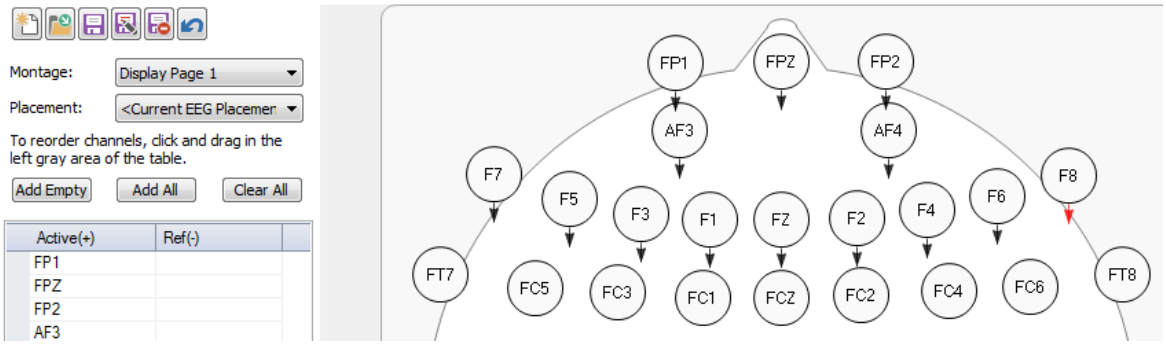
5. Then click the **Save** button to save the changes (or the **Save As** button if you want to use a different name). Click **OK** to exit the Montage Editor.

6. The Tutorial montage has been selected and applied automatically. As with other similar lists, the files above the *Read Only* line are ones you have created; files below are read only files that have been supplied. At the bottom are the montages that are *Invalid For This Group*.

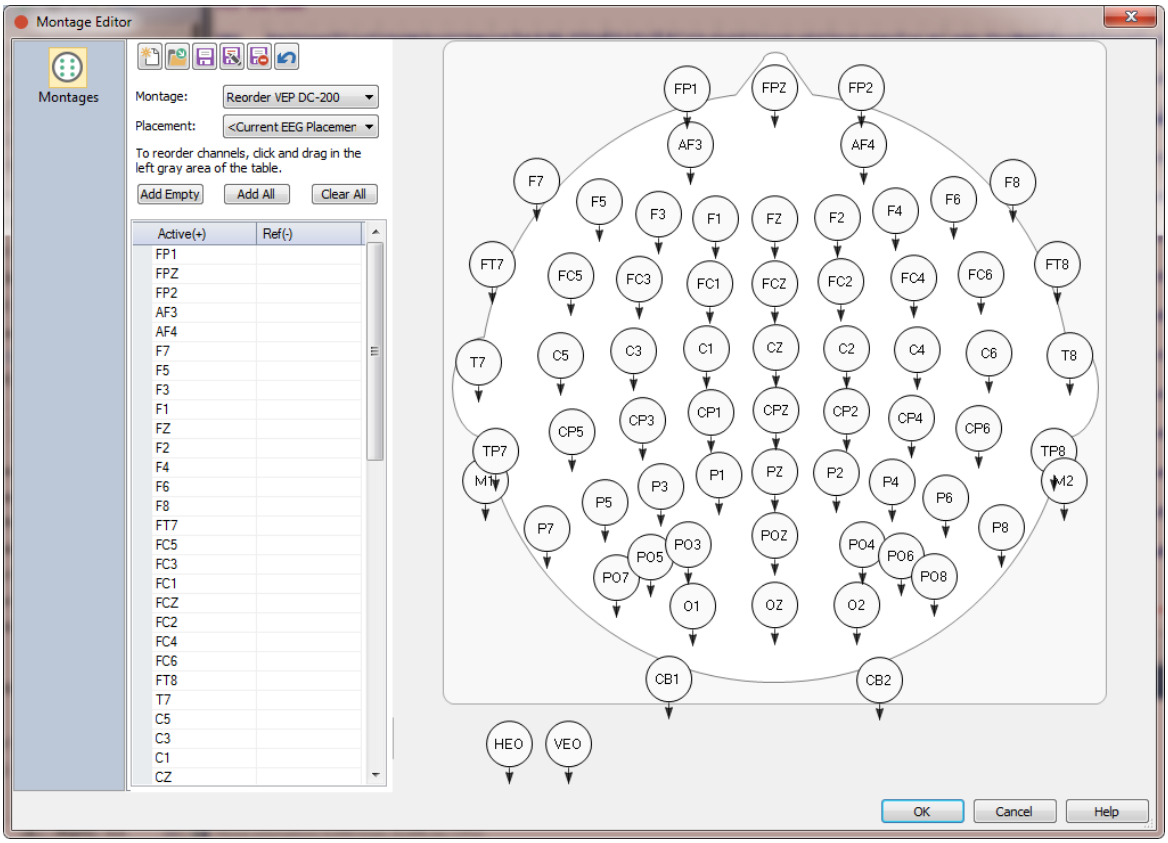


You can in that fashion create any derived montage.

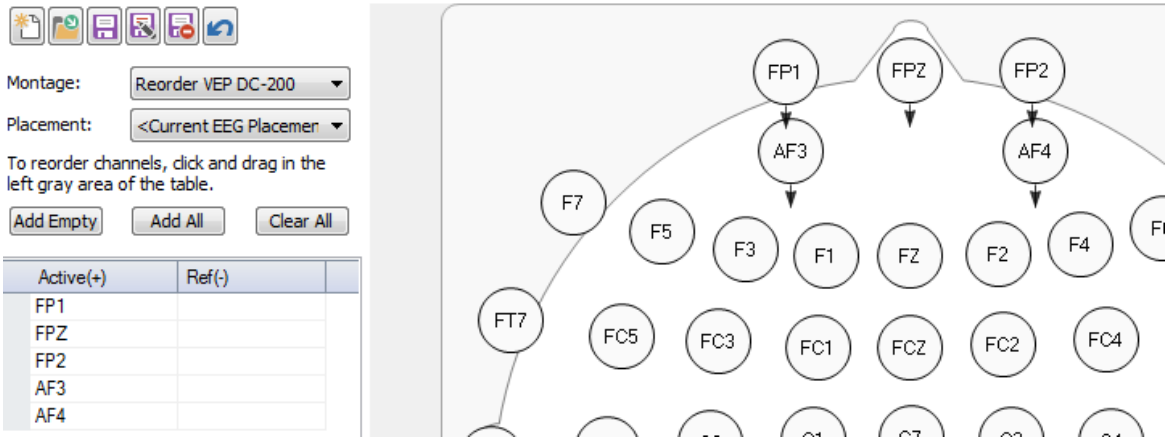
7. If you want to create a display having fewer channels, the process is similar. Return to the Montage Editor by clicking **<Edit>**. Click the **New Montage** icon and enter a file name (*Display Page 1*). Then simply *double-click* on the desired electrodes, in the desired order. Save the changes you made and click **OK**. The Clear All is used to clear the list first, if needed.



8. Reordering the channels can be done in different ways. From the **Options** panel, in the **Montage** drop-down list, there is an option called **<Reorder>**. This opens the Montage Editor where a new file has been created, called "Reorder <File Name>". All of the electrodes appear in the list. Then it is just a matter of dragging and dropping the electrodes in the desired order.

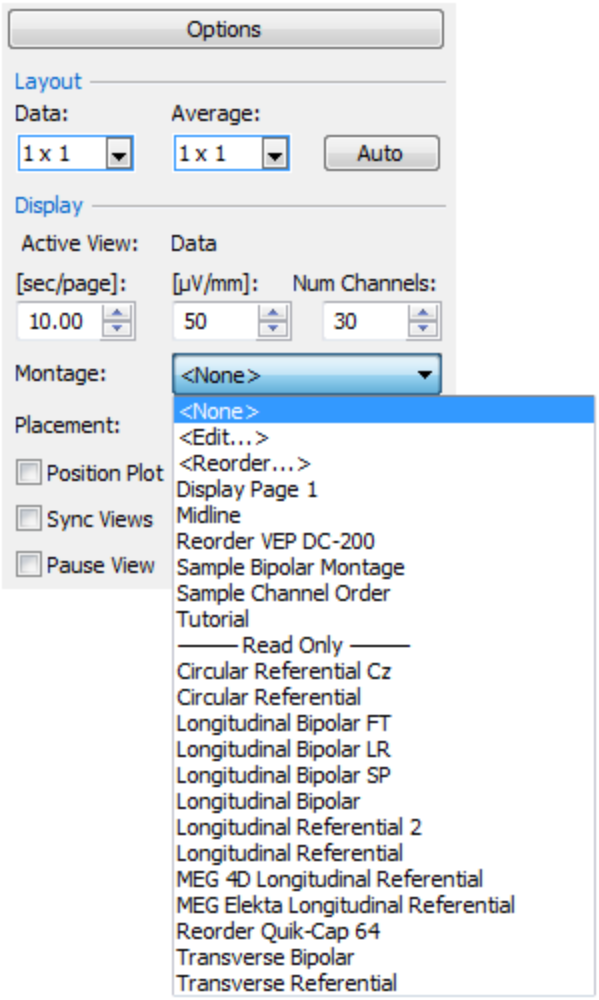


If that becomes too complicated, the alternative is to click Clear All to empty the list. Then *double-click* on the electrodes in the order in which you want them to appear.



Applying Montages

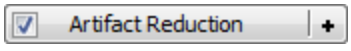
Montages may be applied online or offline. Online, select the montage from the drop-down list under **Options**. You can also access the Montage Editor from the same list.



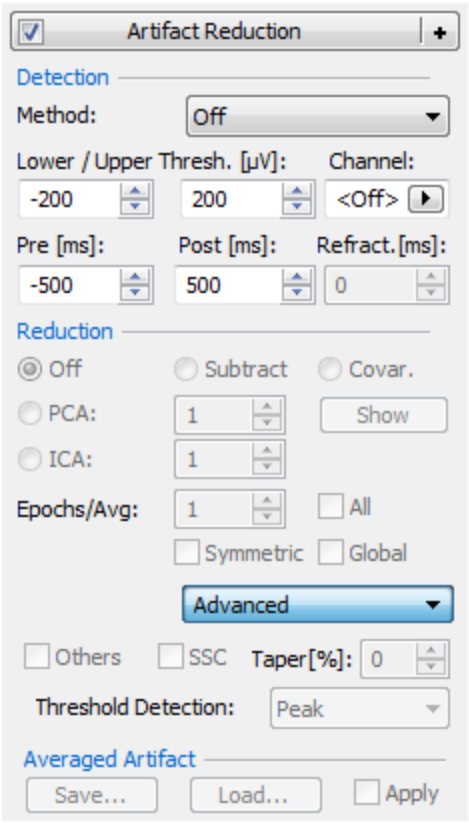
Offline, you may select montages for MEG and EEG data separately, from the **Montages** panel under **Functional Data**. Save the montage selection with the **Study Parameters** if you want it to be applied whenever you open the Study.

2.4.4 Common Artifact Reduction

CURRY 8 has a variety of methods for removing or reducing artifacts. In this session, we will look at some of the common artifacts you will encounter, and illustrate the various ways to remove or reduce them. A later Tutorial deals with gradient artifact and ballistocardiogram reduction.

The 

panel is divided into three parts: artifact **Detection**, artifact **Reduction**, and **Advanced** settings.



Artifact **Detection** has five options for **Method**. **Bad Blocks** is used to detect bad sections in the file automatically, using a voltage threshold. **Threshold** is used wherever the artifacts can be detected reliably using voltage threshold criteria. Blink artifacts, for example, are usually detected easily with a voltage threshold. **QRS Detection** is a special case that is used for reducing pulse artifact (and generally not ballistocardiogram). To use it, the QRS complex must be identifiable in at least one channel. **Event-Codes** is used when there are event codes that mark the artifacts (such as, MR gradient artifact). The **Templates** option uses the template events that are detected using **Template Matching** (which must be performed first). If you define multiple templates, then the first Artifact Reduction panel will use the first template, Artifact Reduction 2 will use the second template, and so on.

In most cases, an averaged artifact is created. The average can be based on **All** of the artifacts in the file, or by using a rolling average of the N most recently detected artifacts, including the current one (**Epochs/Avg**). The rolling average uses preceding artifacts; the **Symmetric** option uses artifacts before and after the current one (must have an even number for **Epochs/Avg**).

The **Reduction** section has several methods - most of the Reduction methods can be used with most of the Detection methods (exceptions will be grayed out). In other words, the detection methods are generally independent from the reduction methods. The Reduction methods include **Subtract**, in which the averaged artifact is subtracted from each artifact that was detected. **Covar.** uses a covariance analysis between the artifact channel and each EEG channel. **PCA** or **ICA** can be performed, and up to five components can be removed from the data with either.

The **Show** option lets you see the averaged artifact or the PCA/ICA components (after scanning). The **Global** option applies the correction to all points in the file when enabled. When disabled, only the artifact intervals will be corrected.

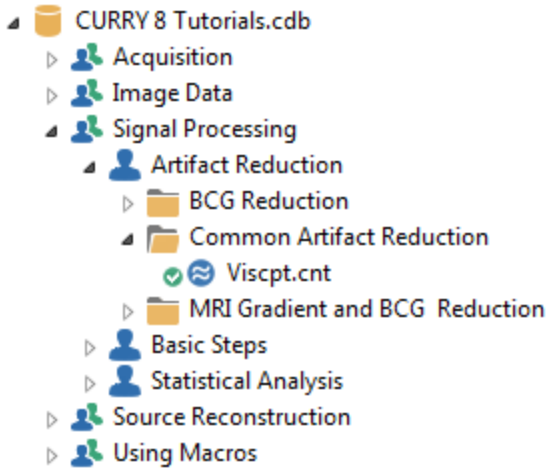
The **Advanced** settings include the **Taper %**, the **Threshold Detection** option (different ways to define the peak location), and some additional options.

Some of these options will be demonstrated below.

If you have a file with multiple types of artifact -- bad sections, blink artifact, heart beat artifact, stimulus artifact, etc. -- the general rule of thumb is to remove the more severe artifact first, then the less severe ones.

Artifact Removal
By artifact *removal*, we are referring to ways in which sections of the continuous data containing artifact can be removed from further analysis, or where epochs can be rejected that contain artifact. Artifact *reduction*, described shortly, keeps the sections of data in the file, while reducing the artifact in them.

The first file we will use is the *viscpt.cnt* file, which is found in the **Common Artifact Reduction** Study.

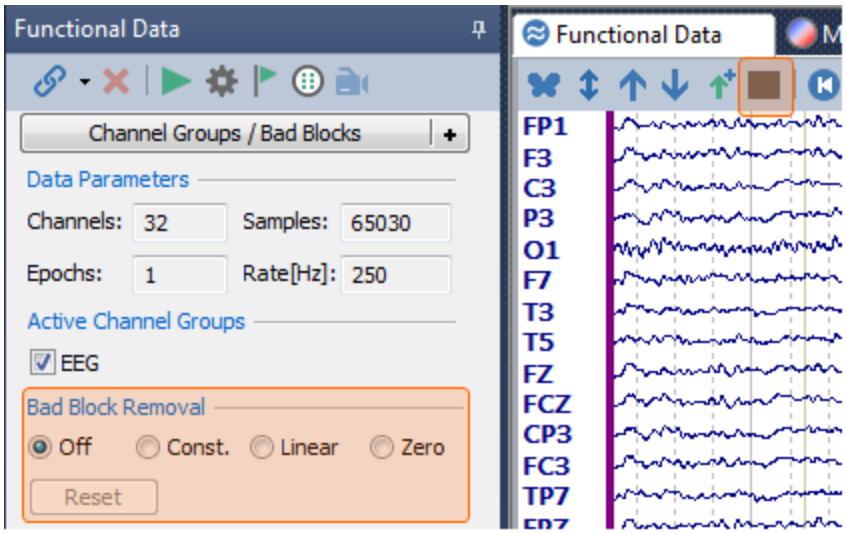


This is similar to a visual P300 recording, with target (Type 1) and non-target (Type 2) stimuli. There are several sections with bad data in the file (due to an electrode pop and high pass filter ringing), and there are blinks through most of the recording. We will first reject the bad blocks, and then looks at different ways to reduce the blinks.

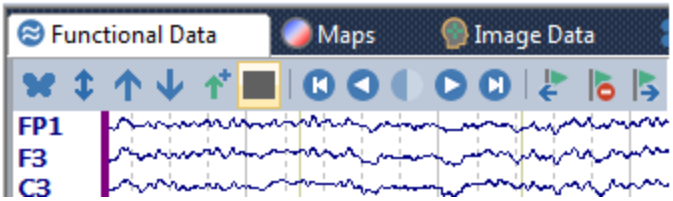
Open the Study.

1. In looking through the file, we see there are some bad sections and we want to remove or reject those sections. If you are having difficulty finding the options in CURRY, try using the Workflow (next to the Database tab). Looking in the **Signal Processing** section of the **Workflow**, we see that there is the Define Bad Blocks line. Clicking it expands the **Channel Groups / Bad**

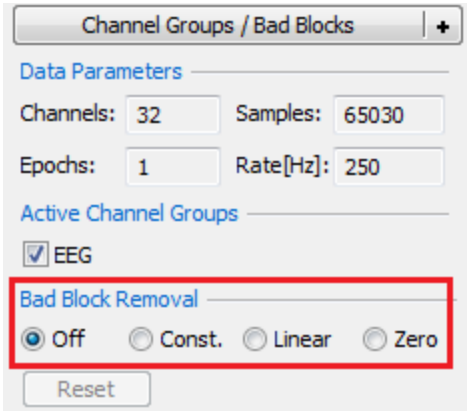
Blocks panel, and flashes the relevant icon on the Functional Data Toolbar , and the **Bad Block Removal** section.



You may manually mark bad blocks using the Bad Blocks icon on the Toolbar that appears when you position the mouse in the upper left area of the Functional Data display (you may also use *Ctrl+Alt+mouse drag* to define the bad blocks).

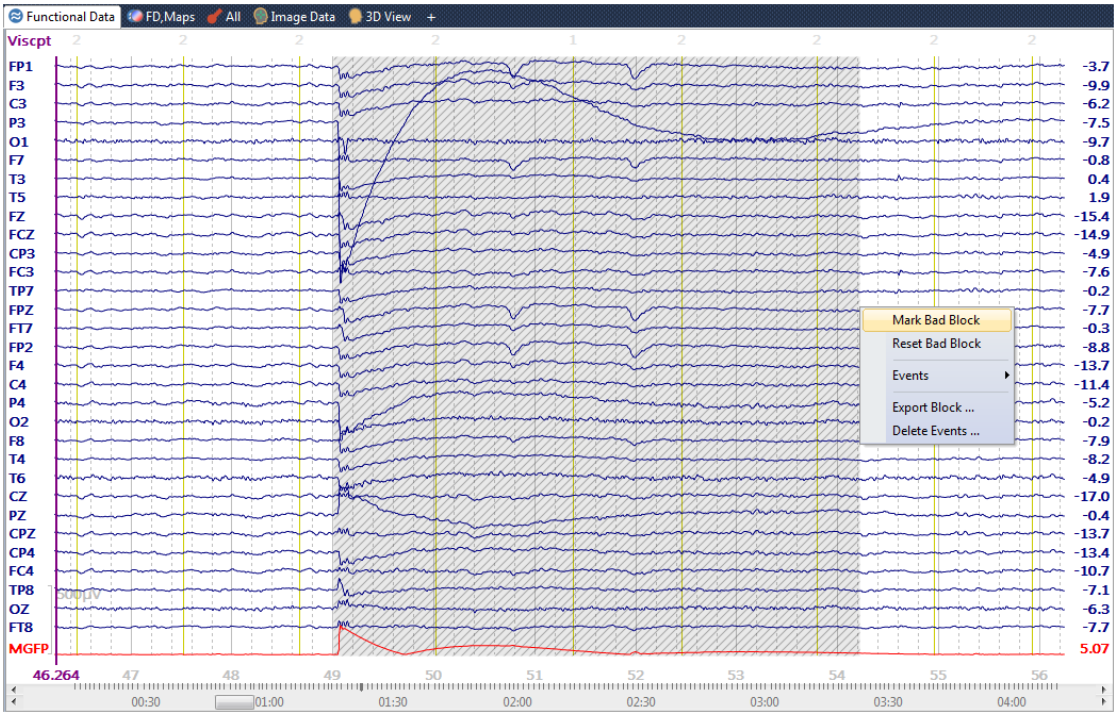


It is the Toolbar icon that will be used here; the Bad Block Removal options will replace the bad block sections you define with flat or sloping lines. Here, we just want to reject the bad sections.



Go to the 49th second in the recording to see the first bad section. An electrode pop occurred at P3.

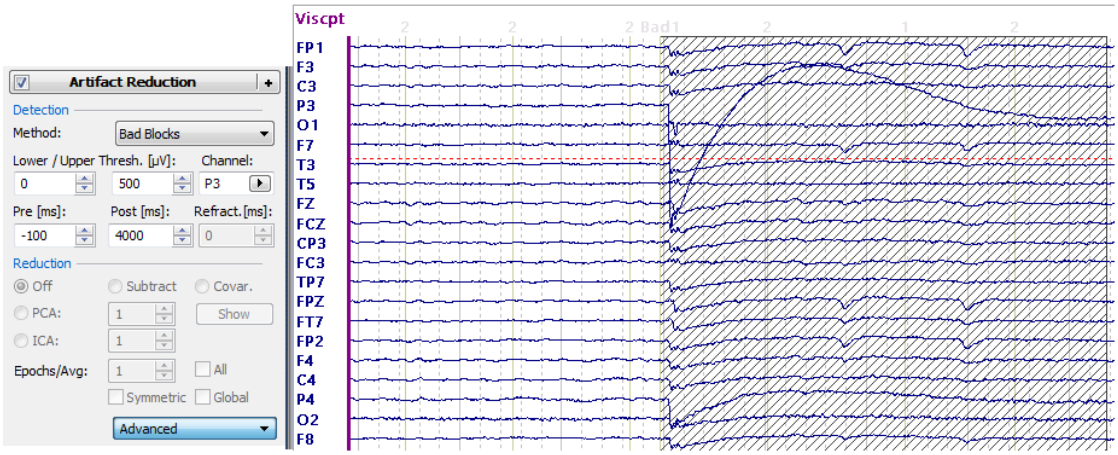
Click the **Mark Blocks** icon from the Toolbar; the cursor will turn into a + sign. You can either click just before and just after the artifact, or, click before the artifact and hold the mouse button down as you drag across the artifact. Release the mouse at the end of it. With either method, a context menu will appear. Select **Mark Bad Block**. The block will remain highlighted, and no epochs will be created that include wholly or partially rejected blocks.



Repeat the process for the remaining artifacts in the file (there are 5 sections with pops). Click the **Mark Blocks** icon again to deselect it when you are through.

Alternatively, you can use the **Bad Blocks Method** in this case to reject the bad sections automatically, which we will just mention at this point.

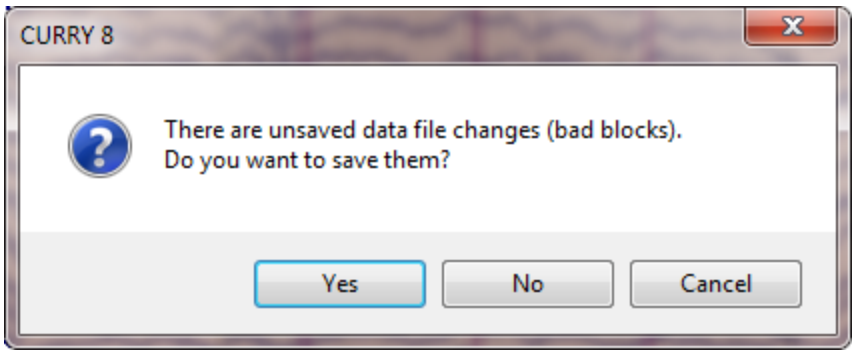
Looking at the example above (all are similar), we see that P3 is the bad electrode. If we measure the voltage at the peak, we see that a voltage threshold of 500μV would easily detect the artifacts. In the other affected channels, the artifact resolves after about 4 seconds. Knowing these parameters, we can set up the **Bad Blocks** method under **Artifact Reduction**, as shown. Note that the **Lower Threshold** was set to **0μV** - this turns the lower threshold Off. This was done to ensure that only the positive values will be used to detect the artifacts. The **Upper Threshold** is represented by the red dashed line (relative to P3). When you click the **Scan Data** button, the bad blocks would be detected automatically.



It was fortuitous that the **Bad Blocks** method could be used with this data file - other files may not have such repetitive artifacts. The Bad Blocks method can also be used to reject sections in the data file that contain blinks. You can thereby exclude those sections, rather than reduce the blinks (as in the next section). If you have a file with very few blinks in it, it may be easier to simply exclude those sections. The options are there for you to choose.

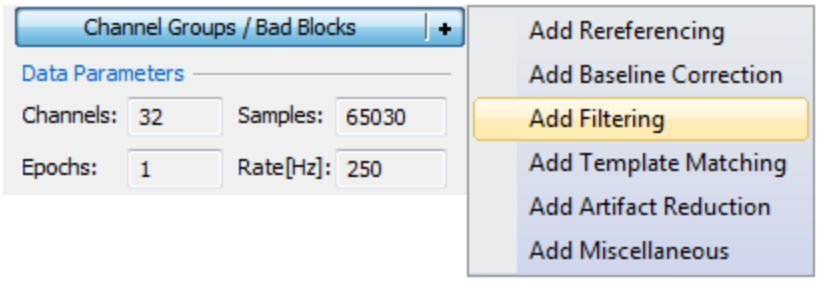
---

2. If you were to close the Study at this point, you would see the message shown below (do not close it now - we will close it later). The bad block designations are saved automatically in the .dpa parameters file rather than the Study Parameters. By saving them, you will not need to redetect them when you open the file in the future. By saving them in the .dpa file, rather than the Study Parameters, you can apply the Study Parameters to other data files that would have their own bad sections. To remove manually all selected Bad Blocks from the continuous data file, click the Reset button (in the Channel Groups / Bad Blocks + panel), or you can go through the file and use **Reset Bad Block** (shown above in the context menu) to mark individual bad blocks as good ones.

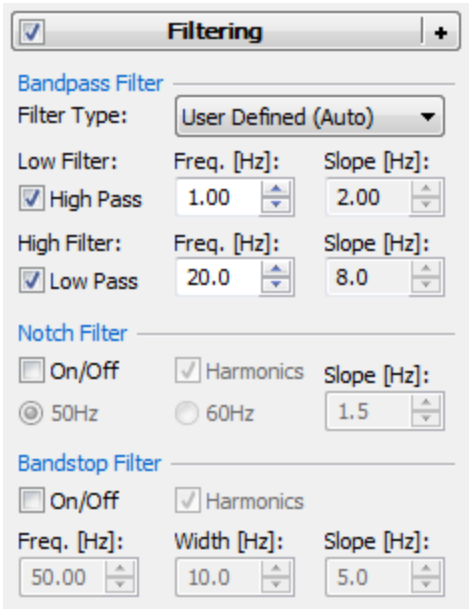


3. If you are creating averages, you also have the option to reject epochs based on voltages that exceed thresholds you define, and/or SNR thresholds you define. These are demonstrated in the **Evoked Response Analysis** tutorial.

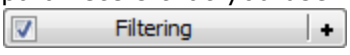
4. We also note that there is some faster activity in some channels, apparently due to neck tension. We would like to filter that out. Looking at the **Workflow**, we see the Filtering (Off) line. Click it the **Filtering** panel opens and flashes. If you are not using the Workflow, click on the + sign at the end of **Channel Groups / Bad Blocks** and select **Add Filtering**.



Set the parameters as shown.



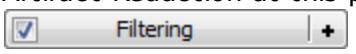
If you plan on using the **Covariance** method for blink reduction, you will obtain better results if you filter the blink channel (e.g., VEOG) using the same parameters that you use for the EEG channels. Filtering in the



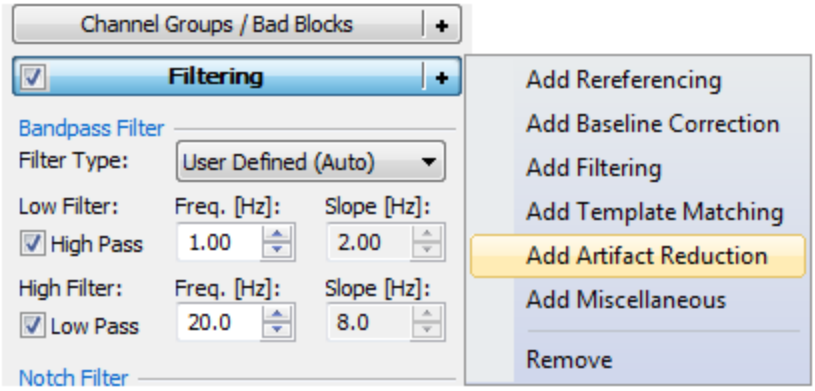
panel affects only the EEG (and MEG) channels, but not the "Other" channels. The VEOG channel is typically an Other channel. You have two options here. One, you can *right click* on the blink channel label and select **Set Filter Frequencies**. Use the same parameters that you used for the EEG channels. If you forget to filter the blink channel, CURRY will perform a check for you. When you select the **Covariance** option, CURRY will check to

see if the filtering is the same for the EEG and the selected **Channel**. If not, you will be asked if you want to filter the Other channel. We will do the latter below.

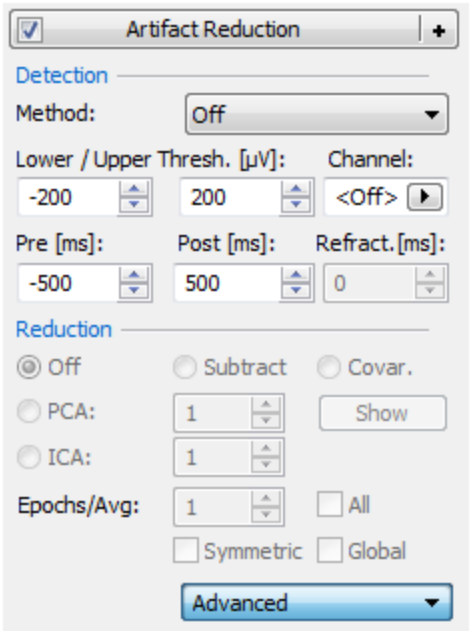
Artifact Reduction

Perhaps the most common artifact you will encounter is blink artifact, which is greatest at the frontal leads and decreases as you move posteriorly. To access Artifact Reduction at this point, click the + sign at the end of the 

bar and select **Add Artifact Reduction**.



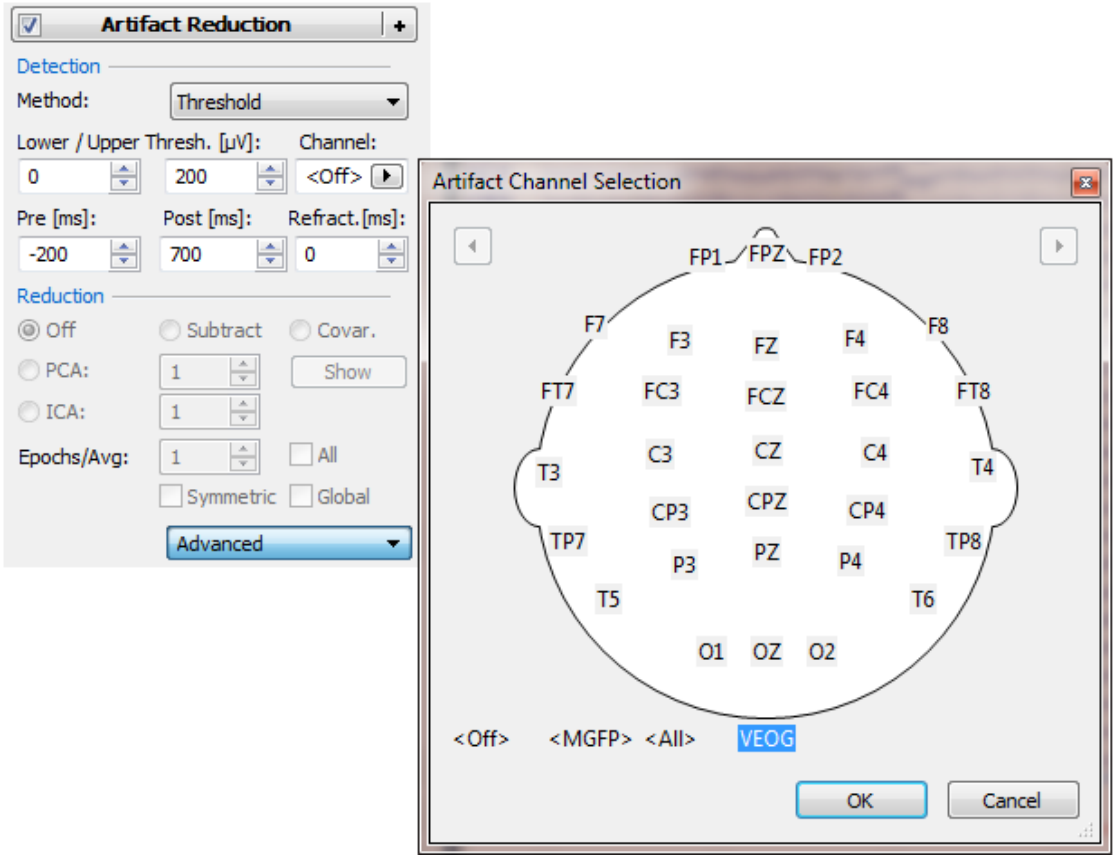
You will see three sections that are relevant for blink reduction: Artifact **Detection**, which contains the options for detecting the artifacts, **Reduction**, which contains the methods for reducing the artifact, and the **Advanced** section, which includes additional parameter settings.



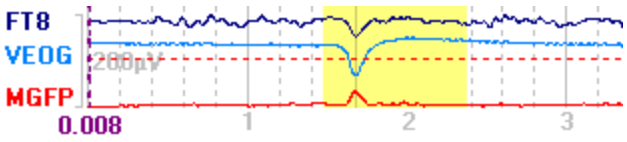
For blinks, there are several methods that can be used, and we will look at some of them. In practice, you should use the method that best reduces the artifact in your particular data files. The most likely method you will use is **Threshold**.

Artifacts are detected using a simple voltage threshold. In this file, we will use the VEOG channel, and we find by manually measuring a few representative blinks that a voltage threshold of 200μV should work well.

5. Enter the parameters as shown. Click the arrow button for **Channel** to see the **Artifact Channel Selection** dialog. You can click on a single channel to select it, use *Ctrl+left mouse* to select several channels, drag a rectangle around selected channels, or click **<All>** to select all channels. Select just the **VEOG** channel for this example and click **OK**.



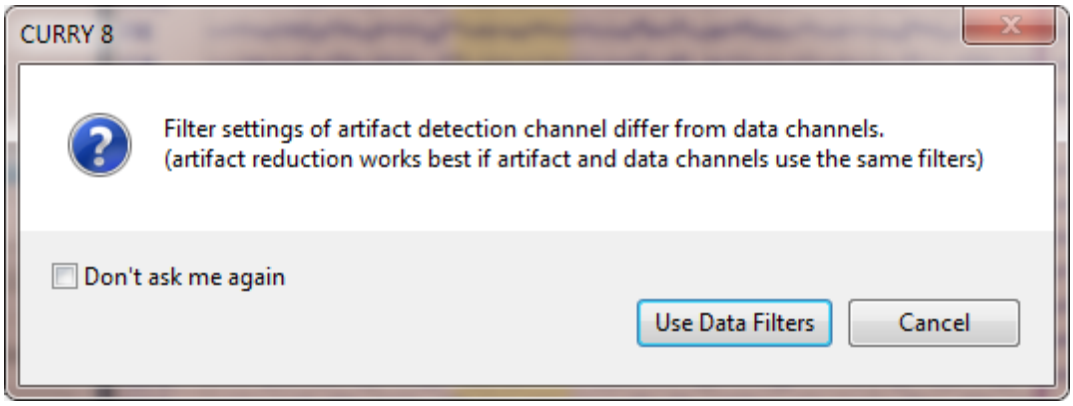
In the data display, we see the dashed line that represents the position of the threshold with respect to the selected channel.



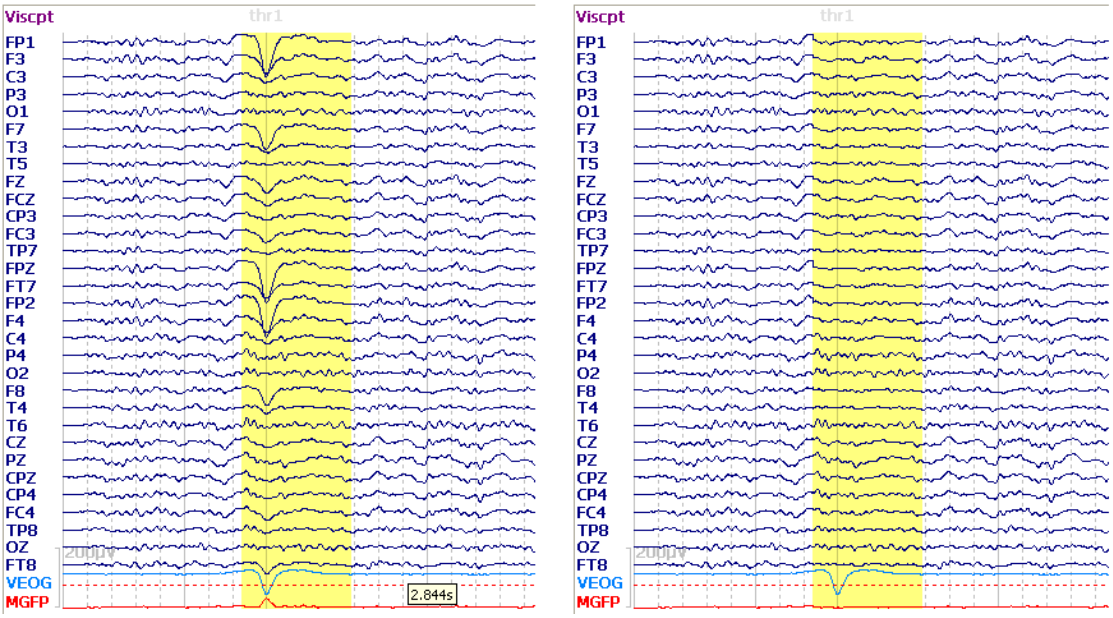
Setting the **Lower Threshold** to **0μV** turns it off, meaning that there is no lower threshold. Otherwise, we would see + and - threshold lines. This was done to ensure that only the positive values will be used to detect the blinks. (It is not really necessary for this file, but it is a good habit to develop). Blinks will be assumed to occur when the voltage on the VEOG channel exceeds **+200μV**. **Pre** and **Post [ms]** define the span of the artifact. The **Refractory** period sets the duration that the program will skip before looking for the next

artifact. The minimum **Refractory** period is the sum of the **Pre** and **Post** intervals. A value of **0** is a special case (and the default), which means to always use the sum, even when the Pre or Post intervals are reduced.

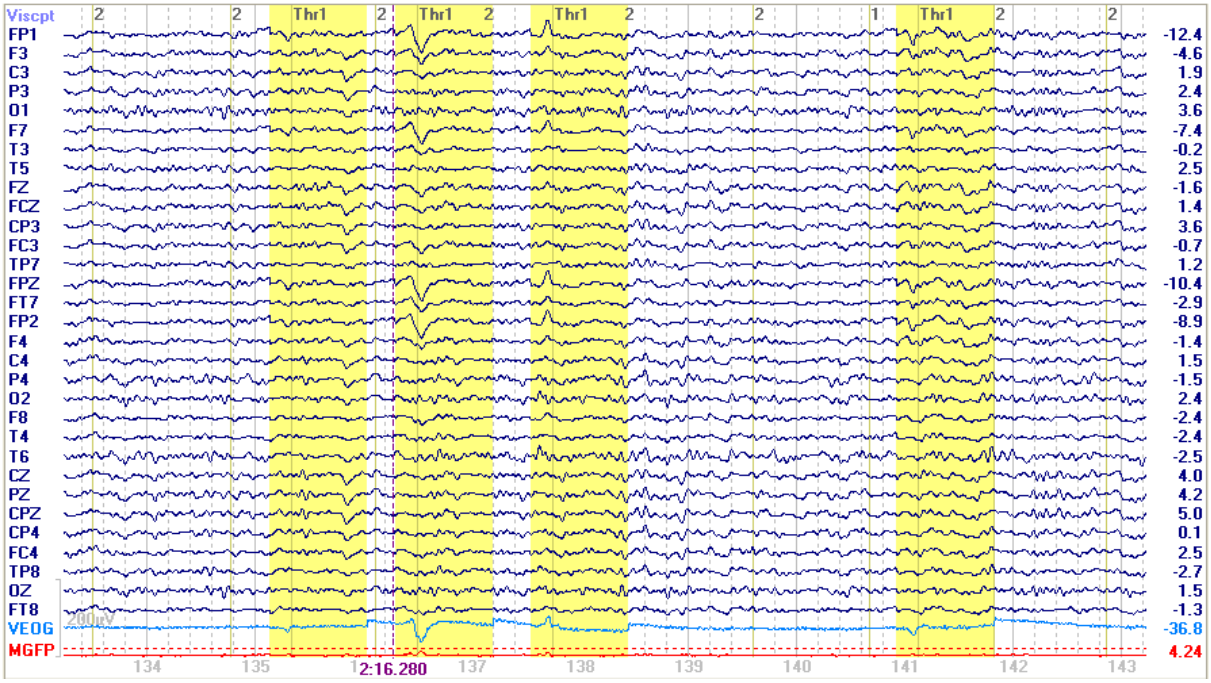
6. Next, we can try different methods for reducing the artifact. At this point, this step can be seen as a preliminary method for assessing the effectiveness of the reduction techniques. Select **Covariance**. This performs a covariance analysis between the selected artifact channel and each of the other channels (using the blinks that are displayed on the screen only). The greater the covariance, the larger the correction value that is used (linear transmission coefficients, similar to beta weights in linear regression). On clicking the Covariance option, we see a message saying that the filtering for the EEG channels is different from the artifact channel (VEOG, set as an "Other" channel).



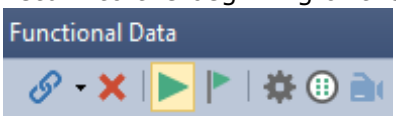
The reduction works best if the filtering is the same. Click **Yes** to set the filters on the VEOG channel. The blink was well removed. (If you scan the file and then select Covariance, you will see the same message if the filtering does not match. In that case, you will need to scan the file again, after clicking Yes).



7. Select **Subtract**. All you will see is a flat line in place of the artifact. The artifact has been subtracted from itself. If there were multiple artifacts displayed, you would see a flat line for the first one, and corrections following that (assuming **Epochs/Avg** was greater than **1**), based on the rolling average that is being created. Advance further into the file to see the correction, using **Epochs/Avg** of **10**. The Subtract option is generally not especially effective with blinks, since the amplitude varies considerably across blinks, so any given blink will be different from the average of all blinks.



Return to the beginning of the file. When you click the flashing arrow



button (not yet), the averaged artifact will be created based on the number you enter for **Epochs/Avg**, or for all artifacts if you select **All** (active after scanning), and that averaged waveform will be subtracted from each detected artifact in the file. For now, select **Off** again to see the blink return.

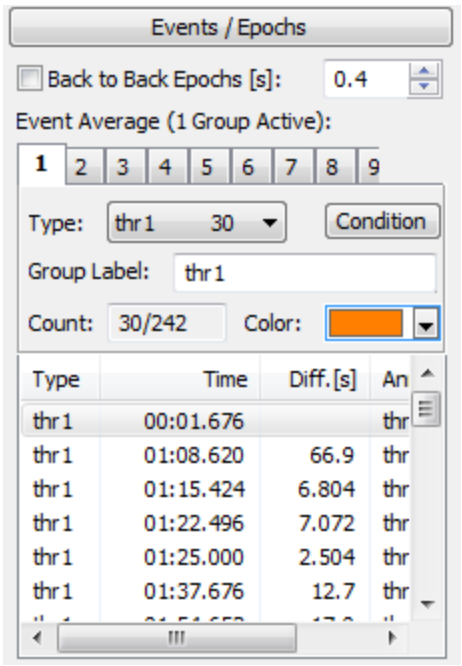
8. Now select **PCA**. Again, the blink disappears. A PCA (Principle Components Analysis) has been performed and the 1st component, typically the blink component, has been removed from the data. Increase the number of components to **5**, and see that additional activity has been removed. You typically want to use only as many components as are needed to reduce the artifact. Projecting additional components could affect the signal that you are trying to preserve. Be conservative in the number of components you select. Select **Off** again to see the blink return.

Note

If blinks occur too closely together, some will be missed. This is because you cannot have overlapping artifact intervals. See the **Missed Blinks?** section at the bottom of the online **Blink Reduction** section above for ways to deal with this.

Now click the flashing **Scan Artifacts** button to detect the blinks and apply the correction throughout the file (prior to clicking , the correction is applied to the visible display only). After the file has been scanned, the button will stop flashing , indicating that it has been scanned. If you change any parameters in this panel - or any other panel (reference, baseline correction, filtering, etc.) - that would affect the results of the scan, the button will start flashing , letting you know that you should scan the file again.

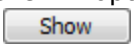
9. If at this point you were to look in the Events / Epochs (next to the Database tab, or click the icon on the Toolbar), with **Type** set to **thr1**, you would see a list of the blinks that were detected. These can be averaged like any other events if you wish to see what the averaged artifact looks like.



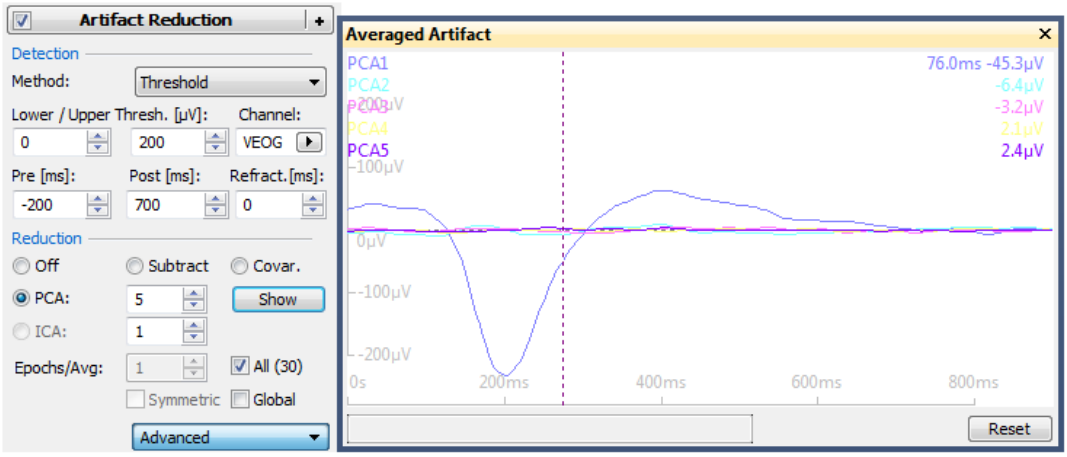
The colored tick marks below the data display now show the locations of the blinks (and the bad blocks in gray).

10. Move to a section of the recording where there are several blinks displayed, such as, the interval from 135s to 142s. Select **PCA** again, set **Components**

to **5**, enable the **All** option

(your count may be slightly different), and click the 

button. The 5 PCA components are displayed. You can see that it is the first component that represents the blink. Increasing the display scale (*mouse wheel*) shows little activity in the other components that could represent blink activity. Therefore, we would remove the first component only. Close the window.

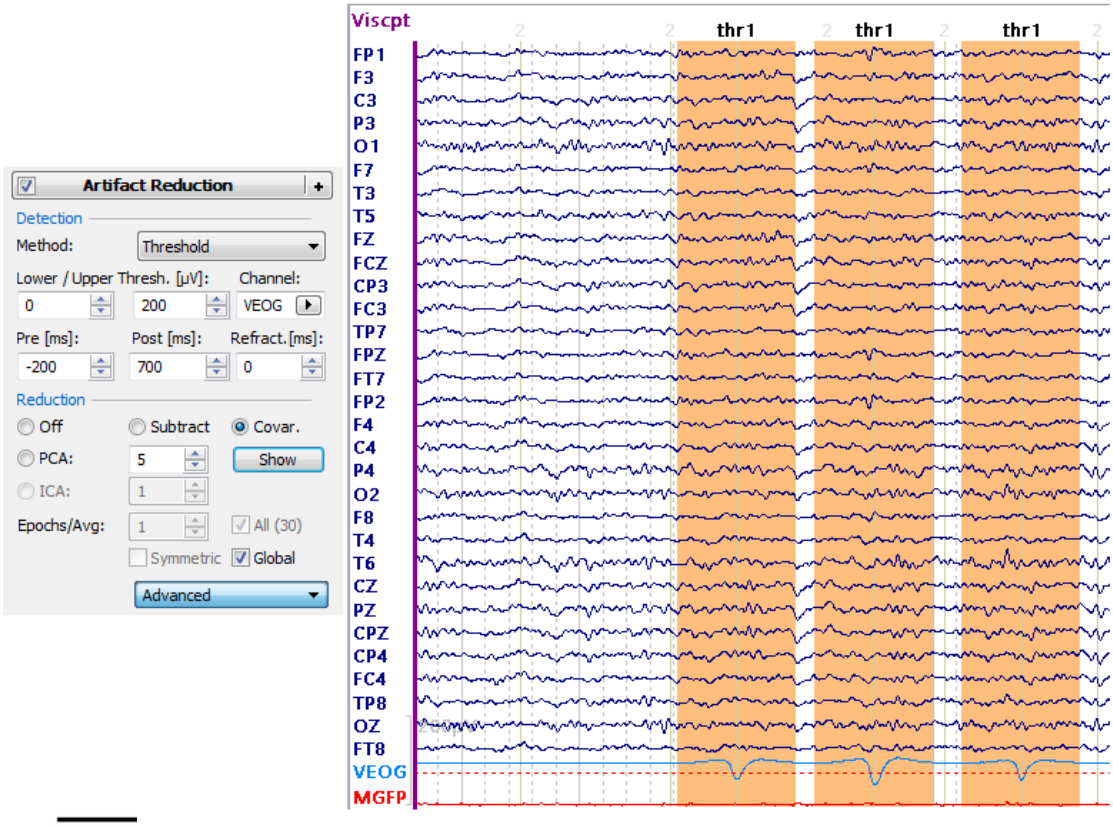


11. Set **Components** to **1**. Now enable the **Global** option

. This applies the correction to all samples in the data file. Otherwise, the correction is applied to the artifact intervals only. This is useful for removing the abrupt transitions that can occur at the beginning and end of the blink interval, and also for reducing sub-threshold blink activity.

12. Switch to the **Covariance** option, leaving **Global** enabled. Go back and forth between the **PCA** and **Covar.** options to see the differences between methods. More of the overall activity is preserved with the **Covar.** option, in this file at least.

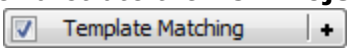
The **Covariance** option, with **All** selected, and with **Global** enabled, most closely approximates the **Ocular Artifact Reduction** method that has been used in the Neuroscan EDIT software for many years.



CURRY 8 is meant to be used from top to bottom (meaning, in this case, **Channel Groups/ Bad Blocks**, **Rereferencing**, **Baseline Correction**, **Filtering**, and so on down the parameter panels to **Frequency Domain**), especially when using **Artifact Reduction**. For example, if you are using PCA or Covariance methods to reduce the artifact, and then you go back and change the Filter Parameters, that will invalidate the PCA and Covariance results. In such cases, you will see the Scan Artifact button flash , indicating that you should rescan the file.

This demonstrates the most common method for reducing blink artifact. A different method is shown next.

Template Matching and PCA Projection

Next, we will demonstrate the **PCA Projection** method after identifying the artifacts using  . This can be used not only with eye blinks, but also with any other artifact - or other feature - that can be detected reliably and where the first PCA component is the artifact (and not something you wish to keep). You do not necessarily have to use Template Matching with PCA Projection - you can use one of the other detection methods (Threshold) as well.

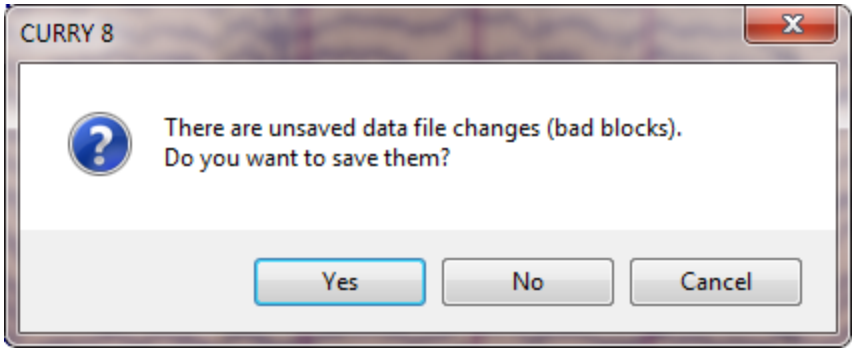
Note

Note that CURRY 8 always uses an internal CAR (Common Average Reference) data when computing PCA in Maps, even if you have turned off the CAR option in

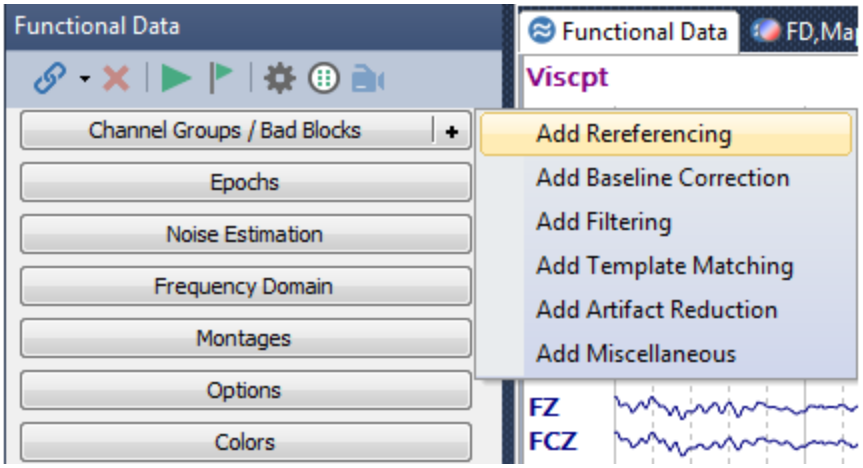
Functional Data. If you are using the PCA results from Maps to project artifact from your data in the **PCA Projection** option under **Artifact Reduction**, you must enable CAR to see the expected effect. If you do not wish to use a CAR for the remainder of your analyses, you should not use PCA Projection.

Note
PCA Projection is the basically the same as the **PCA** option under **Reduction** methods, when **Global** has been selected. The main difference, as seen in the latter part of Step 3 below, is that you have more flexibility in how the PCA is computed (you can use a Timerange other than that set for the artifact interval and you can see more of the results).

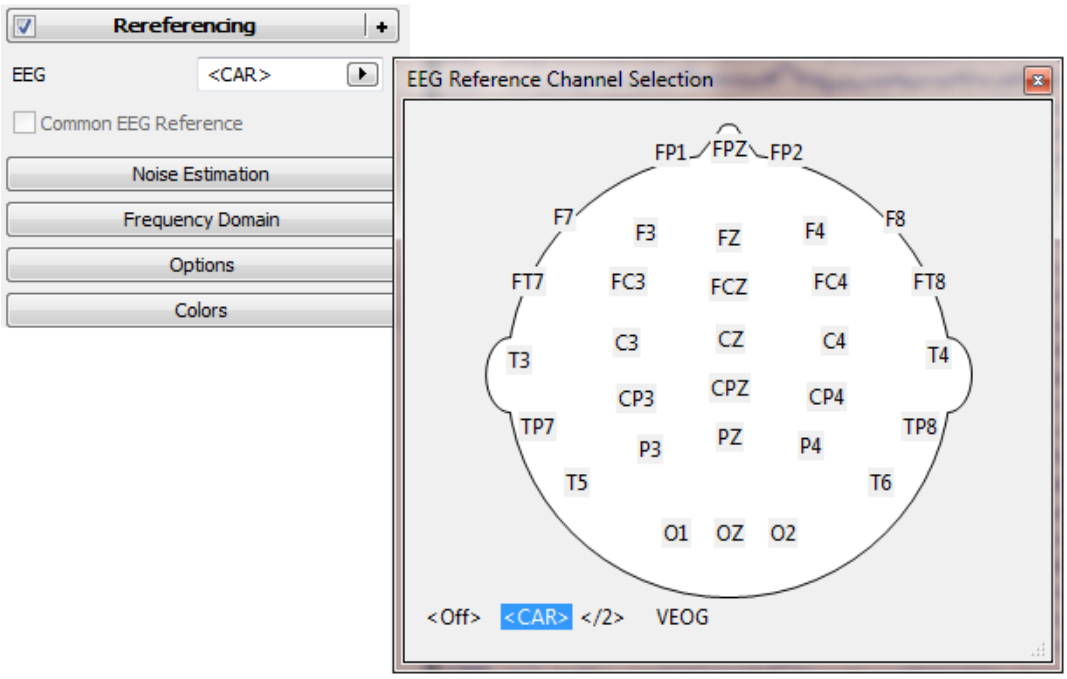
It is simplest at this point to close and reopen the Study. You will be asked if you want to save the Bad Blocks - click Yes. When you open the Study again, the bad blocks will remain.



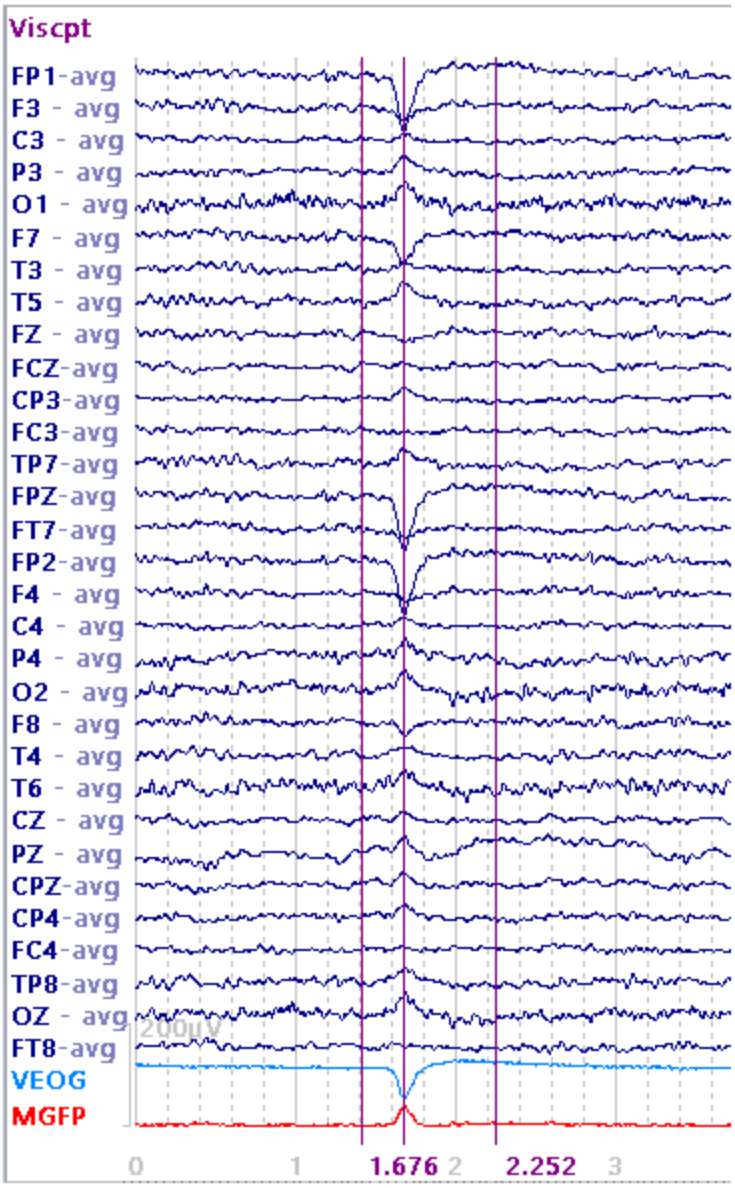
1. First we need to select the CAR (Common Average Reference), for the reasons described just above. From Channel Groups / Bad Blocks, select **Add Rereferencing**.



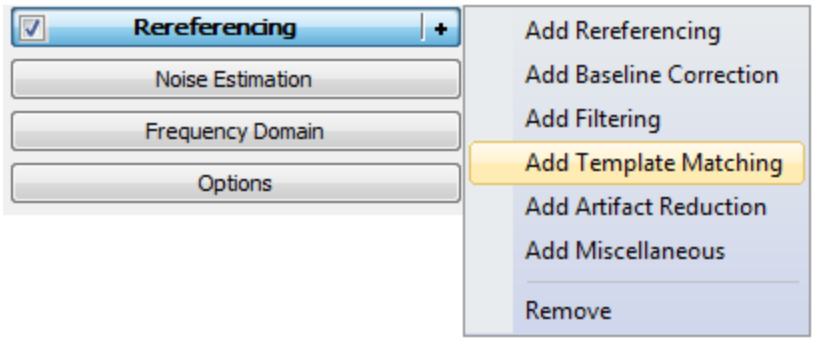
Select the **CAR**.



2. The next step is to define the template. Set the two outer cursors around a blink.

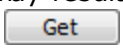


3. From the **Rereferencing** list, select **Add Template Matching**.

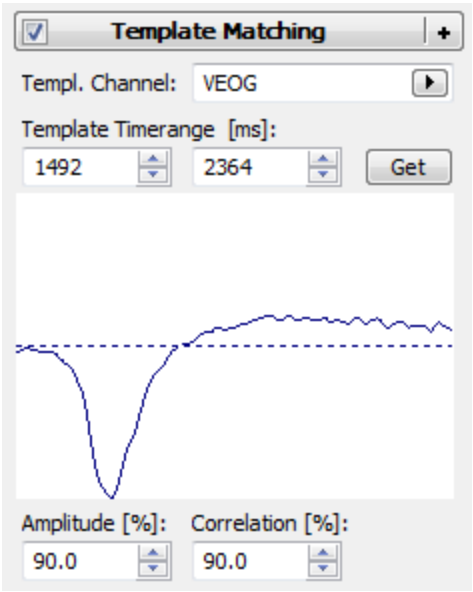


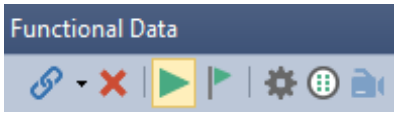
In the

panel, select the **VEOG** channel. The cursor positions will be seen in the **Template Timerange** fields, and the artifact will appear in the window. If you change the cursor positions, you would need to press the

button to have them transferred. If you select a channel before setting the Timerange, the program will use wherever the cursors are positioned, which may result in spurious matches. Reposition the cursors, if needed, and press 

to use the current positions.

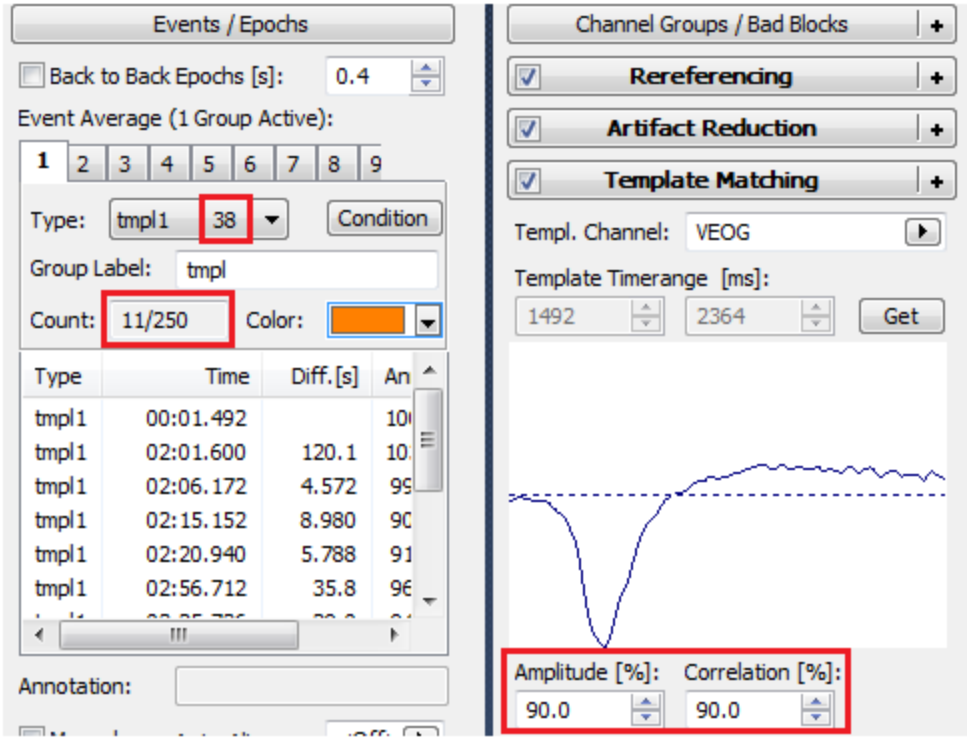


Now click the flashing **Scan Templates** 

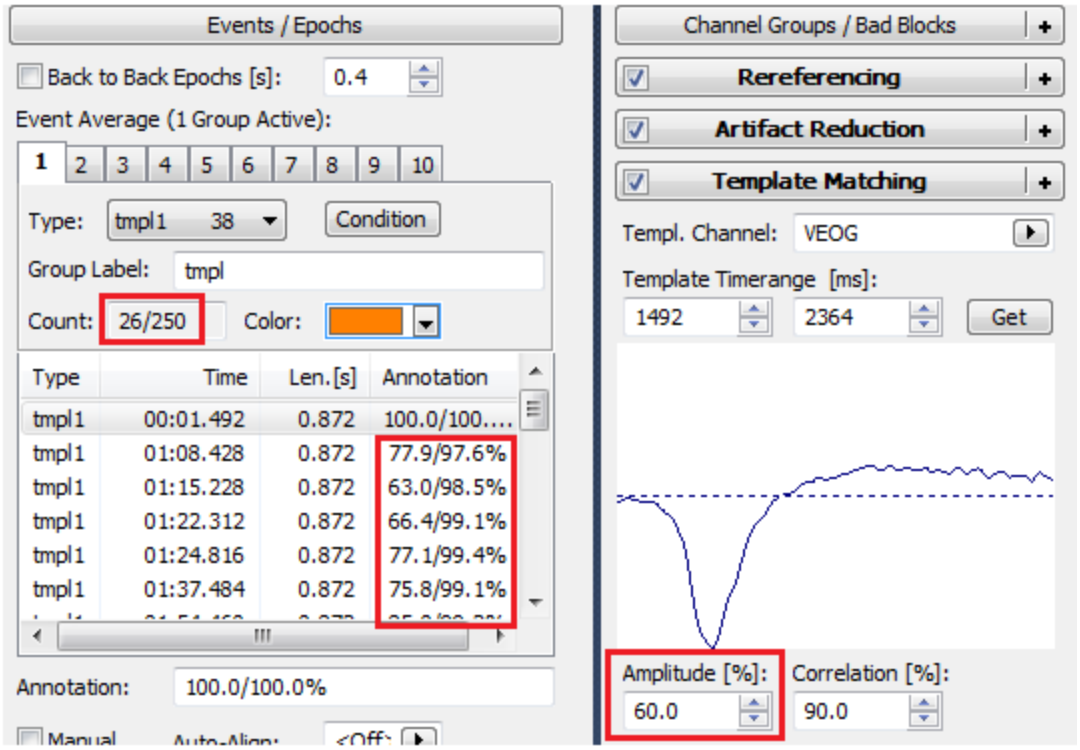
icon at the top of the Functional Data panel. As with other "Scan" buttons, the flashing means that the file has not been scanned yet. Once it has been scanned, you will see the non-flashing green arrow . If you change a parameter that would affect the scan results, such as, changing the Timerange or Channel (or reference, baseline correction, filtering, etc.), the flashing button will reappear and you will need to scan the data file again.

4. Select the

display, and set **Type** to **tmpl1**. We see that 11 blinks have been detected using the **Amplitude** and **Correlation** criteria set above (both at 90.0%). The "38" means that 38 blinks were detected using the lowest Amplitude (30%) and Correlation (50%) criteria. (Your counts may vary, depending on the bad blocks that you have designated). The 250 means that there are 250 total events in the file. The numbers in the **Annotation** field are the Amplitude and Correlation values for the template and each match. If you see the Difference in the third column, rather than the duration, or Length, *right click* on the header and select deselect **Show Durations**, if desired.

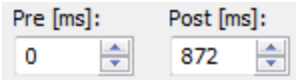


If we decrease **Amplitude** to **60%**, we pick up many more of the blinks. Note that the correlations are all quite high. You can move through the data file to see the blinks that were accepted (use to see just the selected events).

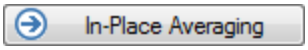


It is not necessary to capture all of the blinks; we will be performing PCA on the average of the ones that were detected. The Event list shows that 26 blinks were detected.

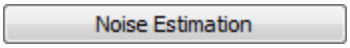
5. To average the blinks, enter the values for **Pre [ms]** and **Post [ms]**. In this case we are using the same values for the blinks that were detected. This is found by looking in the **Length** field in the event list (*right click* in the list and select **Show Durations** of you do not see **Length**). You can use other latencies as well.



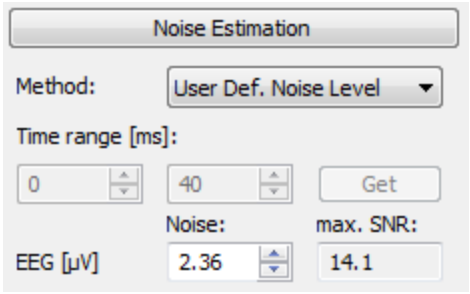
In this case we know the artifacts are well correlated, and looking through the file showed no unusual blinks, so we will not use any of the epoch rejection methods.

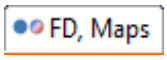
To average the blinks, click the 

button.

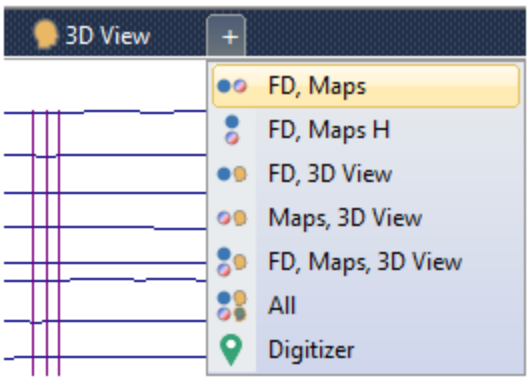
In the figure below we have made several selections. First, when saving the PCA results, as we will be doing, it is necessary to select **User Defined Noise Level** for the **Method** of **Noise Estimation**. Go to 

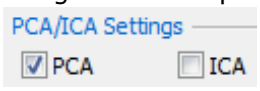
(Functional Data) and select **User Defined Noise Level**.



The 

display was then selected.

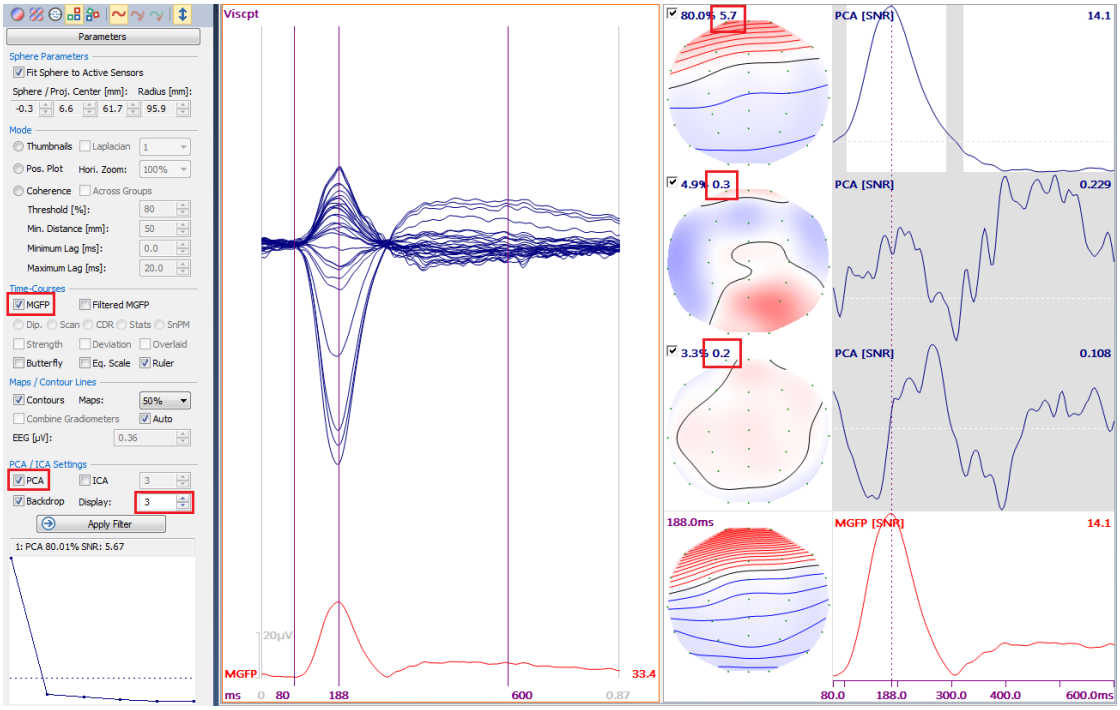


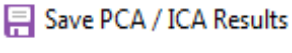
Butterfly Plot was selected for the Functional Data. We used the two outer cursors to set the Timerange to encompass the main part of the blink (80 to 600 ms). We selected 

for the display (in the **Parameters** panel under **Maps**), and set the **Displayed Components** to **3** (only the first one has an SNR > 1.0; SNRs < 1.0 become questionable). As you reposition the outer cursors, you will see the effects immediately in the PCA display. The number of the Displayed Components is also the number of PCA components that will be saved.

was added to the Maps display.

What we are looking for here is to make sure the first component represents the blink, which it does. Then we look at the SNR values for each component (5.7, 0.3, 0.2). Your values may vary slightly (due to the Bad Blocks you selected). The "scree" plot in the lower left corner shows the SNRs graphically (the dotted line is where SNR = 1.0). We also look at the peak of the MGFP to ensure that the contour maps show a distribution consistent with blink artifact.



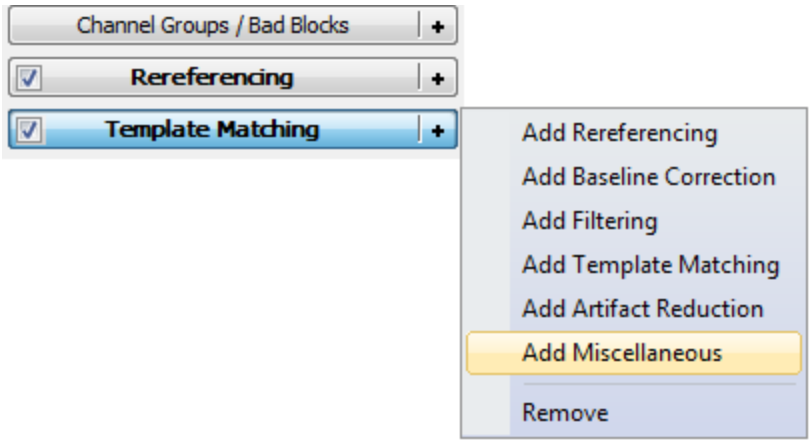
To save the results, go back to the **Workflow** and click on the 

line, or go to **Maps** → **Save** → **Save PCA Results**. Select a folder and enter a file name (*viscpt blinks.pca*). (Save the file to a convenient location, such as your Desktop).

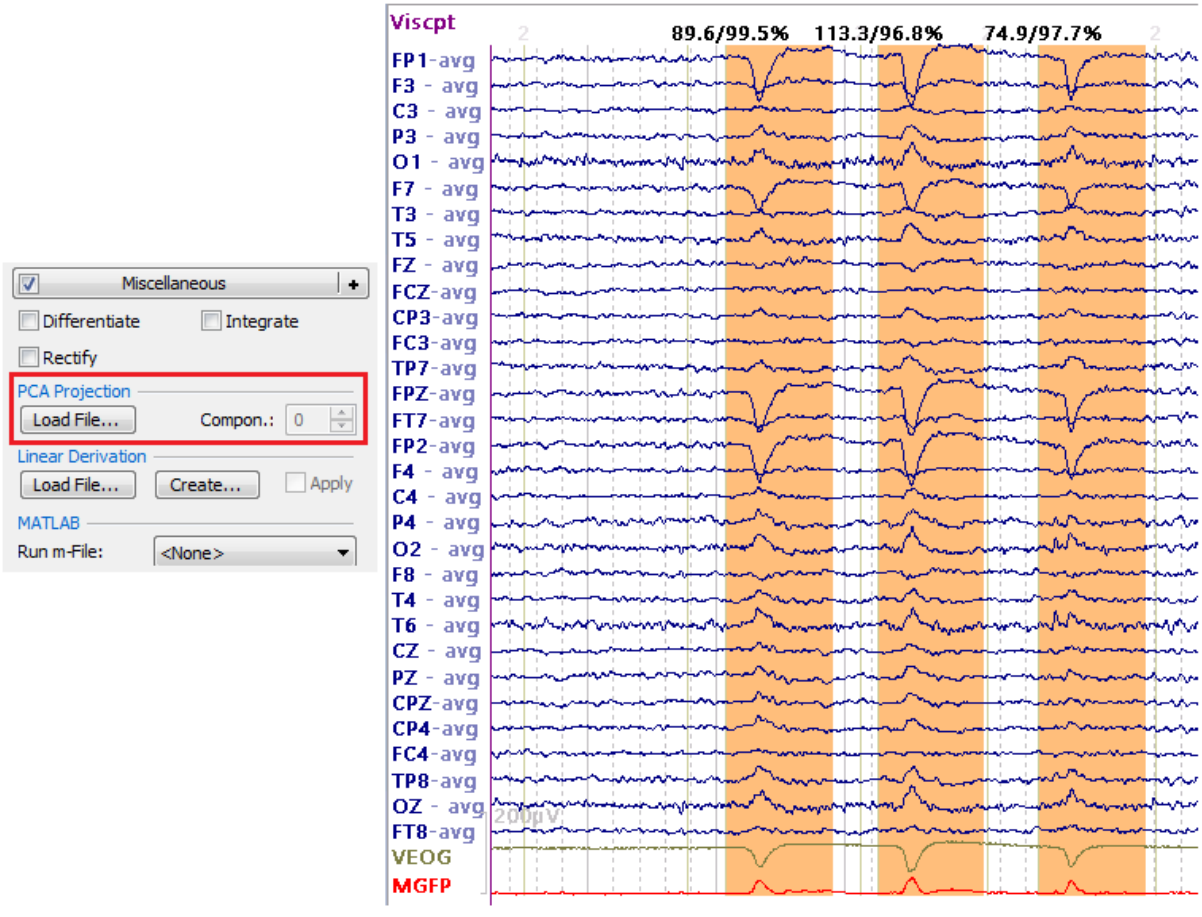
6. Now click

(**Events/Epochs**) to return to the original continuous data.

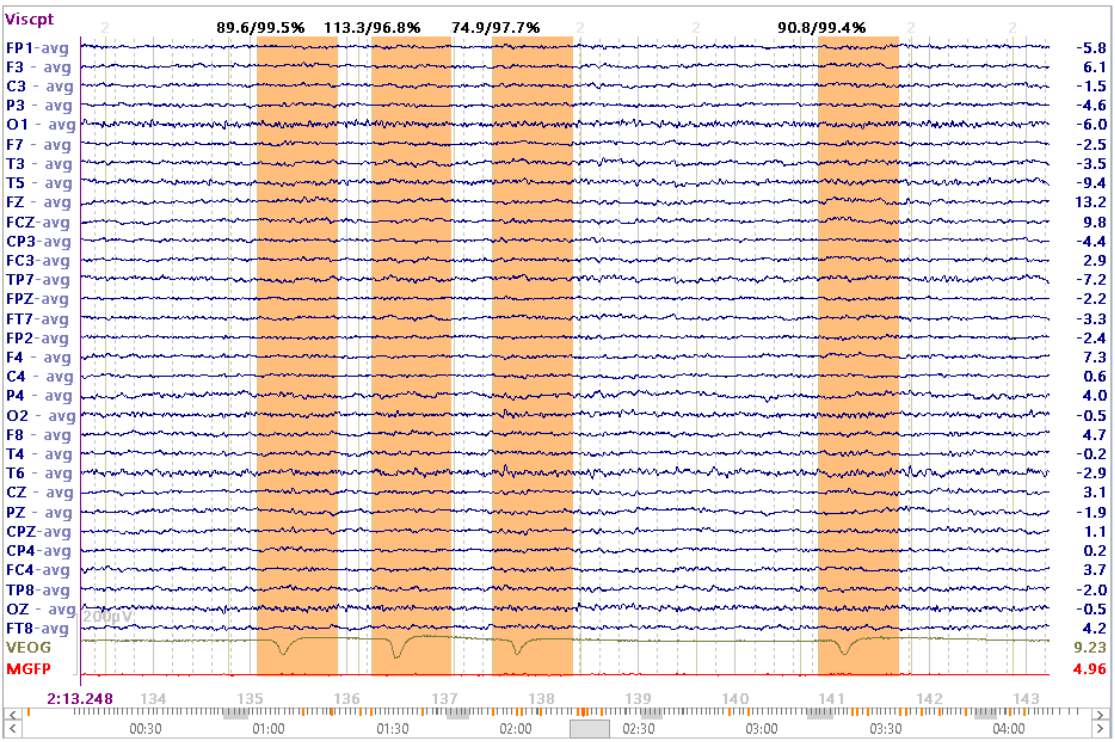
7. From the **Template Matching** list, select **Add Miscellaneous**.



In the **PCA Projection** area, click the **Load File** button and select the file that was just saved. Set **Components** to **0**, and go to a section of the file that has several blinks, such as 135-142 seconds.

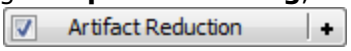


Then increase the number of **Components** until the blink is reduced (**1** is safest in this example). The correction is applied globally.

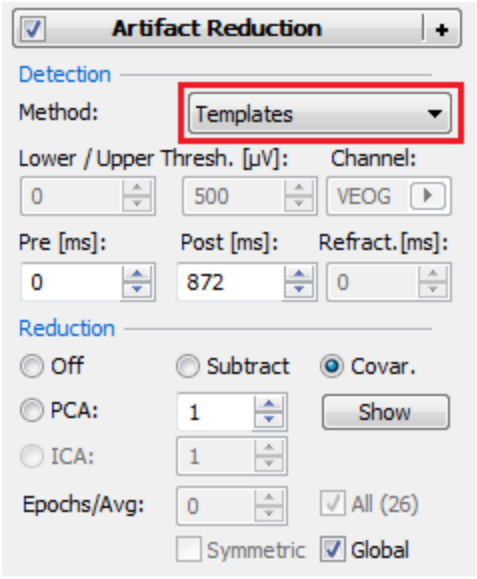


From here you can go on to average the stimulus events to create the ERPs, etc.

The above steps illustrate some of the methods that can be used to reduce not only blinks, but other artifacts as well. With this data file, where we were simply reducing the blink artifact, there were several ways we could have done it, and the results - the averaged ERPs - would have all been very similar. With other files and other types of artifacts, there may be just a single method that will work best, so it is useful to be aware of the possibilities.

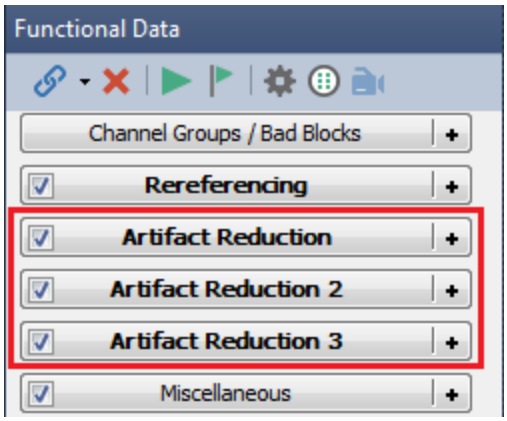
For example, we could have detected the artifacts using **Template Matching**, as above, and then selected the **Templates** option under 

.



The only difference here is that the PCA is performed automatically, where there is no opportunity to fine-tune the Timerange and view the PCA results in detail.

Using Multiple Processing Sequences
You may find that you frequently use multiple Processing Sequences to remove more than one type of artifact. You do this by configuring multiple **Artifact Rejection** sequences (the same may be accomplished with multiple **Template Matching** sequences).



There are a few things to understand in order to use the sequences correctly.

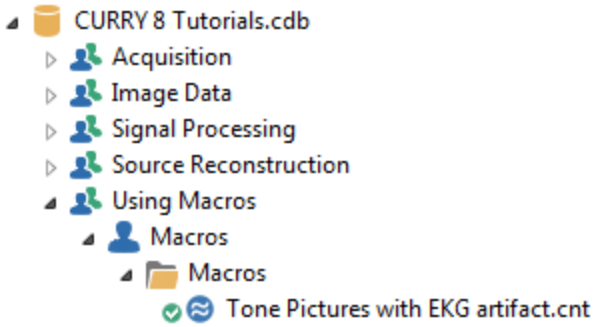
First, when you click the flashing button, each sequence will be scanned, in order. The results of the first pass will be applied to the second sequence, and so on.

Second, if after scanning you change a parameter in the Artifact Detection section, that will affect the results of the current and all subsequent sequences.

Therefore, the button will revert to the flashing button, indicating that you need to rescan the file. If after scanning you change other parameters, including filtering, the reference, baseline correction, etc., these will also affect the scan results, so again the flashing button will appear and you will need to rescan the sequences.

Third, if you select the **All** and **Global** options prior to scanning, any subsequent sequences will use that data. If you enable All and/or Global after scanning, then any subsequent sequences must be rescanned (and the Scan Artifact button changes accordingly to let you know).

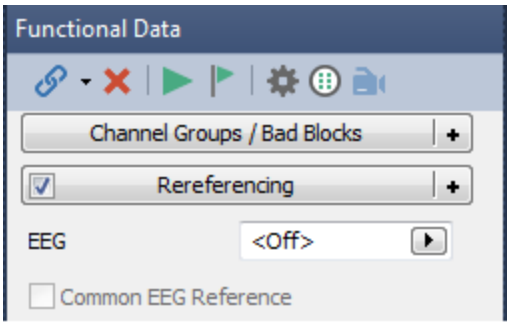
The following example illustrates these points. Open the indicated Study.

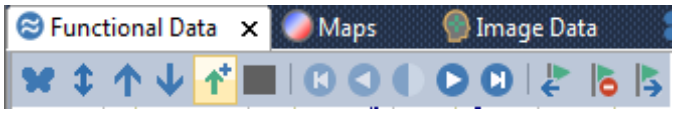


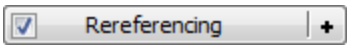
This file contains pulse artifact and occasional blinking. We will set up two Processing Sequences to reduce the EKG and blinks.

1. There are several bad, unwanted, or unused "Other" channels: A2, X1, X2, H+, H-, V-, and EKG- (leaving only V+ and EKG+). Click on their labels to deselect them, and then remove them by deselecting Show Deselected Channels under Options (for Functional Data). If you do not see them, enable Show Other Channels under **Options**.

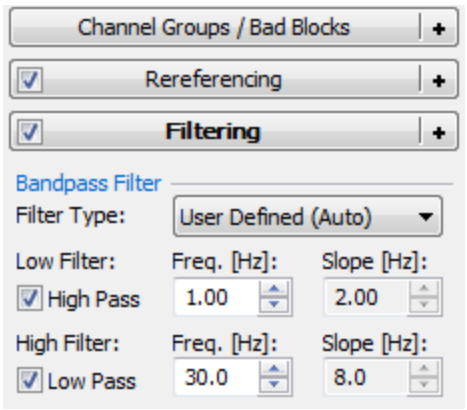
2. If needed, change the **Reference** to **<Off>**. (Click the + at the end of Channel Groups / Bad Blocks + to see the **Add Rereferencing** option).



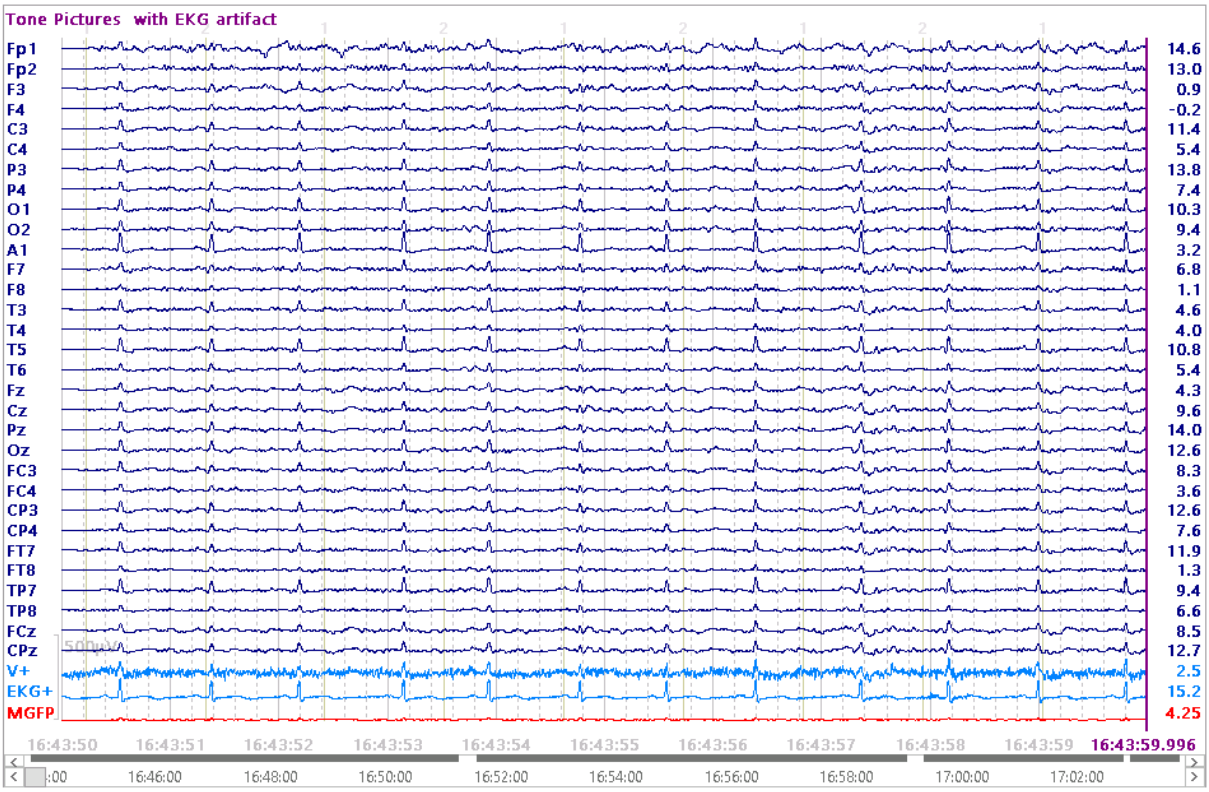
3. Invert the polarity: 

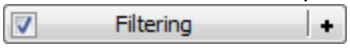
4. Filter the data from 1-30 Hz. (Click the + at the end of 

to see the **Add Filtering** option).

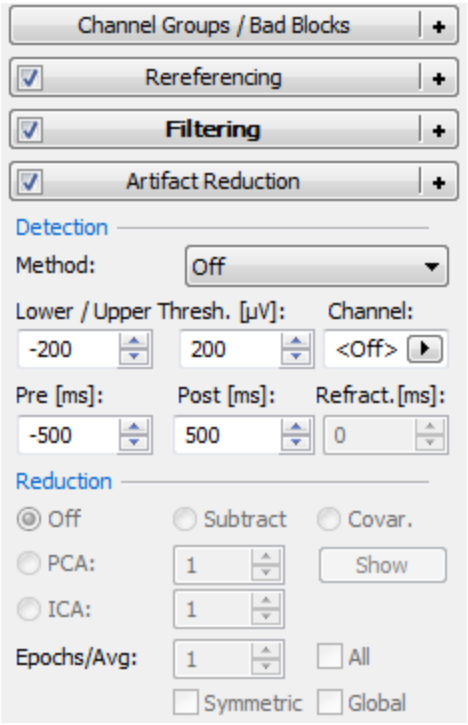


5. With rescaling, the data should now appear as shown.

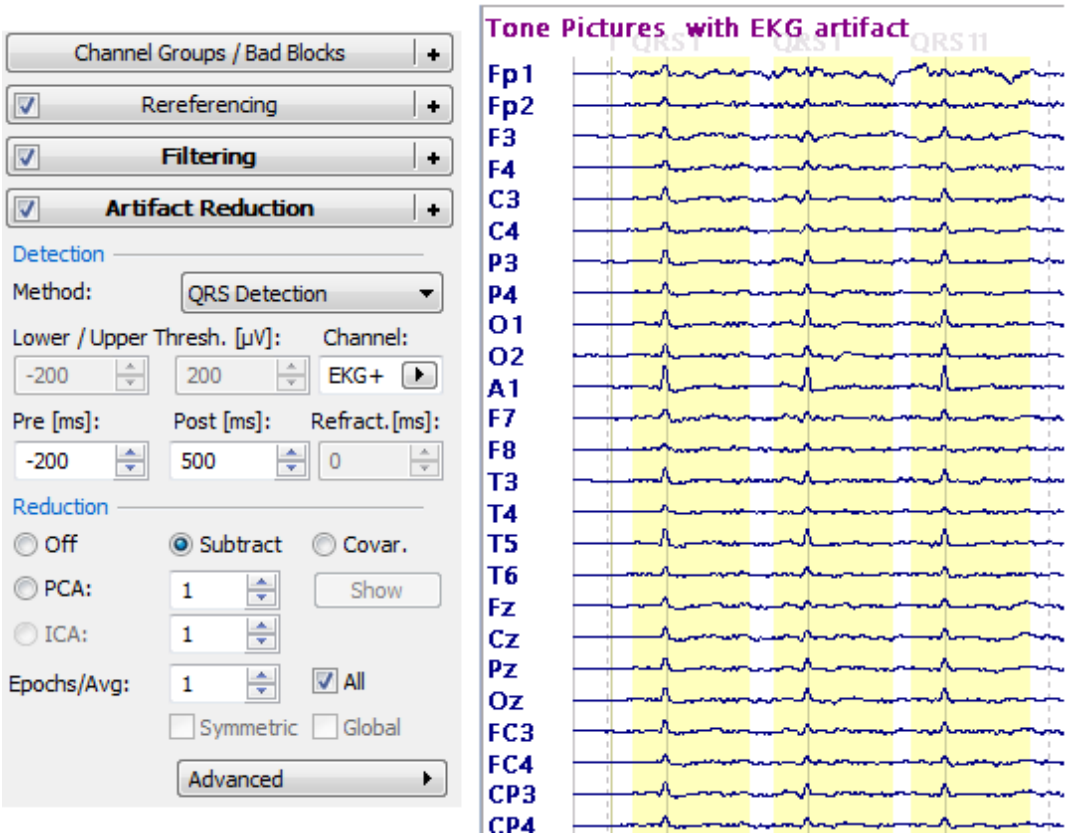


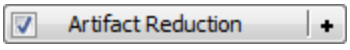
6. We will set the first artifact reduction sequence for the EKG artifact. (Click the + at the end of 

to see the **Add Artifact Reduction** option).



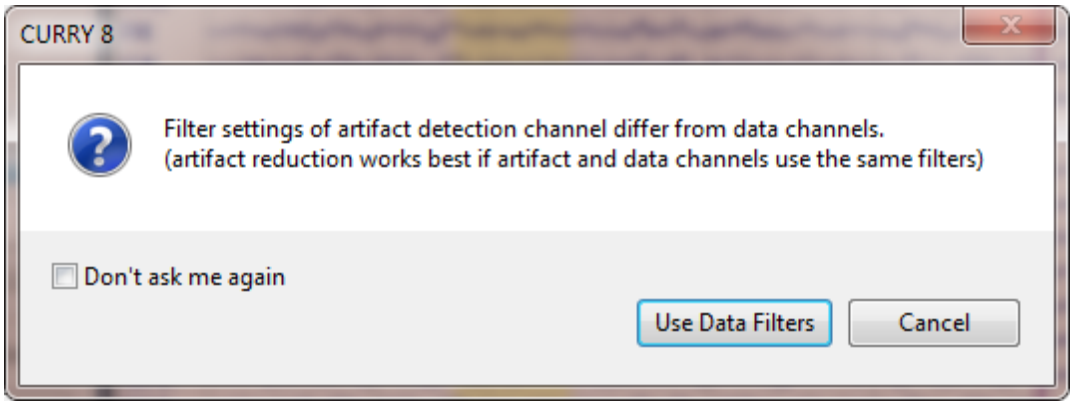
Enter the values as shown. You will see each pulse artifact with a yellow background, as determined by the **Pre** and **Post [ms]** times.



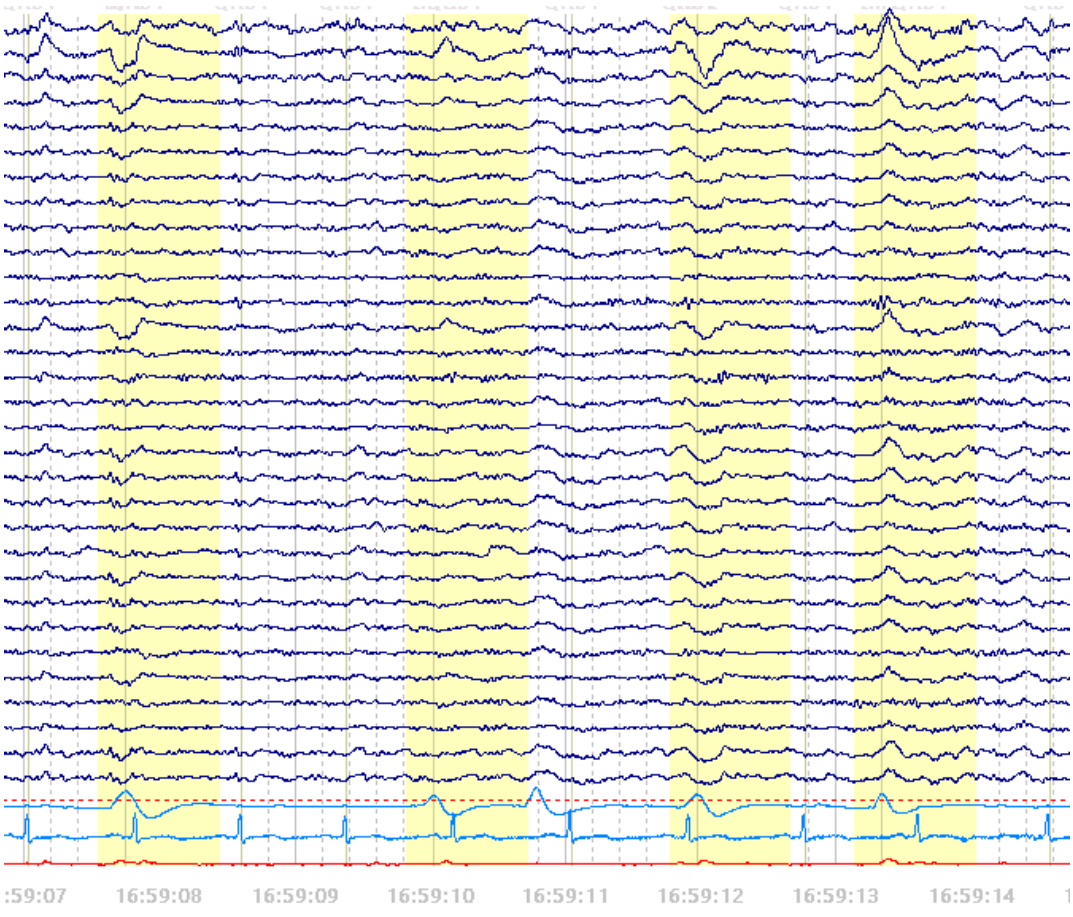
7. Click the + at the end of  and select the **Add Artifact Reduction** option again. Go into the file to about 35 seconds until you see the first blink. Set the parameters as shown.

8. Now click the flashing icon at the top of the Functional Data panel. The file will be scanned twice - once for EKG and once for blinks.

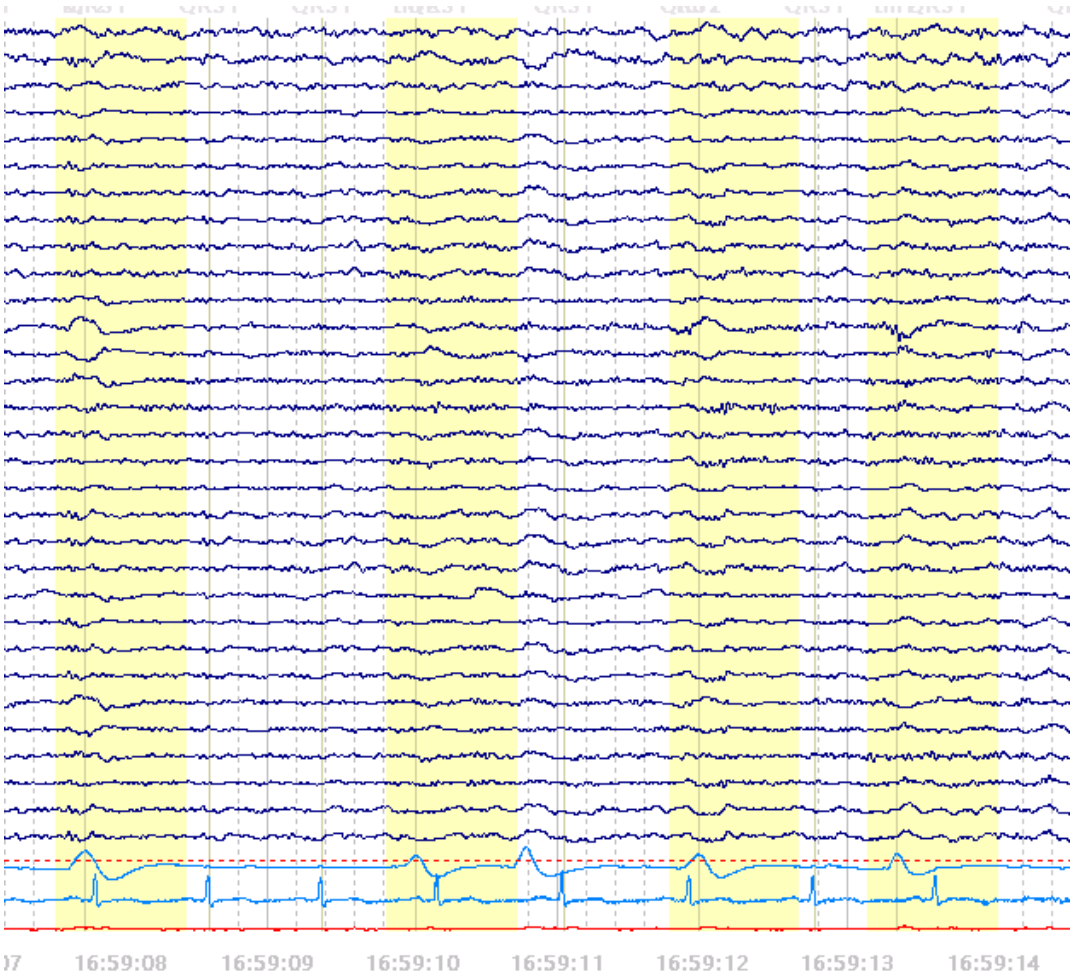
You will see the following message, saying the filtering is different for the blink channel(s). Click **Use Data Filters** to apply the same filtering to it. This will require rescanning of the last sequence.



9. In looking through the file, we see that there are some sections where the correction was not optimal.



In that case, try switching to PCA, with a single component, to see if the reduction improves, as it does. No method is 100% effective with all files, or throughout a given file. It will take a little trial and error to determine which reduction method works best with your data files.



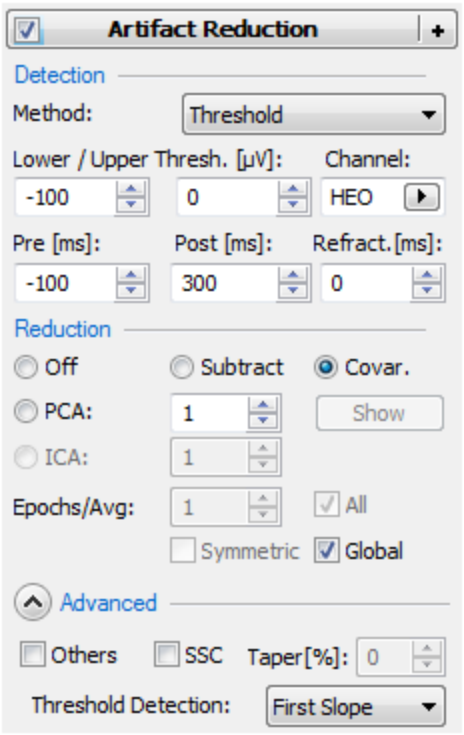
10. The file is now ready for further processing. To make a point, let's say that we now realize that we should have filtered the file with a 20 Hz LP filter instead of 30 Hz. Go to the **Filtering** panel and make the change. You will see the flashing icon at the top of the Functional Data panel, meaning that it is necessary to rescan the file. Anytime you make a change that will affect the results of the scan(s), you will see the flashing arrow indicating you should rescan the file.

Horizontal Eye Movement Reduction

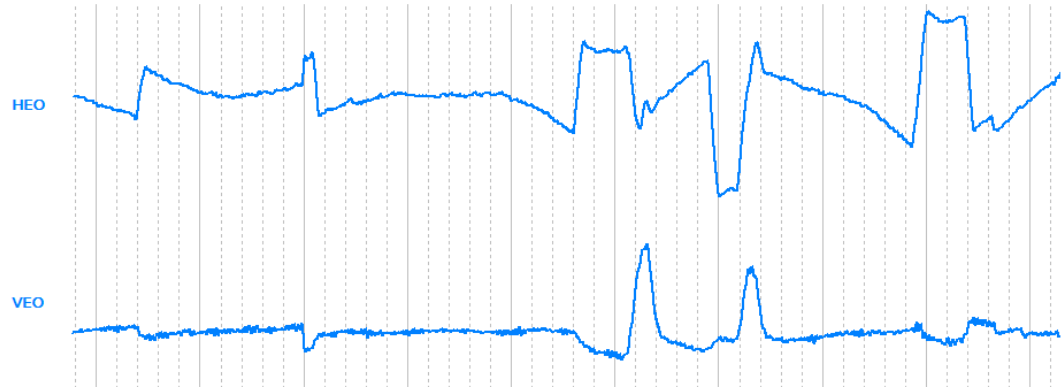
Generally, horizontal, or lateral, or saccadic eye movements are better avoided than reduced. This is usually accomplished by having a fixation point (eyes open recordings), or by asking the person to try to focus on a spot on the wall

(with eyes closed), and reminding them to fixate when you see their eyes wandering in the recording. In some cases, however, the subjects may be less compliant, or the eye movements may be an integral part of the study. In these cases it is necessary to reduce the eye movement artifacts in the EEG channels.

If you get lucky, you may find that all or at least most of the lateral eye movements are similar, as shown. If that should happen, you can use parameters similar to those shown. You do not need to capture the entire artifact - you want to use the most stable section for the Covariance computations. If possible, filter the EEG and artifact channels first (using the same parameters). You will be asked if you want to do this when you select **Covar**. You may also want to select **First Slope** for **Threshold Detection**. Otherwise, the maximum value between the two threshold crossings will be used (if you have selected **Peak**).

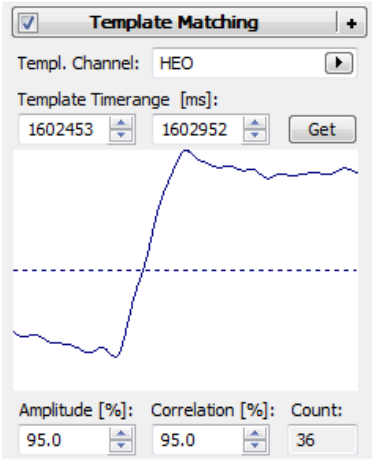


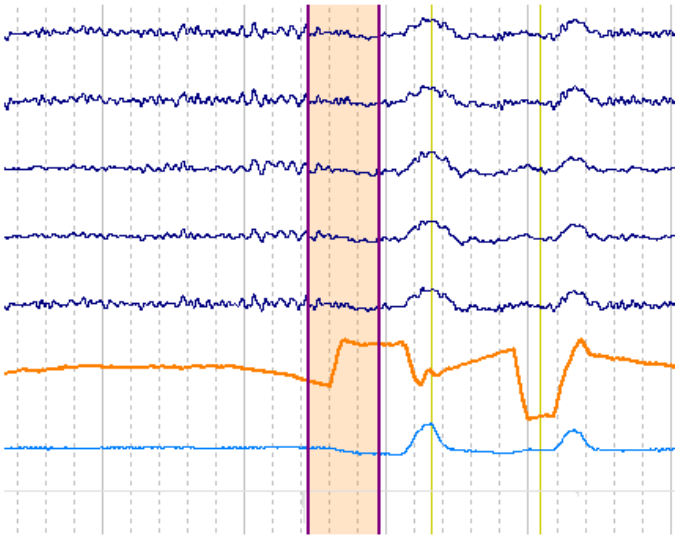
More likely, however, you may see all kinds of movements and blinks combined in the recording.



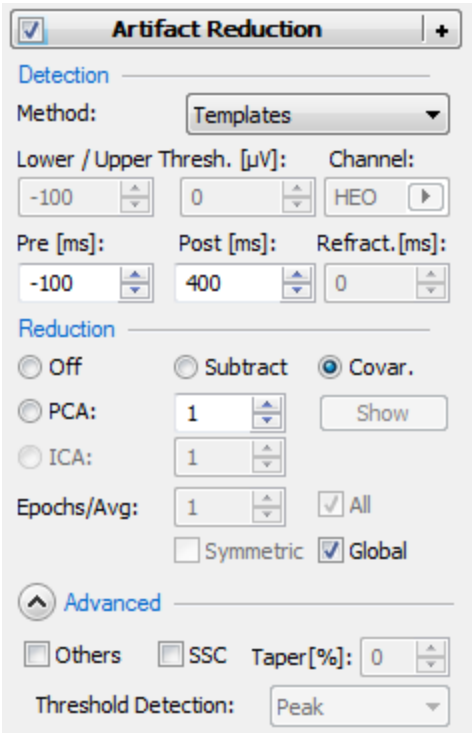
The *blinks* can be reduced as usual, using the **Threshold** option, as described above. A voltage threshold for the HEO channel will not be as effective. In this case, the best thing to try is **Template Matching** and then **Artifact Reduction**.

Start by **Filtering** the EEG and artifact channels using the same parameters. After that use **Template Matching**. For the template, select a segment of a regularly occurring artifact, such as shown below. For the covariance analysis, you only need a stable part of the artifact. It may help to increase the **Amplitude** and **Correlation** criteria to select only the most similar examples. Ideally, you want the averaged artifact to be as clean as possible, as this will result in the best correction factors (linear transmission coefficients, similar to beta weights). In reality, however, the **Covariance** transform is extremely robust, and sufficient results can be obtained with very few artifacts in the average artifact, or even just one! Then **Scan** the file for matches.

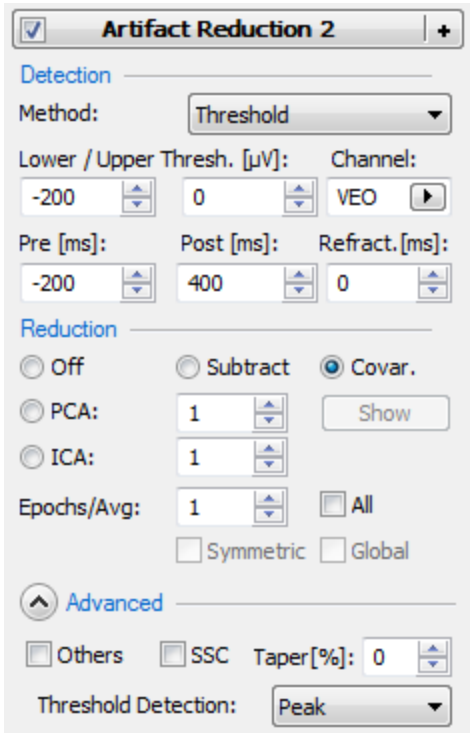




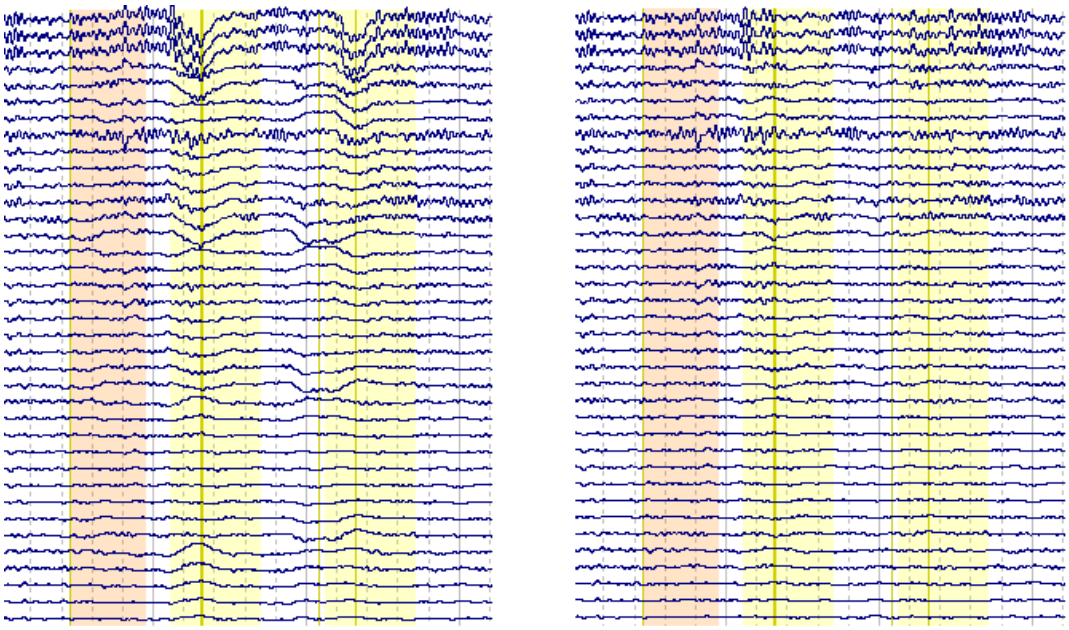
Then use **Artifact Reduction**, where you select **Templates** for the **Method**. Use **Covariance**, with **All** and **Global** selected for Reduction. The **Pre** and **Post** parameters will vary depending on what you selected for the template interval.



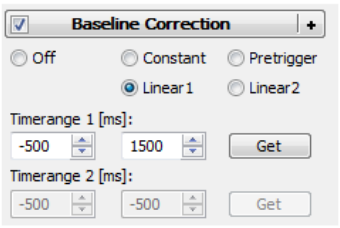
Use a second **Artifact Reduction** to reduce blink activity, as usual.

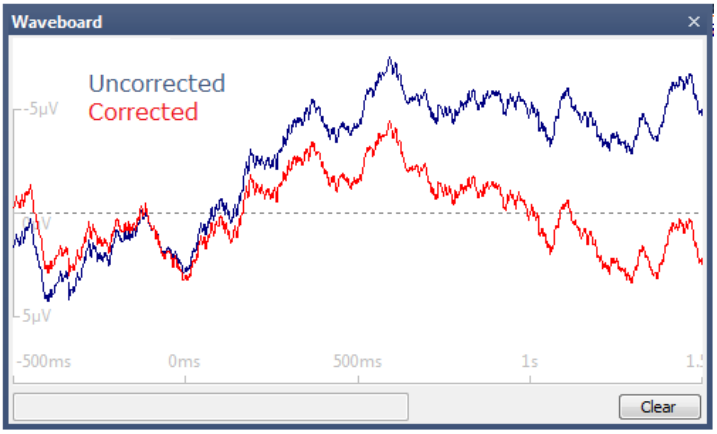


Below are the results following both reductions, with the original data on the left and the corrected data on the right.



Despite your best efforts to reduce the eye movement artifact, it is not uncommon to see some residual artifact. If you go ahead and average the epochs, the artifacts may average out, or become even more reduced. Even then, however, you may still see residual artifact in the averages, and this will appear as drifting, usually in the fronto-temporal channels (F7 shown below). This can be reduced further if you use the **Linear** option(s) under **Baseline Correction**. This subtracts out the linear component, if present. In this example, the entire interval was selected; you may find that another interval(s) works better with your data.





These steps have been shown to effectively reduce eye movement and blink activity in the files we have tried. You may need to adjust the parameters as needed to get the best results with your files.

2.4.5 MRI Gradient and Ballistocardiogram Reduction

It is helpful to keep in mind that any given EEG channel that is recorded in the magnet will contain three or more separate signals that are combined into the single signal that

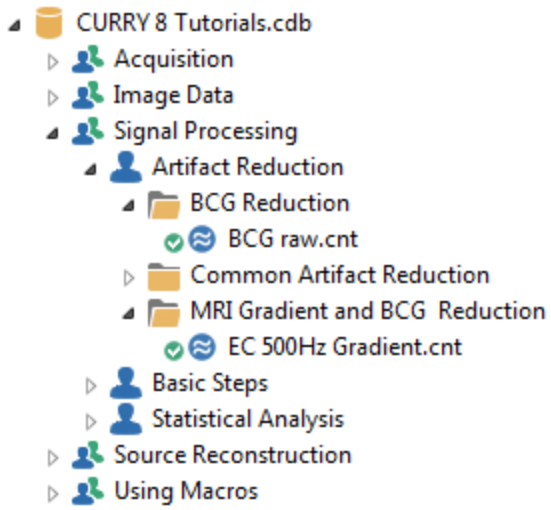
you see. First, and having the greatest amplitude, is the gradient artifact. That must be reduced in order to see the other signals, and this needs to be accomplished without distorting the remaining signals. Next in voltage (typically) is the ballistocardiogram (BCG) wave, which is an exaggerated EKG signal. While the gradient artifact is in most cases a fairly stable artifact across TR blocks, BCG can be fairly stable across the recording, or it can vary, sometimes appreciably throughout the recording. After reducing the BCG, you are left with the EEG, which if course is constantly varying. Additionally, you may encounter pump noise artifact that appears as bursts of faster frequencies. The task is to reduce the various larger artifact signals while preserving as much as possible the lower amplitude EEG signal. Given that there are typically more variables than constants, this can be an imperfect equation to solve, and the goal is to get the best EEG possible, realizing that it may not be possible to obtain completely unaltered EEG signals.

Removal of MRI gradient artifact is generally a straight-forward procedure, when there are events placed accurately at the beginning of each TR Block and the artifact does not vary across blocks. TR Blocks are averaged together and then subtracted from subsequent TR Blocks. The artifact subtracts out, leaving the EEG and BCG. Reducing BCG is more challenging, as the BCG artifact can vary across time.

There are two general approaches you can take. One, you can focus on reducing the gradient artifact first, and then save the gradient corrected continuous data. Retrieve that file and then reduce the BCG. In the other method, you reduce the gradient artifact and then the BCG without saving the continuous data in between. Why not just do it the latter way? Reducing BCG is more challenging, there are different approaches you can try, and it may take some experimentation to find the best combination of parameters for your data. If you want to go back and change some previous parameters, that may affect the gradient correction as well, requiring you to do it over again. Sometimes its easier to start with the gradient corrected file, and then focus solely on the BCG.

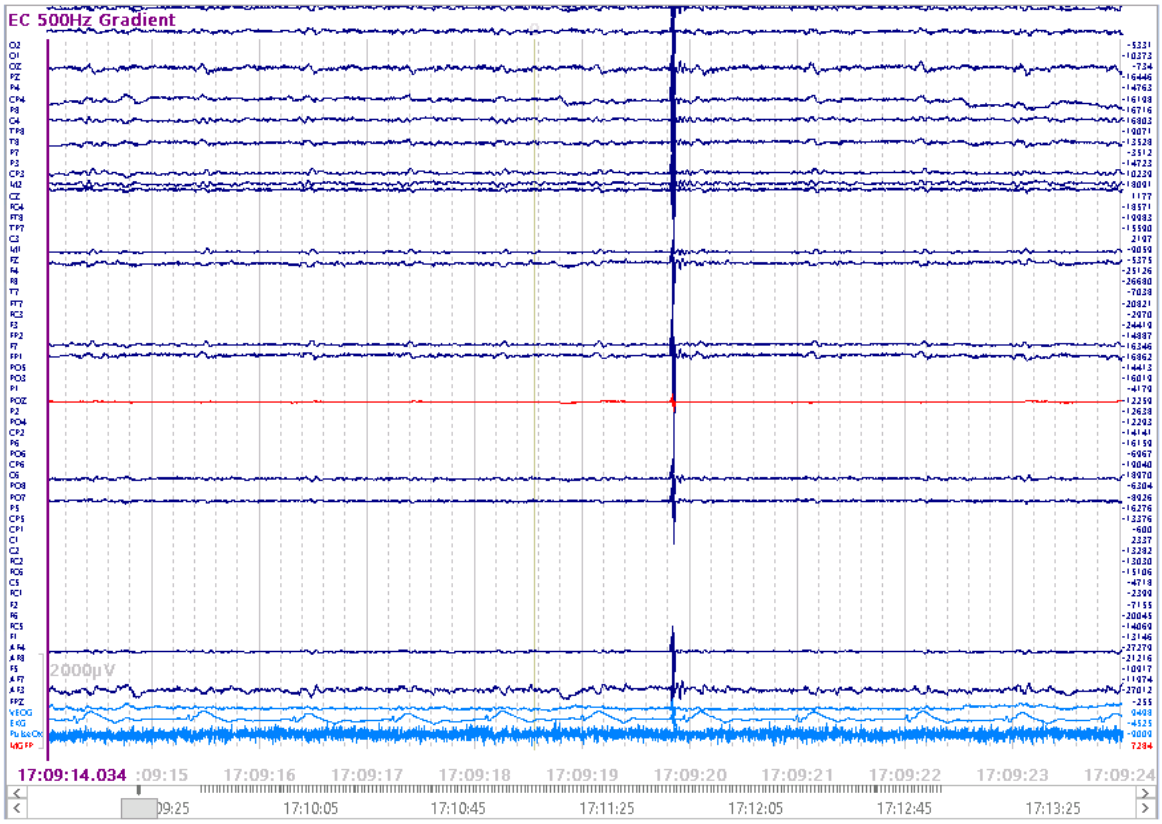
For this example, we will use the former method first, then briefly show the steps for the latter method.

There are two Studies containing separate data files that we will look at. These are found in the *CURRY 8 Tutorials* Database, as shown below. One has gradient and BCG artifact; the other has BCG artifact only (the gradient artifact was removed previously).

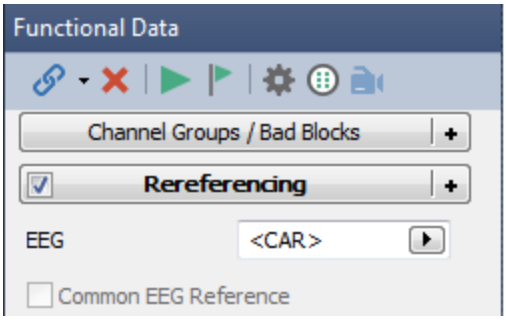


Gradient Artifact Reduction

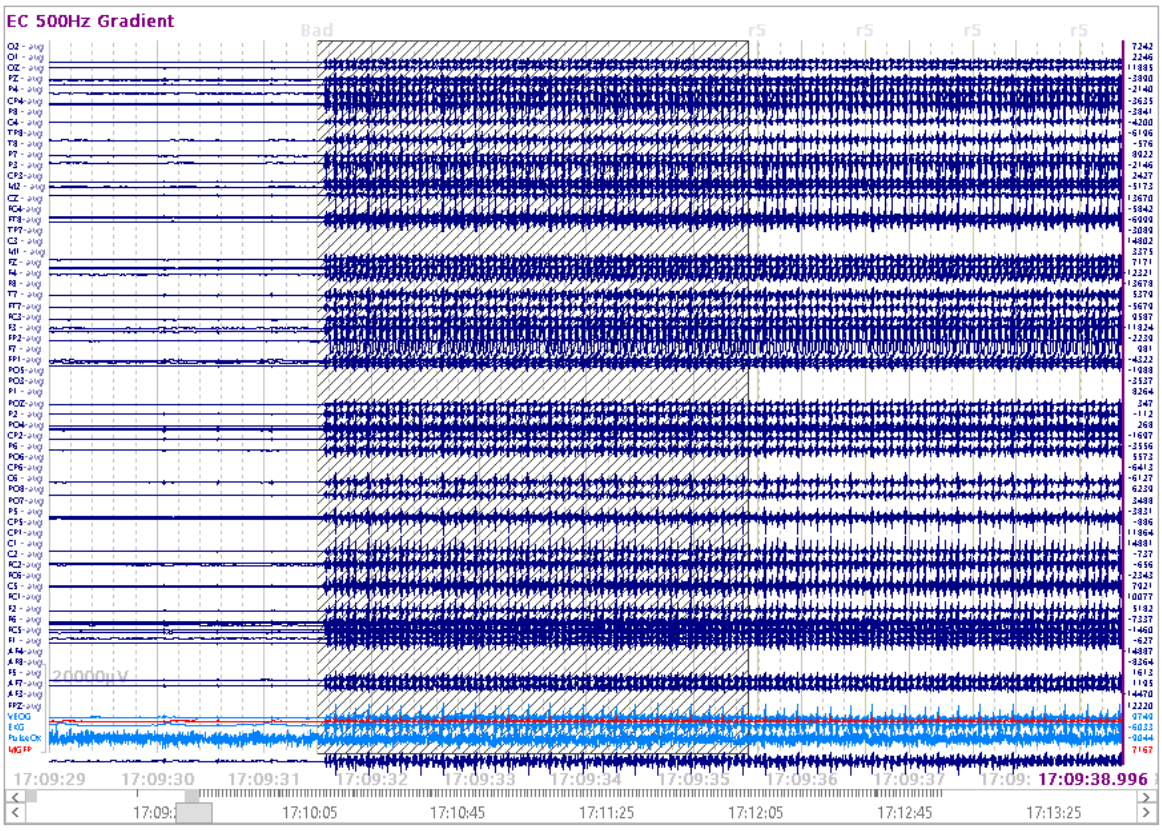
We will demonstrate with a representative file recorded at 500 Hz (with clock synchronization). The start of each TR Block is indicated by a response event Type 5, and the TRs are 1000 ms in duration. The first figure below shows a section prior to the gradient artifact, using the *EC 500 Hz Gradient.cnt file*. Baseline Correction is not recommended with gradient reduction, and may adversely affect the results. The DC offsets will be removed in the correction process.



1. If the file does not appear with a **Common Average Reference** (CAR), select it from the **Rereferencing** panel (which you may need to add to the list).



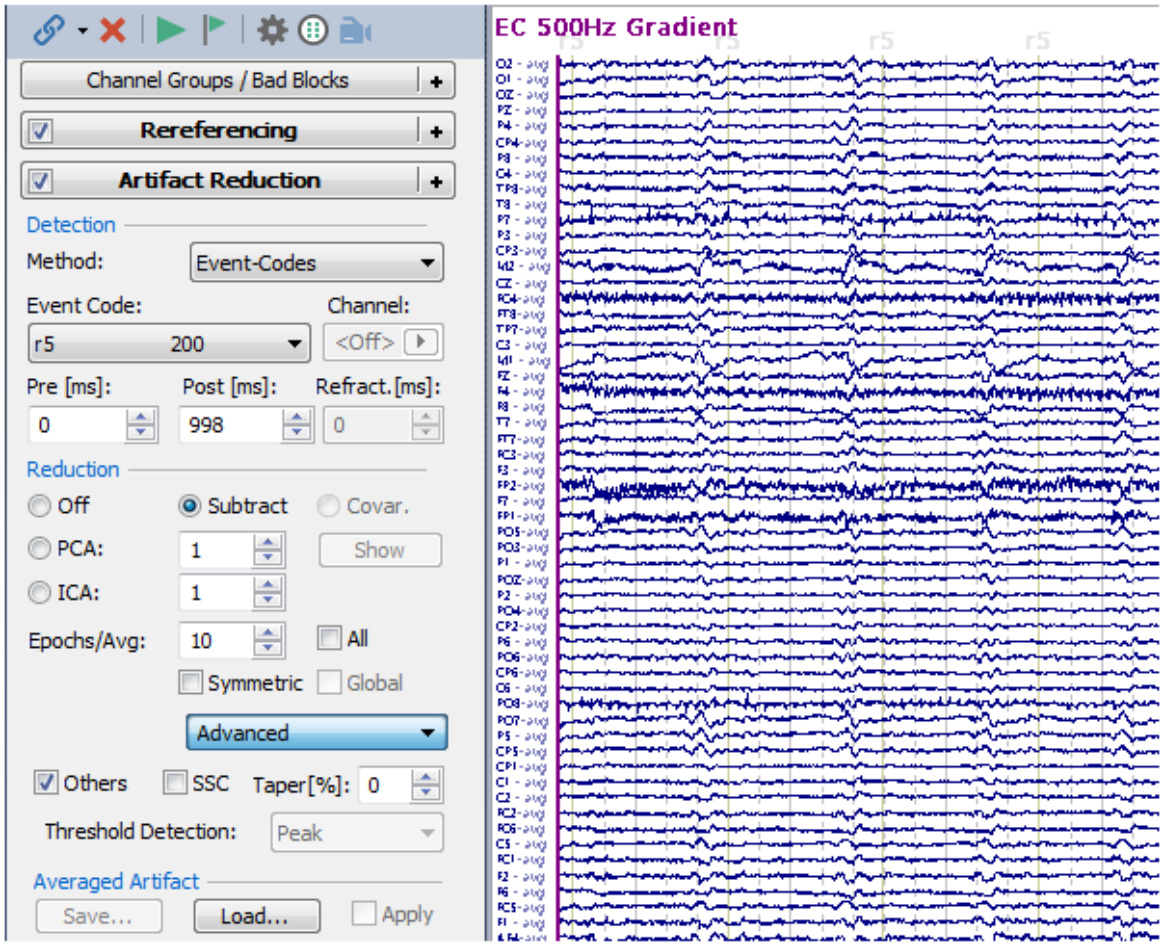
2. We will now go through the file, designating any bad sections (using **Mark Block** ; see for example **Common Artifact Reduction**, step 2). There are just a few bad sections in the file, including one at the very beginning. Note that the gradient artifact actually starts before the initial r5 event. We will mark that section as a bad block to exclude it from subsequent analyses. Deselect the button when finished.



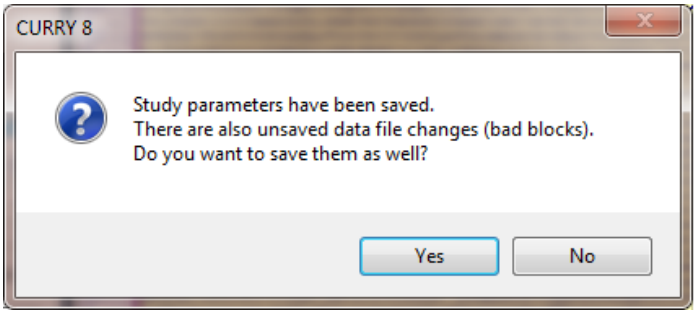
3. To reduce the gradient artifact, add an Artifact Reduction panel and select **Event-Codes** for the **Method**. Select the **r5** events. In this case, the TR Blocks are **0** to **998**ms (zero-based scale). Set **Epochs/Avg** to **10** (or larger number - even numbers recommended) and select **Subtract**. When the events are r5's (as opposed to some other event), CURRY will autodetect the TR interval and set the Pre and Post

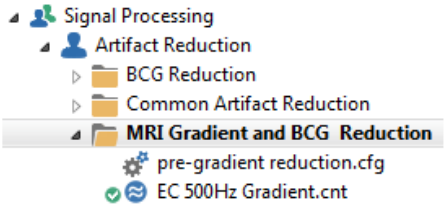
times automatically. The **Others** option is enabled, as these are the typical settings you would use (to correct the Others channels also). **SSC** (SubSample Correction) is not needed with this file; it is used when there is jitter in the placement of events with respect to the artifacts.

Move to a middle section of the file and see the greatly reduced gradient artifact.

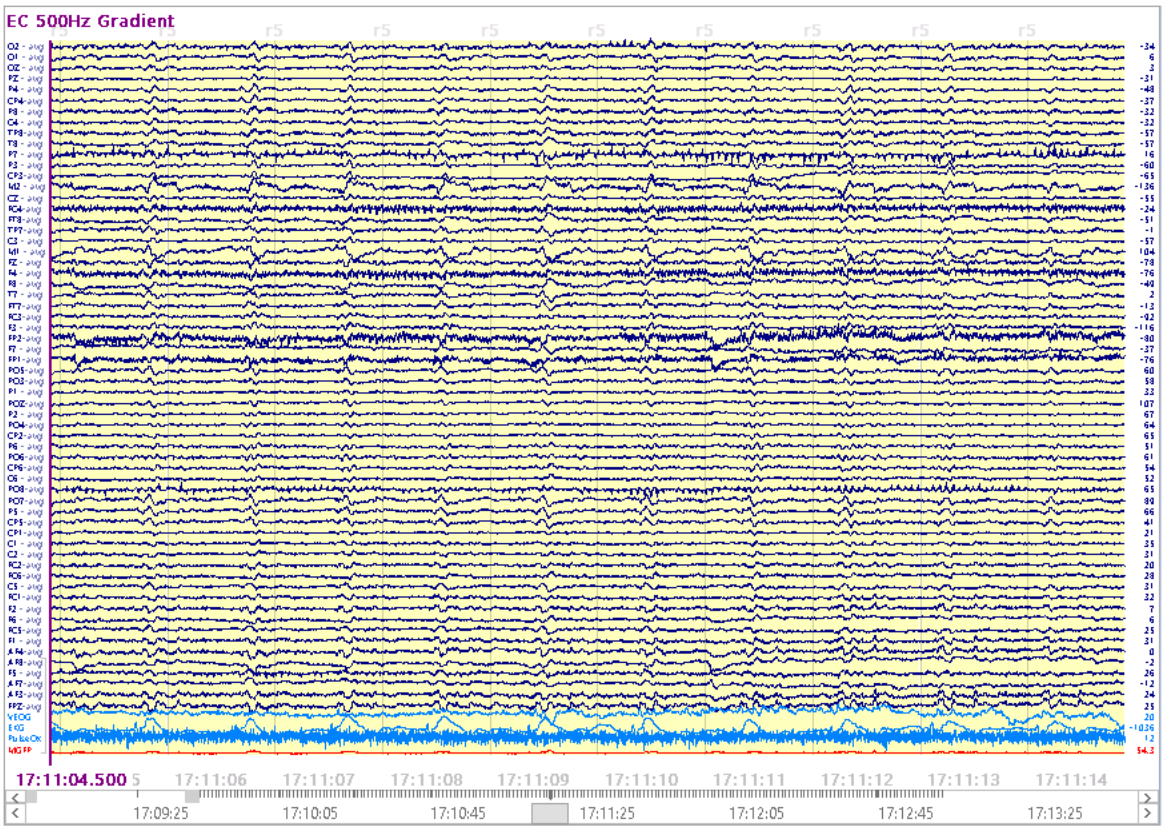


3. This is a good point to save the **Study Parameters** (click and enter a file name, *pre-gradient reduction.cfg*). When you open the file again, everything to this point will be preserved. You will be asked if you want to save the Bad Blocks - say Yes.

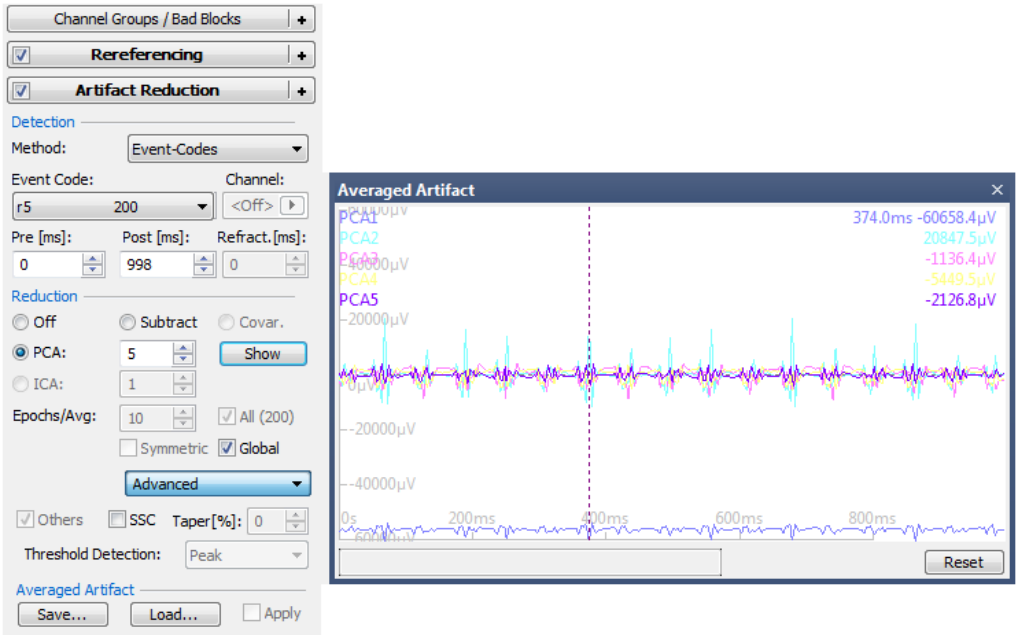




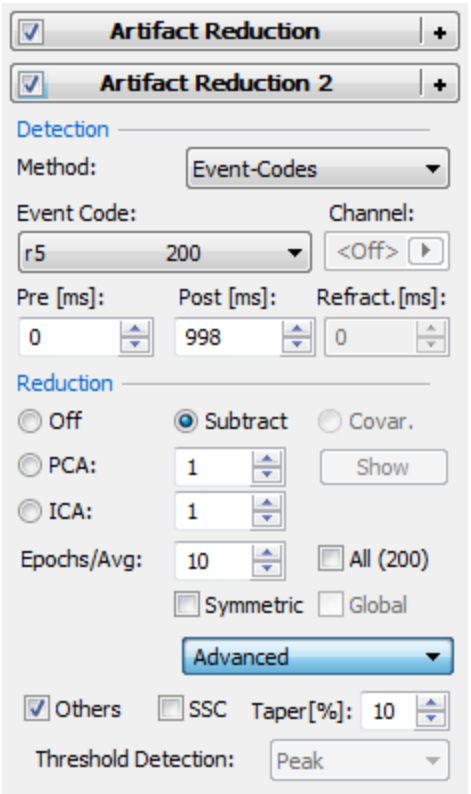
4. Now click the flashing Scan Artifact button . When the scan has been completed, move again to a middle section of the file. The artifact is now removed. No filtering has been applied (note the fast activity), and BCG is seen.



We will digress here for a moment to mention a modification to the above procedure. In this variation, do a PCA analysis first, followed by the usual Subtraction method as the second step in the Artifact Reduction sequences. For the PCA step, use the regular TR interval. Click the **Show** button to see the 5 components, and decide how many represent the gradient artifact (which may well be all 5). After scanning, use All and Global (or whatever works best).

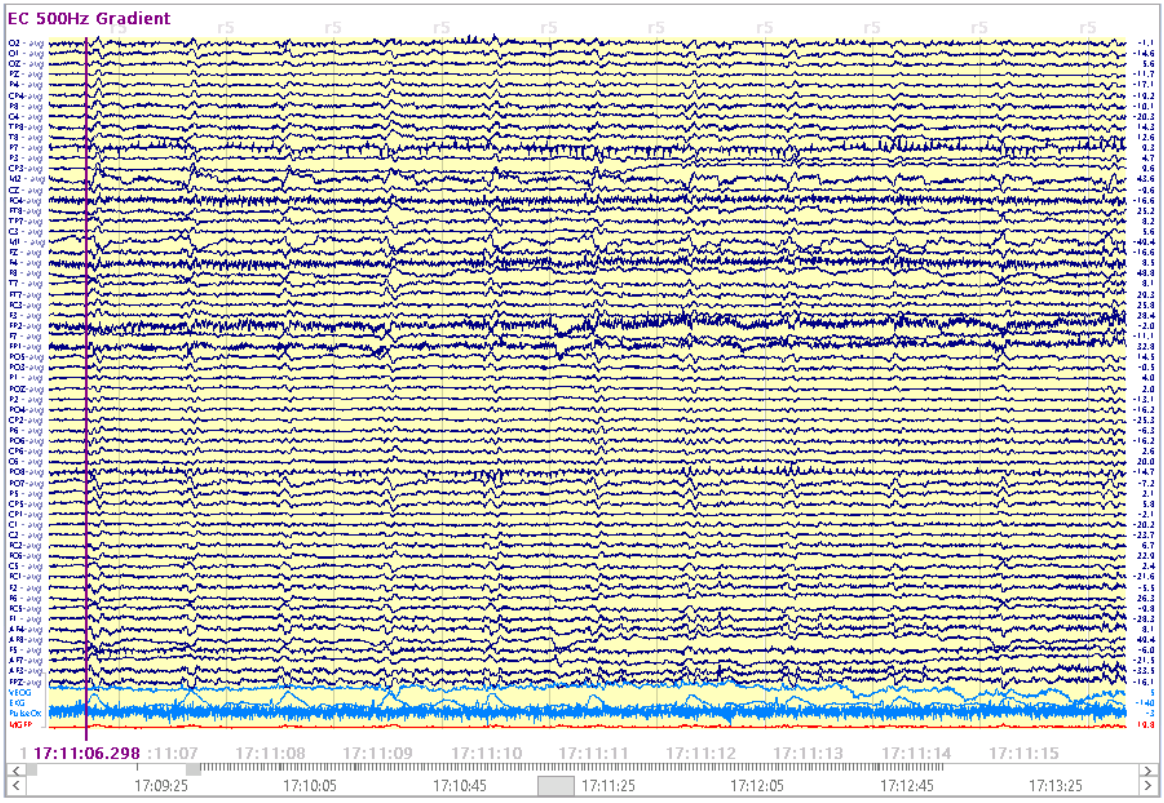


In a second Processing Sequence, set the parameters as usual for Subtraction, and Scan the data as usual. Use some number of **Epochs/Avg** or All, depending on which works best. Based on our analyses so far, this method appears to do a better job of reducing the faster activity, without doing any High Pass filtering.

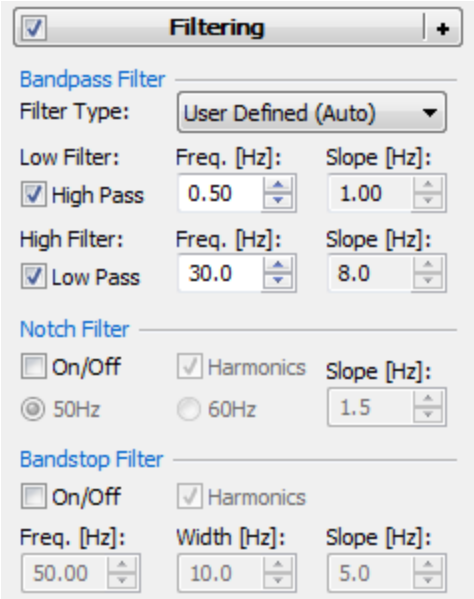


---

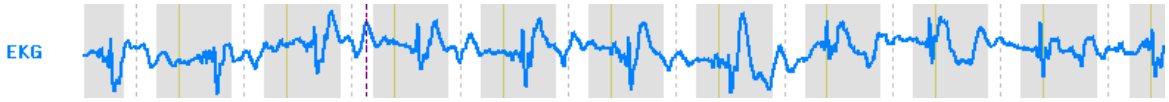
6. Now we see the file with the fast frequency noise (probably a combination of EMG and pump noise artifact) and BCG.



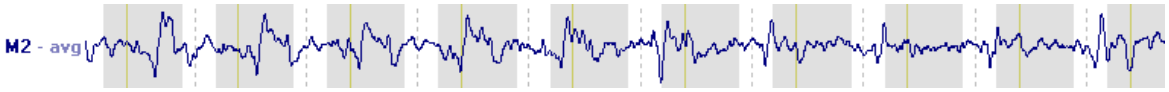
Add a **Filtering** panel and set the filters as shown. What you will use with your data depends of course on the band width of interest.



7. Now we need to *detect* the BCG and then use one of the methods to *reduce* it (described shortly). There are two ways to detect the BCG artifact. One is to use a simple voltage threshold (**Threshold Method** under **Artifact Reduction**). This requires a channel, typically the Pulse Oximeter (Pulseometer) channel, where a voltage threshold will reliably detect the artifacts, with no or few false positives. In this file, there is no Pulse Ox channel, and the activity on the EKG channel varies too much for a single voltage threshold. High Pass filtering of the single EKG channel would help.

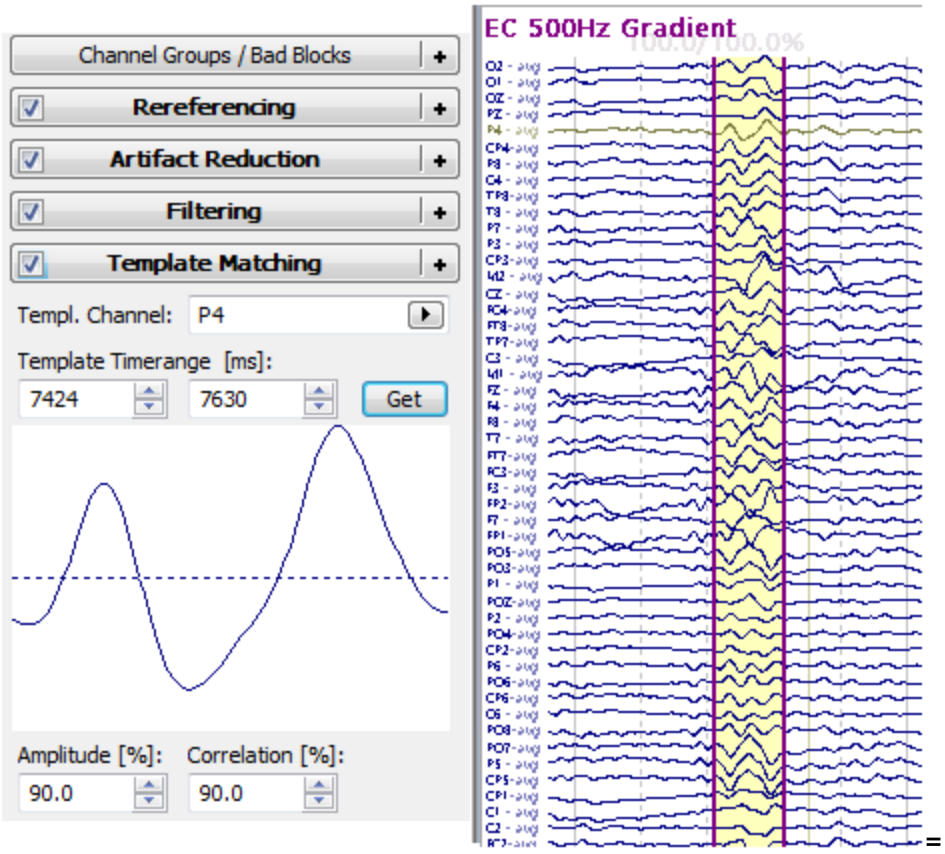


It would also be difficult to use a good EEG channel, such as M2. With enough experimentation with the voltage threshold and refractory period, you might detect most of the BCGs, but there would be false positives and missed artifacts.

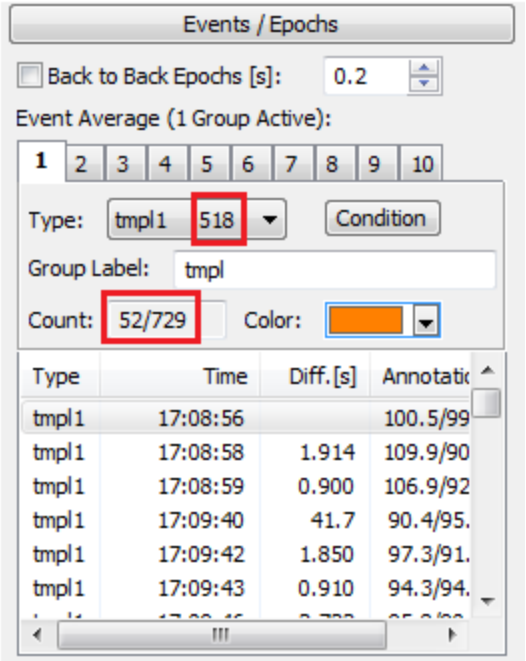


The other method uses **Template Matching**, which is the one we will use. It also may have some false positives and missed artifacts, but it is easier to use, in this case.

Add a **Template Matching** panel, select **P4** (for example) as the **Template Channel**, and set the two outer cursors to define a Timerange around a stable looking section of the artifact. Then click the **Get** button. Always be sure that the displayed artifact contains both positive and negative values. Otherwise, the detection may not be very reliable. Then click the **Scan Artifact** button .

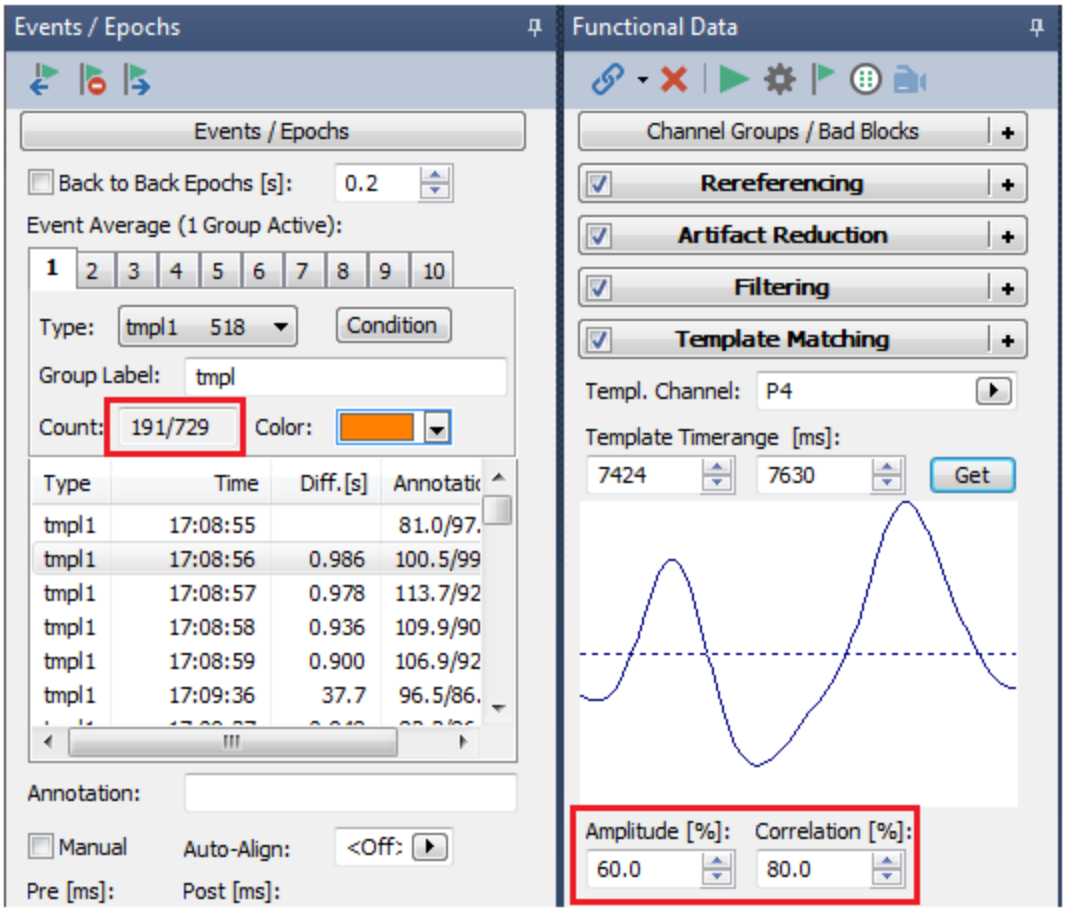


8. Display the **Events / Epochs** list , and note that there were 518 matches, and 52 of them have been listed (your numbers will vary depending on the Timerange you selected and the rejected blocks). This means that 518 matches were detected with the least allowable Amplitude and Correlation criteria of (30% and 50%, resp.), and that 52 matches met the 90% criteria. There was a total of 729 events in the file.

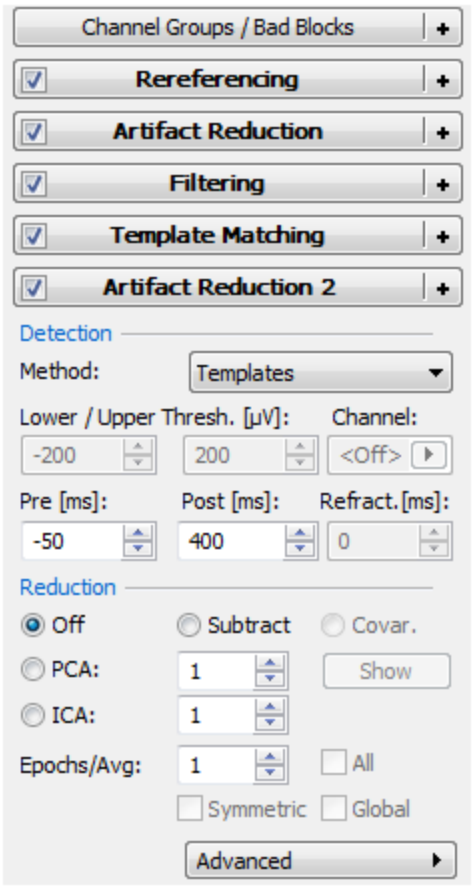


Reduce the **Amplitude** criterion to **60**% and the **Correlation** criterion to **80**%. We now see that 191 matches appear in the list

. For the analysis we will be doing, it is not necessary to detect all of them, and it is better to have some missing than to permit poorer matches.

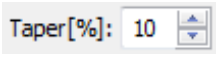


9. Now, there are another couple of ways we can proceed. We will do the easier way here, and demonstrate a different way in the second example below. Add another **Artifact Reduction** panel, and set the parameters as shown. Go to a section of the file where the gradient artifact had been.

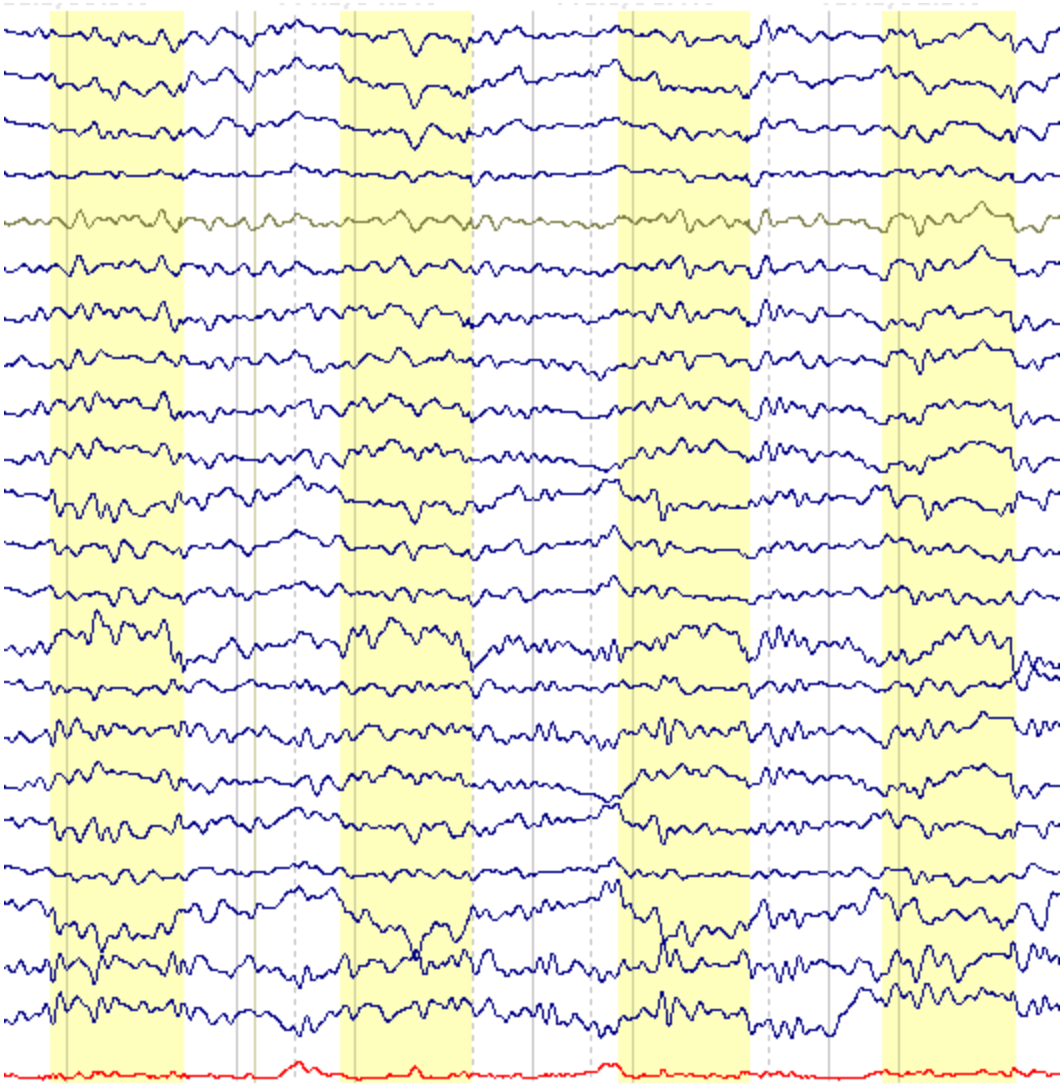


Click the **Subtract** and option with **Epochs/Avg** set to **10** to get an idea of how the correction will appear, and then click the **Scan Artifacts** button . Now it is a matter of finding the reduction method that works best. Enable the

option and note the slight difference.

Try **Subtract** with **10 Epochs/Avg** compared to **All** detected BCG artifacts. Try **Subtract** with **All** compared to **PCA** with **All**, where you also vary the number of PCA **Components** that are removed. Try **PCA** with **All** enabled where you compare the correction with and without the **Global** option on. The Global option will apply the PCA correction to all data samples in the file. Otherwise, only the sections where the artifacts have been detected are being corrected. Increasing the number of PCA components may make the data look better, but there is a possibility that you may overcorrect the data, and affect the actual components of interest (throwing out the baby with the bath water). Generally, PCA with Global On may be more effective than Subtract, since not all BCG artifacts are detected. Subtract corrects only the detected artifacts; PCA with Global corrects all points in the file. If you are seeing sharp voltage jumps at the ends of the epochs, add a small Taper 

(in the **Advanced** section). Try different methods to see which works best for you.



Once you decide on the best combination of parameters, you should save the **Study Parameters** , or else save the corrected data file (**Functional Data** → **Save** → **Save Data**). If you save the Study Parameters and then reopen this study, you will need to press the **Scan Artifacts** button to get back to this point.

Some Tips for Gradient Reduction

In the ideal world, gradient and BCG reduction will be similar to the examples included in this tutorial. However, we have seen exceptions, due to differences in scanners and scanning protocols. In some cases, there will be a trial and error process for finding the best parameters to use. The more you understand about how the corrections work, the faster this process will go.

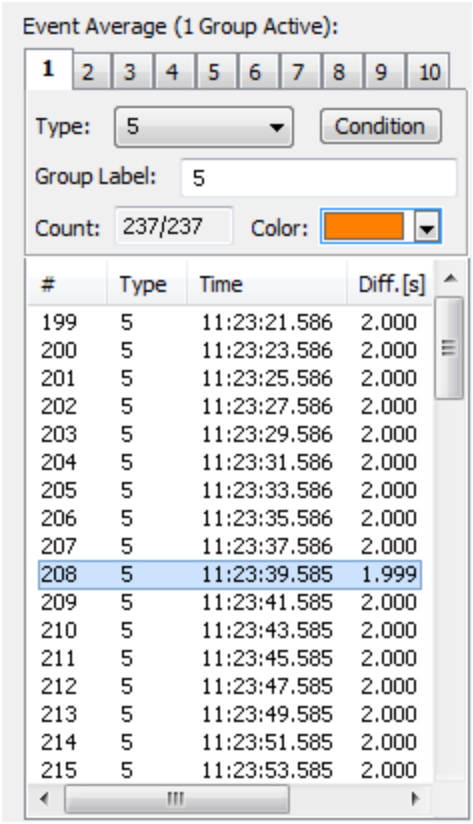
As mentioned at the top of this tutorial, gradient reduction works well when the events are placed accurately at the beginning of each TR Block, and the artifact does not vary across blocks. In some cases, one or both of these conditions may not be

met satisfactorily. It is important to recognize when these situations occur, and to know what can be done to still perform the correction, if possible. We have occasionally encountered user files that cannot be corrected, mainly due to the use of atypical scanner protocols that result in inconsistent gradient artifacts across TR blocks.

The examples below are meant to make you aware of how features in CURRY can be used.

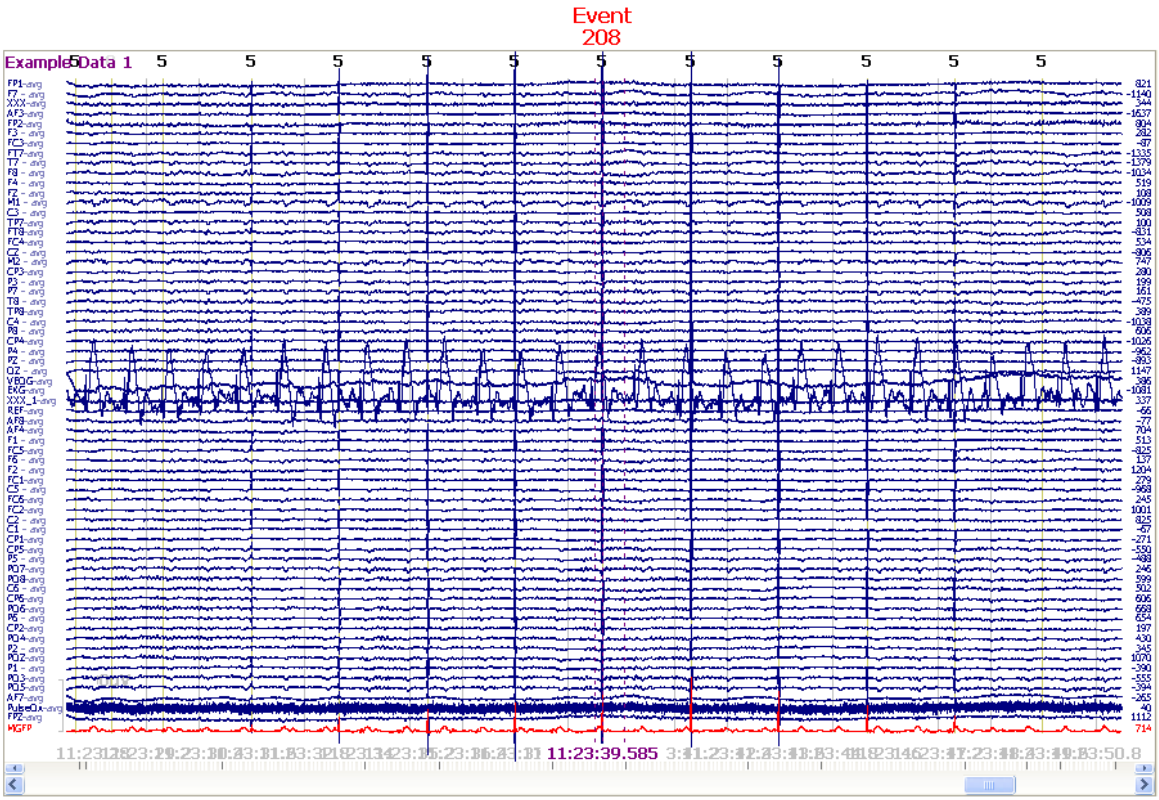
One of the useful things to do is to look at the **Events / Epochs** list after you have selected the **Type** code for the gradient artifact (5 in this case). *Right click* and deselect **Show Durations** (if needed) so that you are seeing the differences (**Diff.[s]**) in time between the successive events. In some cases, it is helpful to select **Show Indices**, which adds an event counter for the first column.

In this example, there is a constant difference of 2s between all events, with the exception of the 208th event, where the difference was 1.999ms.

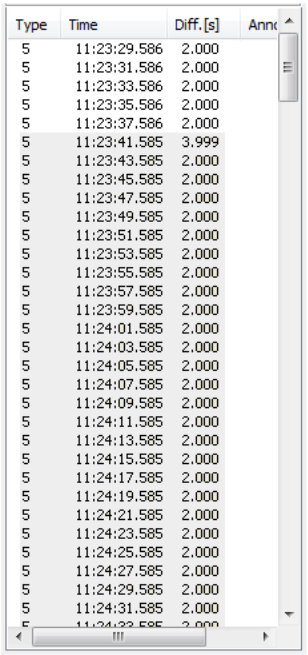


#	Type	Time	Diff.[s]
199	5	11:23:21.586	2.000
200	5	11:23:23.586	2.000
201	5	11:23:25.586	2.000
202	5	11:23:27.586	2.000
203	5	11:23:29.586	2.000
204	5	11:23:31.586	2.000
205	5	11:23:33.586	2.000
206	5	11:23:35.586	2.000
207	5	11:23:37.586	2.000
208	5	11:23:39.585	1.999
209	5	11:23:41.585	2.000
210	5	11:23:43.585	2.000
211	5	11:23:45.585	2.000
212	5	11:23:47.585	2.000
213	5	11:23:49.585	2.000
214	5	11:23:51.585	2.000
215	5	11:23:53.585	2.000

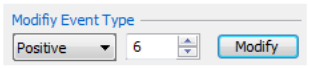
If you perform the correction as is (where **Epochs/Avg** was set to **10**, and **SSC** enabled), you will see a spike artifact appear before and after the event, due to the shorter TR block and the rolling average. If you save the corrected file and then open and filter the data, you can reduce the amplitude of the spikes. You might also use PCA to reduce the artifacts.

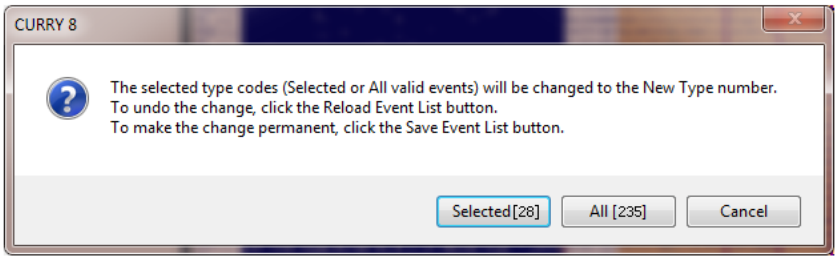


Another option is to create a **Bad Block** to encompass the bad event. Then, in the **Event List** highlight (you can use *Shift+click*) all of the events after the Bad Block. Change those codes to, for example 6, using the **Modify Event Type** field. Click **Selected [N]** to the message.

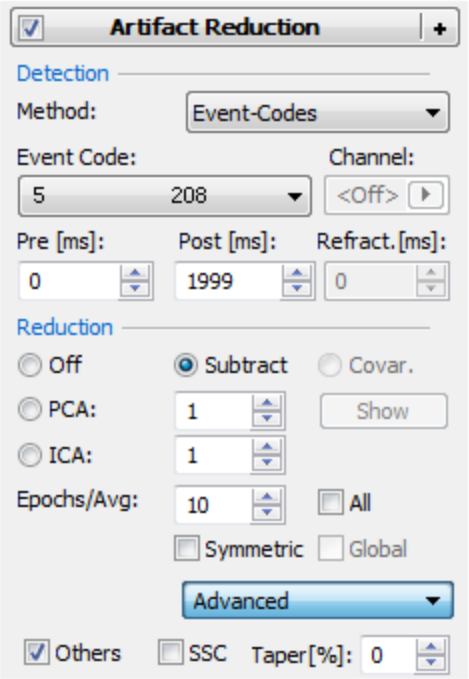


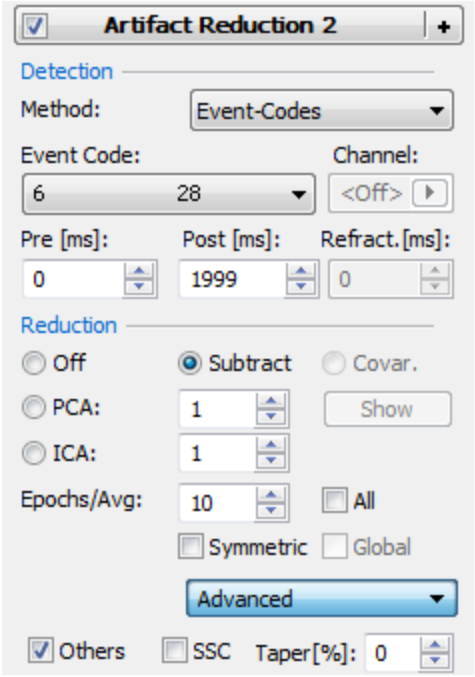
Type	Time	Diff.[s]	Anno
5	11:23:29.586	2.000	
5	11:23:31.586	2.000	
5	11:23:33.586	2.000	
5	11:23:35.586	2.000	
5	11:23:37.586	2.000	
5	11:23:41.585	3.999	
5	11:23:43.585	2.000	
5	11:23:45.585	2.000	
5	11:23:47.585	2.000	
5	11:23:49.585	2.000	
5	11:23:51.585	2.000	
5	11:23:53.585	2.000	
5	11:23:55.585	2.000	
5	11:23:57.585	2.000	
5	11:23:59.585	2.000	
5	11:24:01.585	2.000	
5	11:24:03.585	2.000	
5	11:24:05.585	2.000	
5	11:24:07.585	2.000	
5	11:24:09.585	2.000	
5	11:24:11.585	2.000	
5	11:24:13.585	2.000	
5	11:24:15.585	2.000	
5	11:24:17.585	2.000	
5	11:24:19.585	2.000	
5	11:24:21.585	2.000	
5	11:24:23.585	2.000	
5	11:24:25.585	2.000	
5	11:24:27.585	2.000	
5	11:24:29.585	2.000	
5	11:24:31.585	2.000	



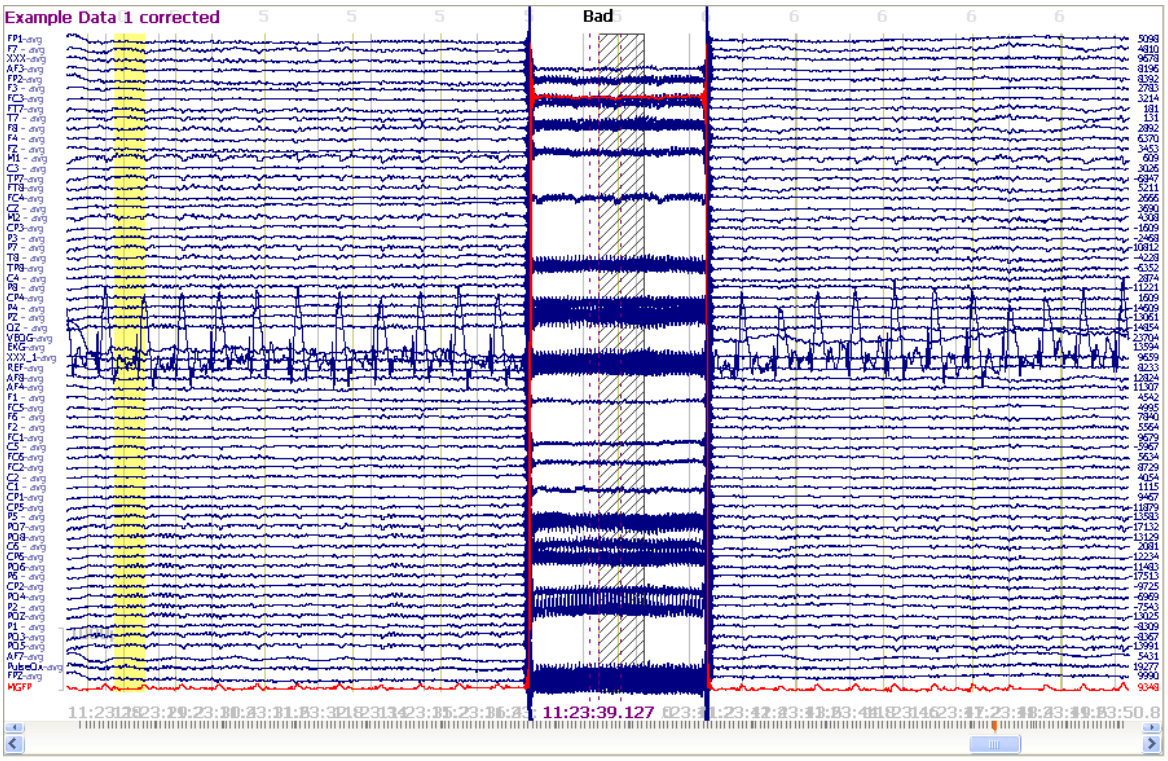


Now you can use two **Processing Sequences** for **Artifact Reduction** to correct the 5's and then the 6's.





Save that file, filter it, and you will see the corrected data except for the TR blocks that contain parts of the Bad Block (note the type 5's before the bad block, and the type 6's after it). This method avoids the spike artifacts seen with the previous method.



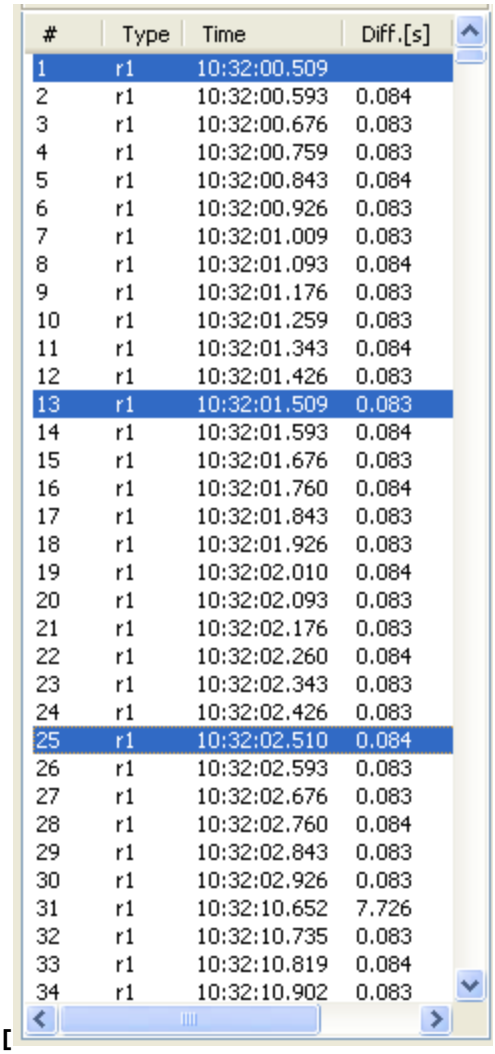
In some cases you may have events for the individual slices, rather than for the TR blocks. That will work if the duration between each slice is exactly the same, and if the gradient artifact is the same for each slice. That is not always the case. In the example below, you can see that the events come at every 0.0833333ms. With an AD Rate of 1000 Hz, you will see that the difference between events will be either 83ms or 84ms. That will not work well for correction.

#	Type	Time	Diff.[s]
1	r1	10:32:00.509	
2	r1	10:32:00.593	0.084
3	r1	10:32:00.676	0.083
4	r1	10:32:00.759	0.083
5	r1	10:32:00.843	0.084
6	r1	10:32:00.926	0.083
7	r1	10:32:01.009	0.083
8	r1	10:32:01.093	0.084
9	r1	10:32:01.176	0.083
10	r1	10:32:01.259	0.083
11	r1	10:32:01.343	0.084
12	r1	10:32:01.426	0.083
13	r1	10:32:01.509	0.083
14	r1	10:32:01.593	0.084
15	r1	10:32:01.676	0.083
16	r1	10:32:01.760	0.084
17	r1	10:32:01.843	0.083

Moreover, the gradient artifact is different for each slice; however, in looking at the actual gradient artifact for each event, it was apparent that the artifact repeated in groups of three, giving a duration of 250 ms. If the TR block is a multiple of that, say

2000 ms, then you can use 0-1999ms as the **Pre** and **Post** times in **Artifact Reduction**, where the **Post** time acts like a refractory period. Events in between will be ignored. You can also try 0-249ms, for example, for the Pre and Post times.

In unusual cases, you also have the option to select the beginnings of the TR events manually (*Ctrl+click*). Then use **Modify Event List** to reassign those event codes. After selecting the new codes in the event **Type** field, you can then proceed with Artifact Reduction.



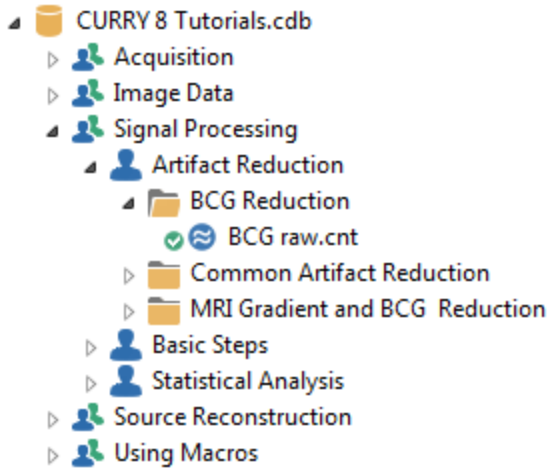
#	Type	Time	Diff.[s]
1	r1	10:32:00.509	
2	r1	10:32:00.593	0.084
3	r1	10:32:00.676	0.083
4	r1	10:32:00.759	0.083
5	r1	10:32:00.843	0.084
6	r1	10:32:00.926	0.083
7	r1	10:32:01.009	0.083
8	r1	10:32:01.093	0.084
9	r1	10:32:01.176	0.083
10	r1	10:32:01.259	0.083
11	r1	10:32:01.343	0.084
12	r1	10:32:01.426	0.083
13	r1	10:32:01.509	0.083
14	r1	10:32:01.593	0.084
15	r1	10:32:01.676	0.083
16	r1	10:32:01.760	0.084
17	r1	10:32:01.843	0.083
18	r1	10:32:01.926	0.083
19	r1	10:32:02.010	0.084
20	r1	10:32:02.093	0.083
21	r1	10:32:02.176	0.083
22	r1	10:32:02.260	0.084
23	r1	10:32:02.343	0.083
24	r1	10:32:02.426	0.083
25	r1	10:32:02.510	0.084
26	r1	10:32:02.593	0.083
27	r1	10:32:02.676	0.083
28	r1	10:32:02.760	0.084
29	r1	10:32:02.843	0.083
30	r1	10:32:02.926	0.083
31	r1	10:32:10.652	7.726
32	r1	10:32:10.735	0.083
33	r1	10:32:10.819	0.084
34	r1	10:32:10.902	0.083

These are all examples of the features that may be useful when performing gradient reduction with difficult data files.

We will now move on to BCG reduction.

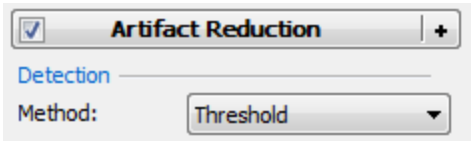
BCG Reduction

The second example, in the *BCG Reduction* Study folder, is included as a fairly simple example that is good for trying different methods.

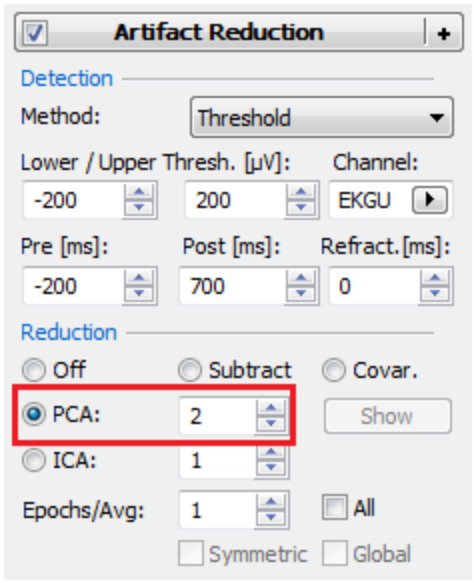


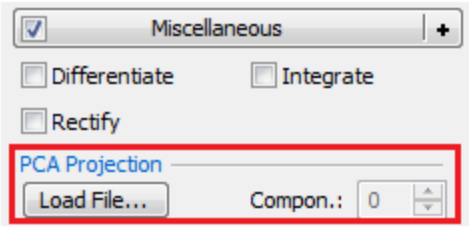
The gradient artifact has already been removed, and the BCG is fairly constant throughout.

There are several ways to detect and reduce BCG artifact. For detection of BCG, you can use a voltage threshold method - if you have a channel that provides reliable detection, or a template matching method, as described above.



You can use PCA to reduce the artifacts, using either of two methods.

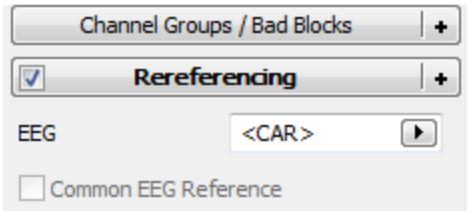


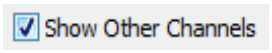


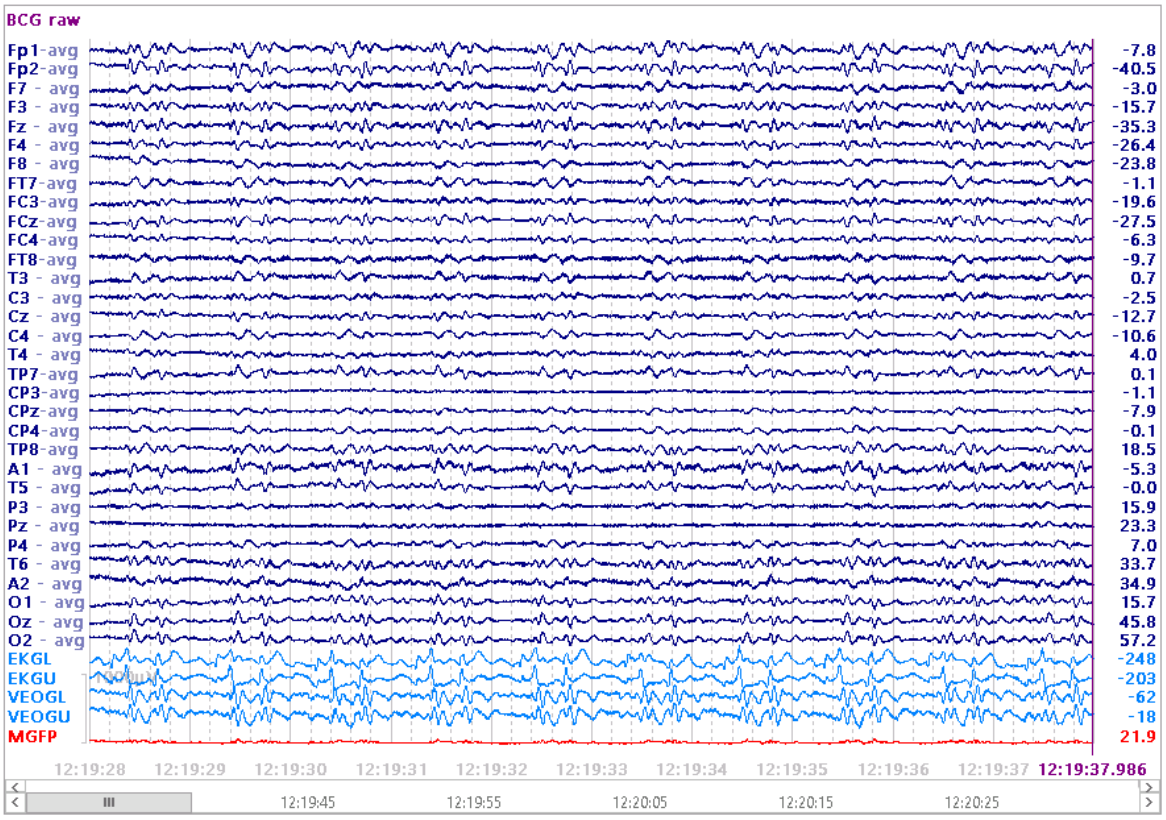
You can also use the **Subtract** and **Covariance** options, with a fixed numbers of **Epochs/Avg**, or **All** detected artifacts, with or without the **Global** option. So there are many variations on ways to reduce BCG. The way that works best will depend on the data you have, namely how stable the BCG artifact is over time and how it can be detected reliably.

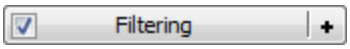
Open the study.

1. If you do not have the Common Average Reference (CAR) already selected, select it now.

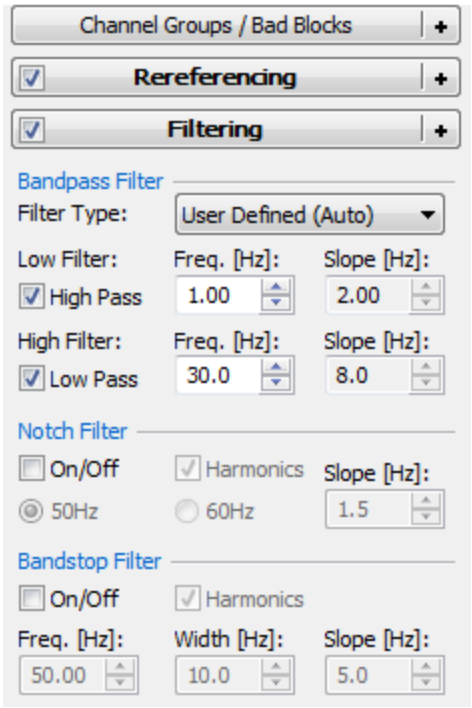


Enable  under **Options**, if needed. Note that the **EKGL**, **EKGU**, **VEOGL**, and **VEOGU** channels appear in a different color. This means they were designated as "Other" channels in the Functional Data Import Wizard. As such, they will be excluded from the PCA, but we can still use them for detection, if desired.

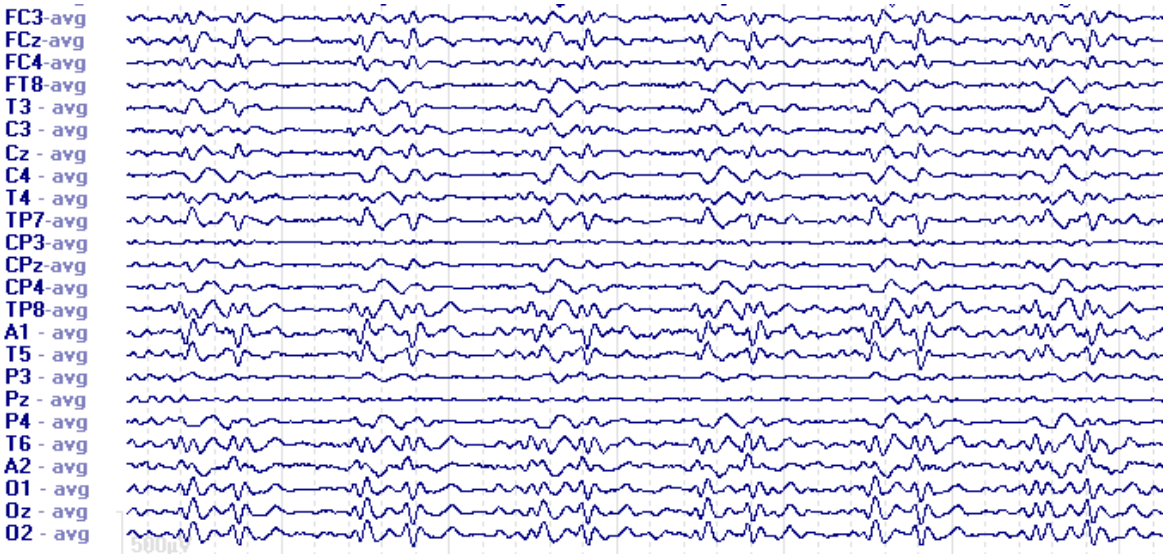


2. We note that there is a lot of fast frequency noise on several channels. Add the 

and select **User Defined (Auto)**. Enter the parameters shown, as needed.

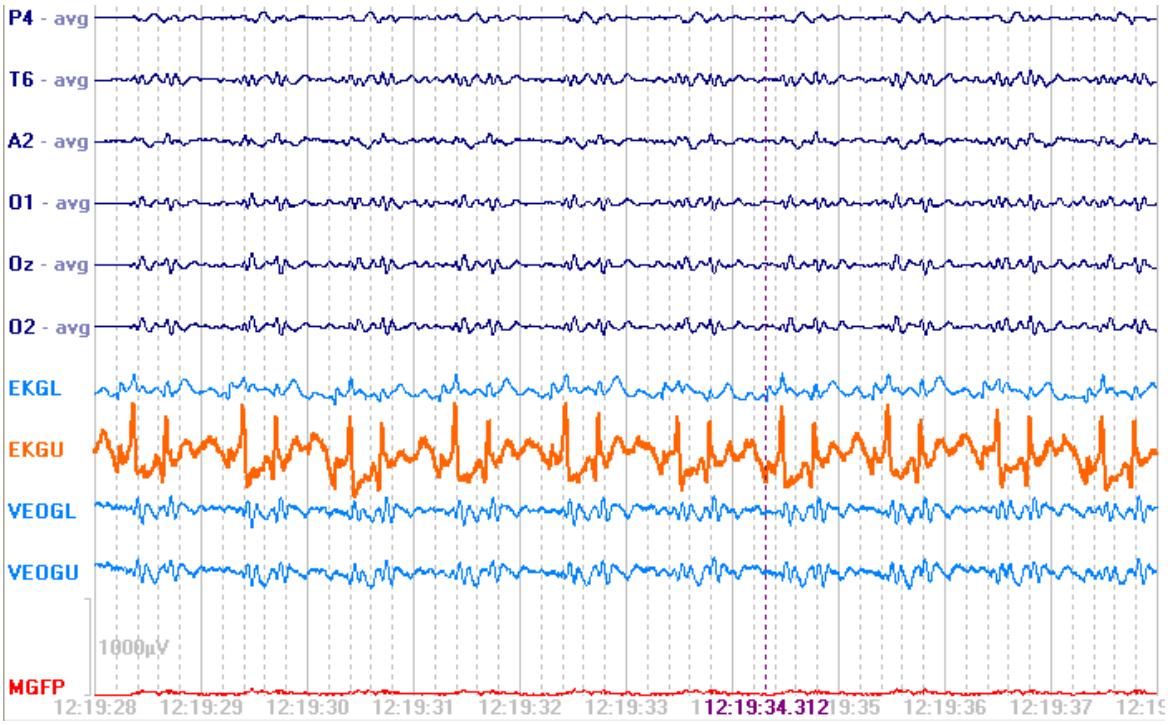


The BCG is clearly evident in most channels.

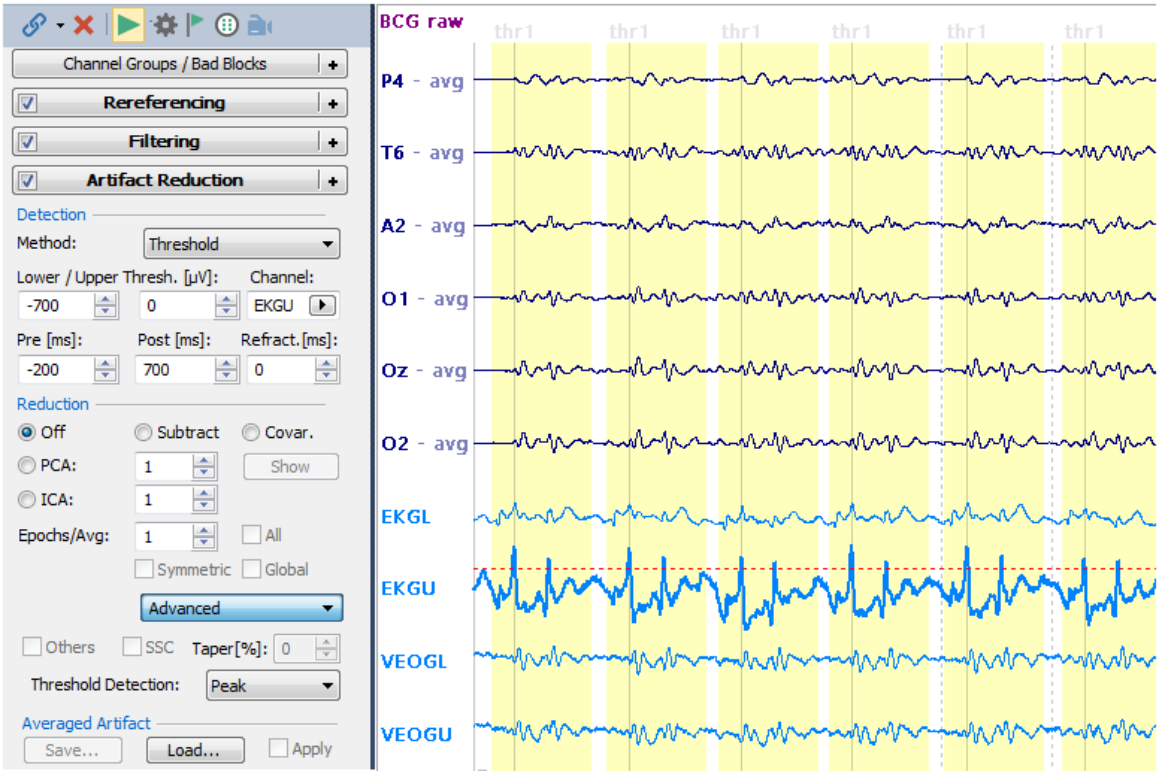


Save the **Study Parameters** at this point (use the default name) because we will return to the file in this state later to use a different method.

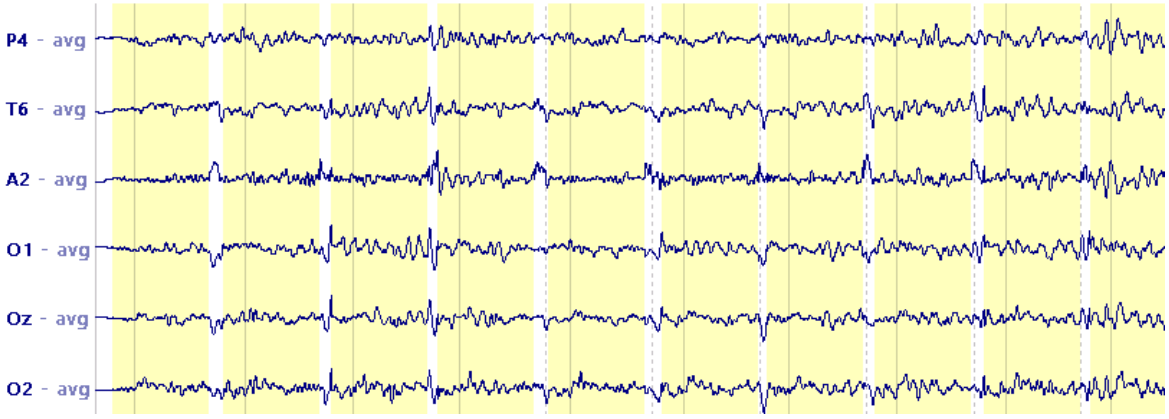
3. Expand the Options panel and decrease **Max. Displ. Chann.** to **10** (you can also position the cursor in the data display and use *Shift+mouse wheel* to change the number of channel displayed). Rescale to see the **EKGU** channel clearly (to rescale a single channel only, position the mouse over the channel label and rotate the *mouse wheel*). We will need amplitude and time measurements for the voltage threshold. Negative voltages are "up" in the display. A **Lower Threshold** of about **-700** will reliably detect the initial peak throughout the file. The artifacts are generally about 1000 ms apart, and a Refractory period of about 900 ms should be sufficient (the minimum).



4. Add an Artifact Reduction panel. We will use the **Threshold** method to identify the BCG artifacts. Select **Threshold** and select the **EKGU** channel. The dashed red line shows the position of the threshold with respect to the selected channel. Setting the **Upper Threshold** to **0** turns it off - note that the dashed line for it disappears when set to 0. **Pre** and **Post [ms]** were set to encompass most of the BCG artifact. The **Refractory** period cannot be less than the sum of the **Pre** and **Post [ms]** latencies; no additional peaks will be detected during the Refractory interval (a Refractory of 0 ms means the sum of the Pre and Post times).

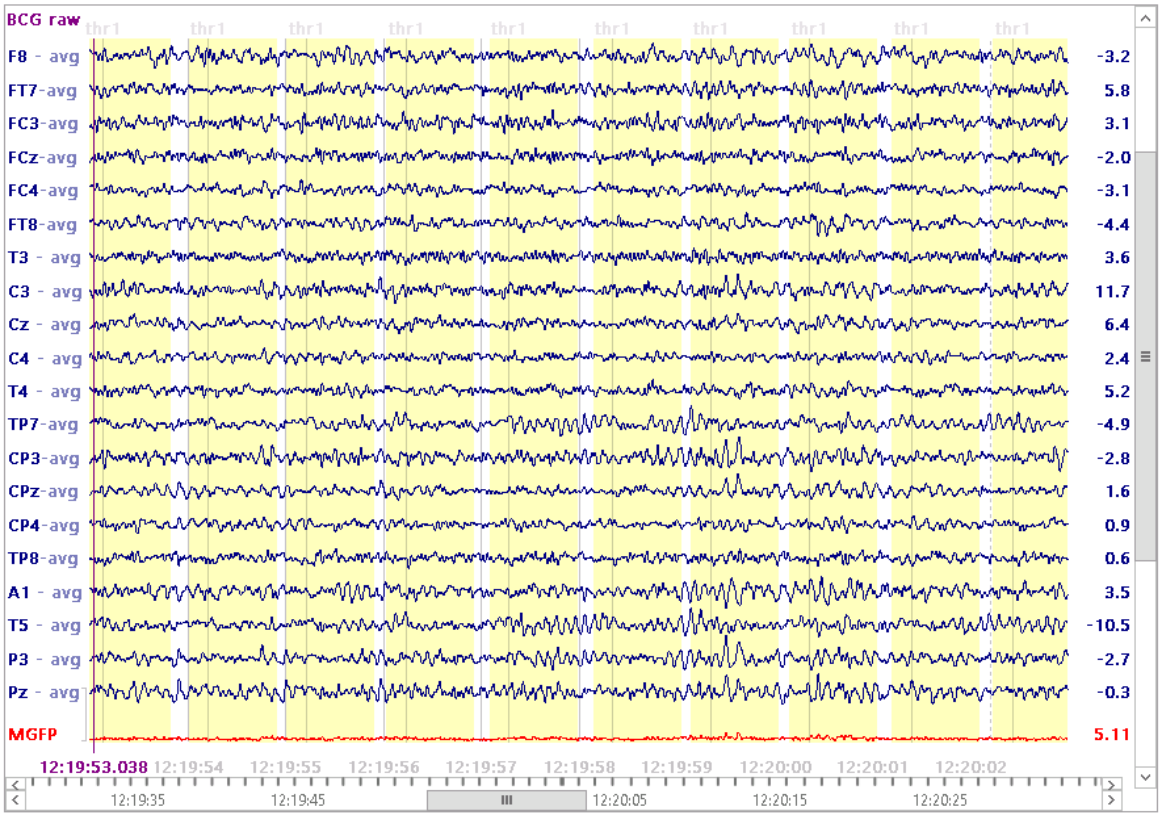


5. To get an idea how effective the correction will be, enable **PCA** and increase the components to **3**. Rescale the display. Note that the areas in yellow are corrected, but not in the intervals in between. This will be addressed shortly. For now it looks like PCA should be effective. You can also try increasing the number of **Epochs/Avg** and/or selecting **Subtract** (Subtract works well if the BCG is fairly constant).



Click the flashing button.

6. Select **PCA** with **3** components, if needed. Enable **All** to use all of the detected artifacts for the artifact average. Enable **Global** to apply the correction throughout the file. This corrects the data in the intervals between the BCG artifacts as well. Now we see clean EEG. Alternate between **Off** and **PCA** to see the results.



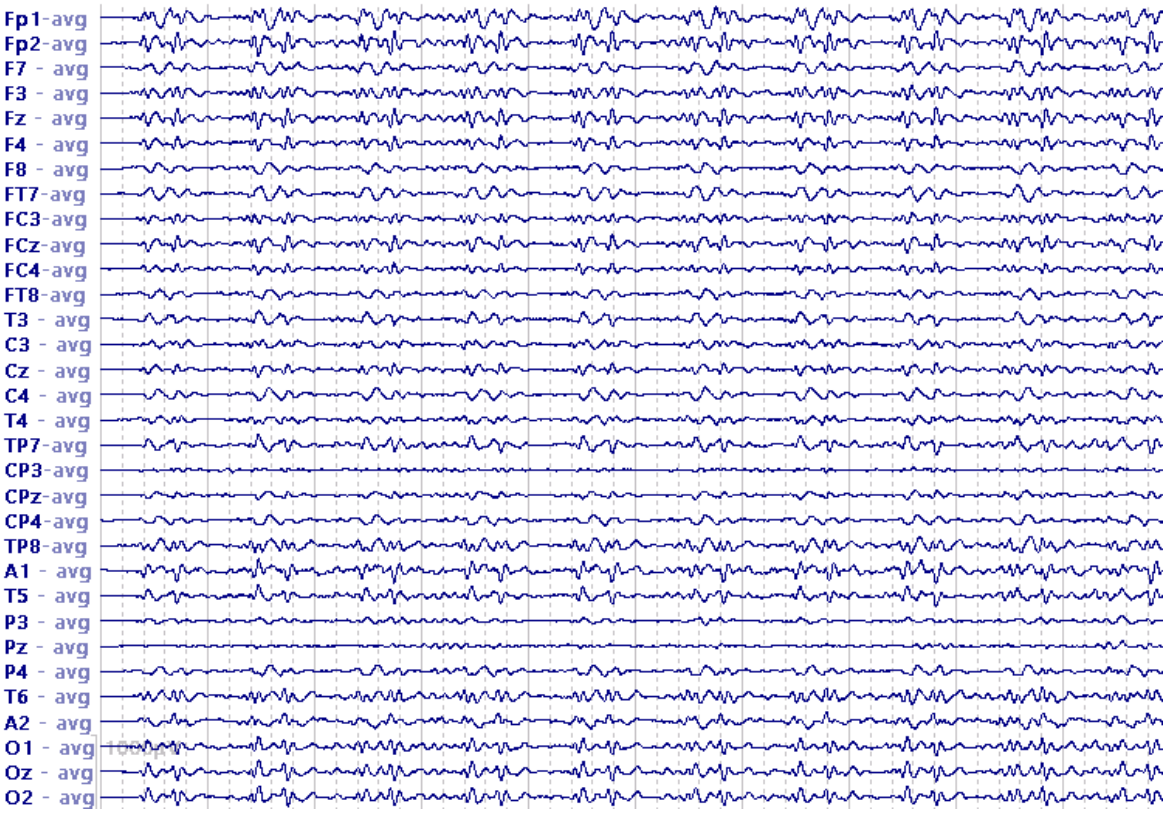
If there were stimulus events in the file, you could go on from here and do the averaging as usual.

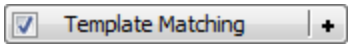
In the next example file, there was no Pulse Ox channel, but there were EKG channels, and one of them was adequate for threshold detection of the BCG artifacts. What happens if you have no Pulse Ox or EKG channels, and the EEG channels have BCG, but not where threshold detection can identify them reliably? Then use **Template Matching**, as in the first example above. In that example, we used Template Matching to detect the BCG artifact, and the Templates method in Artifact Reduction prior to reduction.

There is a variation on that procedure that provides a little more flexibility, and this uses the **PCA Projection** approach.

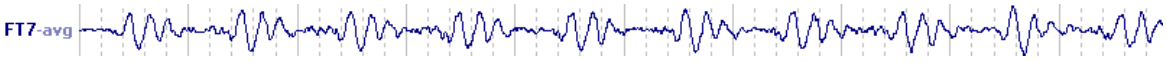
Close the Study and reopen it. Since we saved the Study Parameters, we will not have to repeat the initial steps (filtering).

1. For this example, we will pretend there are no artifact channels at all. Expand the Options panel and deselect **Show Other Channels**. The artifact channels will be removed from the display.



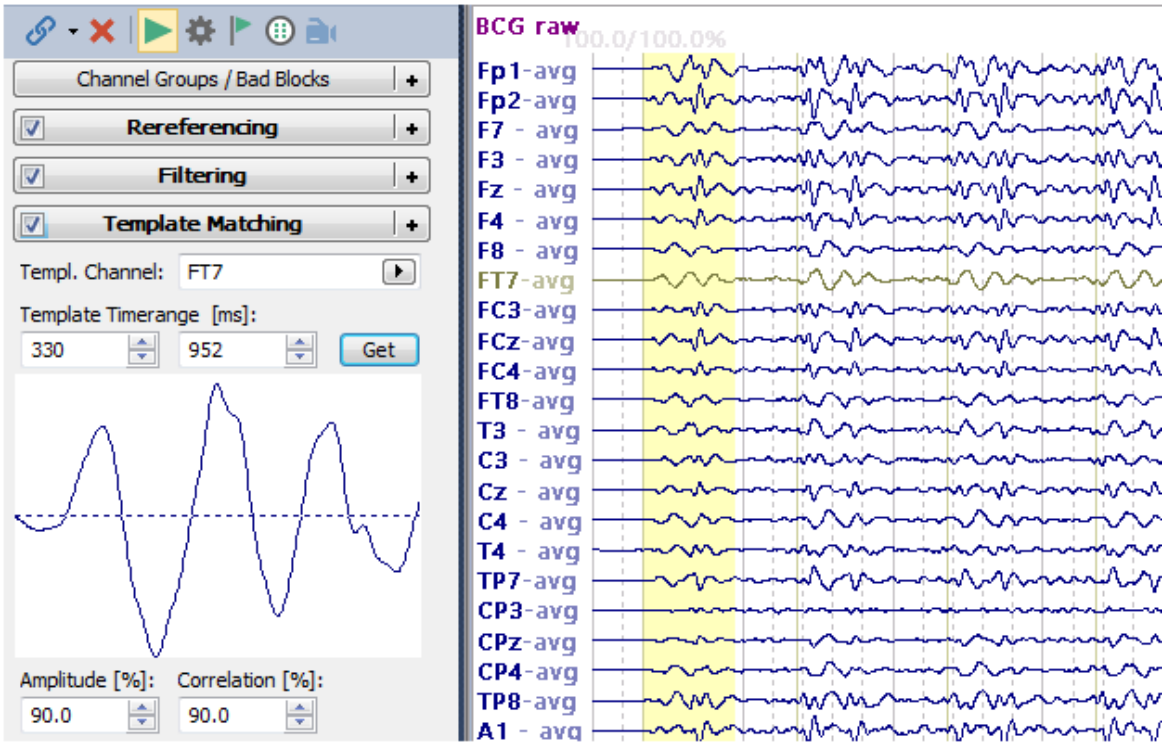
2. Now we need to create a template. Add a 

panel. FT7 has a stable looking artifact, although almost any channel should work.



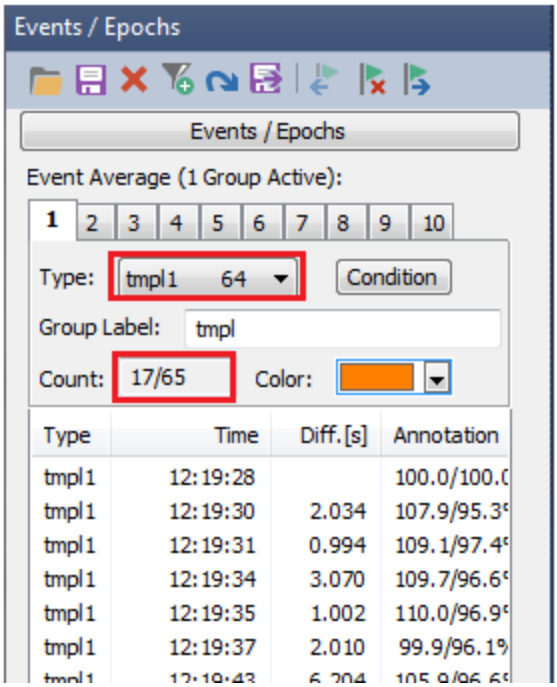
Enter **FT7** as the **Template Channel**. Position the outer two cursors to define a Timerange that encompasses an artifact. Press the

button to transfer the latencies and see the artifact.

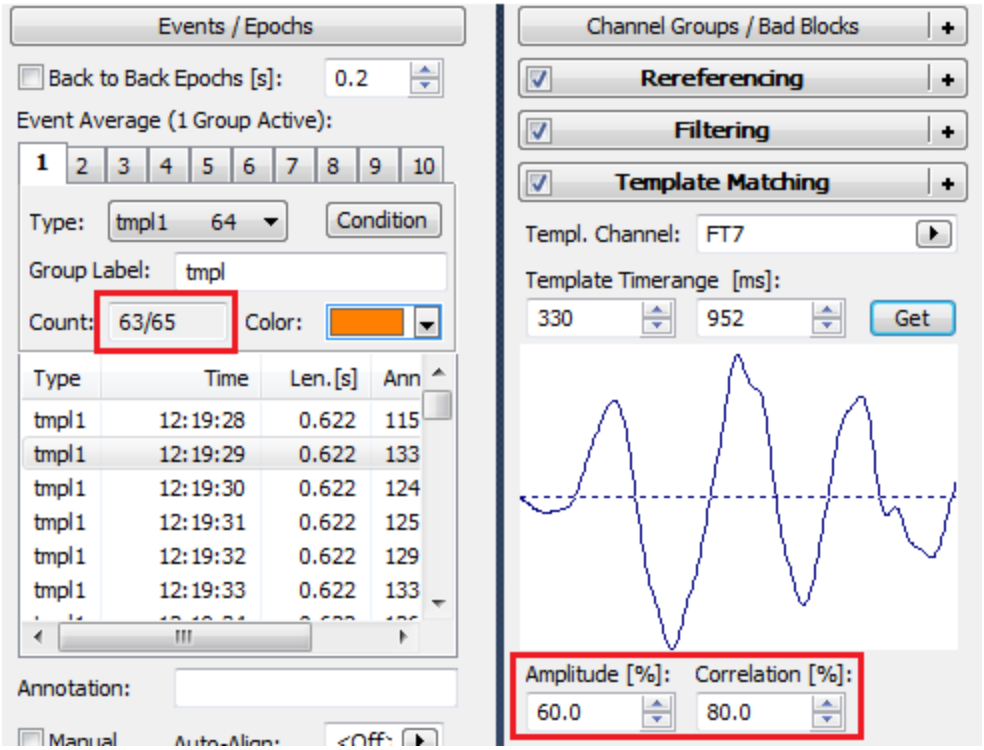


Then click the flashing button.

3. Go to the list, in the panel, and select "tmpl1" for the **Type**. There were 64 events detected with the minimum Amplitude and Correlation criteria of (30% and 50%, resp.). With the 90% settings that we used, 17 were detected. There were 65 total events in the file.



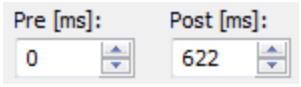
If we decrease **Amplitude** to **60%** and Correlation to **80%** nearly all of the artifacts will be detected (63).

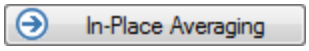


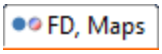
You can tell which events are detected by looking at the tick marks below the data display. When all are detected, there will be evenly spaced hash marks throughout the file. The missed one is in gray at the end.

4. The variation with this approach is that we will average the artifacts, do the PCA, save the results, and then apply **PCA Projection** to the continuous data.

In the **Averaging** list, we will use the displayed **Pre** and **Post [ms]** times to define the span of the BCG artifacts we will average. (*Right click* in the event list and select **Show Durations**, if needed, to see the **Lengths** of the intervals - 622ms in this case).

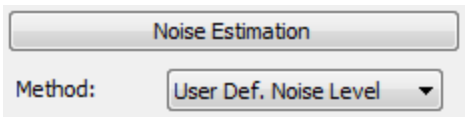


Then click the 

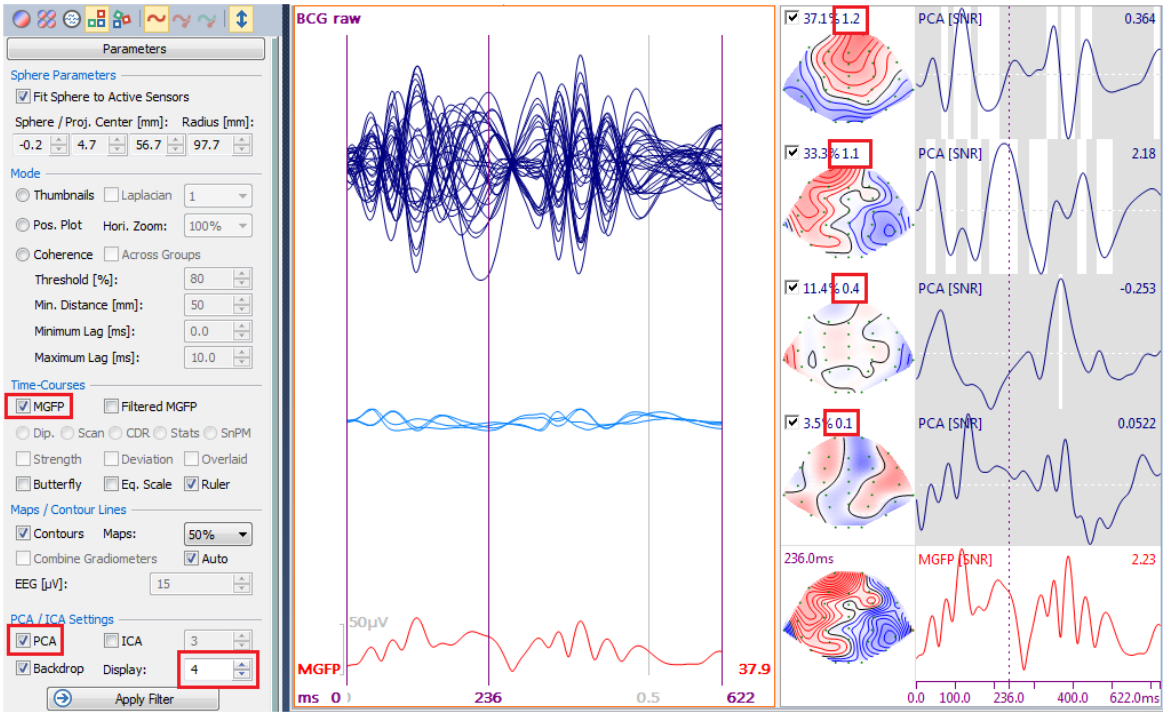
button to create an instant average of the BCG artifacts. We selected the **Butterfly Plot** and the 

display.

5. Whenever you save the PCA results, it is necessary to use the **User Defined Noise Level** for **Noise Estimation**. Expand the **Noise Estimation** panel and select the option.

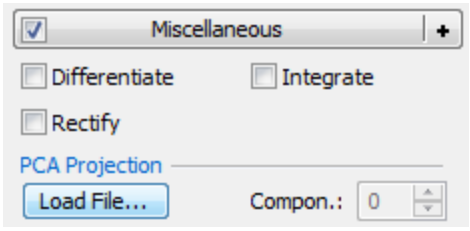


6. We then selected a Timerange encompassing the entire interval (use *Ctrl+double click* to spread the two outer cursors automatically). In the **Parameters** panel for **Maps**, enable **MGFP** and **PCA**, and select **4 Displayed Components**. In the maps display (looking at the SNRs), we see that there are 2 marginal components, with SNRs just over 1.0.

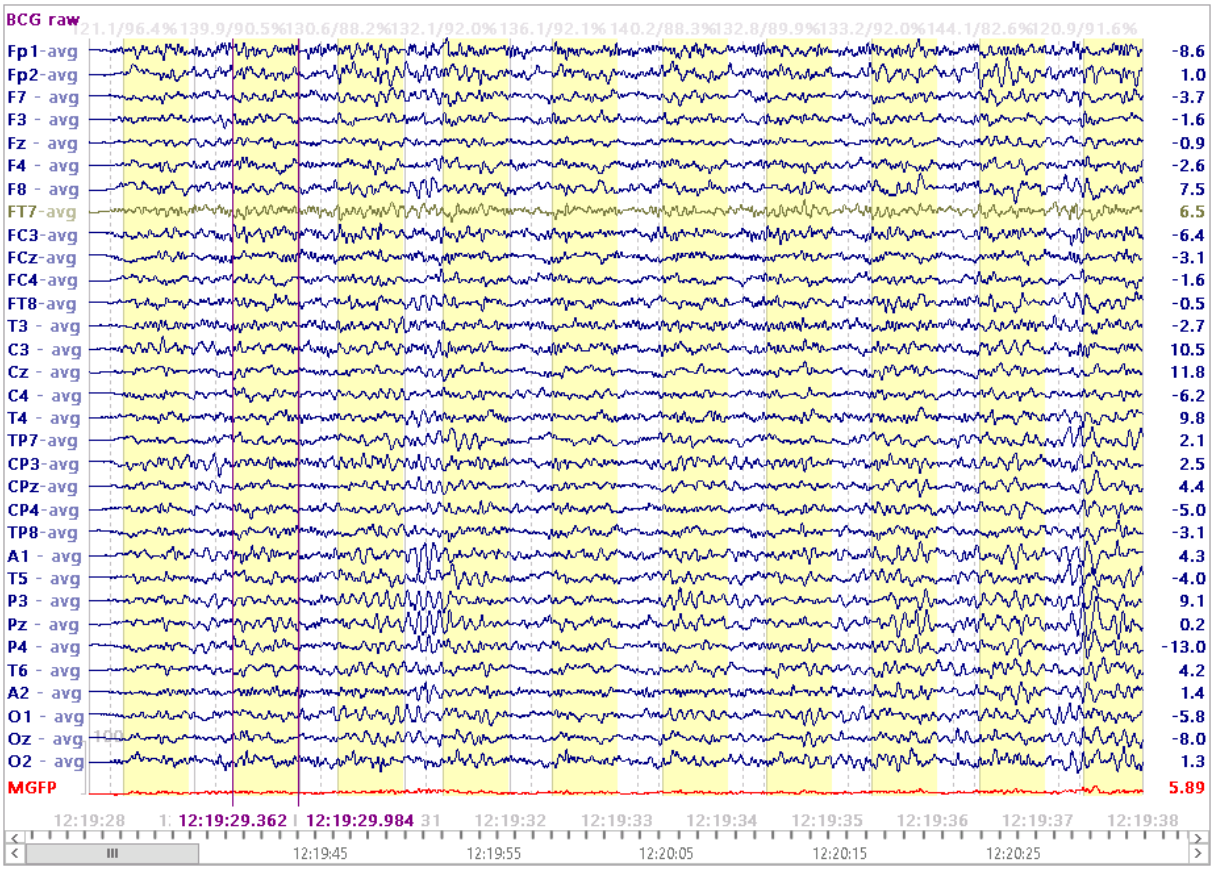


From the Workflow select Save PCA / ICA Results (or **Maps → Save → Save PCA Results**), save the .pca file (giving it a name of your choice). Then click the In-Place Averaging button (at the bottom of the **Events / Epochs** panel).

7. Add the Miscellaneous panel, and use the **Load File** button to select the .pca just saved. Vary the number of **Components** that are projected from the data file. Use as few as possible to avoid over-correcting the data.



In this file, 3 components reduce the BCG substantially on all channels.



In this Tutorial we demonstrated several methods for reducing gradient artifact and BCG; these can be used with other types of artifacts as well. Generally speaking, Subtract and PCA both work well when the BCG is fairly stable across the recording. PCA is better when the BCG varies. ICA generally tends to overcorrect, you cannot correct between the BCG artifact intervals, and it is more time consuming. Nevertheless, you should try the various options with your data and with differing parameters to determine the best method.

2.4.6 Evoked Response Analysis

There are several things that need to be understood in order to use the CURRY software most effectively. There are different paths you can take to create epochs and averages, and the path you need to follow depends on what you want to accomplish.

These are the four main paths to go from continuous data to averaged data.

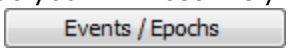
1. You can create in-place averages without applying any of the epoch rejection methods. No epoched file is created or saved. In this case you are simply averaging all of the epochs for each event type (relying on the Artifact Reduction methods to reduce artifact, if desired). The results are averages for each event

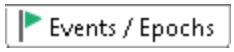
group. This method gives the fastest results, although not necessarily the cleanest results.

2. You can create in-place averages using any of the epoch rejection methods (in addition to the Artifact Reduction methods, if desired). 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.

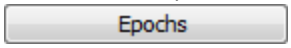
3. You can create an epoched file excluding epochs that are rejected on the basis of voltage thresholds, FFT power thresholds, Noise Statistics (SNR), or any combination of the methods. The epochs are rejected prior to creating the epoched file. This gives you a clean file that may then be used for averaging or single file statistics. This method takes a little longer than the first two methods because another file is created and cleaned.

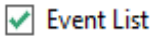
4. You can create an epoched file that contains *all* of the epochs. Open that file and then reject epochs on the basis of voltage thresholds, FFT power thresholds, Noise Statistics (SNR), or any combination of the methods. This gives you a clean file that may then be used for averaging or single file statistics. This method differs from the 3rd one in that you can see all of the epochs before rejecting any of them.

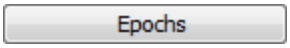
There are three panels that you will most likely be using with time domain data (after **Artifact Reduction**): the 

panel, found under the 

tab, the

panel under **Events / Epochs**., and the 

panel, found under **Functional Data**. The first two may also be accessed from the Workflow option 

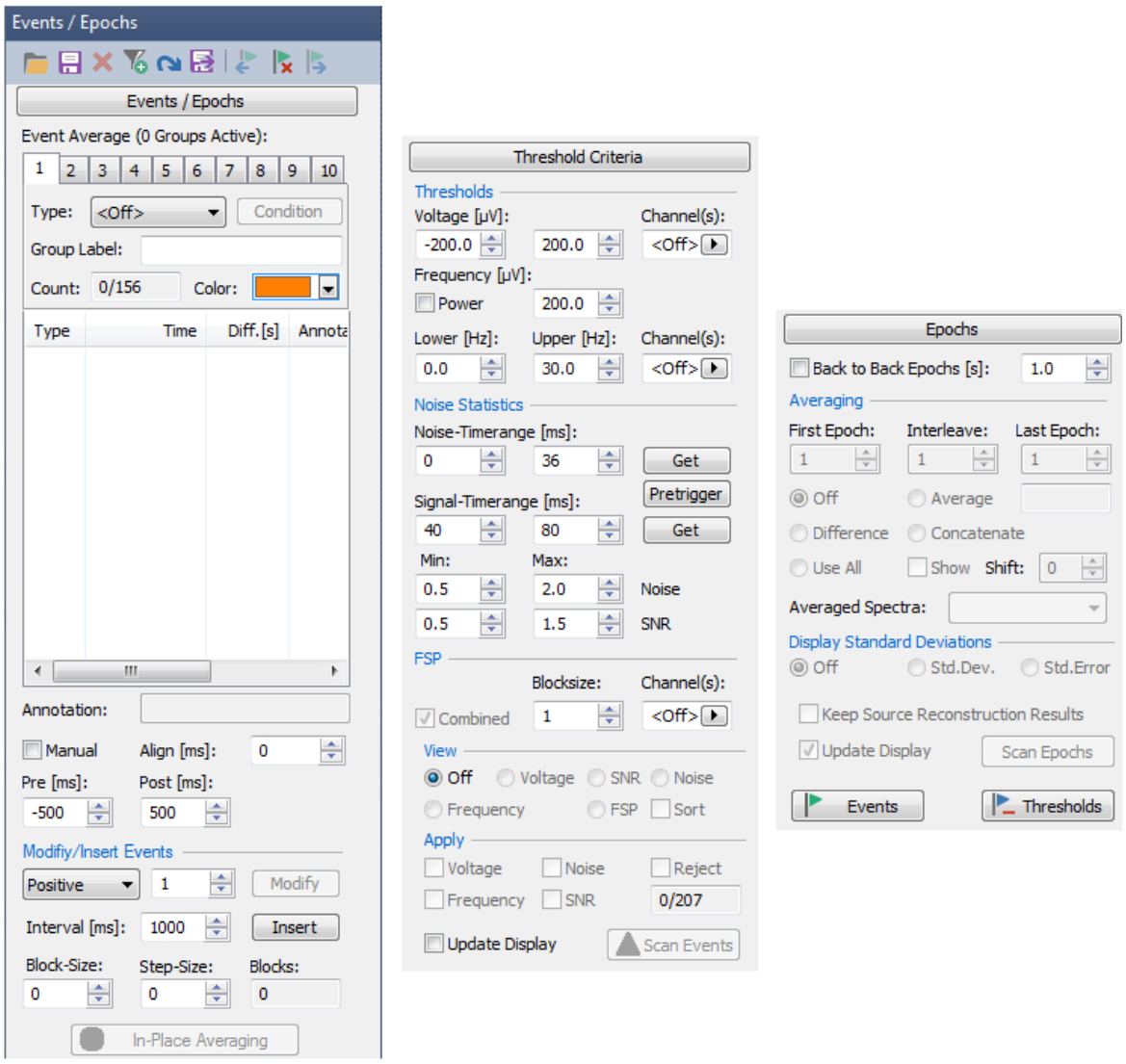
under **Signal Processing**, or the 

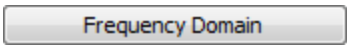
panel buttons:

and

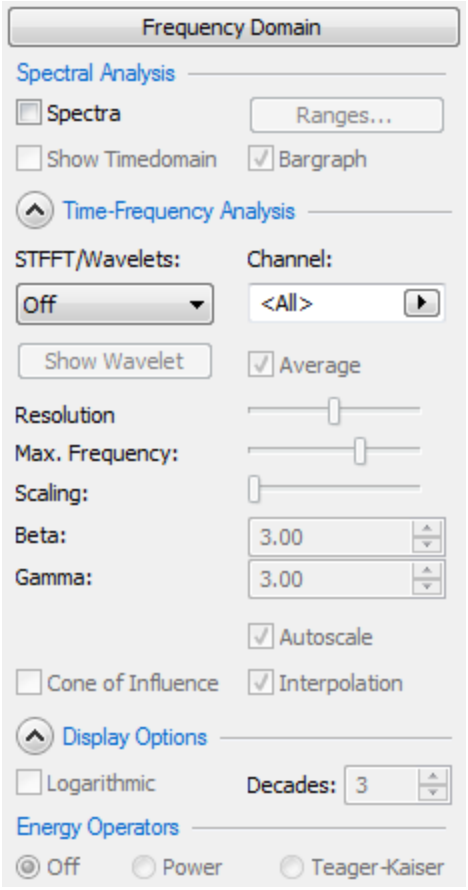
. The

panel is also accessed from the Events icon on the Functional Data Toolbar.



With Frequency domain data, you will also be using the 

panel, found under **Functional Data**.



One of the first questions is: do you want to create back-to-back epochs, or create epochs that are around stimulus, response, or other events in the continuous data file? If all you want to do is create back-to-back epochs (as you would use for spectral FFT analyses), you need only to enter the duration of the epochs and then enable the **Back to Back Epochs** option. See the **Spectral and Coherence Analyses** tutorial for an example.

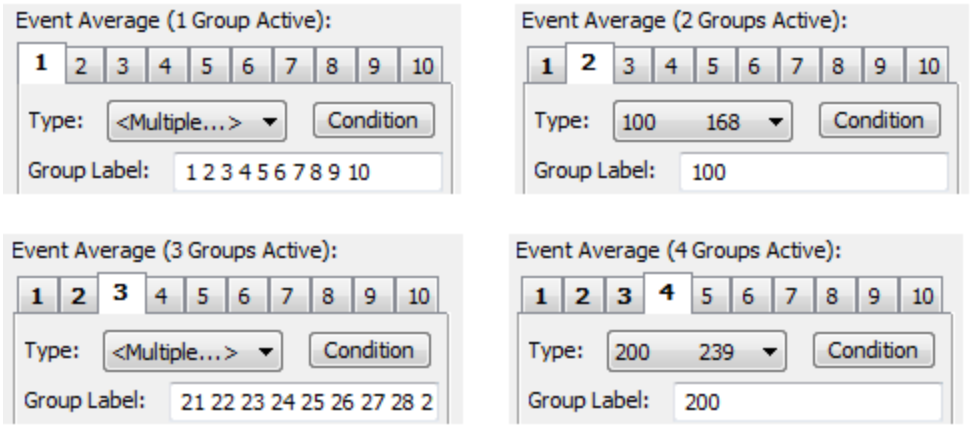
If you want to create epochs around events that are in the continuous data file, there are other things to consider. After performing the pre-processing options (baseline correction, filtering, artifact reduction, etc.), the next step is to go to Events / Epochs. Here you define which events you want to use - singly or in combination. There are two important buttons: In-Place Averaging (at the bottom of the panel) and the **Export Epochs** icon (at the top of the panel).

In-Place Averaging will create *averages* for the event groups you define (e.g., Type 1, Types 5-10, etc.). The averages for the 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 - that step is bypassed. You have the option to reject epochs using various criteria, or not. An example will be presented below.

The averages are seen with the original event codes and number of epochs that went into the 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. Four averages will be created.

This is a situation where the Group Label field is especially relevant. Here you can redefine the labels that you will see in subsequent steps. In this example, the Group Labels are created automatically.



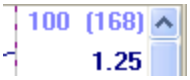
A small problem will occur for Event Group 3 because the text string does not fit in the space allotted (the string may not be seen, or it may not be seen in its entirety). In this case, it is recommended that you use a different Group Label, such as "events 21-30". For consistency's sake, we changed the Group 1 label to "events 1-10".

After averaging the epochs for each group, you will see, in the upper right corner of the data display, event information in the form: Group Label (number of epochs).

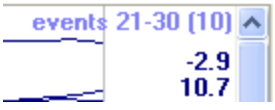
If the first group had a single epoch for each of the 10 event types (1-10), you would see the following:

The (10) indicates there were 10 epochs averaged.

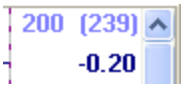
In the second group, there was the single type 100, and there were 168 of them.



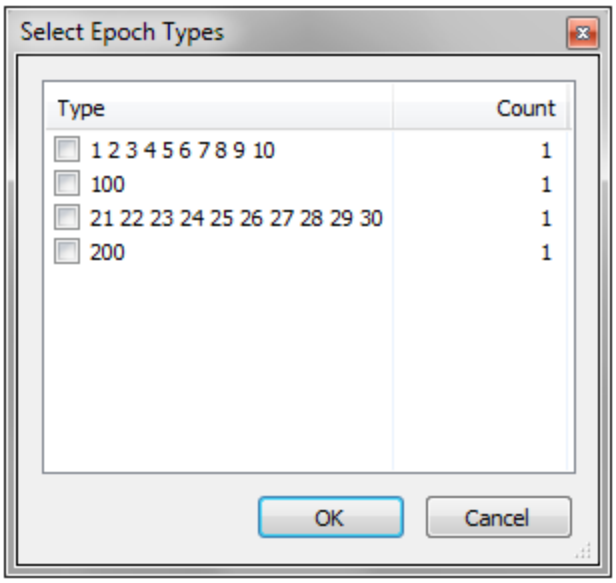
The third group in this case again had single epochs for each of the events from 21-30.



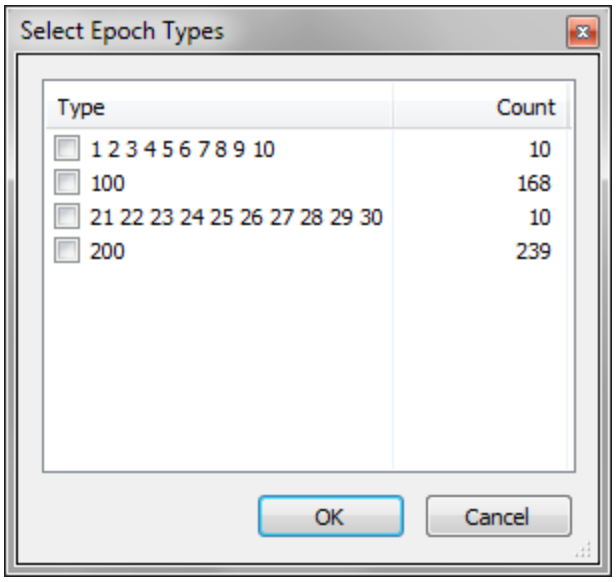
Lastly, the fourth group contained only event type 200, and there were 239 of them. You would then see the following.



If you used multiple events that created a text string too long to fit in the data display, you can still see which event types were in which average. Go to the **Events / Epochs** panel and look at the drop-down list for **Event Type**. If there are more events than will fit in the window, click the **<Multiple...>** option to see the entire list. Incidentally, here you can combine the averages to make new [unweighted] averages.



The **Export Epochs** icon will create a new file that contains all of the epochs *for all event groups*. You may exclude epoch using artifact rejection criteria, or you may save all of the epochs. When that epoched file has opened, you will be able to use the epoch rejection methods seen in the Threshold Criteria panel above. You can also select any single or combination of Group types 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, each with a Group code seen in the upper right corner of each epoch. If you select the second group (100s) for **Event Type**, in the Events / Epochs panel, and then click the In-Place Averaging, button you will see the average for all event type 100s. You may configure multiple groups, and the group averages will be created separately. The Counts (10, 168, 10, and 239) are the number of epochs in each group. By clicking the corresponding check boxes, you can include selected event code groups in a single average. These will be weighted averages (unlike when you average the average files).

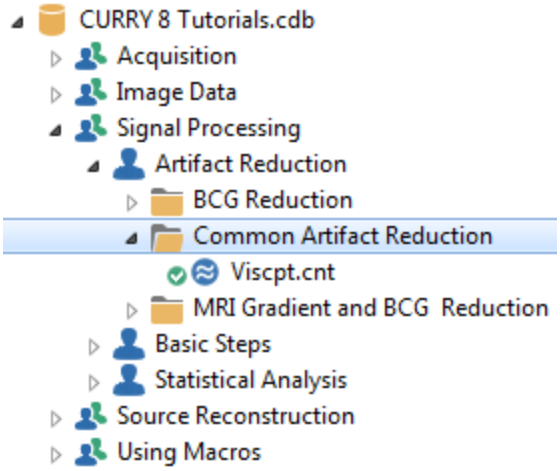


We will first demonstrate the quickest and easiest way to obtain averages.

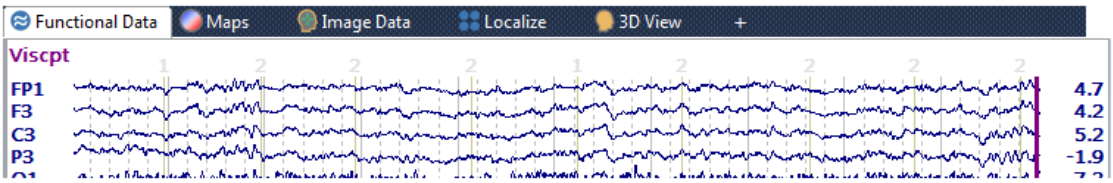
If you are not familiar with finding your way around in CURRY, please make use of the **Workflow**. Examples for using it are included in the steps below, but see also the **Workflow** tutorial.

In-place Averaging without Epochs

1. Locate the Common Artifact Reduction study shown below and open it.

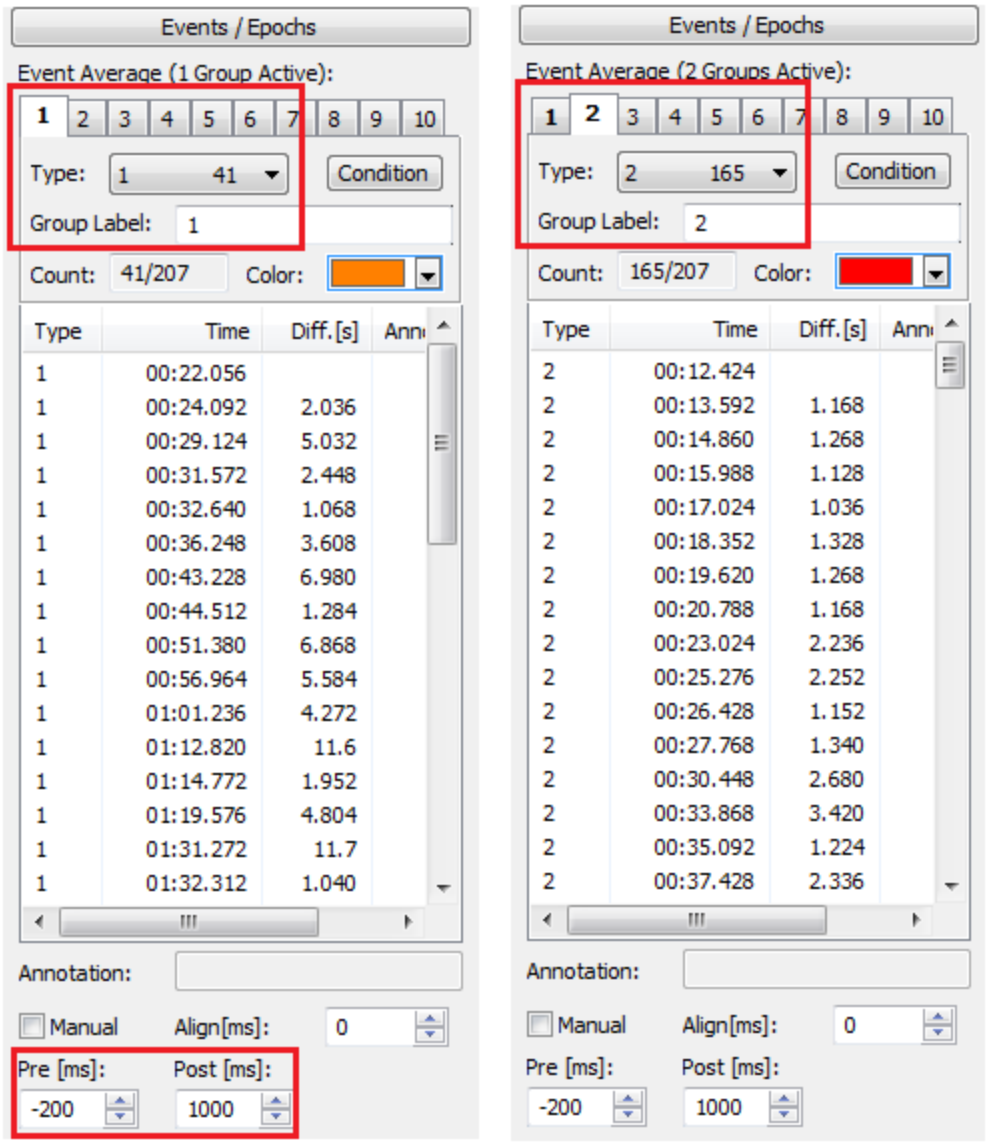


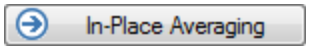
2. For this tutorial, all we care about are the Type 1 and Type 2 events in the file. We will ignore the artifacts and simply create the averages for the 1s and 2s (this is similar to a visual P300 recording where the 1s are the targets).



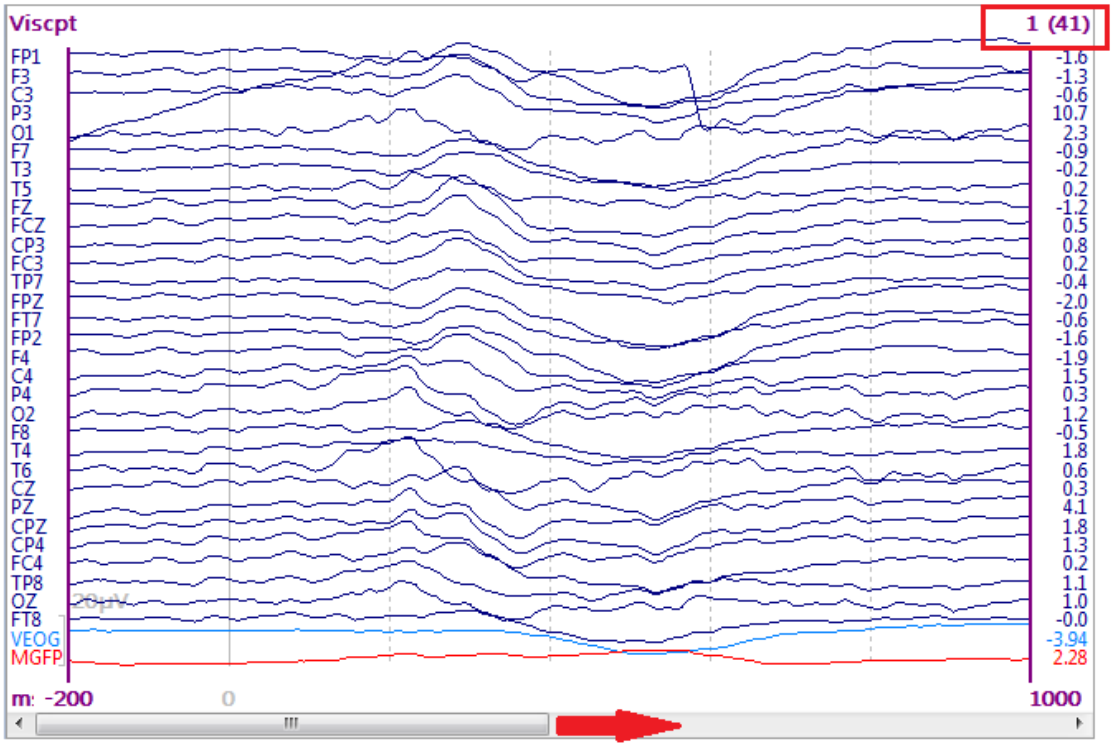
3. With this file we will create "in-place" averages. There are two paths we could take. One is to simply create the averages using all of the epochs in the file, and the other is to reject the bad epochs and then create the average. We will do it both ways.

First, we will create two event groups. From the Workflow, select Event List from the **Signal Processing** options, or click the at the top of Functional Data. In the Events / Epochs panel, set **Type** for the **1s** in Group 1, and set **Type** for the **2s** in Group 2. Set the **Pre [ms]** and **Post [ms]** fields to define the epoch interval, which in this case will be **-200** and **1000 ms**. You only need to set this once for the Groups; all Groups must use the same values.



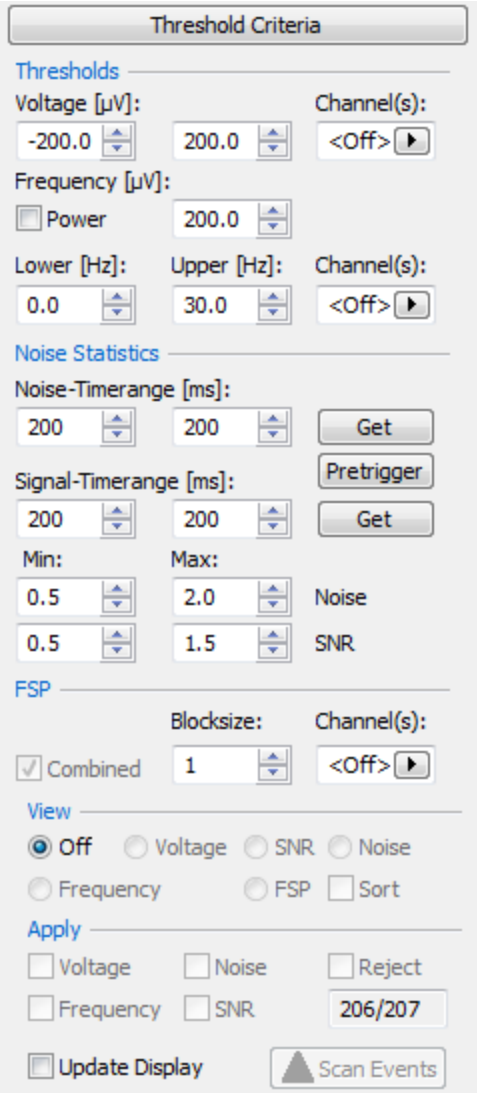
4. Now click the 

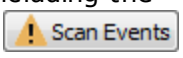
button. The averaged files will shortly appear. In the top right corner you can see the Type code and the number of epochs that went into the average. Grab and drag the slider bar at the bottom to see the other averaged file. These are the two "Instant" averages (that can be saved, etc).



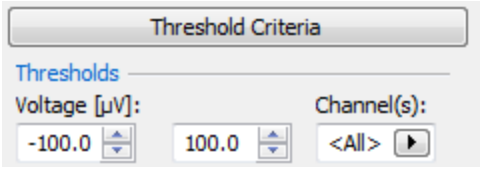
5. Now we will return to the continuous data without saving anything. Click the In-Place Averaging button at the bottom of Events / Epochs.

We will now create the averages again, but this time we will reject epochs that fall outside of criteria we set. Expand the Threshold Criteria panel (bottom of Events / Epochs). Take a moment to note the sections in it. First, you may use Voltage thresholds, based on actual waveform voltage or FFT voltage, to reject epochs. The Noise Statistics section offers another way to reject epochs, based on whether the SNRs (Signal to Noise Ratios, or just Noise) are too low or too high. The Fsp section is used primarily with ABRs and will not be discussed here. Then there is a section to View the results and then to Apply the results.

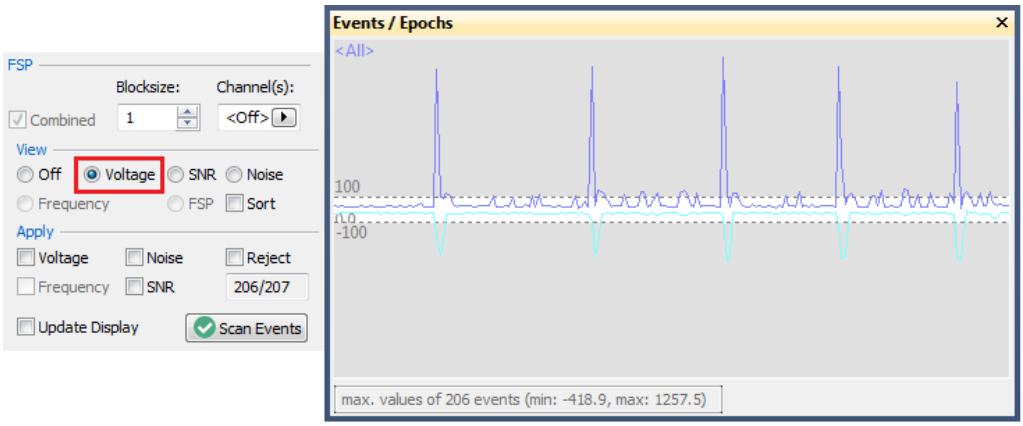


6. Let's say we want to reject any epoch where any channel has any voltages greater than **100** or less than **-100µV**. Set the values as shown, including the **<All>** selection (click the arrow and select **<All>**). Then click the 

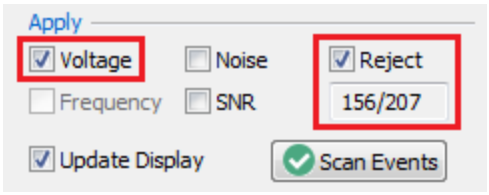
button at the bottom.

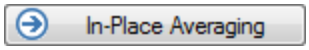


7. After the file has been scanned, you will see the **View** and **Apply** areas become active. Click the **Voltage** option for **View**. You will see the results in the Waveboard. The white region in the middle shows the accepted voltage range. The gray areas are the rejected voltages. The large peaks correspond to bad regions in the data file. If you *double-click* on one, you will be taken to that epoch. You can adjust the thresholds just by changing the Voltage values as you did above.



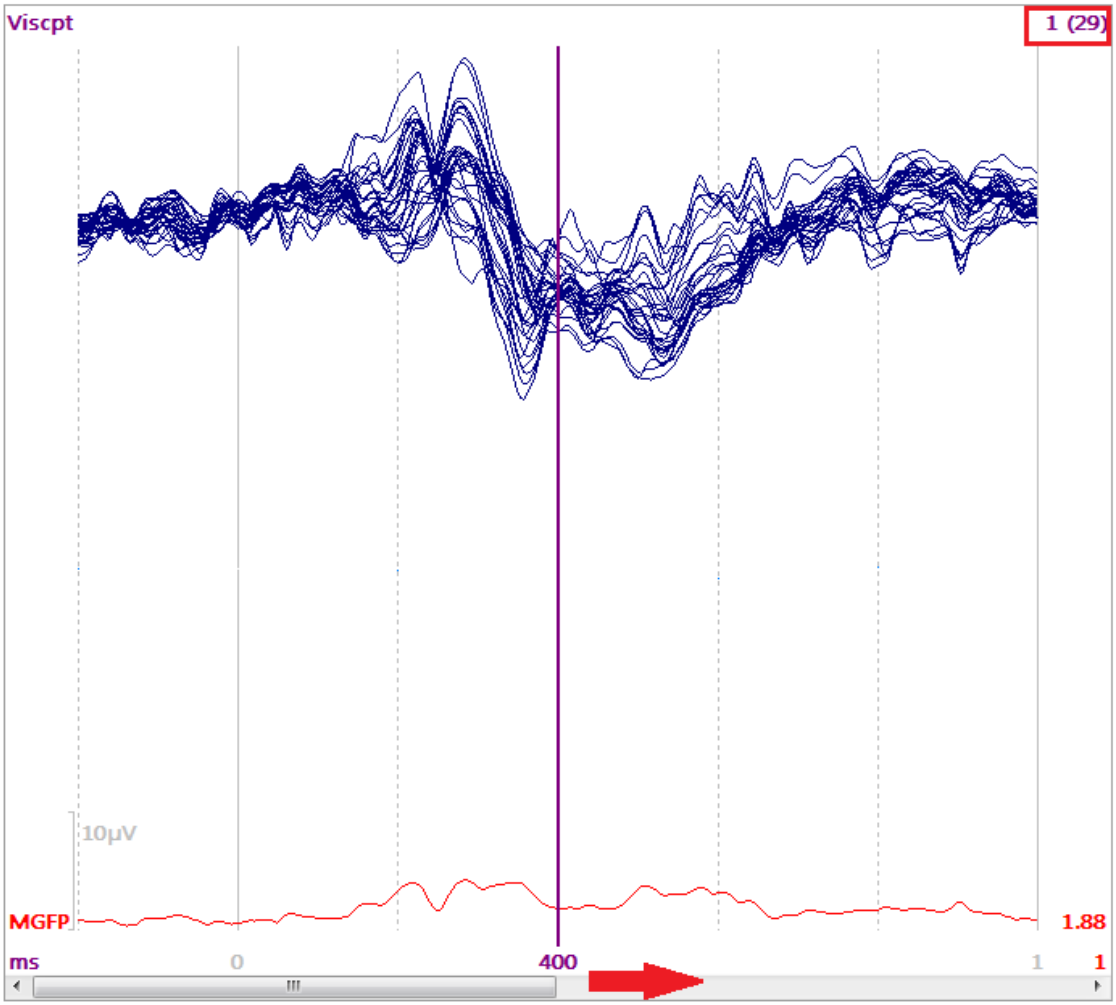
8. In the **Apply** fields, select **Voltage** and **Reject**. We now see how many epochs remain after applying the voltage criteria. Close the Waveboard.



9. As before, click the 

button in the

panel. The averaged files will again shortly appear. They appear much cleaner with the bad epochs removed. As above, note that you initially see the first event group, the Type 1s, and that there are 29 epochs that were included in the average. Drag the slider at the bottom to see the average of the Type 2s.

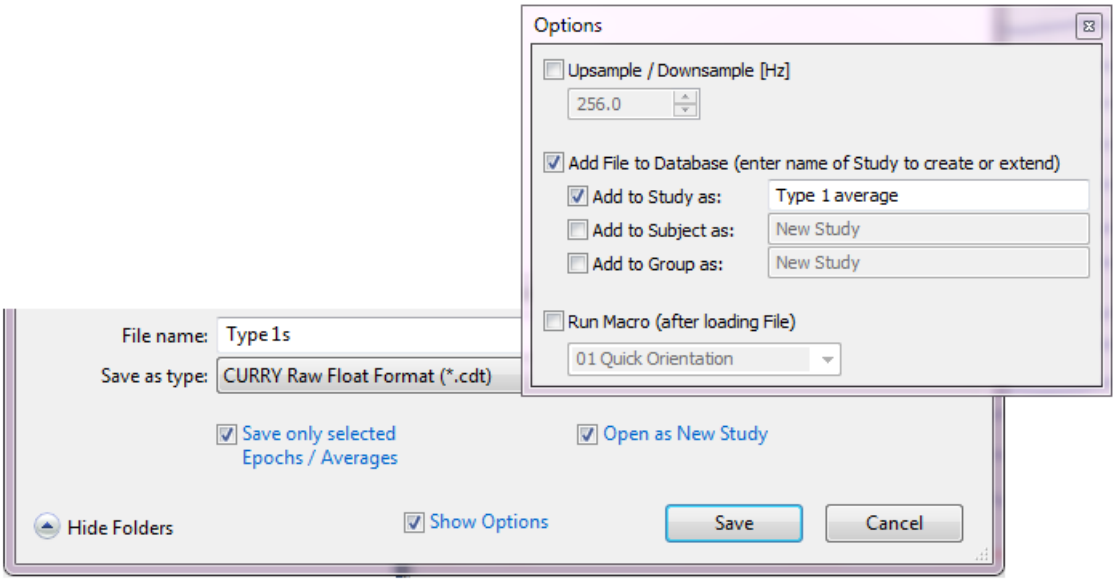


10. To save the averages, you may use the Save Functional Data option in the **Signal Processing** section of the **Workflow**, or you can go to **Functional Data → Save → Save Data**. Before doing that, you need to realize that if you save epoched file now, *you will be saving both averages in a single file*. Generally, you will want to save these as separate files, so the Type 1s are in one file and the Type 2s are in a different file. If you have ten averages, you would likely want all of them to be in separate files. To to that, you need to select only the average that you want to save, and you do that by *deselecting* all other epochs.

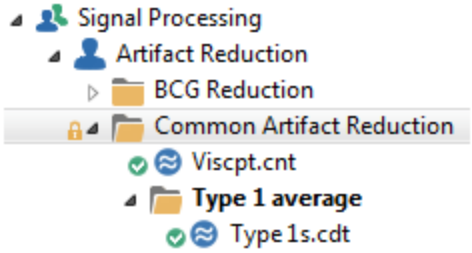
In this case where there are only two averages, it is an easy process. You can deselect the one you are not saving by displaying it and pressing the *spacebar*, or by *right clicking* and selecting Toggle Actual Epoch Space, or by clicking the icon. The deselected epoch(s) will have a gray background (unless you change it to a different color). Save the selected epoch (do not do it yet), and then select the second epoch while deselecting the first and then save that one. In some cases it may be easiest to *right click* and select Invert Epoch Selection.

If you have multiple files, it is helpful to use Deselect All Epochs and then select only the one you want to save.

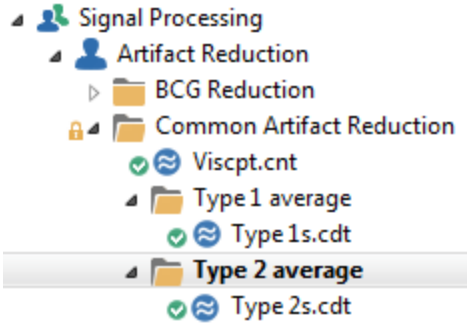
11. In this case, deselect the second average and select only the first one. After selecting Save Functional Data from the Workflow, note the options at the bottom of the **Save Data** window. **Upsample / Downsample [Hz]**, in the **Show Options** dialog, is where you can decimate the data file (downsampling). Be sure that the **Save only selected Epochs / Averages** option is enabled. If you are using a Database, you will likely want to create a folder for the average data files. You can add it at the Study, Subject, and/or Group levels. Select whether you want to see the file after you save it (**Open as New Study**). Enter the information as shown and click **Save**.



These settings create the folder in the Database, as shown.



Close that Study. Deselect the first average and select the second one. Save that file using **Type 2s** as the file name and **Type 2 average** as the folder name. You will see that average and also the addition to the Database.



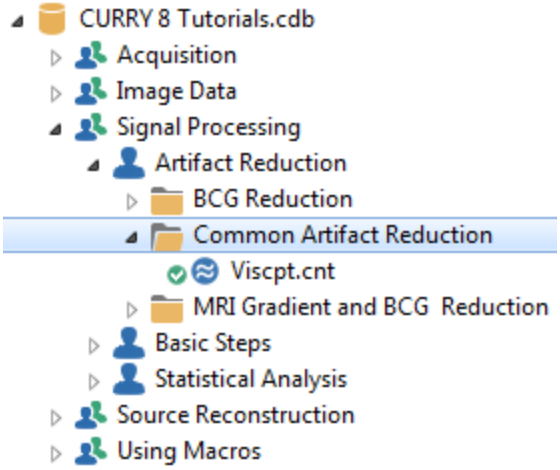
Close all of the studies.

This tutorial has illustrated the quickest way to generate averages using all epochs, or only those epochs that were not rejected by the Voltage method, and then save the averages.

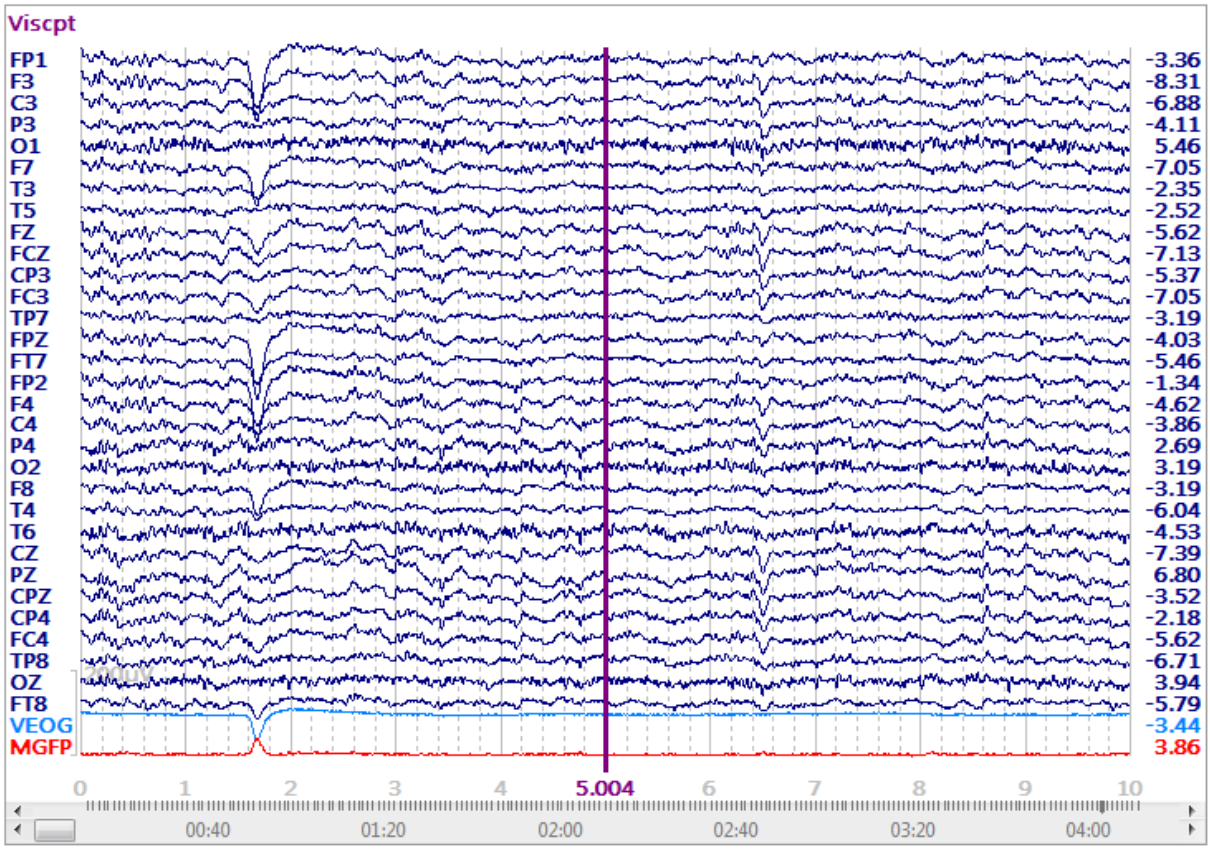
As shown above, it is possible to create the average data directly from the continuous data, without ever seeing the epochs. If preferred, you have the option to save the epochs and then perform additional processing and averaging.

Continuous to Epochs to Averages
There are two ways you may go from the continuous data, to an epoched file, and then to the final averages. Basically, you may reject bad epochs before you save the epoched file, or you may save all of the epochs and then reject the bad epochs from the epoched file. You may also do both by rejecting bad epochs before creating the epoched file and then again after creating the epoched file, if desired. We will demonstrate both in the following example.

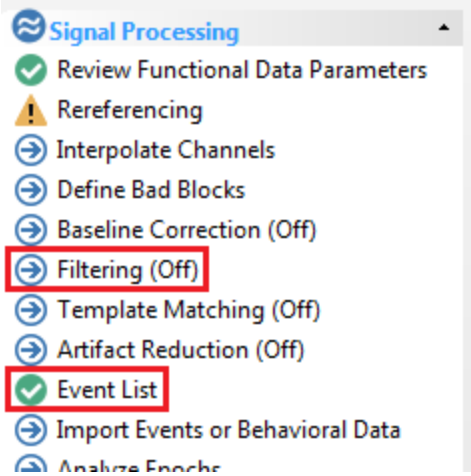
1. Locate the **Common Artifact Reduction** study in the *CURRY 8 Tutorials* Database (same as above; the folders that were created have been removed).



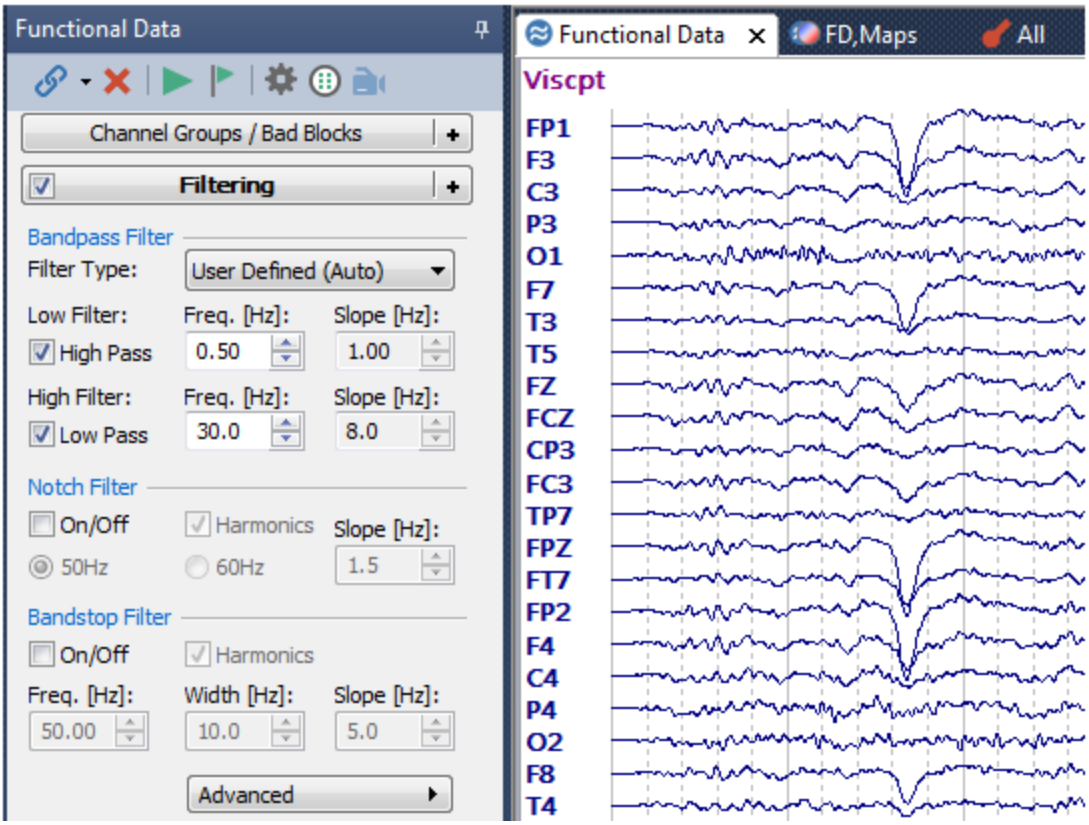
2. Open the Study and the Functional Data will be displayed. Again, the file is similar to a visual P300 recording where the Type 1s are the targets and the Type 2's are the distractors. We will leave the artifacts in the file (electrode pops and blinks) so there will be plenty of epochs to reject.



3. If you are using the **Workflow** as a guide, start by asking yourself what is it that you want to do? In this case, we will do some filtering and we will be using the Event List. We would ordinarily use Artifact Reduction, but we will leave the artifact as is for now.

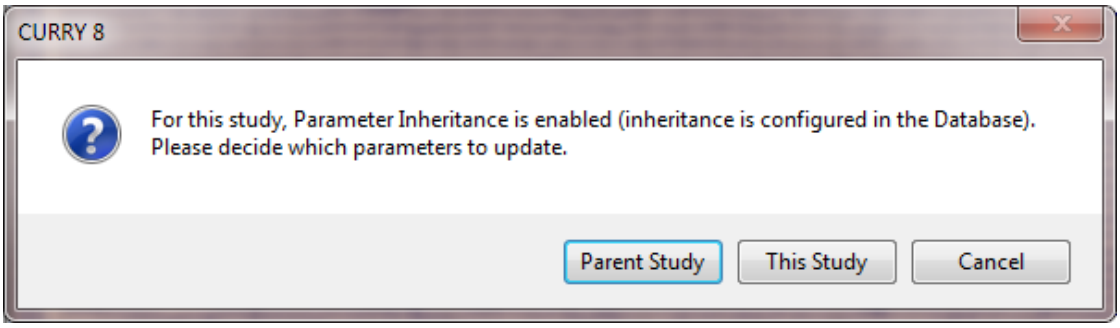


4. From the Workflow, select the Filtering (Off) option. This displays the Filtering panel. Select **User Defined (Auto)** for **Bandpass Filter**. Enter, for example, **0.5 Hz** for the **Low Filter**, and **30 Hz** for the **High Filter**. (The slope for a filter should not exceed twice the Frequency; **User Defined (Auto)** sets the slopes automatically). Filtering is applied immediately when you change the parameters.

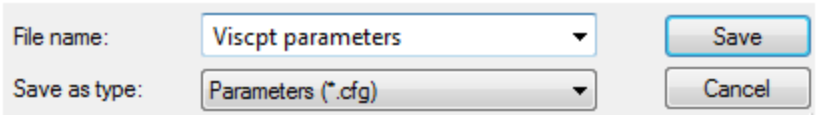


This would be a good time to save the **Study Parameters**. Saving the Study Parameters will create a .cfg file that contains all of the parameter settings in the program, including the changes we have just made, namely, the filter settings. If we had marked Bad Blocks, we would have the option to save them when the study is closed. These are saved to a different file. The Study parameters will be applied the next time you open the Study, and you will not need to perform the operations again. Click the **Save Study Parameters** icon on the Toolbar.

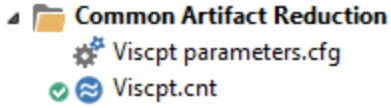
In some situations, you will see the following dialog, asking if you want to save the file in the parent study, or in the current study. If we had multiple studies below a parent study, and we wanted to apply these same settings to all of the "child" studies, we would click **Parent Study**. If you want to save the file with this study only, click **This Study**.



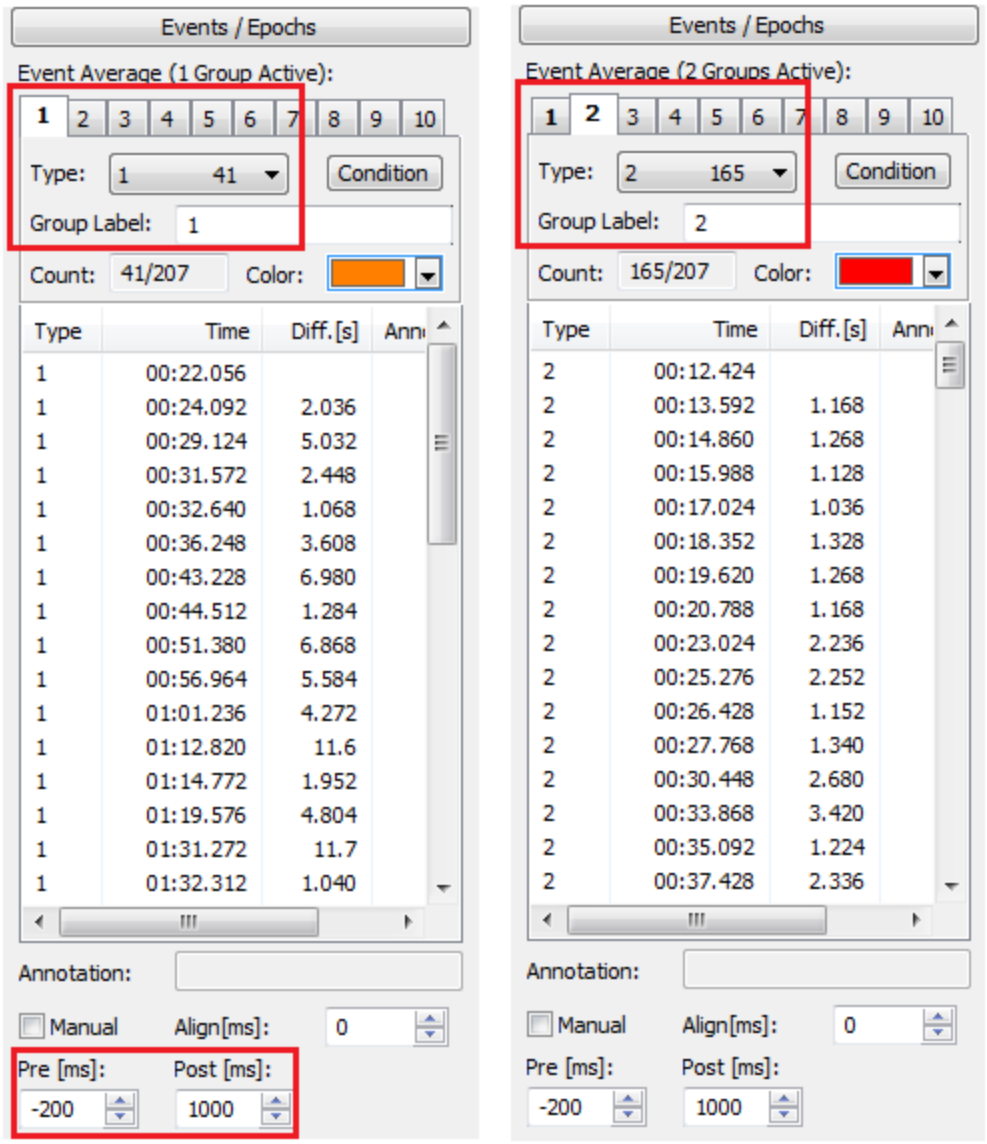
A Save As dialog will appear. Enter a file name for the .cfg file (or use the default name, which uses the study name). The file will be saved to the folder where the data file is located (unless you change it).



The file has been added to the Database automatically.

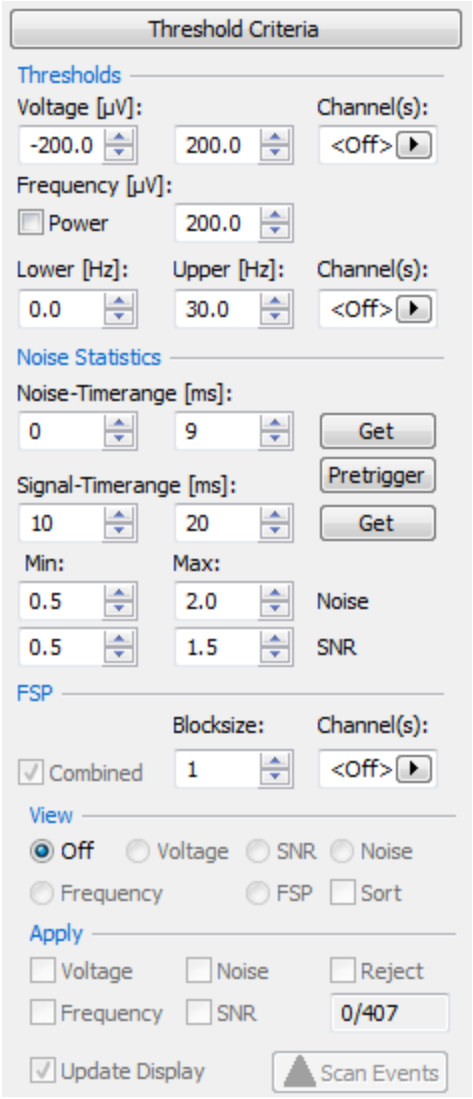


5. Next, click Event List from the **Workflow** list, or click the button from the top of the Functional Data, or click the Events / Epochs tab in the lower left area (adding it if need it), or click the Events button in the Epochs panel. Any one will display the Events / Epochs panel. As above, select **Event Average** group **1**. Select **1** from the **Type** drop-down list, so that only the Type 1 events will be listed. There are 41 Type 1 events in the file. For the second Group, select Type 2. There are 165 Type 2 events in the file. Set the **Pre [ms]** and **Post [ms]** fields to define the epoch interval, which in this case will be -200 and 1000 ms. You only need to set this once for the Groups; all Groups must use the same values.



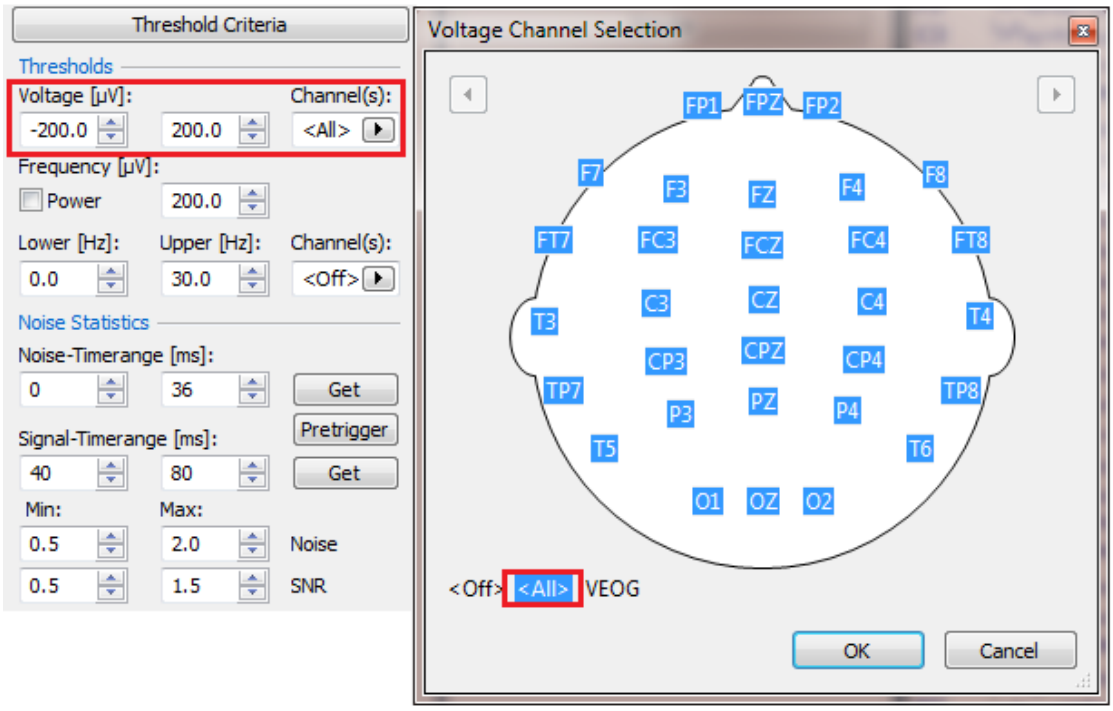
6. In the previous example above, we created averages that included all epochs, and we created averages where epochs were rejected according to criteria we set. We did that without ever seeing or saving any epochs. In this example we will reject some of the epochs before saving the epoched file, and then reject more of them afterwards (for demonstration purposes).

Expand the Threshold Criteria panel, below Events / Epochs.



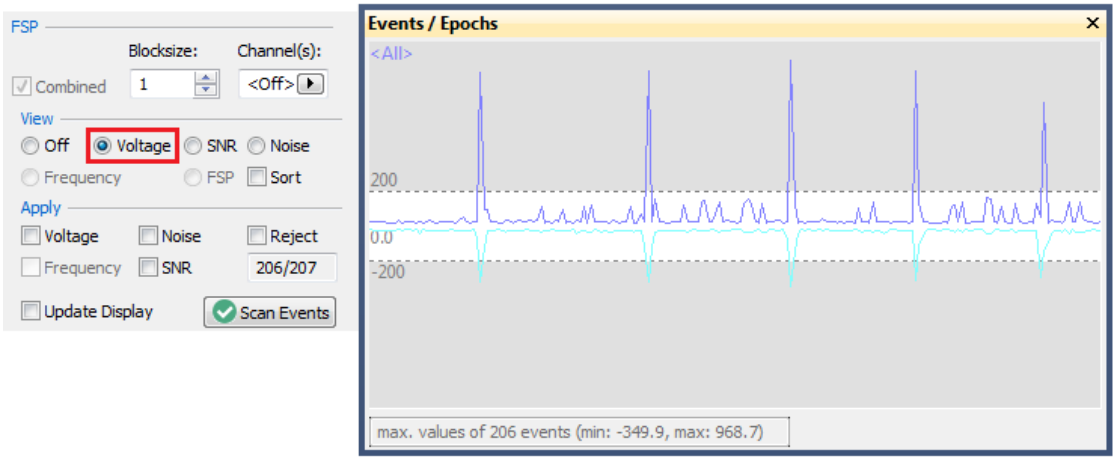
For this example we will use the conventional **Voltage** thresholds first, and then use **Noise Statistics** later with the saved file. You may apply either, neither, or both.

7. Set the voltages for **-200** to **200µVs**. In the **Channels** dialog, select **All**, if needed. The artifact channels were excluded in this example, but you may include them as well using *Ctrl+click*. Any EEG channel that has a voltage anywhere in an epoch greater than 200µVs or less than -200µVs will cause the epoch to be rejected.

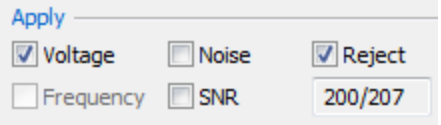


Then click the Scan Events button. (If you deselect Update Display, the process will go faster).

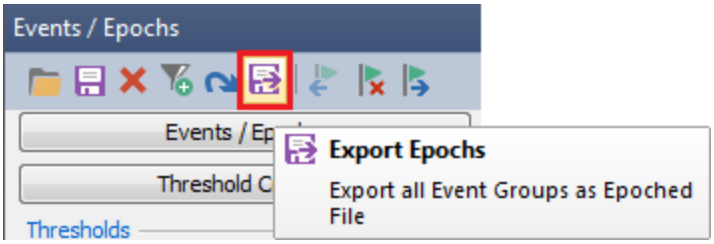
8. When the scan is finished, select **Voltage** in the **View** section. The Waveboard now displays the voltage for All channels across epochs. The white area in the middle is the accepted range; the gray area is the rejected range. These may be adjusted using the same fields in which they were set. *Double-click* on an epoch, such as a peak, to go to that epoch. In this case, we will keep the thresholds as they are. Basically, we are rejecting the epochs containing the large artifacts, while keeping the epochs containing blinks. (Ideally, you would remove or reduce both of these from the continuous data file; we are doing it this way to illustrate the functionality).



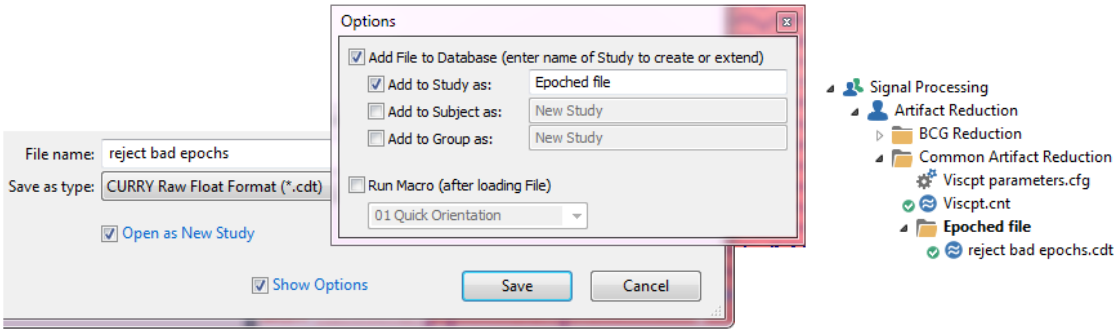
In the **Apply** section, select **Voltage** and **Reject**. We now see that 200 epochs remain. Close the Waveboard when finished.



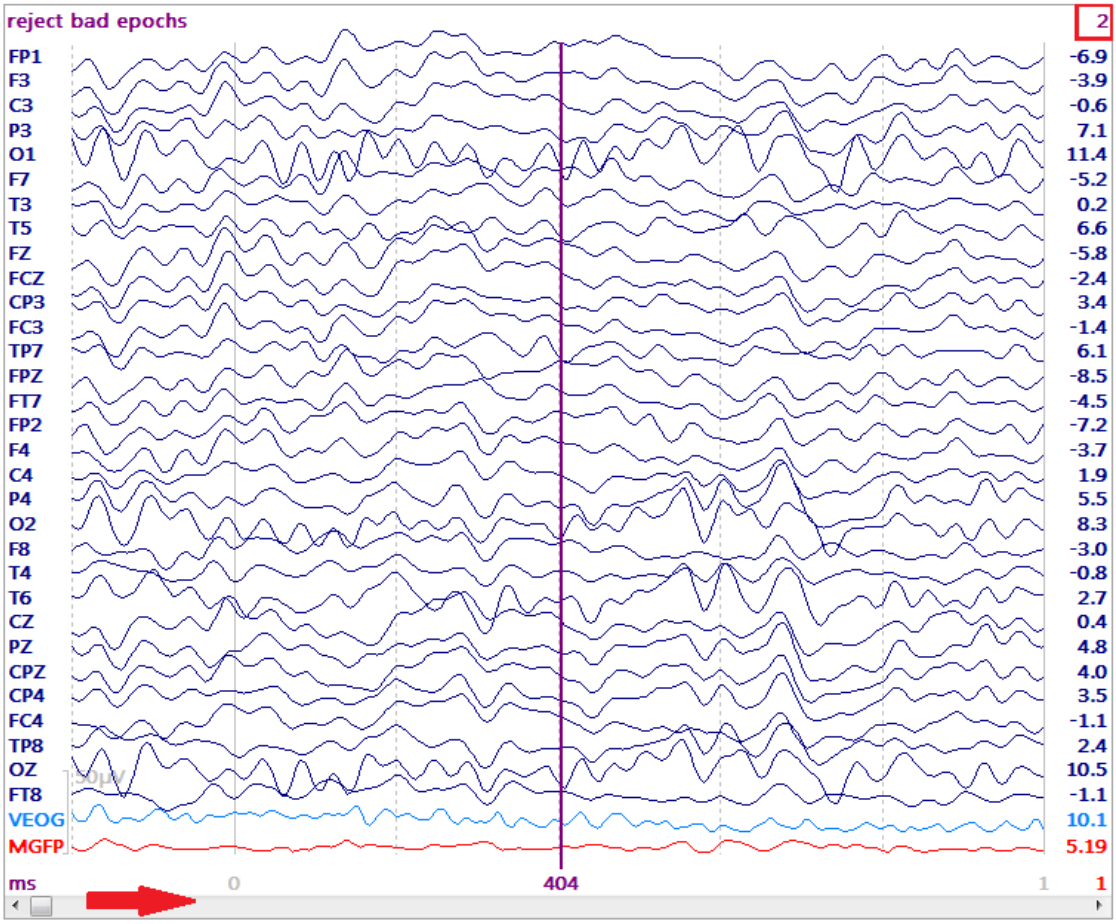
9. At the top of the **Events/Epochs** section, locate and click the **Export Events** icon .



In the Save Data window that appears, enter a file name, such as *reject bad epochs*. Add a folder to the Study called *Epoched file*. Enable **Open as New Study**. Click **Save**. The file is added to the Database.



When the scan is finished you will see the individual epochs. Drag the slider at the bottom to see the epochs, or you can use the buttons (or keyboard *arrow* keys). The number in the upper right corner displays the Type.

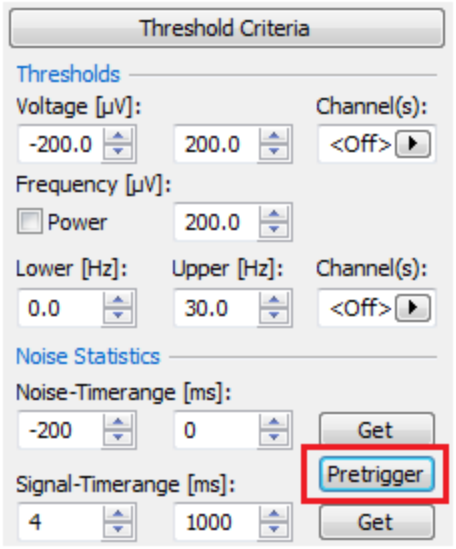


10. Now we will reject epochs that contain remaining artifact. We could use the **Voltage** threshold again, with more stringent criteria. For demonstration purposes, we will use the **Noise Statistics**. In the Threshold Criteria panel, look at the **Noise Statistics** section. Briefly, CURRY will compute the SNRs (Signal to Noise Ratios) for each epoch using all channels. Generally speaking, the greater the SNR, the better the data in the sweep. If some epochs have abnormally low SNRs, this indicates that the signal (the data in the Signal Timerange) is low in comparison to the noise (the data in the Noise Timerange). So, if SNR is low for a given epoch, then either there is more noise in that epoch or less signal. On the other hand, if there is unusually high voltages in the Signal Timerange, due to some artifact, this will inflate the SNR abnormally.

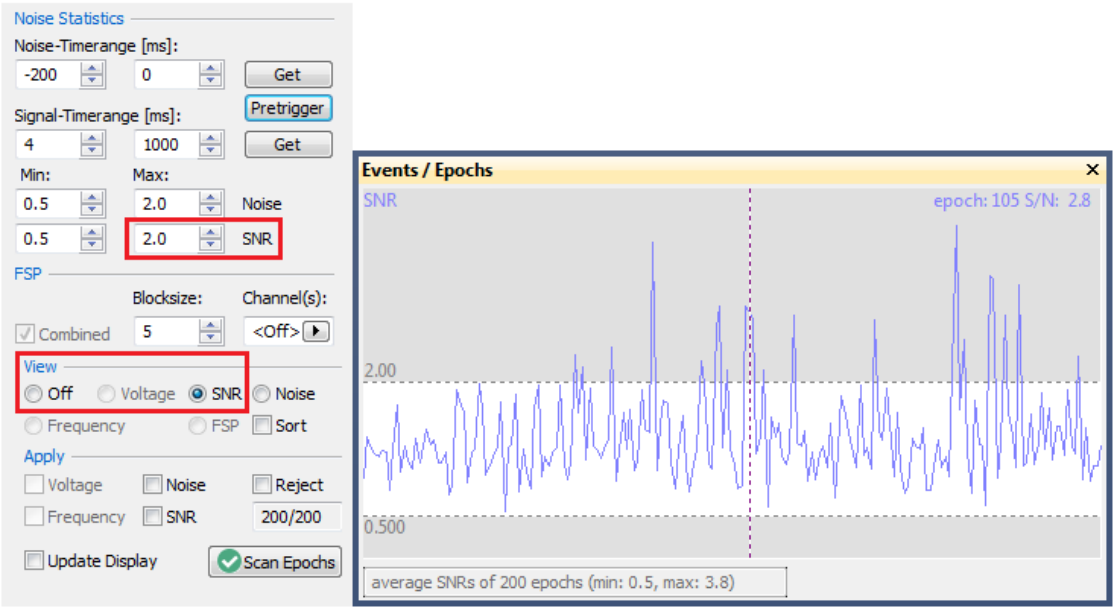
Note

When you use the **SNR Rejection** method, it is recommended that the pre-stimulus interval be the same duration as the post-stimulus interval (so the frequency components of the two intervals will be the same). It was not possible with this data file, as the stimuli were presented too close together.

Click the Pretrigger button for **Noise Statistics**. This sets the Noise and Signal Timeranges.

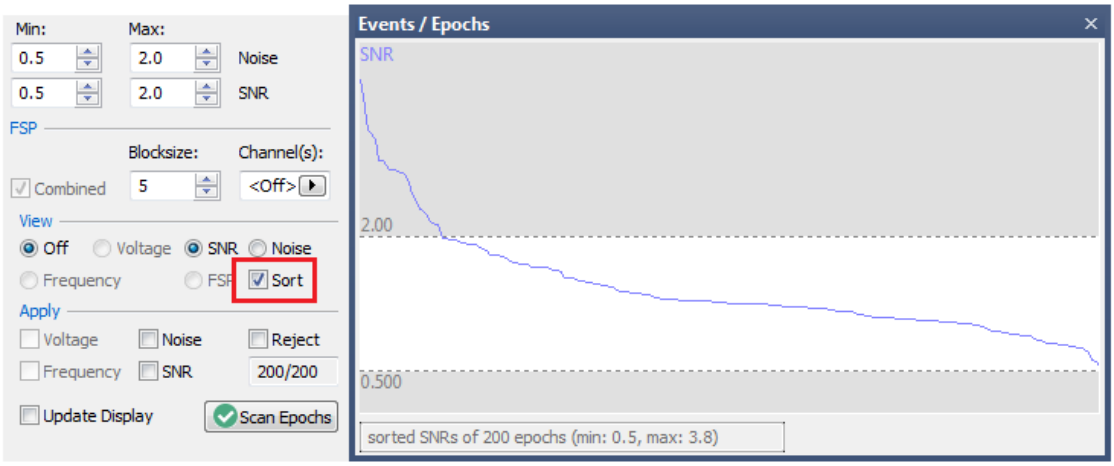


11. Then click the Scan Events button. (If you deselect Update Display, the process will go faster). When the scan has been completed, click the **SNR** option for **View**. The SNR upper criterion was increased to 2.0 to allow more epochs to be accepted. As above, you can *double-click* on a peak to see that epoch. The peaks in most cases here are due to blinks.

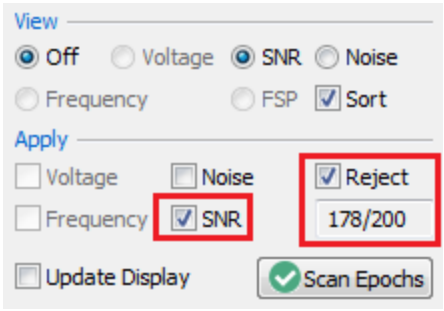


The setting of the Min and Max thresholds is somewhat arbitrary. There are no absolute rules to follow. It is helpful to view some of the outlying epochs to determine what is causing the atypical values, and then decide whether to include or exclude epochs having those values. Using the same thresholds for all subjects allows you to say that epochs having SNRs within a given range were accepted for averaging, thereby providing a different criterion than regular voltage thresholds. Using different Min and Max values across Subjects becomes difficult to describe in a research paper.

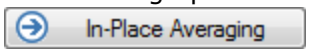
12. It is also useful to select the **Sort** option, which displays the SNRs from largest to smallest.

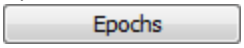


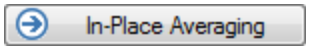
13. To apply the criteria, select **SNR** and **Reject** in the **Apply** section. We now see that 178 epochs remain. Close the Waveboard.



If you look at the bar below the data file, you will see the rejected epochs as gray bars, much like the bad blocks you see with continuous data files.

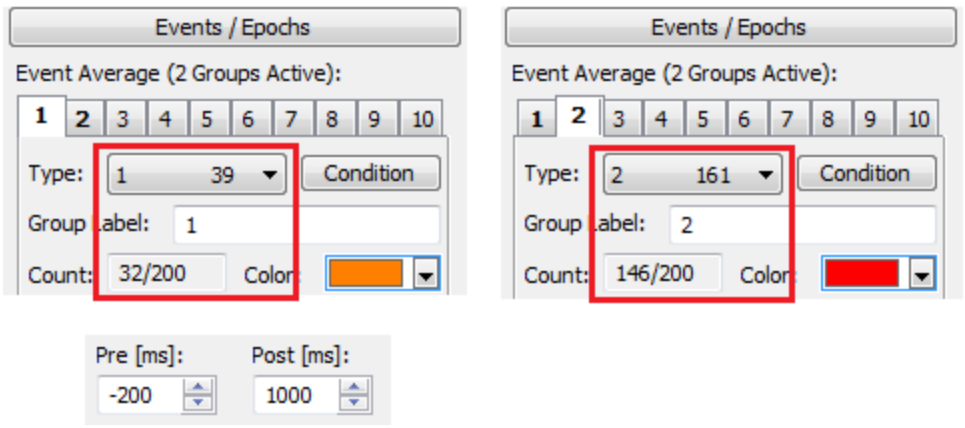
14. Next, we can now average the remaining epochs. There are two ways to do this. The main one is to use the 

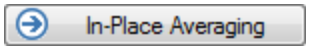
button, as was described above. Alternatively, you can use the **Average** option under 

. We will demonstrate both so you can see the differences, starting with the 

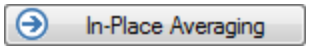
button.

15. Set Group 1 for the Type 1 events and Group 2 for the Type 2 events, as we have done before. The numbers in the Count field show the number of remaining epochs (note that we already rejected epochs). Be sure to set the Pre and Post fields to -200 and 1000 ms.



16. Then click the 

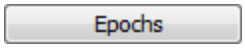
button to see the averages, as before, which you can go on to save individually.

The advantages of using the 

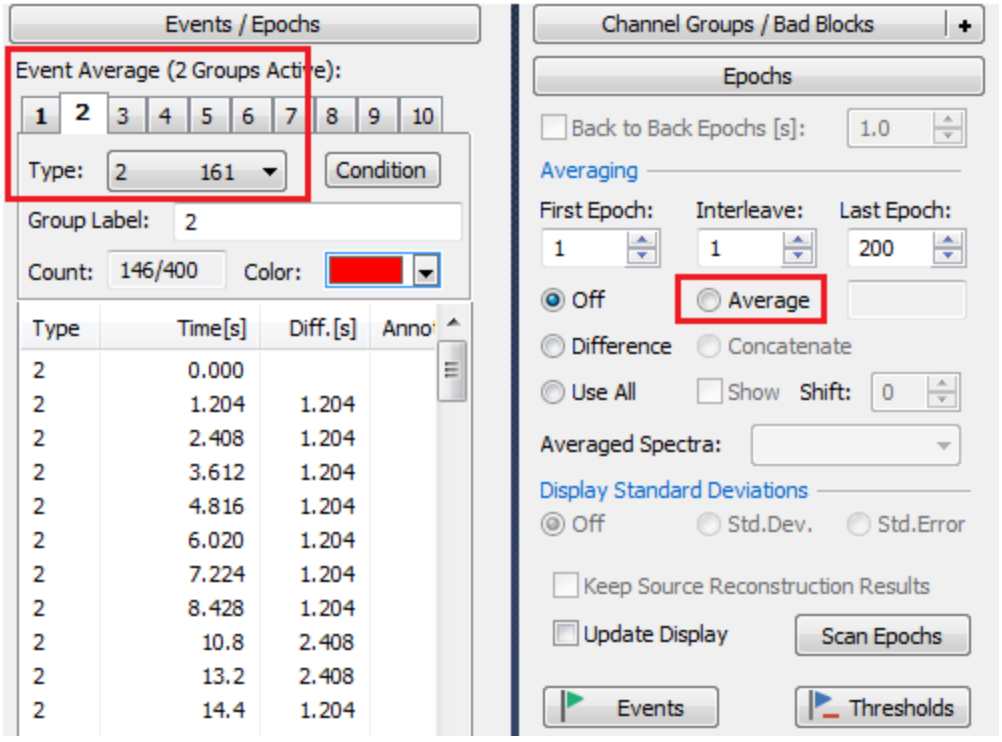
button are that you can configure the event groups in the same way as when you are using continuous data. This is not the case with the **Average** option, as we will see shortly. Also, you may change the Pre and Post times for the epochs.

17. Click the

button to return to the epoched file. Expand the

and 

panels. We will be using the **Event Average** fields and the **Average** option.



There are some things that need to be understood to use this method correctly.

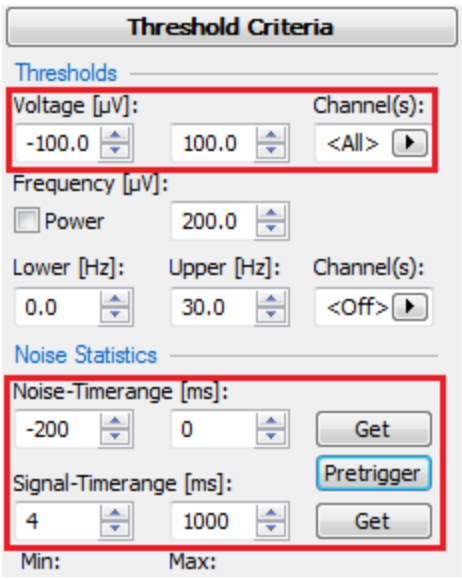
1. When you click **Average**, you will get the average of ***ALL of the epochs*** that you have selected in the Event Average groups. In other words, if you select the Type 1's for Group 1 and the Type 2's for Group 2, you will get a single average of the accepted Type 1s and 2s, not separate averages for each. If you were to add a third group where you selected both Type 1s and 2s, you would still get the same average of all Type 1s and 2s.

2. If you do not select any type codes in the Event Average groups, you will also get the average of all of accepted epochs.

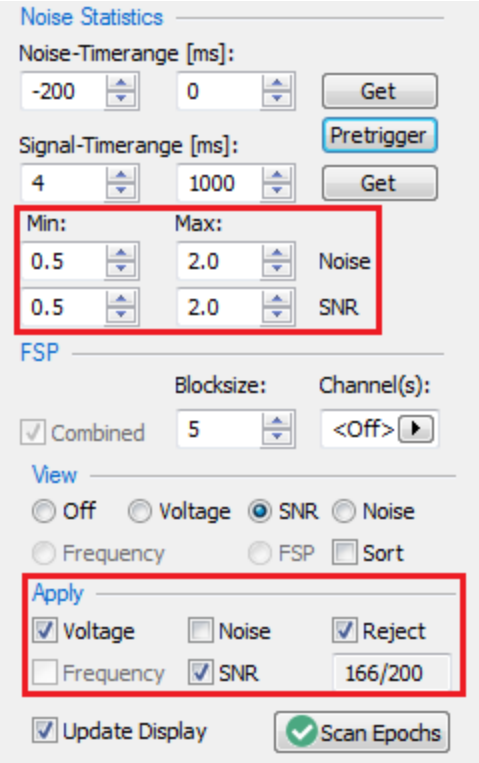
3. The best way to use this method is to use only a single Event Average group. Select a single type code, like the Type 1s, and only the Type 1s will be averaged. Select the 1s and 2s, and they will be averaged together, and so on. If you create the averages one at a time, combining type codes as desired, you can then save the final averages one at a time.

4. If you will be using the epoch rejection criteria under Threshold Criteria, you should use Scan Events with all related types so you can set the thresholds based on all epochs, and then you will likely need to scan again for each individual type code (described below).

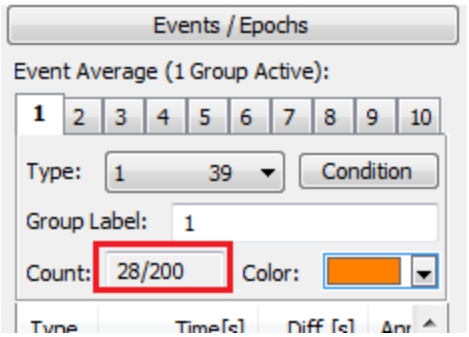
15. To demonstrate, we first want to set the thresholds based on all epochs. Select Type 1 for Group 1 and Type 2 for Group 2, as usual. Make sure the **Pre** and **Post** times are at **-200** and **1000** ms. Set the threshold criteria as shown. Then click Scan Events.

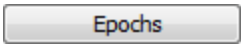


Set the **Min** and **Max** thresholds as shown, and **Apply** the **Voltage** and **SNR** criteria. Be sure to enable the **Reject** option. Now the good epochs remain.

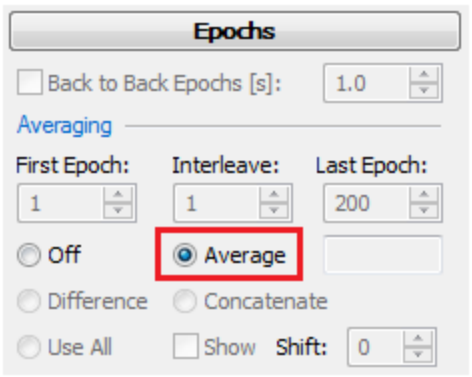


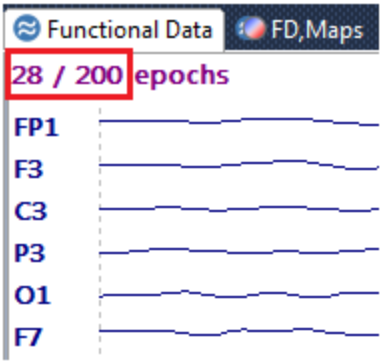
16. Now you must go back to the **Event List** and select only **Group 1**, with **Type 1** (Turn Group 2 Off). The **Count** field will show the number of good epochs.



Now click **Average** under 

. You will see the average, with the number of epochs in the upper left corner. You can then save the file, as usual. Note that when you use the Average option, you will be averaging ALL of the type codes you selected in the Event List, as described just above.



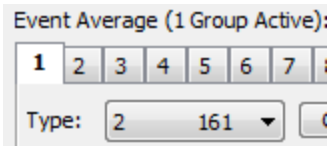


17. To average the next group, you will need to do the following:

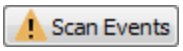
    a. Set **Average** to **Off**

.

    b. Select the second Type code for the first Group.

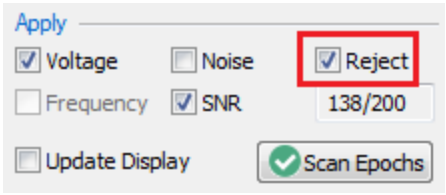


    c. Go to

and click 

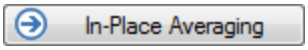
again.

    d. Enable the **Reject** option, and close the Waveboard.



    e. Enable

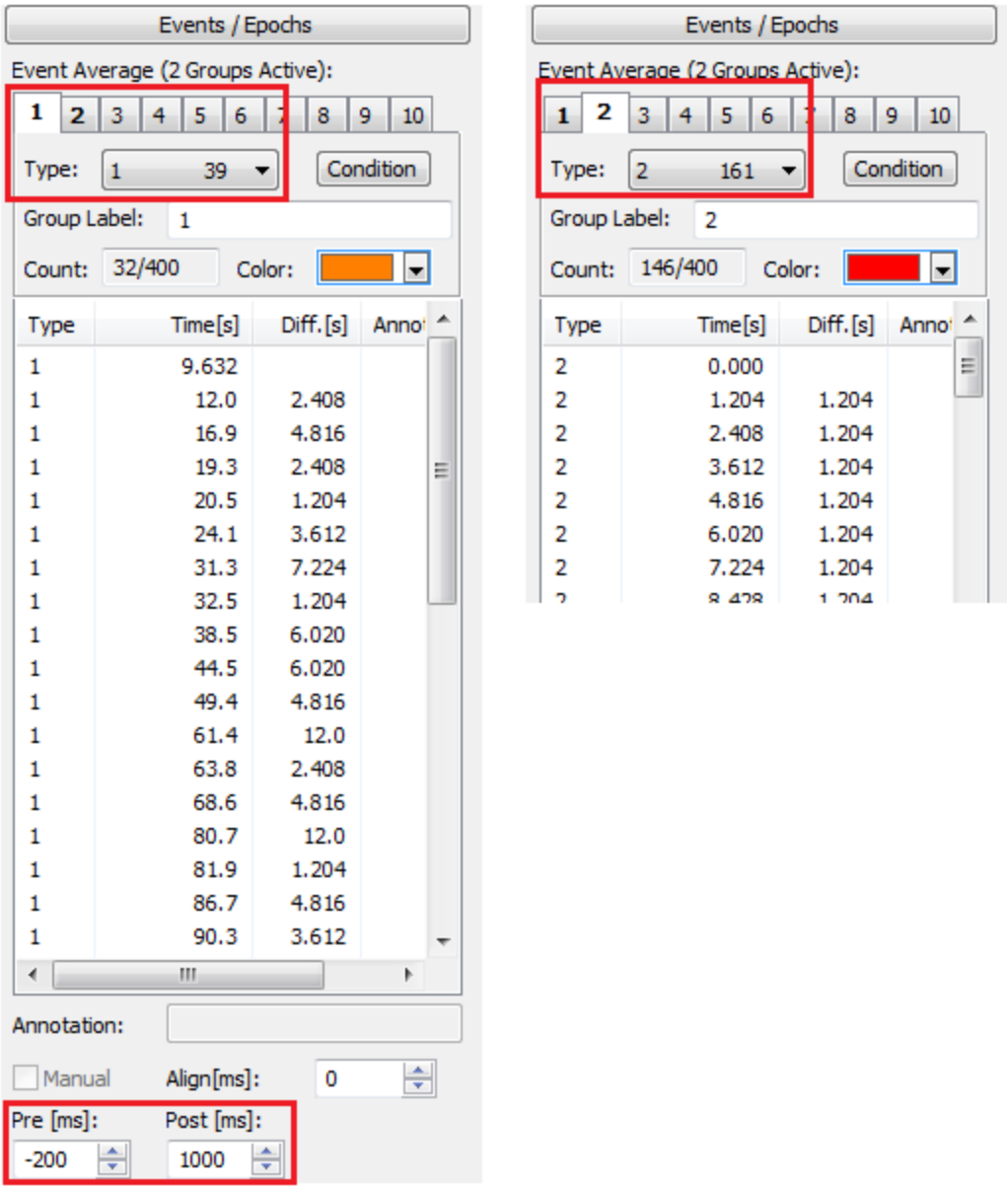
again to see the new average, which you can then save as usual.

Again, the advantage to this method is that you can use the First and Last Epochs as well as Interleave options. Otherwise, the 

method is much easier.

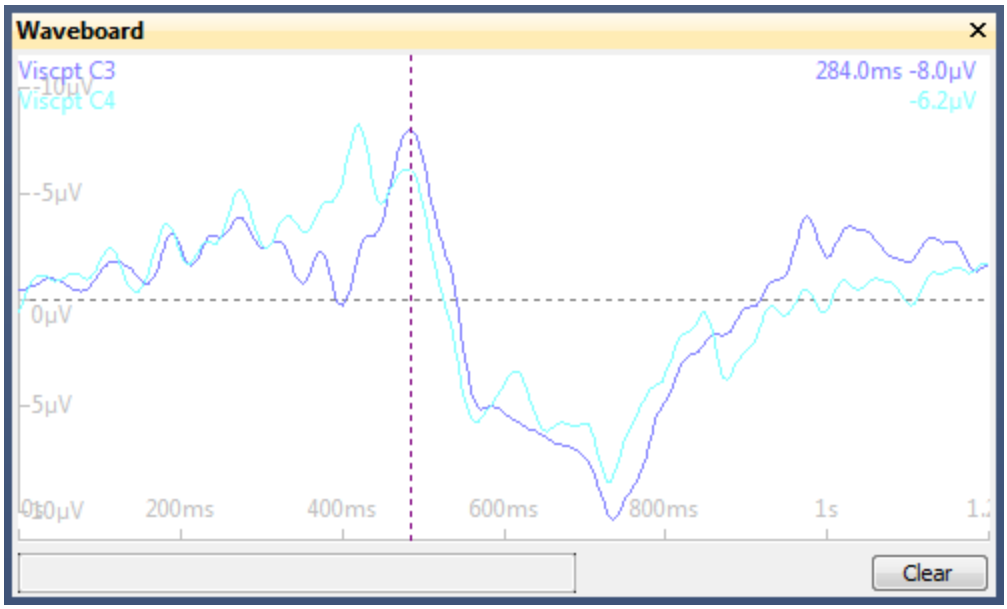
Comparing Files and Channels
At some point you will want to compare, or overlap, channels from the same data file or across data files.

1. Close any Studies you have open, and reopen the same Epoched Study we have been using. Go to Events / Epochs and set up the Type 1s and 2s as we have been doing, with the -200 to 1000 ms epoch interval.



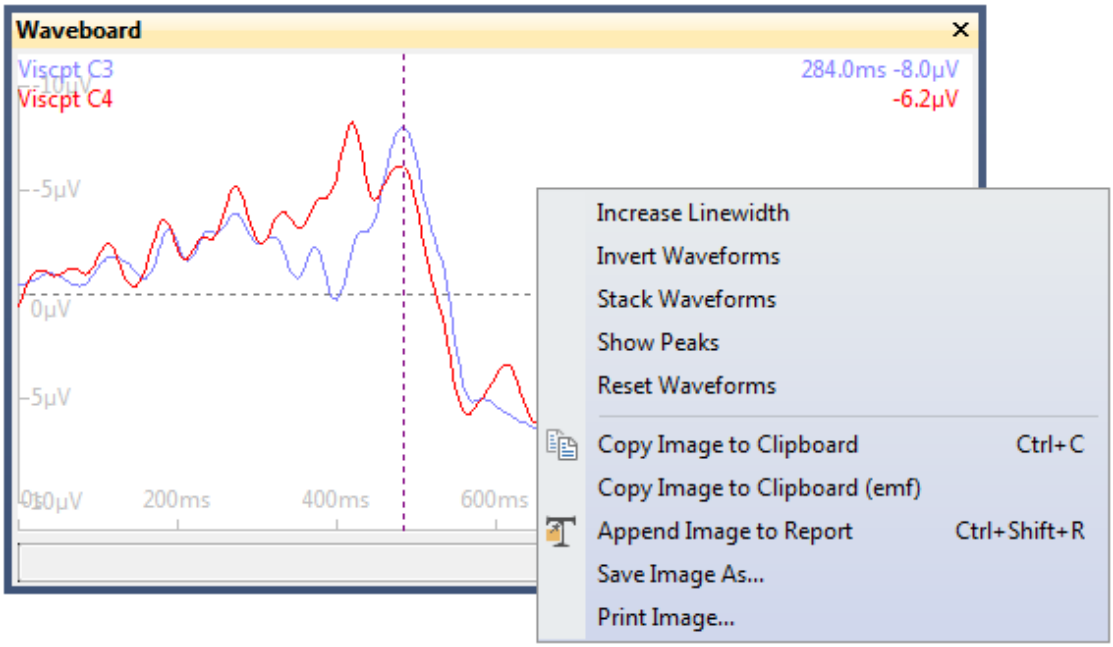
2. Click on the In-Place Averaging button to create the in-place averages.

In the first average, let's say we want to compare (superimpose) C3 and C4. *Right click* on C3 and select **Send to Waveboard 1** (there are three Waveboards you can use). Then do the same with C4. You will see the two wave forms in the Waveboard. The cursor gives the time point and voltage for the first wave form you send.

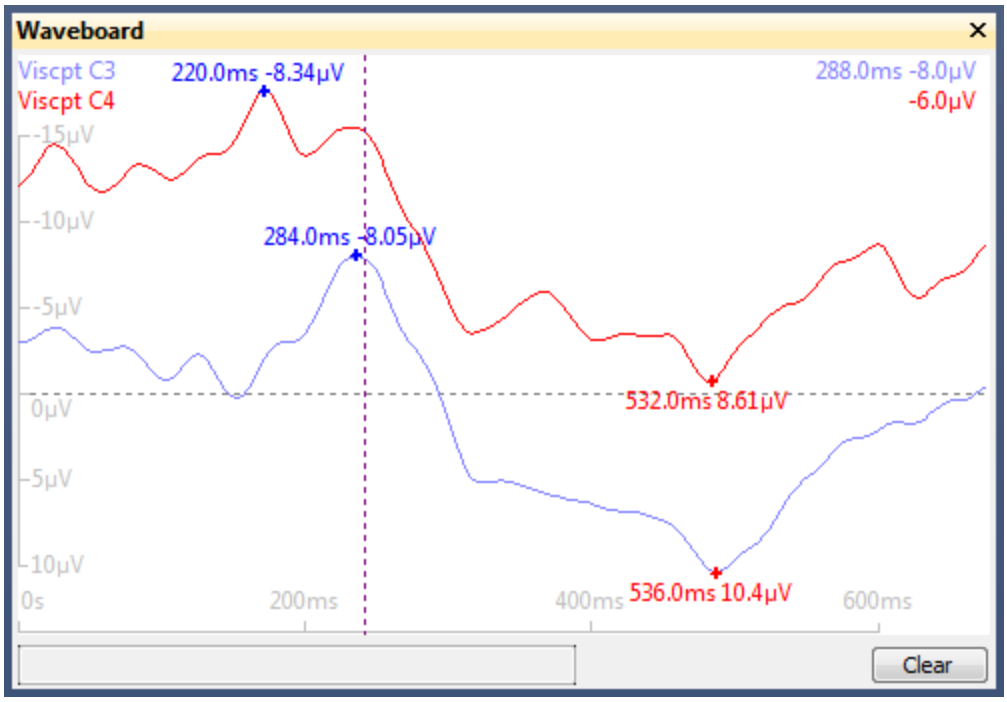


The color for C4 is not ideal, so right click on the *Viscpt C4* label, select **Color**, and select a different color. The *mouse wheel* adjusts the scaling.

Right click elsewhere in the display to access the context menu. The options are largely self explanatory (refer to the User Guide if needed).



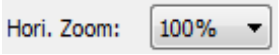
There are a few combination keys that are very useful. *Shift+drag* will move the entire contents of the waveboard. *Ctrl+mouse* wheel repositions the second waveform, so that you can see them not superimposed. Shift+mouse wheel expands / constricts the x axis, allowing you to zoom in to selected areas. With a little practice you can obtain the display you want.



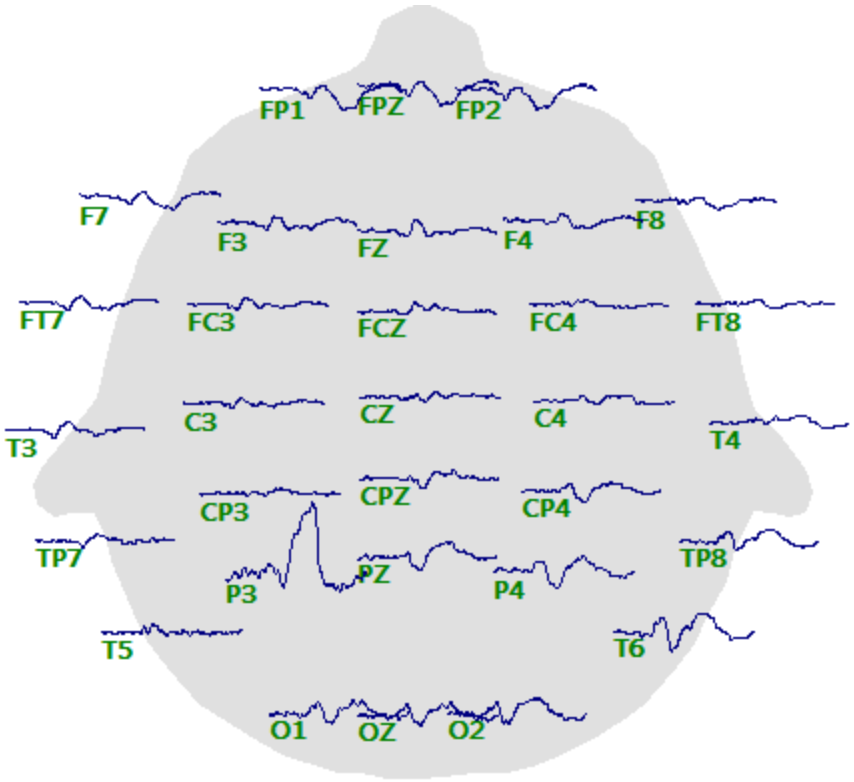
3. Clear and close the Waveboard. Now we will compare the 2 files. To compare two or more averaged data files, you need only to place them in the same Study and open it (assuming the files are all compatible).

In the Functional Data display, use *Ctrl+double click* to spread the outer cursors all the way apart. Select the

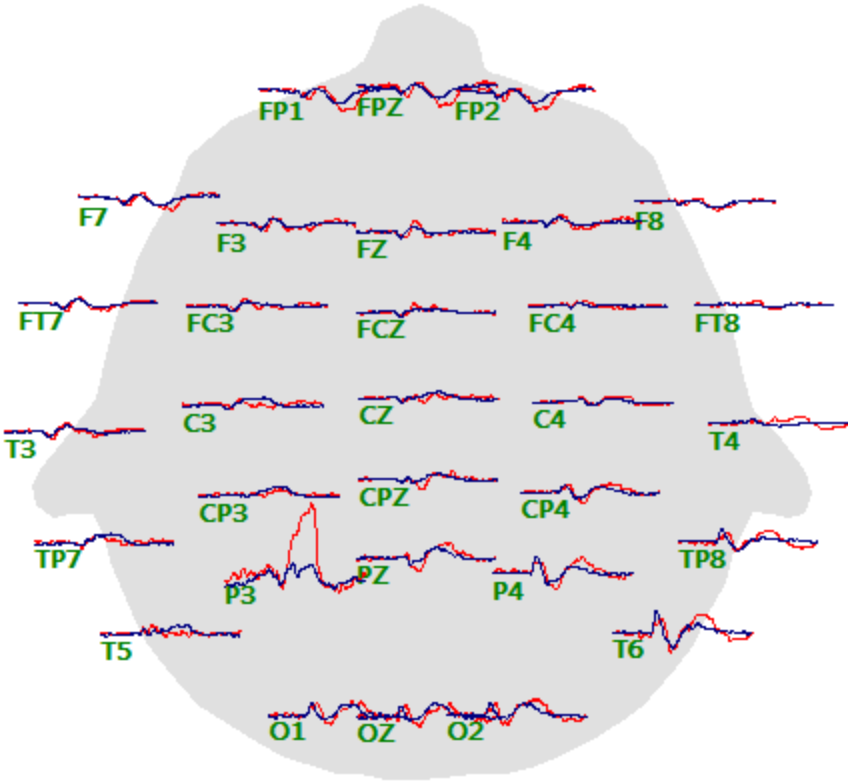
display option. From the Maps toolbar, click the **Position Plot** icon.

You will now see the waveforms displayed for the first file. Use the *mouse wheel* for scaling and the 

options to extend / constrict the x-axis. Use the mouse wheel, positioned over an electrode label, to extend / constrict just that channel. You can also drag the channels around by the labels.



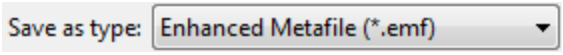
4. To superimpose the second file, *right click* in the Maps display and select **Keep Waveforms**. Then, in the Functional Data, move the slider at the bottom to display the second average file. You will now see the two files superimposed. The dark blue is the second file, and the red is the initial file.



Right click in the display and select **Reset Waveforms** and **Reset 2D Positions** to restore the original display.

In this way you may overlay up to five epochs. The epochs can be group averages, individual epochs, or the effects of operations that you perform. For example, display the waveforms, select **Keep Waveforms**, and then perform an operation such as filtering. You will see the original and filtered data.

Incidentally, you can save the **Maps** display as an enhanced metafile (*right click* and select **Save Image As**, where you select



for the file type). Open that file in, for example, Word, *right click* on it, and select **Edit Picture**. You can then modify the individual components of the display.

The basic steps in creating and displaying averaged evoked potentials were illustrated.

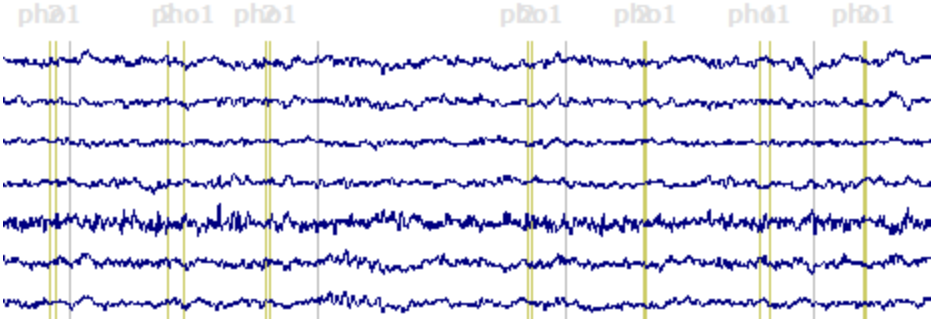
2.4.6.1 Epoching and Averaging with StimTracker

The newest version of STIM2 uses the Cedrus StimTracker in place of the STIM Audio System unit. With that system the CURRY acquisition software (or ACQUIRE) will receive pairs of stimuli: the TTL pulses from the STIM computer, and the directly measured auditory and visual stimulus events from the StimTracker. The STIM TTL pulses are seen in CURRY as regular events with type codes from 1-247. (Responses from the Cedrus Response Pad are received with type codes of 248-255, and converted automatically to type codes of r1-r8). Auditory events from the StimTracker

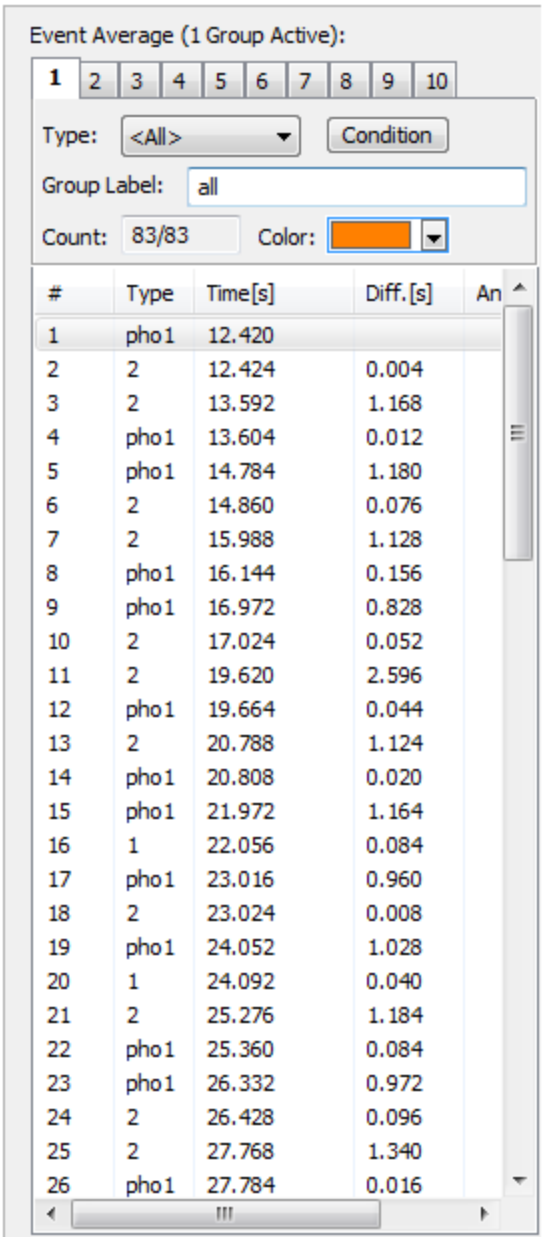
will have the type code of *aud1*, and visual events will have the type code of *pho1* (and *pho2* if two light sensors are used). If you have a MagLink or MicroMaglink system, the pho2 events will be seen as r5 events, which are from the scanner.

Each auditory or visual stimulus that is presented will therefore have two events associated with it. The StimTracker event codes are more accurate, as they are measured directly as they are presented. In CURRY, the TTL pulses are aligned with the StimTracker pulses, that is, the latencies of the TTL pulses are replaced with those from the associated StimTracker events.

In this demonstration file, you will see the pairs of TTL events (types 1 and 2) with a pho1 event. Normally, the pairs will be closer together than in this test file, usually only a few milliseconds apart (up to about 20 ms or so), and the TTL's will typically precede the pho1's. (See also the *StimTracker Test* section of the *STIM^2 User Guide* for a more thorough test).

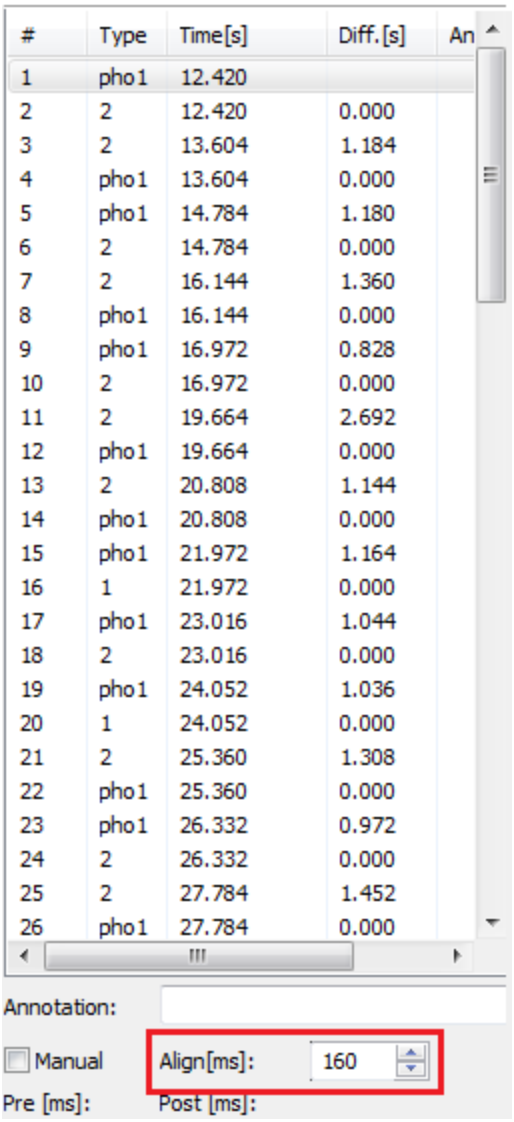


In the **Event List**, **All** events were selected. The **Show Indices** option (from the context menu) was enabled to add the line numbers.



#	Type	Time[s]	Diff.[s]	An
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	
21	2	25.276	1.184	
22	pho1	25.360	0.084	
23	pho1	26.332	0.972	
24	2	26.428	0.096	
25	2	27.768	1.340	
26	pho1	27.784	0.016	

Looking at the first 2 lines, you can see that the pho1 event preceded the type 2 event by 4ms. On line 3 and 4, you can see that a type 2 event preceded the pho1 event by 12ms. And so on. If you look down the list of differences, the largest discrepancy (in the entire list) is 156ms, which again is atypical in real data files. Set the **Align[ms]** field to a number slightly larger than the greatest discrepancy (**160**ms in this case). The Times in the Event List are updated automatically. The Time for a given type code is replaced with the Time from the nearest pho1 event.

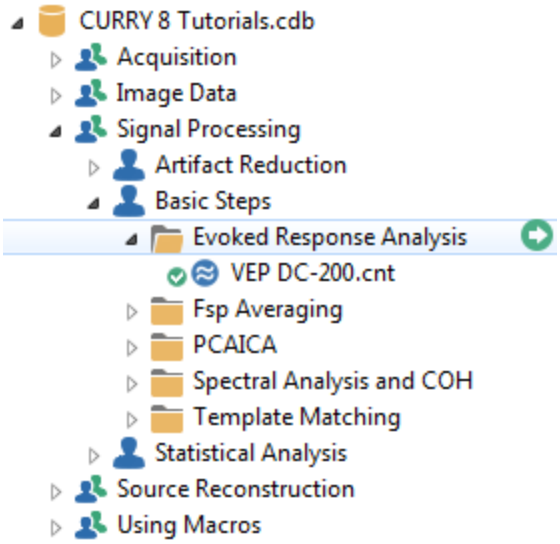


You can now go ahead with creating epochs or averages, using the numerical type codes as usual. To revert back to the original times, enter 0 in the Align[ms] field.

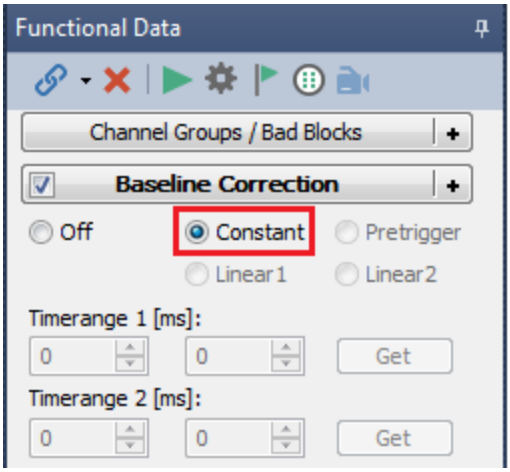
Click the button at the top of the panel to save the adjusted event file, overwriting the existing .cef file.

2.4.6.2 2D and 3D Mapping

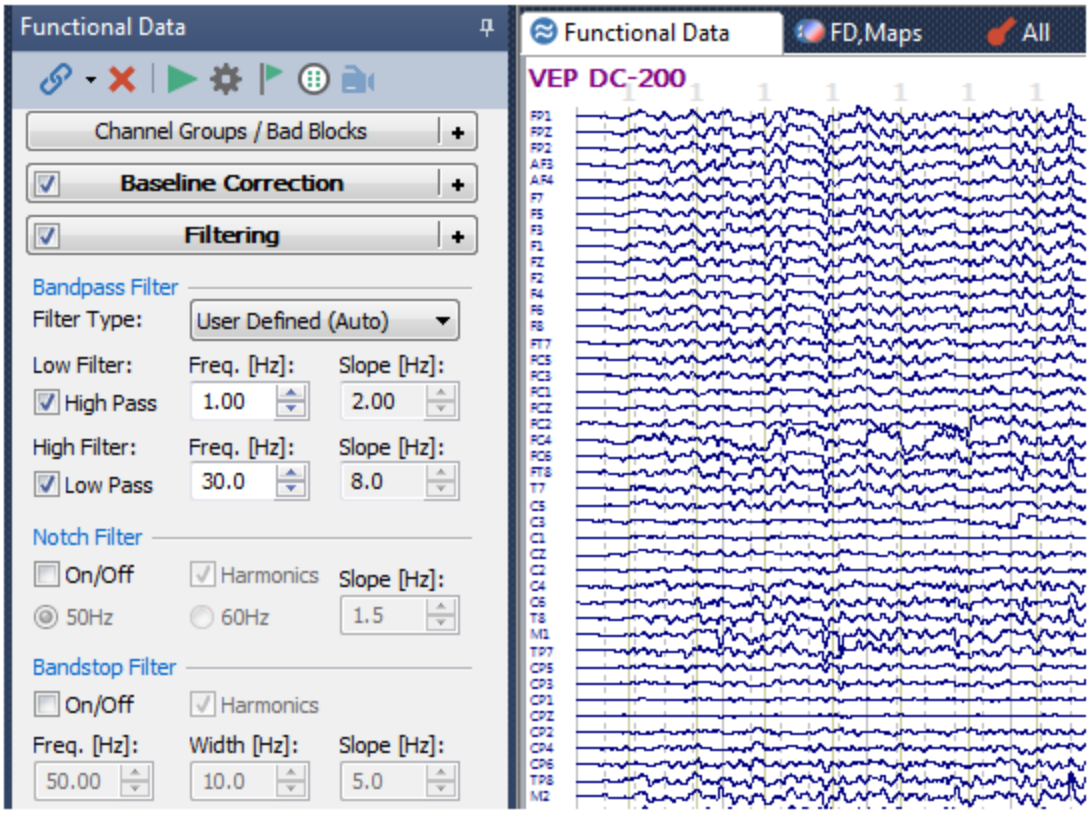
The EEG data can be mapped in 2D and 3D. For this tutorial, we will use the averaged results from the Evoked Response Analysis Study, although you can use other data files if you wish.



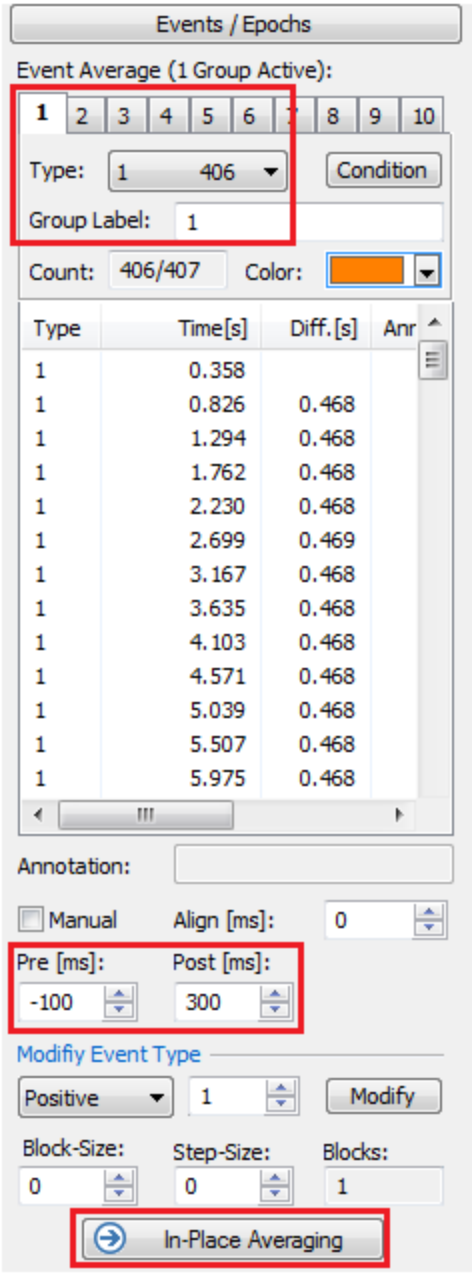
1. Open the Study. This is a recording of a basic VEP. Filtering was from DC to 200 Hz for the recording, and we see that the channels all have DC offsets. The first step is to add the **Baseline Correction** panel and select the **Constant** baseline correction.



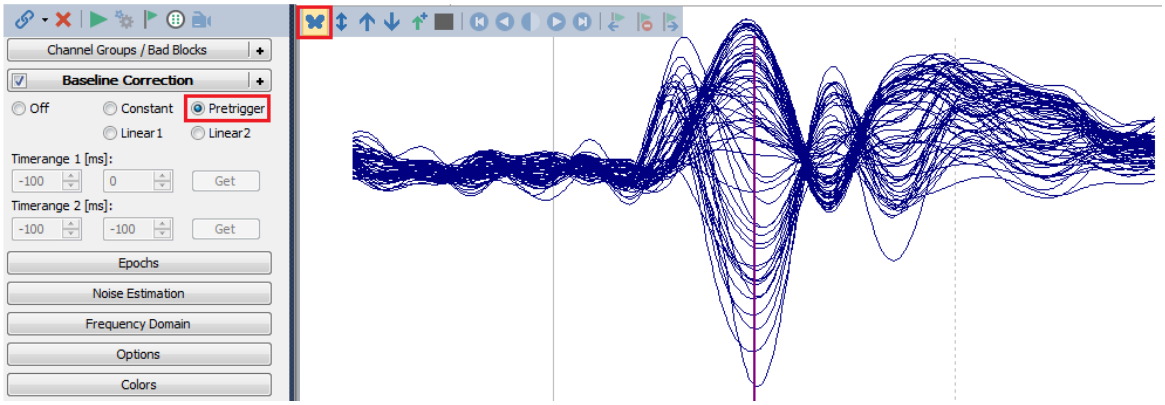
2. Next add the **Filtering** panel and select **User Defined (Auto)**, with **1-30 Hz**. Use the *mouse wheel* to rescale the data.



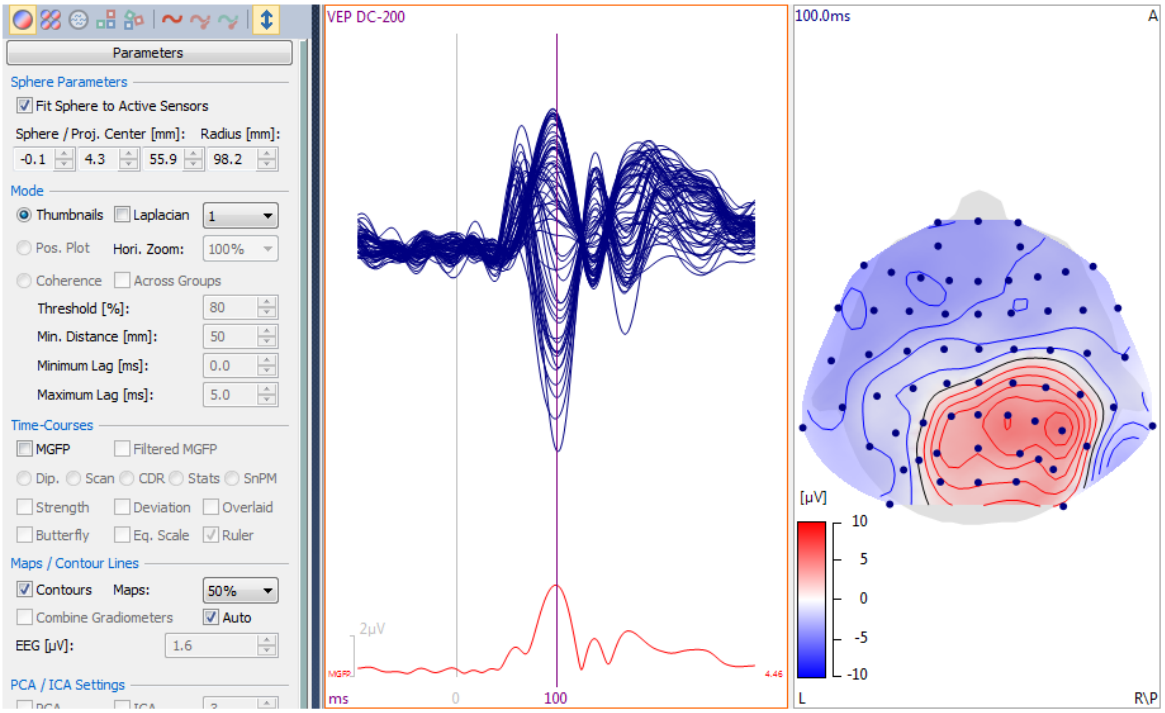
3. There are a few bad sections in the recording that we will ignore for this demonstration. Open the Events / Epochs panel. Select **Type 1**, set the epoch interval to **-100** to **300 ms**, and click the In-Place Averaging button to create the in-place average.



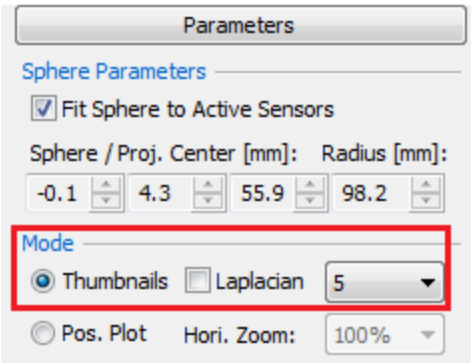
4. Select the **Butterfly Plot**, add the **Baseline Correction** panel, and in it select the **Pretrigger** option.



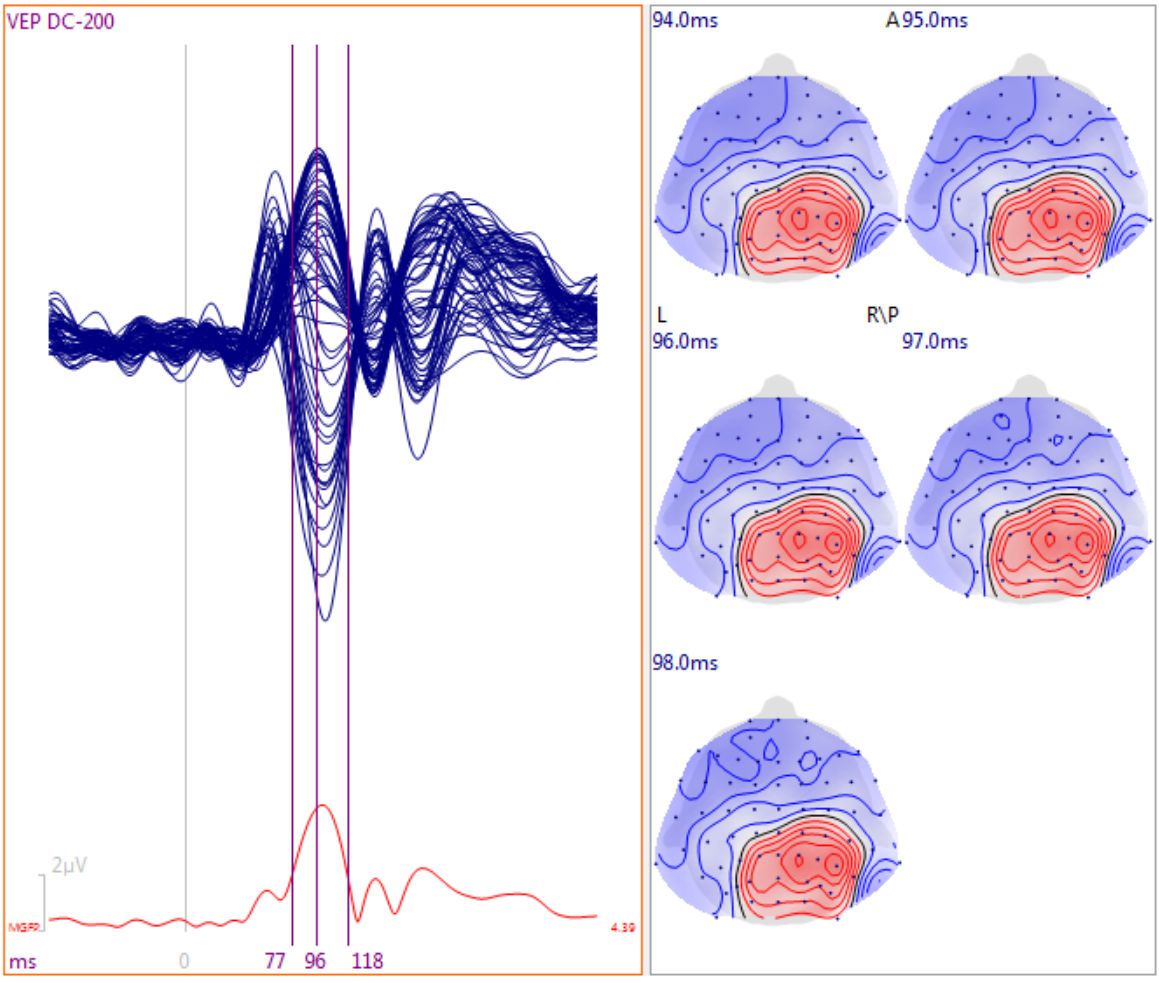
5. Select the FD, Maps display tab, you will see the following.



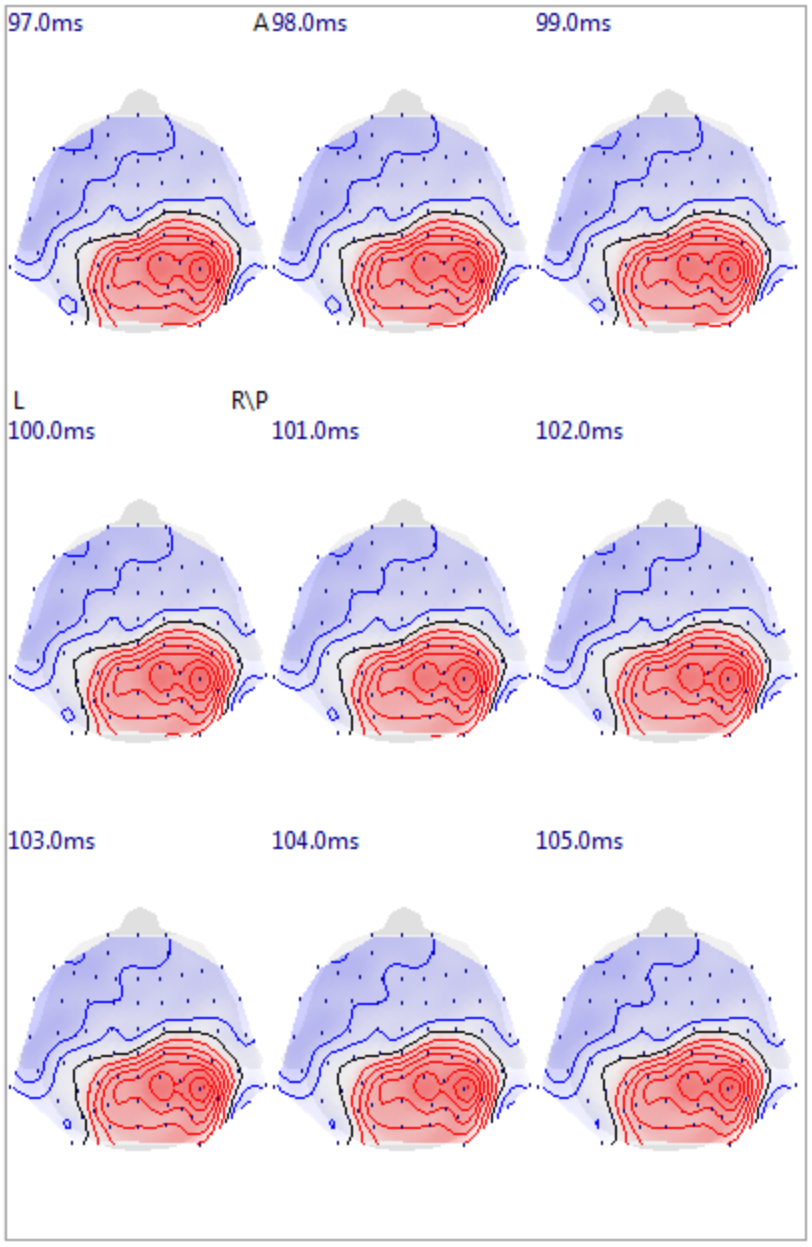
6. There are a few things to understand. First, there are the 3 vertical cursors in the Functional Data (superimposed at this point), and second, there is the number of **Thumbnails** that is displayed (1). Thumbnails are found in the **Parameters** panel for **Maps**. Increase the number to **5**.



We will spread the outer cursors to encompass the large MGFP peak (you must deselect **Tracking Mode** in the context menu to do this). You can use *Ctrl+left arrow* on the keyboard to move the left cursor, and *Alt+right arrow* to move the right cursor.

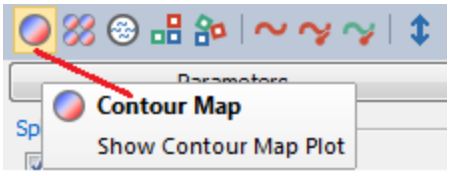


Now select **9** for the number of **Thumbnails**. Which 9 maps are these? They are the maps around the middle vertical cursor. In this case, the middle cursor is placed at 101ms, which is the center map. The others are the 4 data points before and the 4 data points after the middle cursor (the AD Rate is 1000 Hz, so there are data points every millisecond).



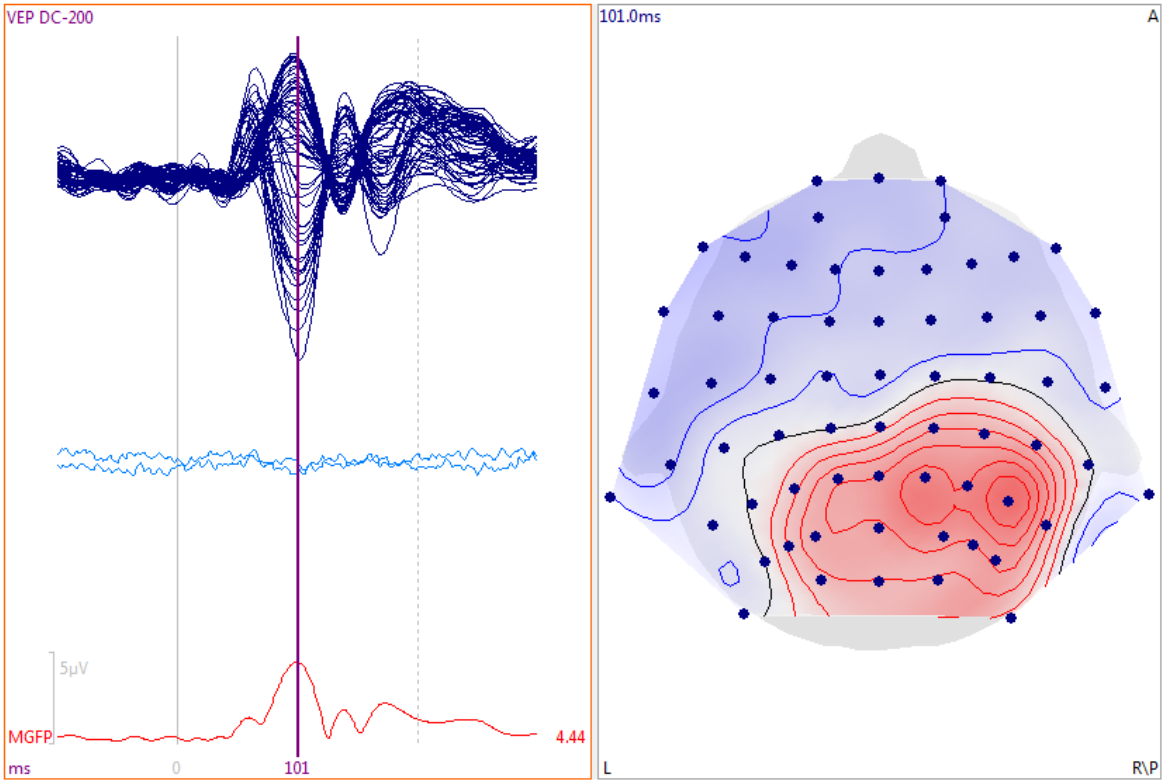
Select **All** for **Thumbnails**. Now you see all maps for data points between the two *outer* cursors.

If you want only a single map, corresponding to the middle cursor position, you can select **1** for **Thumbnails**, or, you can click the **Contour Map** icon on the Toolbar.

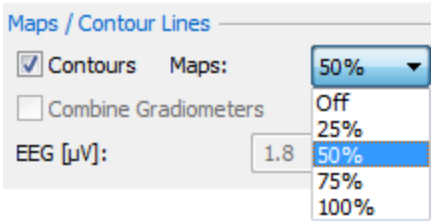


7. Enable **Tracking Mode** again (context menu or *double click* in the Functional Data), and all 3 vertical cursors will be superimposed at the same latency. Now when you move the vertical cursors, the single map will track with that. If you are not in

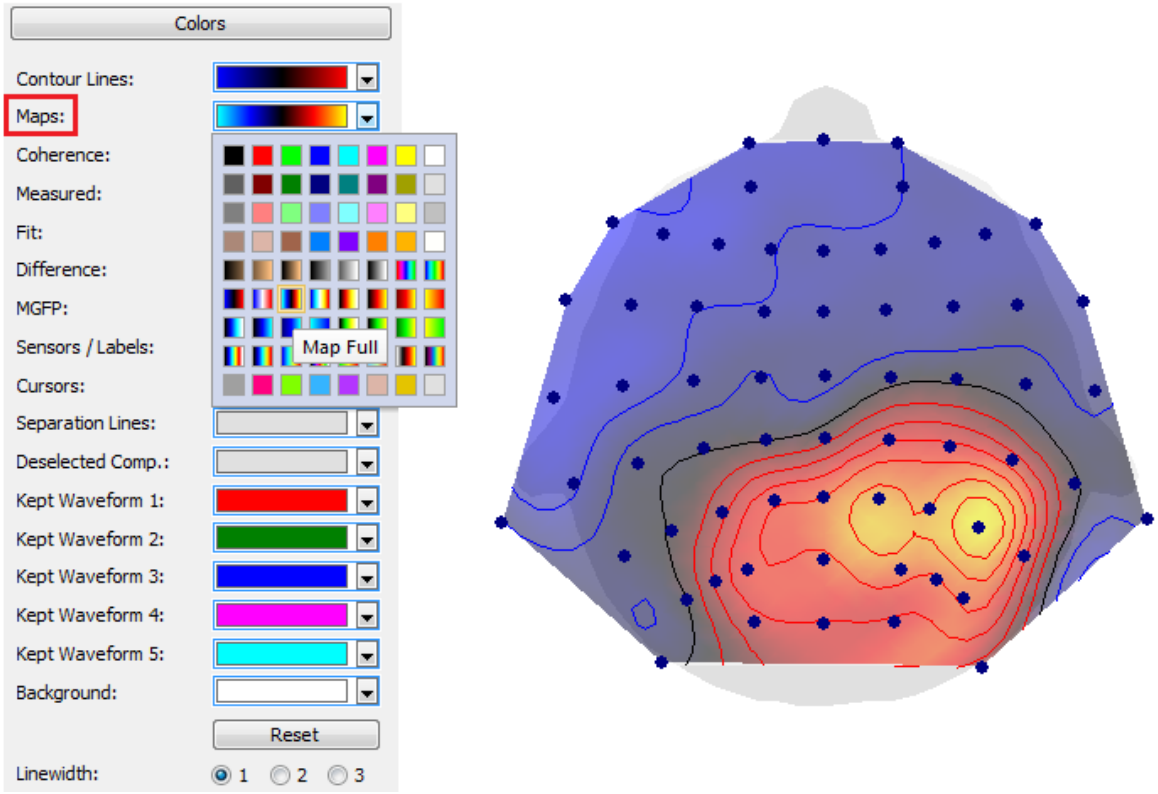
Tracking mode, where the outer cursors are spread apart, the single map will track with the *middle* cursor.



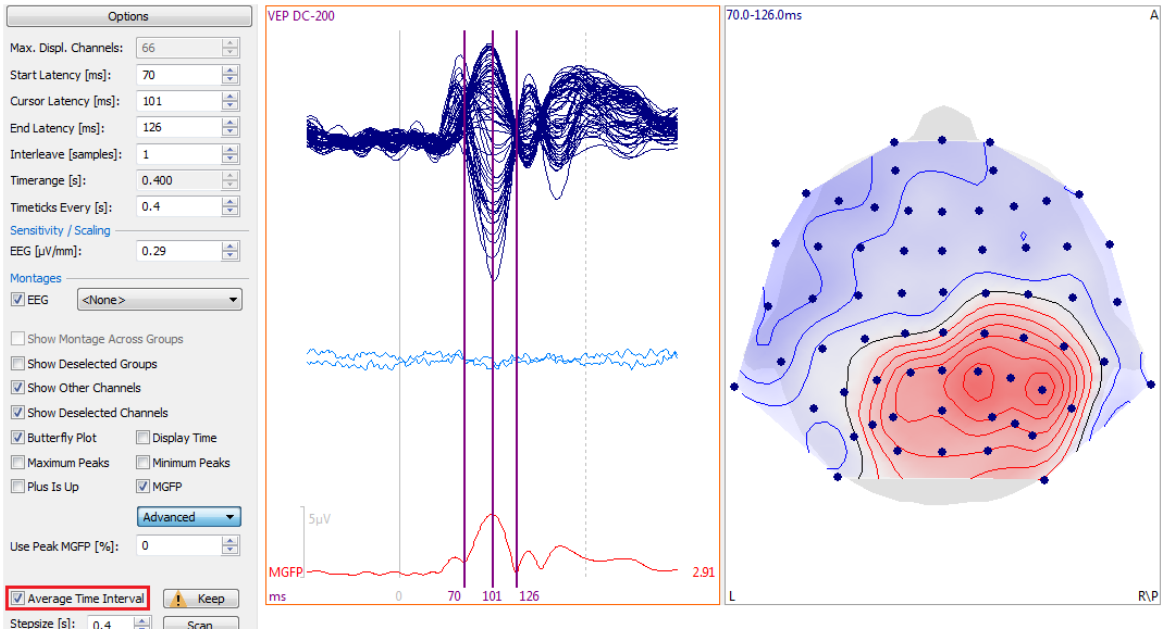
8. Transparency (or the intensity of the map color) is controlled with the **Maps** option.



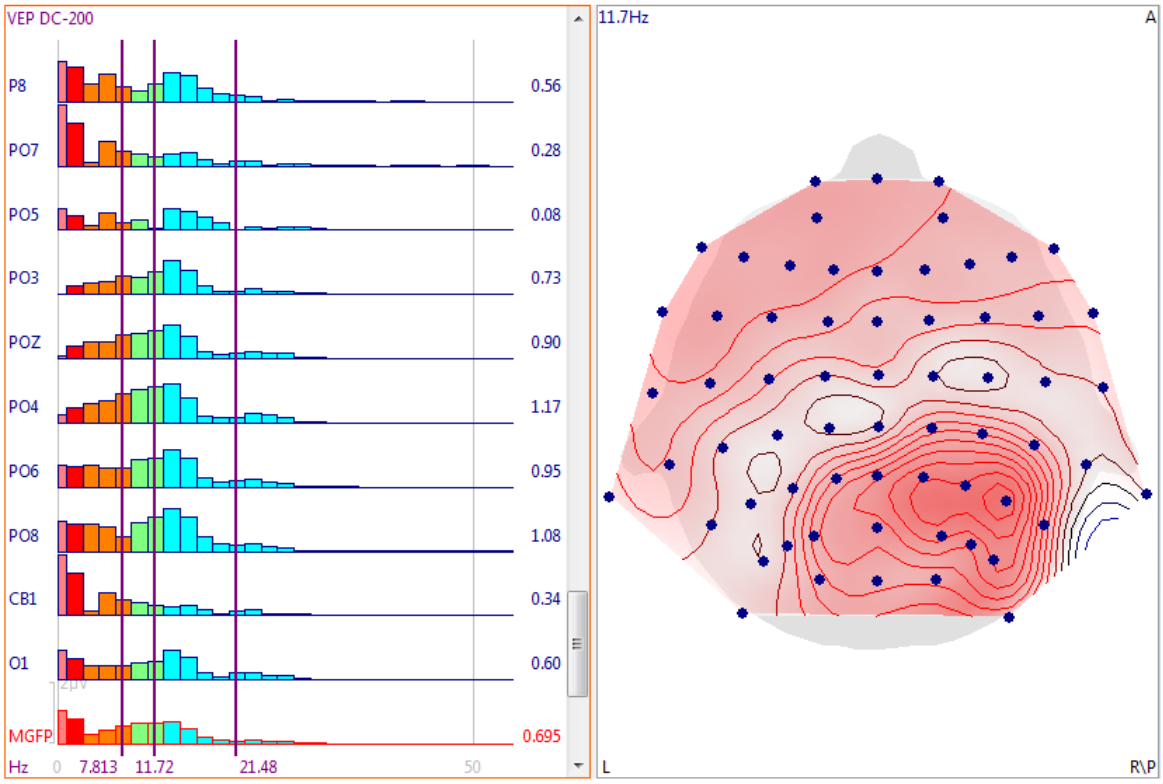
9. The color scheme can be selected from the **Colors** option for **Maps**, under **Maps**.



10. Let's say that instead of mapping a single point, we want to map the average of all points within a Timerange. To do this, set the outer cursors to define the Timerange. In the **Options** panel for **Functional Data**, enable **Average Time Interval** (in the **Advanced** section). Now the map shows the average of the data points for each channel in the Timerange. The middle cursor now has no function.



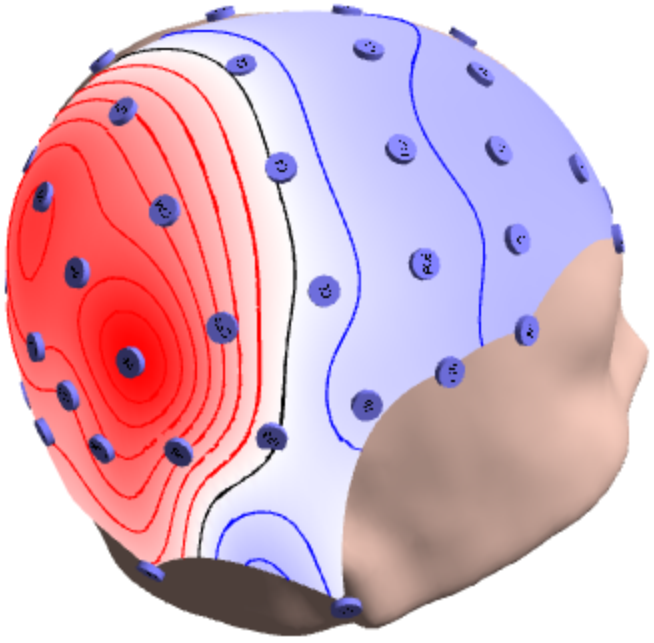
11. We are displaying time domain data so far, but the steps are the same if you have frequency domain data (enable **Spectra** under **Frequency Domain**, adjust channels, zoom in). With **Average Freq. Interval** disabled, the map corresponds to the position of the middle cursor.



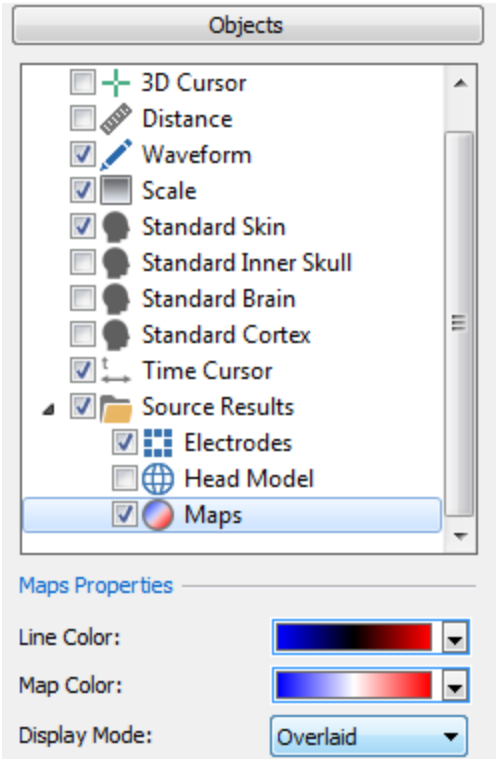
With **Average Freq. Interval** enabled, the maps is the average of the frequency bins in the Timerange.

12. 3D Mapping

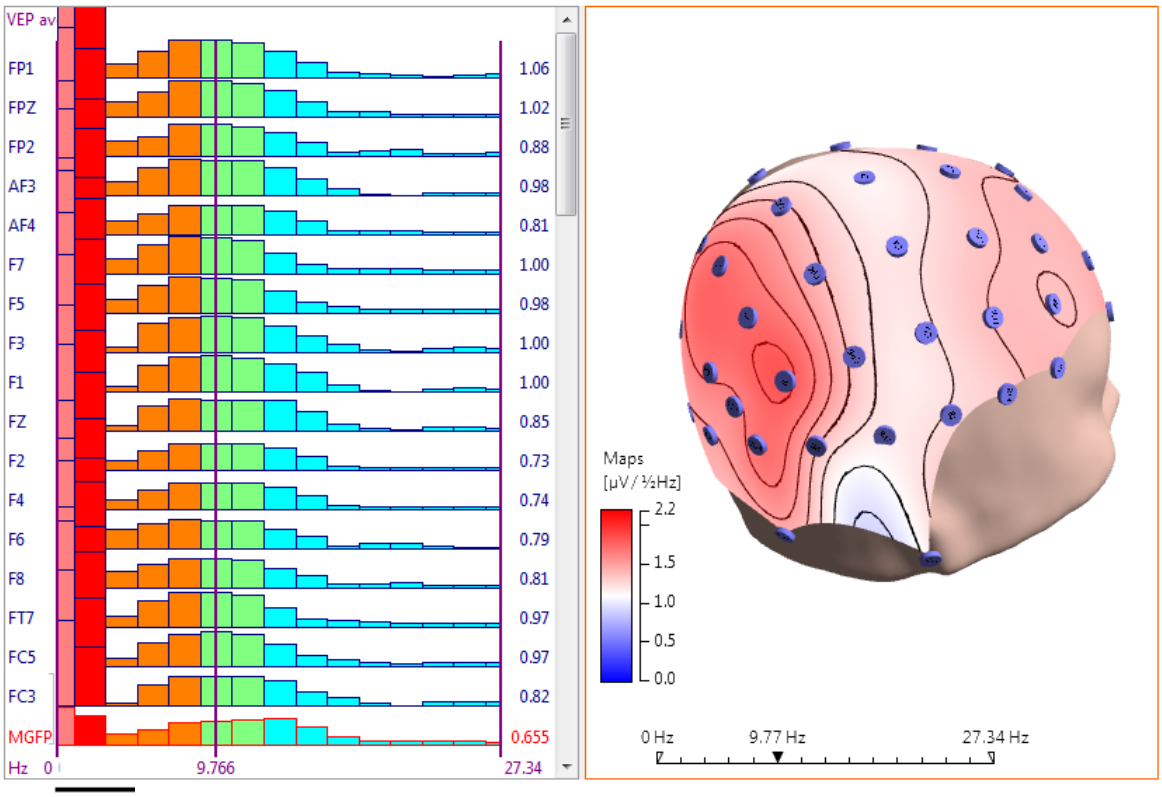
uses the same conventions described above.



In this case, with the time domain data, we enabled the display of the **Standard Skin** (100% Transparency), and selected **Overlaid** for **Display As** in the **Maps Properties** to display the contour lines as well as the color shading. Select a different mapping color scheme using **Map Color**.



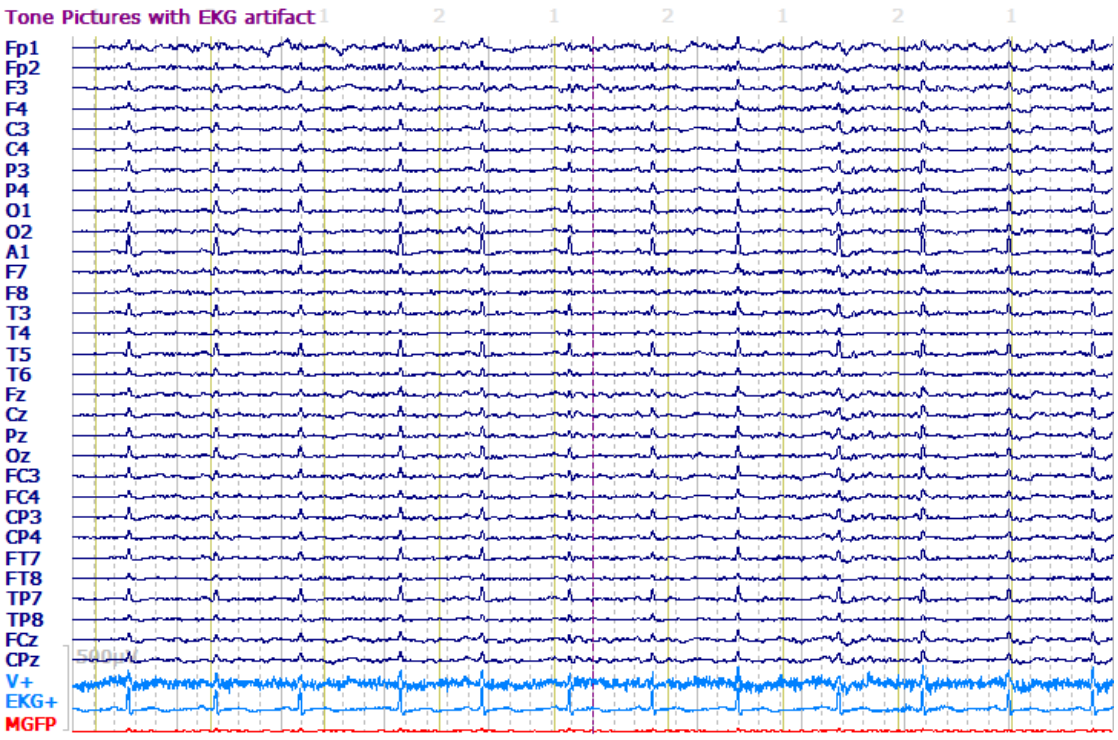
Mapping in the frequency domain in 3D uses the same steps as above.



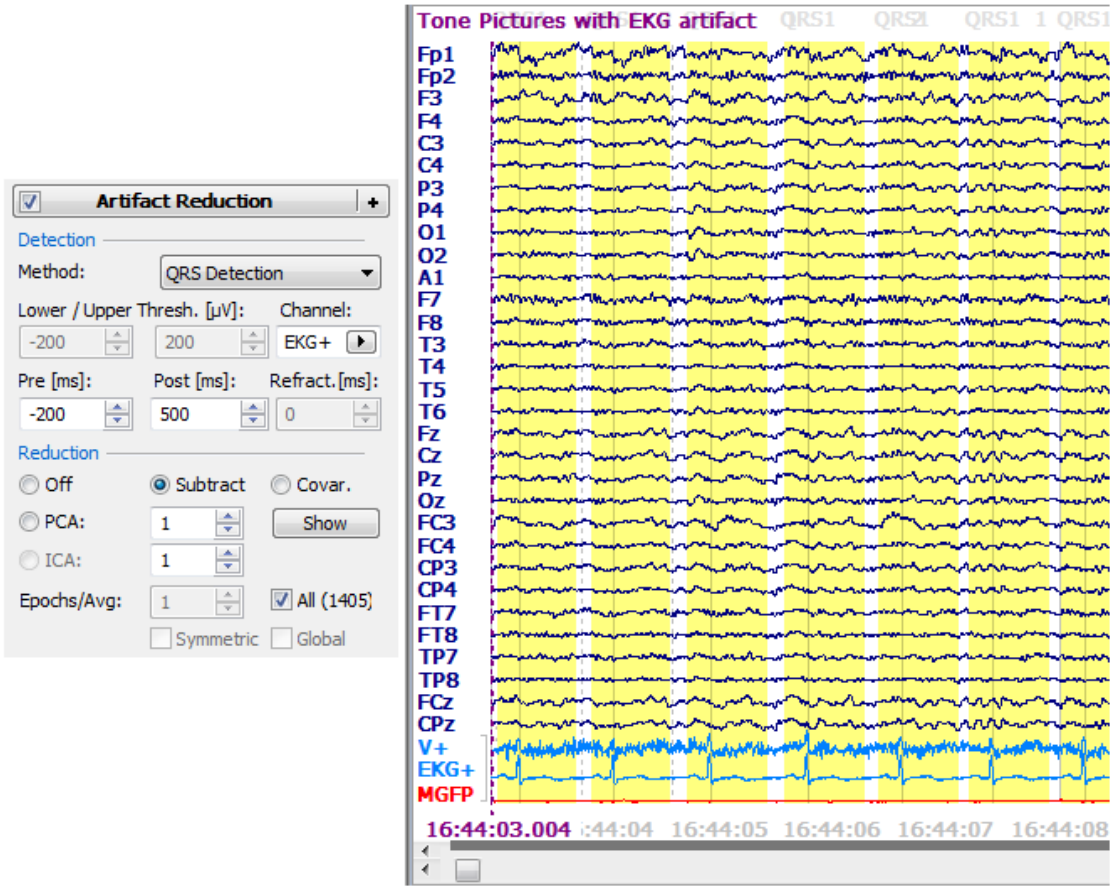
2.4.6.3 Removing Pulse Artifact

In the data file we will be using shortly, there is no EKG channel and no other channel in which the pulse artifact has an amplitude large enough to make it possible to be detected using a voltage threshold criterion.

If there were an EKG channel, with a well developed QRS complex, like in the figure below, it would be a simple matter. Note the well defined EKG artifact (in the EKG+ channel).



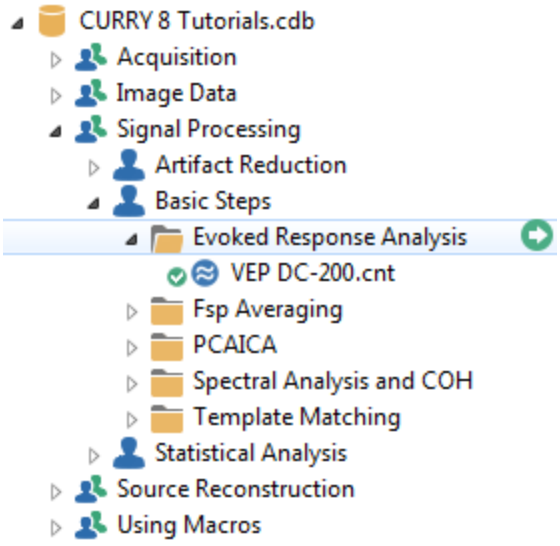
In this case, we would use **QRS Detection** and the parameters shown to reduce the pulse artifact.



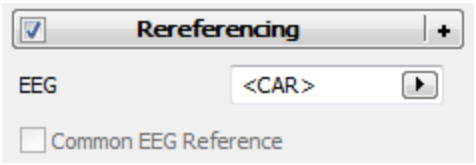
However, in this data file, there is no EKG channel, and the QRS Detection method does not reliably detect the pulse artifact. It will still be possible to reduce at least most of the pulse artifact. The problem lies in the detection of the artifacts. A simple voltage threshold will detect most of the pulses, but some will be missed and there will be some false positives. We will illustrate how to use the **Threshold** method, and then use **Template Matching** and **PCA Projection** as another method.

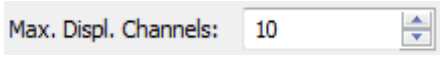
Voltage Threshold

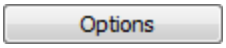
1. Open the file in the *Evoked Response Analysis* folder.

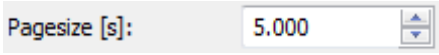


2. Select the Common Average Reference (**CAR**) from the **Rereferencing** panel.



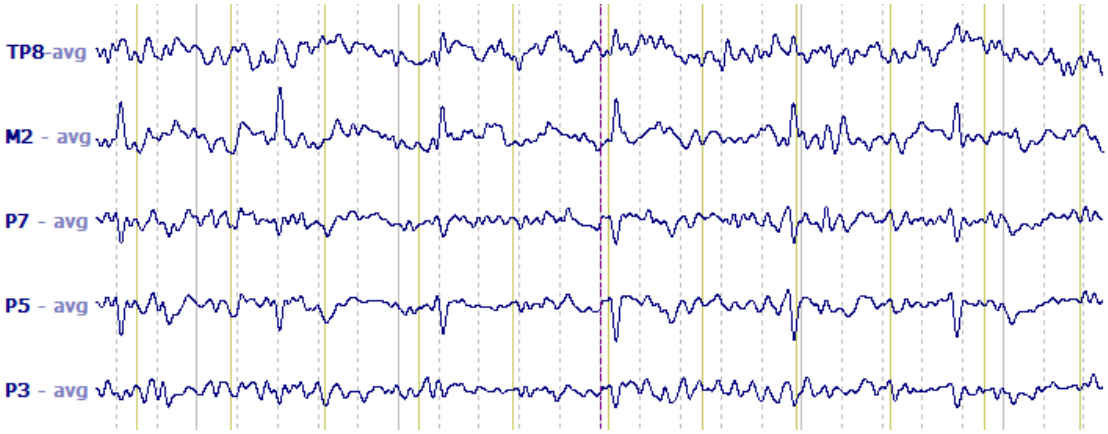
3. Reduce the number of displayed channels to **10**, using the 

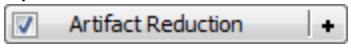
parameter under 

, and a **Pagesize** of **5** 

.

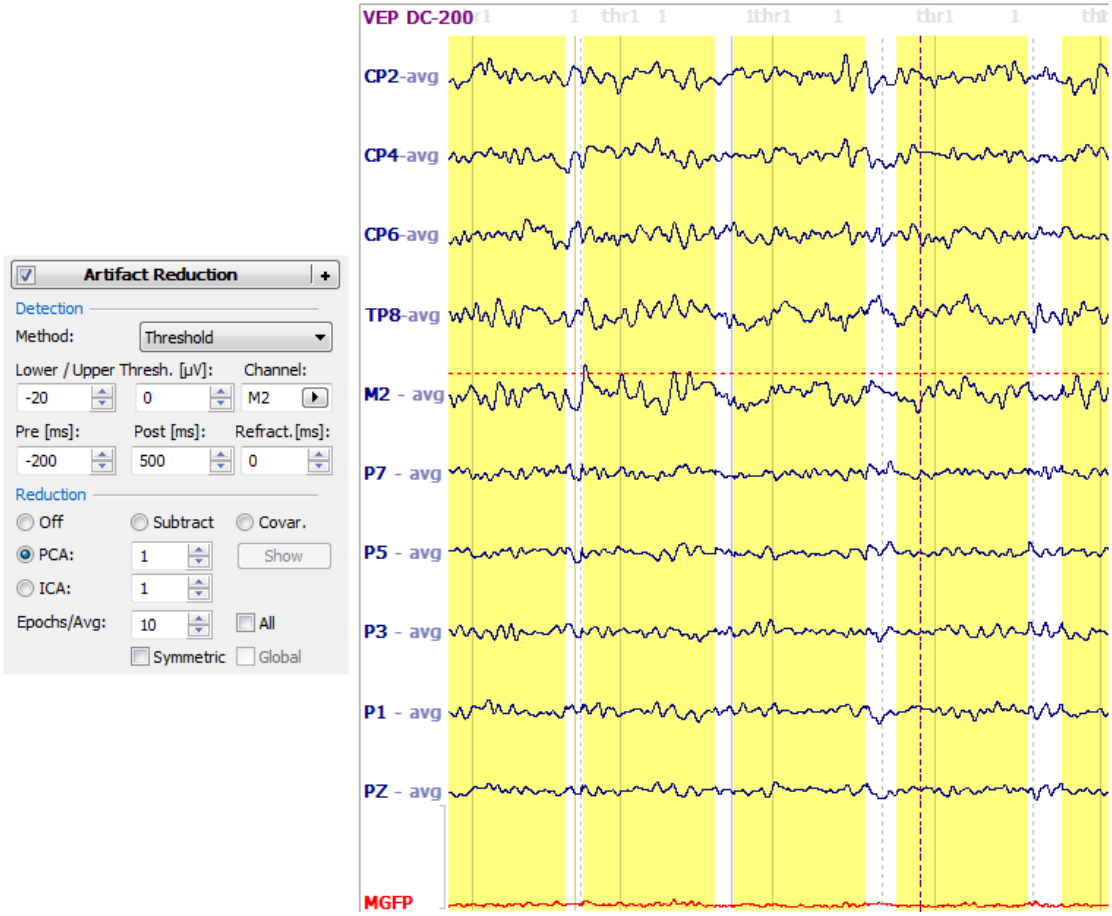
4. **Baseline Correction** was performed (**Constant**). **Filtering** was applied (**1-30 Hz**). Use the scroll bar on the far right to select the channels you wish to see. The pulse artifact is most prominent in the M2 channel.



5. Measuring some of the peaks shows that a threshold of about -20µV may pick up most of them. In the 

panel, we selected the

Threshold option. We entered **-20** for the **Lower** threshold, and **0**μV - for the **Upper** one (to turn it off). The **M2** channel was selected. **Pre** and **Post** times of **-200** and **500**ms were entered - these define the duration of the artifact with respect to the peak. Increase **Epochs/Avg** to **10**. The immediate effect of these parameters is seen in the data display when you click, for example, the **PCA** option.



6. Next, we decide which **Reduction** method to use. Unless there is an *a priori* reason to select one method over another, this requires a "try it and see" approach. Try the different reduction methods - **Subtract**, **Covariances**, **PCA** and **ICA** (with different numbers of components). After a little testing, the **PCA** method with **1** component appears to remove the artifact without greatly affecting the other data.

The correction is being applied only to the data in the display. To apply it to the entire file, click the flashing button at the top of the **Functional Data** panel. Then click **PCA** with **1** component. Try enabling the **All** and **Global** options.

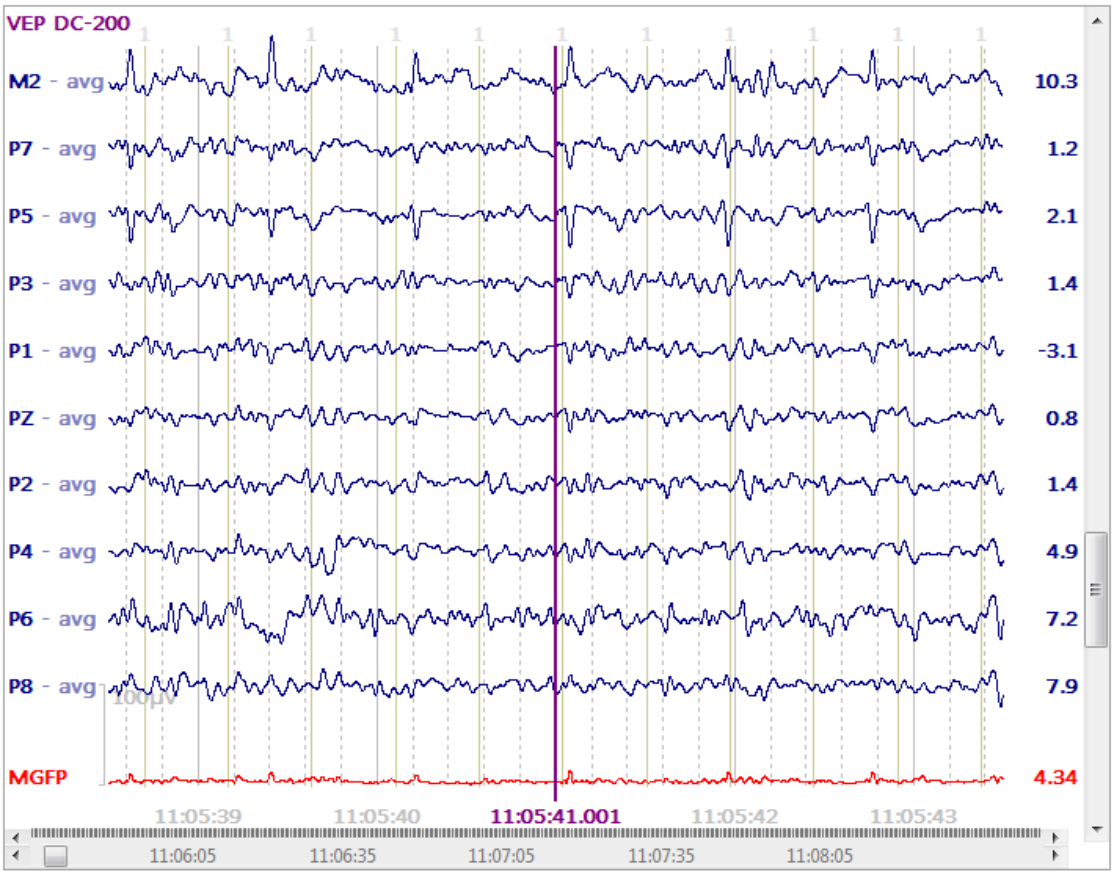
Check different places in the file. Again, without an EKG channel, there will likely be some missed artifacts as well as some false positives. Tweaking the Lower Threshold might include a few artifacts that had been missed, but that will also increase the possibility of false positives. You can remove the false positives by

stepping through the file using the Event buttons on the Toolbar , and rejecting the false positives.

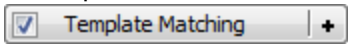
Check all channels and different sections in the file to assess how well the artifact was reduced. You can then go ahead and perform Averaging, etc.

Template Matching and PCA Projection

Another approach we could apply uses **Template Matching** and **PCA Projection**. This is the same data file, prepared as described above (close and reopen the study before proceeding), including the **CAR**, **Baseline Correction**, and **Filtering**.

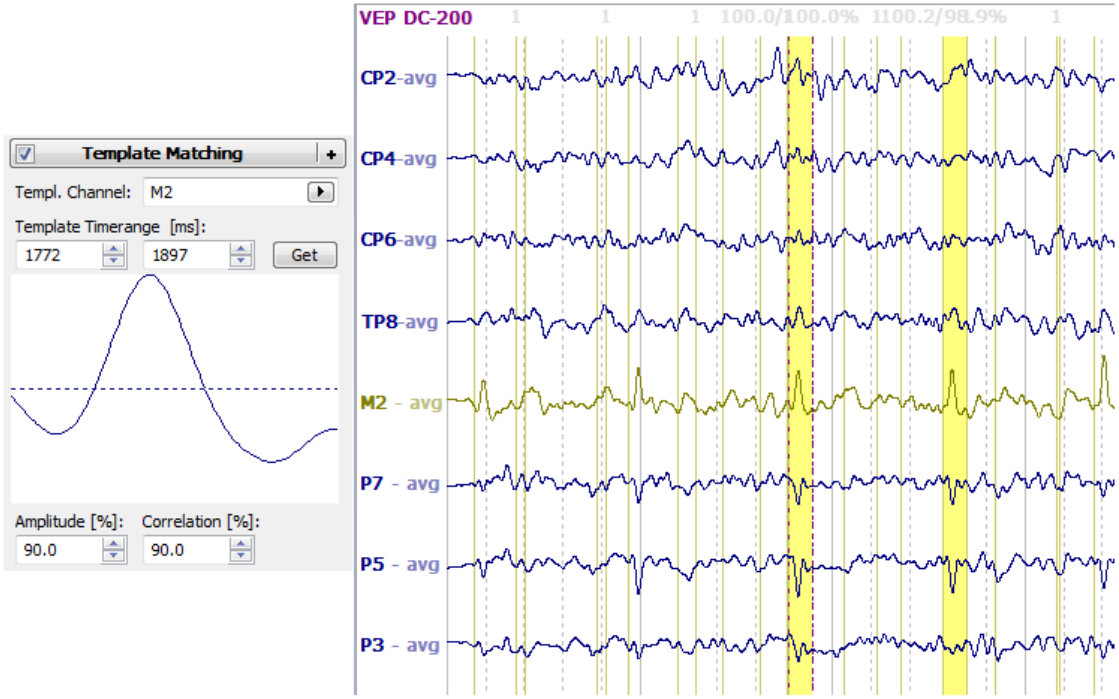


1. The first step is to detect the artifacts, and in this case we will use **Template Matching**. In later steps we will average the artifacts and perform PCA decomposition. Therefore, it is not necessary to detect every artifact - they will be averaged together to get an averaged artifact. We do not want any false positives. Enough of them in the averaged artifact could distort the topography of the artifact.

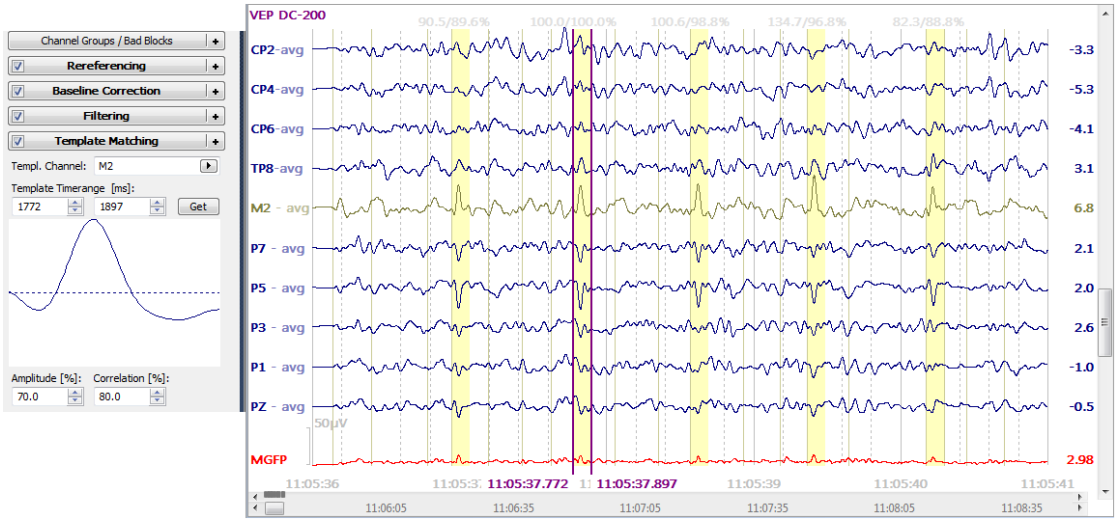
The two outer cursors were placed about one of the larger pulse artifacts to define the template. Set the 

parameters as shown. **M2** was

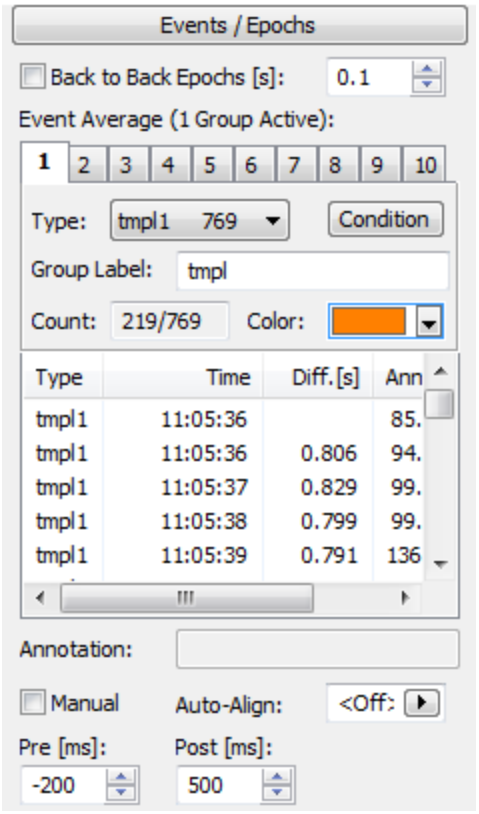
selected as the **Template Channel**. Here it is important that there be both positive and negative numbers in the displayed artifact. The algorithm does not work well if the valences are all positive or all negative. Click the flashing button.

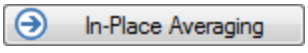


2. Now it is a matter of adjusting the Amplitude and Correlation parameters so that only the artifacts are detected. Again, this does not need to capture every one, but we do not want any false positives. Here we have reduced **Amplitude** to **70**% and **Correlation** to **80**%, and most of the displayed peaks were detected. We then go through the remainder of the file to ensure there are few or no false positives. When you encounter a false positive, you can either increase the amplitude or correlation criterion in order to remove it (the amplitude and correlation values of each event are displayed - increase a criterion beyond that value). Or, you can use the event buttons on the Toolbar to step through the events and delete the false positives.



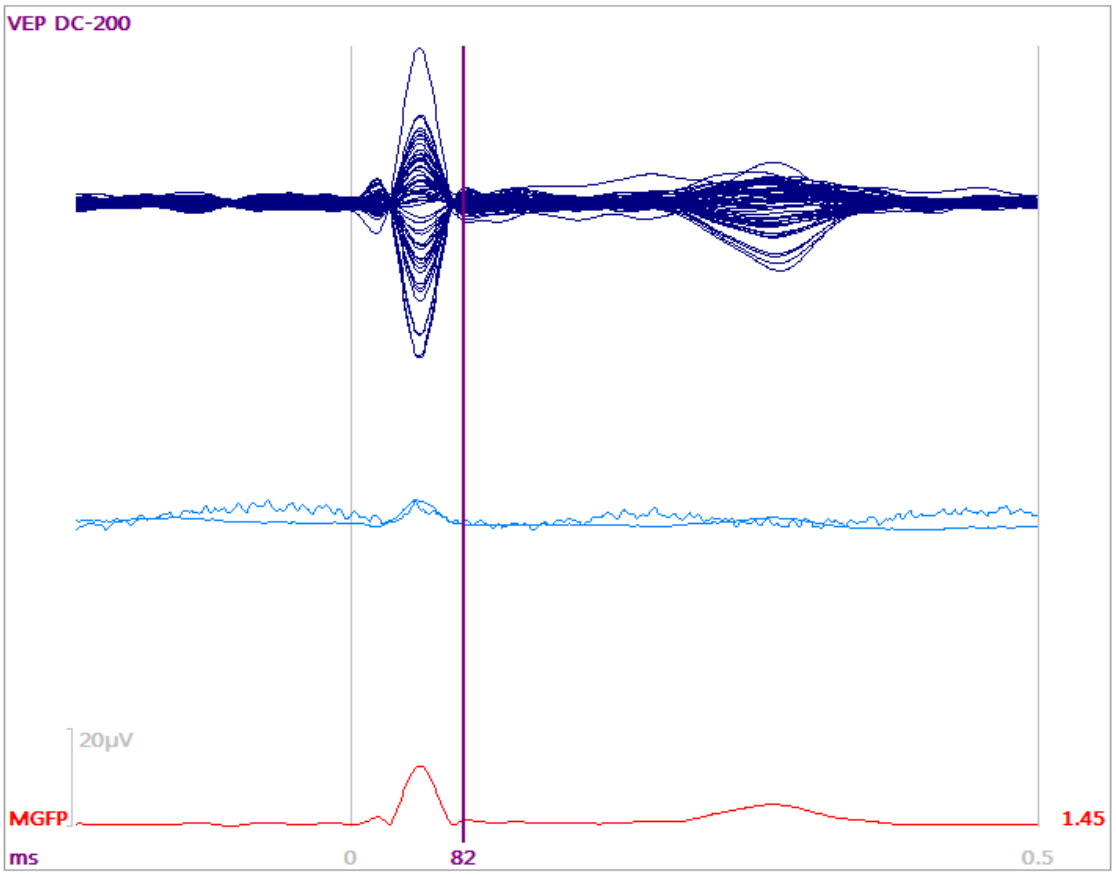
3. When only acceptable Events remain, go to the **Event List** and select the "tmpl1" events. Set the **Pre [ms]** and **Post [ms]** fields as desired. In this case we are using **-200** to **500**ms to save not only the R wave, but the full PQRST complex.



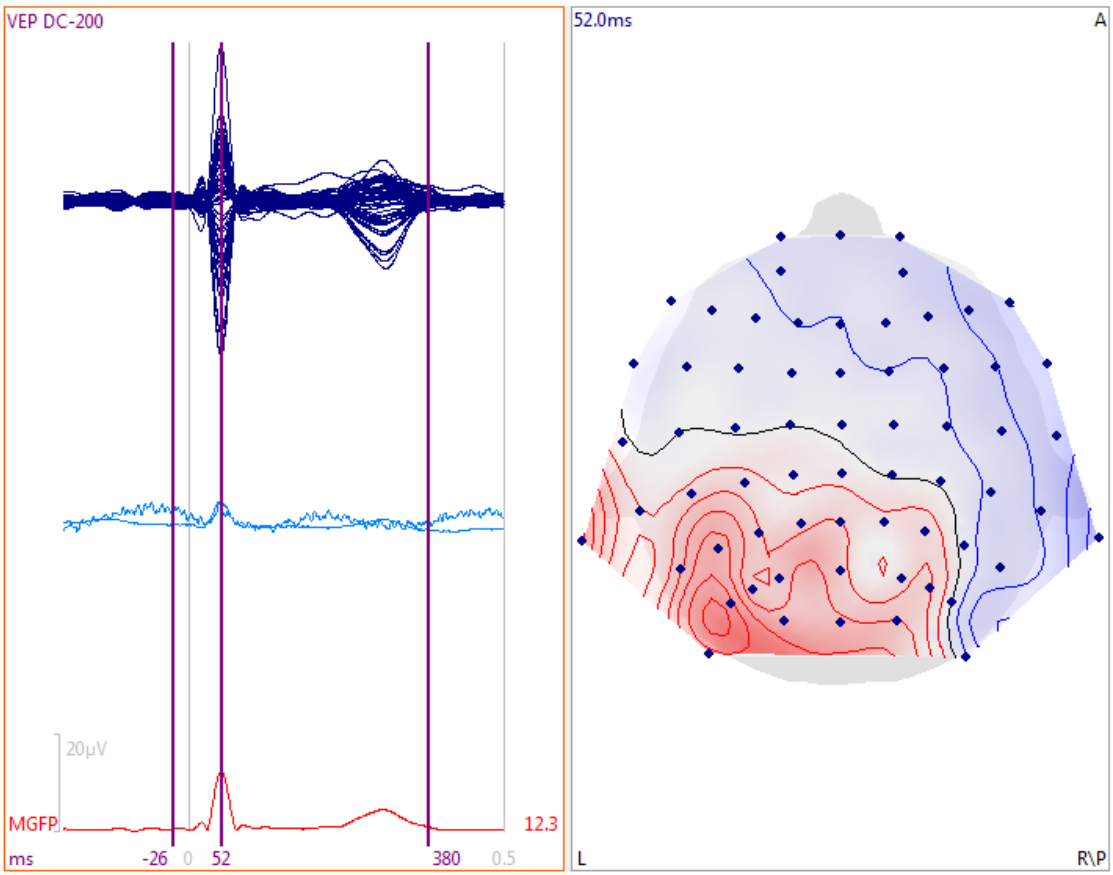
Then average the artifact epochs by clicking the 

button at the bottom. We have already reviewed the individual artifacts, so there is no need to use the SNR method for averaging (although you certainly could).

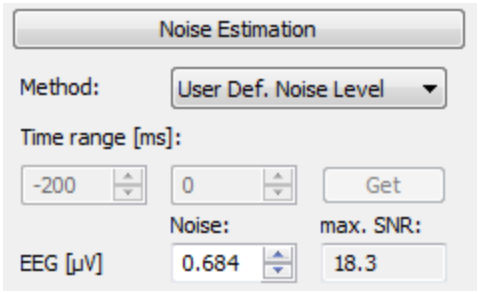
4. The **Pretrigger Baseline Correction** was applied, and the **Butterfly Plot** was selected. We see a very clean averaged pulse artifact. The artifact channels (blue lines) were displayed by selecting **Show Other Channels** under **Options** (**Functional Data**).



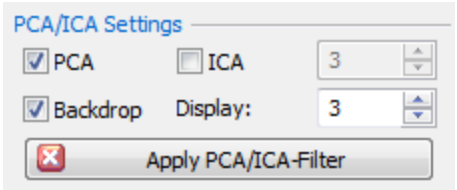
5. Select the FD, Maps display. The two outer cursors were placed to encompass the artifact. Position the middle cursor to see the distribution of the R wave, if desired.



6. Go to Noise Estimation (**Functional Data**) and select **User Defined Noise Level**. This is required for PCA artifact reduction.

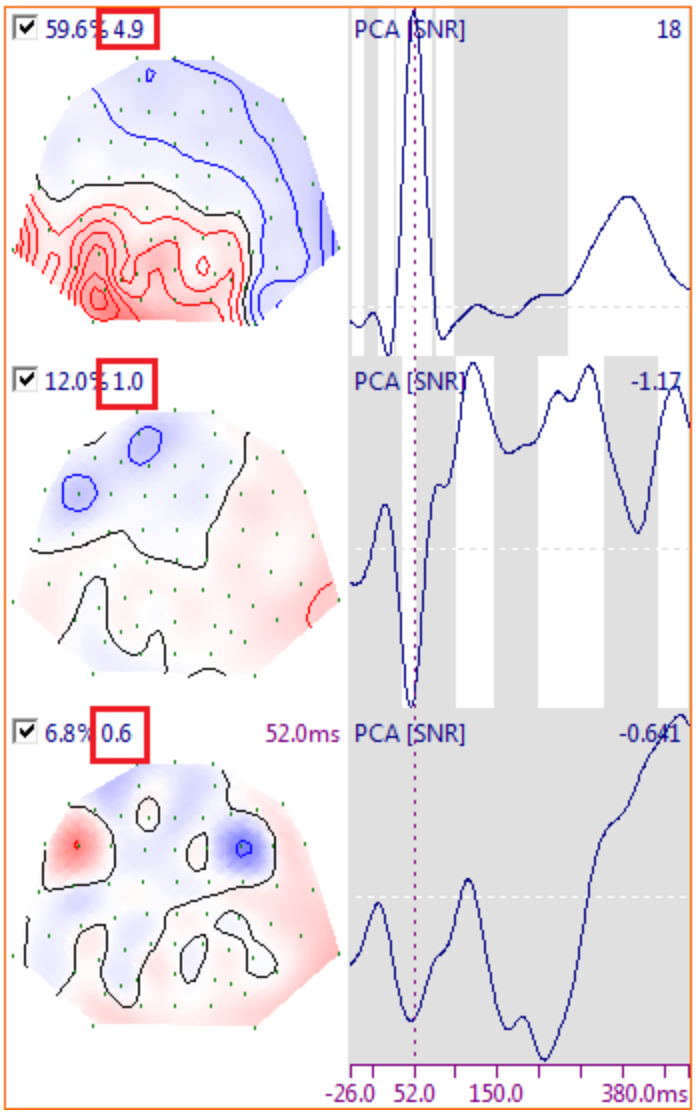


7. Select **PCA** with **3** components displayed (in the **Parameters** panel for **Maps)**.

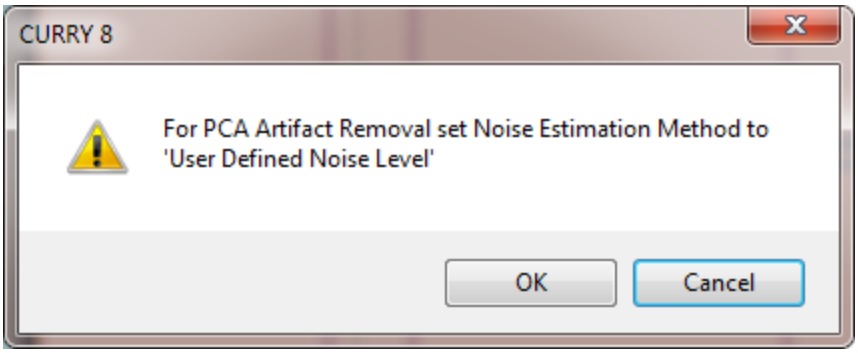


8. We see there is one main component (SNR = 4.9) and one marginal one (with SNRs greater than or close to 1.0). Your values should be similar, but not

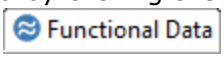
necessarily identical (depending on the Timerange you selected, and any other parameter differences). The gray areas are those in which the point-by-point SNRs are within ±1.0.



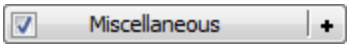
9. Save the PCA results by going to **Maps → Save → Save PCA Results**., or save them from the **Workflow** option Save PCA / ICA Results . Use *PCA comps.pca* for the file name. If you did not set the **Noise Estimation** method to **User Defined Noise Level**, you will get an error message reminding you to do so.



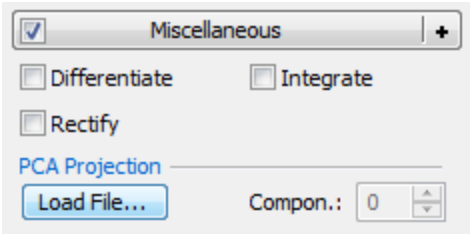
10. Return to the original CNT data by clicking the

button below the **Event List**. Select the 

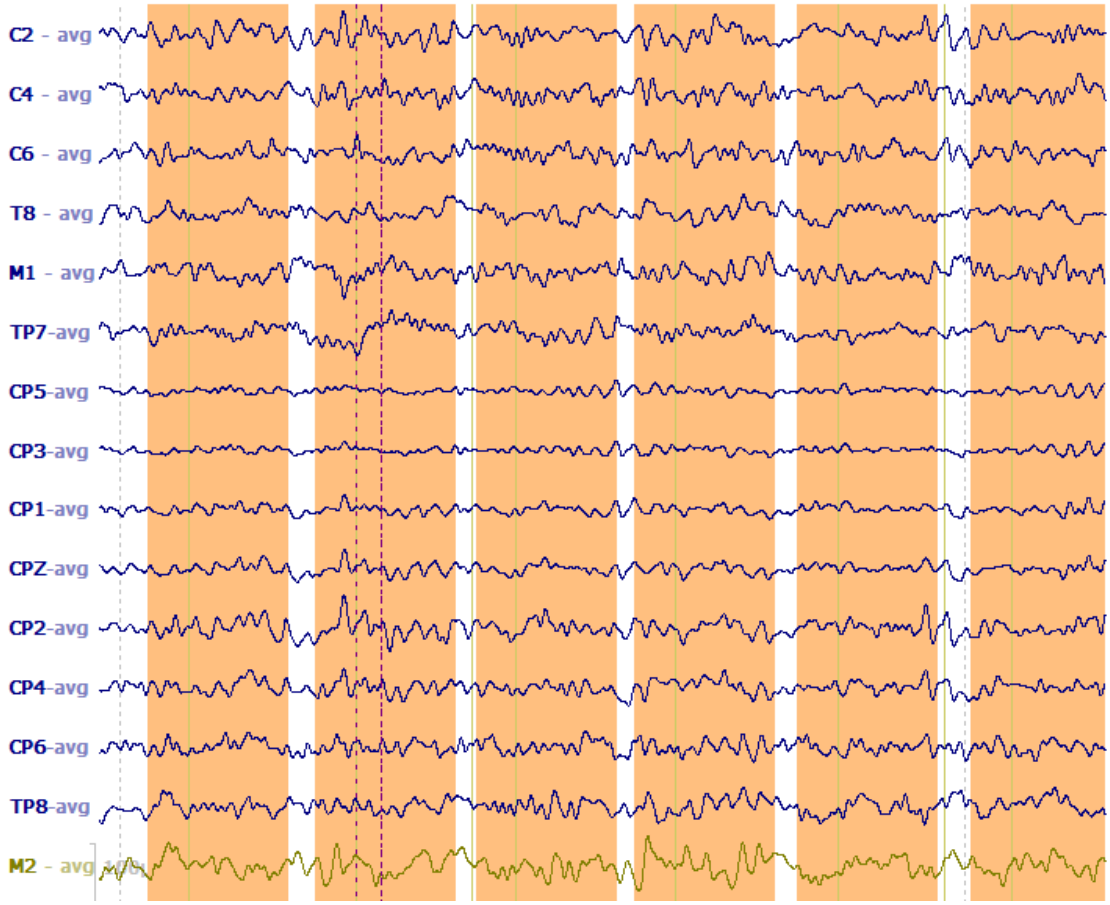
display , if needed, and scroll down to see the **M2** channel again.

11. Add a 

panel, and click the **Load File** button under **PCA Projection**.

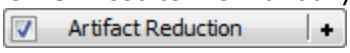


Then select the PCA results file you just saved. Set the **Components** field to **0** to see the artifacts in the file. Increase Components to see each one being projected from the data file. It is recommended that you use as few components as possible in order to reduce the artifact (which may be 1). If increasing the components does not affect the artifacts, do not include them in the projection as you may be affecting the data in unexpected ways. In this example, 1 component was sufficient for reducing most of the pulse artifact.

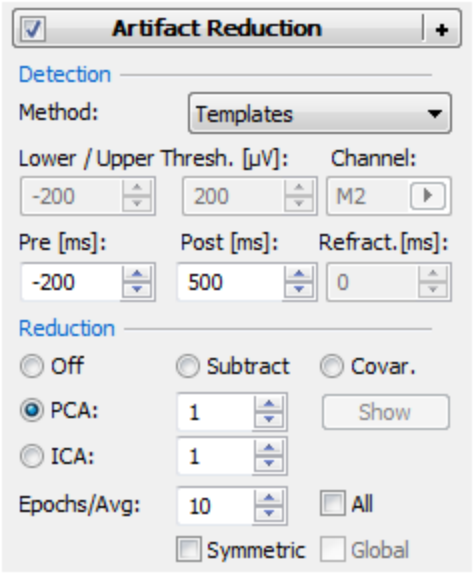


With the artifact reduced, you can then go on and average the sweeps, etc.

Again, this particular file was atypical in that there was no EKG channel, and the voltage threshold method missed some beats and falsely detected others. Normally this will not be the case, and the basic QRS Detection method described at the beginning of this section will be very adequate.

12. In this example, we went through the somewhat longer process of averaging the template matches manually and creating the PCA results file manually. A faster method is to use the **Templates** option under 

. The first Artifact Reduction will automatically use the tmpl1's, the second will use the tmpl2's and so on.

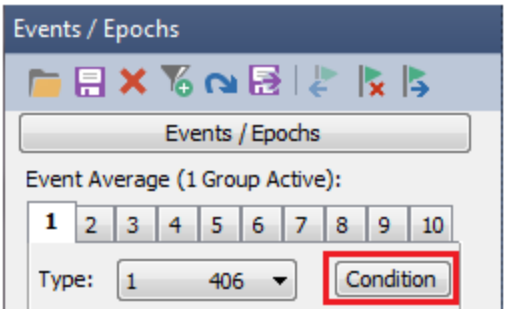


After scanning the data, you have the various options for reducing the pulse artifact, including PCA, with up to 5 components. The longer method was used in this example primarily to demonstrate how to use it. It provides somewhat more control over the process, and lets you see more completely what is happening. The shorter version may work just as well.

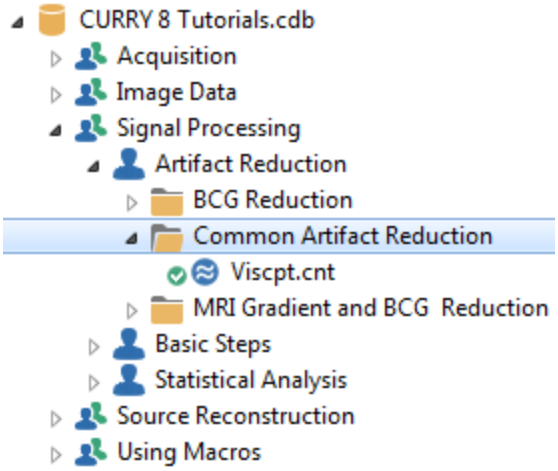
2.4.6.4 Conditional Statements

Just like with the online **Averaging** tutorial described above, you can impose conditions on which epochs are added to the averages you create offline (see that section for more examples). A complete description of all fields is found in the *CURRY 8 User Guide*.

When you are creating the averages offline, the conditions are defined using the Condition button found in the Events / Epochs parameters.



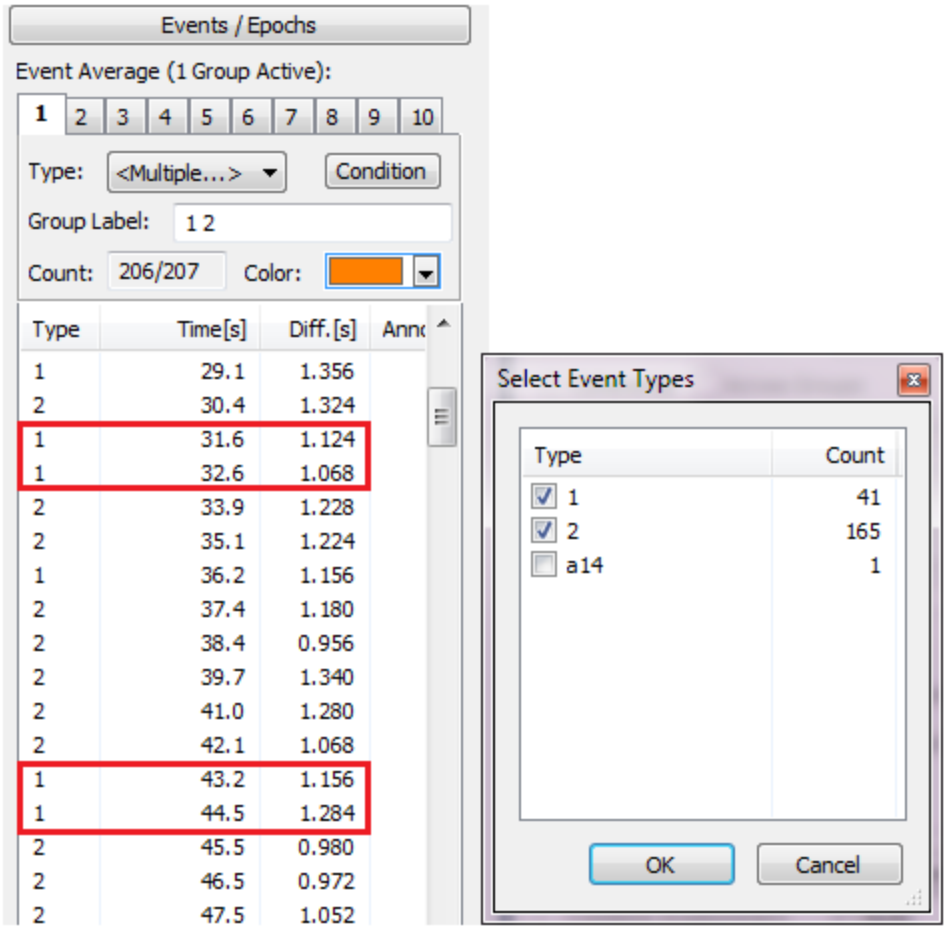
For this quick example, we will use the Study shown below.



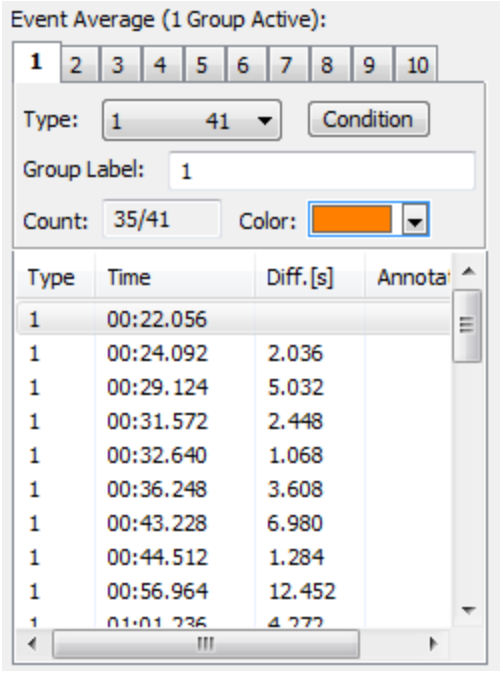
In this case, we have already designated bad sections (created in a previous tutorial). If you do not mark the bad sections in the file, your counts will be somewhat different.

1. Open the Study and select the Events / Epochs. Select **<Multiple>** for **Type**, and select the Type **1** and **2** events. This step is for demonstration only.

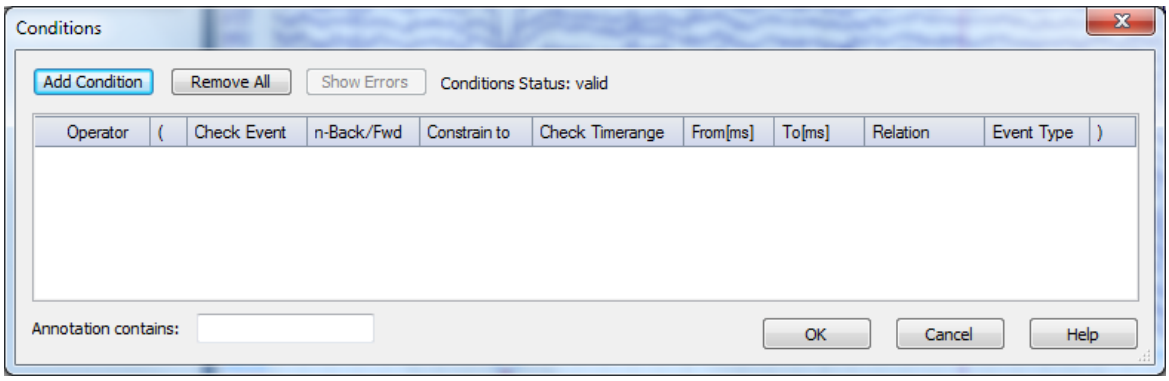
The paradigm used in this recording was an N400 study, where there were target stimuli (1's) and non-target stimuli (2's), similar to a P300 paradigm. In this case, we decided to exclude any Type 1's from the average if they were preceded by a Type 1. Two examples are seen in the Event List below. There are two other examples in the recording, plus one instance where there were three Type 1's in a row (and we want to include only the first one in each case).



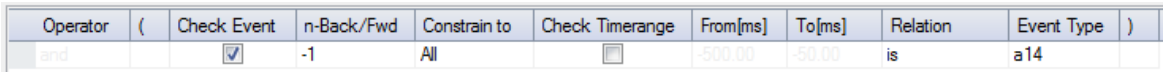
2. Set **Type** for **1** only. There are 41 of them, including the ones in the Bad Blocks, and 35 not in the Bad Blocks. The ones in the Bad Blocks will be excluded when you average the epochs.



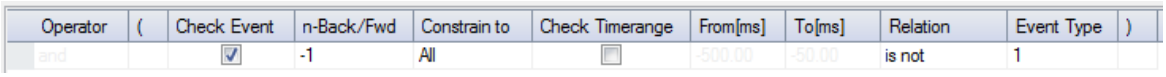
3. Click the Condition button to see the Conditions window.



4. Click the Add Condition button to create a new line.



5. We want to tell the program to include only those (Type 1) epochs that are not preceded by another Type 1 event. Make the changes as shown.



Operator. This field is inactive when there is just the single line; it connects two lines using "and" or "or".

Parentheses ( ). Parentheses are not needed in this example.

Check Event. In this case we are looking for events, so the option is enabled. You must select either **Check Event** or **Check Timerange** (or both).

n-Back/Fwd. In this example we are interested in the preceding event, so select **-1**.

Constrain to. Constrain to is linked with Event Type. Not needed in this case, so select **All**.

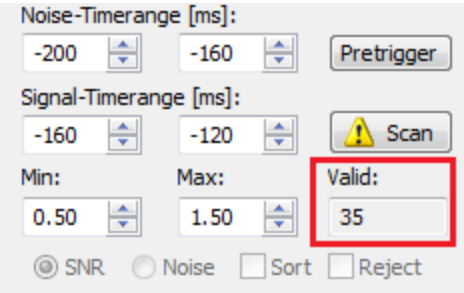
Check Timerange. Not needed.

From/To[ms]. Not needed.

Relation. Select "is not" since we do not want the previous type to be a Type 1.

Event Type. Select Type **1**.

Click **OK** to close the window. Notice that the **Valid** field is now showing 31 epochs, where it had been 41. There were 4 epochs that overlapped the Bad Blocks, 4 epochs with Type 1's immediately preceding the current Type 1, and 2 epochs that overlapped bad blocks and had type 1's before them. Therefore, 10 were excluded (6 bad blocks first, and then 4 that were excluded by the conditions).



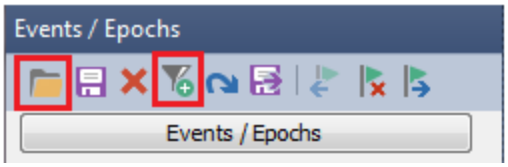
All events in the file are registered - not just the one you have selected. Otherwise, all Type 1 events are preceded by Type 1 events, and all but the first one would be rejected!

In practice, the program looks at the first event in the file, which happens to be a Type 2. It is ignored since the Conditions have been applied to Type 1 events only. When the first Type 1 event is encountered, the program looks back to see if the previous event was also a Type 1. It wasn't, so that epoch goes into the average. When the second Type 1 Event is encountered, the program looks back to the previous event. If it was a Type 2, the epoch is included. If it was a Type 1, the conditions are applied and the epoch is excluded.

In the case where there were three type 1's in a row, the second and third ones were within a Bad Block, and they were rejected before the conditions were applied.

Merging the Behavioral Data. If you have STIM2, you will note that a .dat file is created that contains stimulus, response, response accuracy, etc. information. In EDIT (in the SCAN software), you merged this with the continuous data file in order to gain access to information that was otherwise not available. If you have a stimulus

presentation system other than STIM2, you may have response information on the stimulus presentation computer, but no responses in the continuous data file (because there is no way to send them). In that case you can emulate a .dat file to include the information, and merge that in CURRY 8. In some cases, it is preferable to modify the event file created in EDIT (.ev2), or create your own .ev2 file. Both file types can be imported into CURRY 8 using the **Load Event File** or **Merge Behavioral Data File** buttons at the top of the **Event List**. (The Import Events or Behavioral Data option on the **Workflow** list will highlight these buttons).



For example, if you have a STIM2 system and have merged the behavioral data ( ) with the continuous data file, you will see the events in the continuous data display. 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.

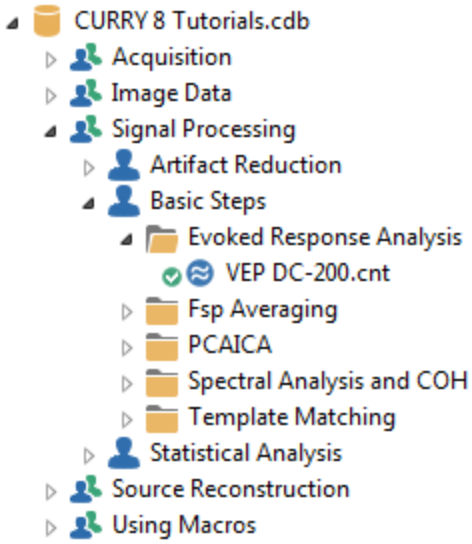
The same response events will also be seen in they Event Type column. If you want to include epochs where there are correct responses only (and these are always type 1's), select r1. This naming convention is also seen for **Artifact Reduction** when you select **Event-Codes** for the **Method**, and also in the **Event Type** field in the **Epochs / Averaging** panel.

To make the merge permanent, click the **Save Event List** button .

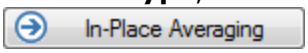
2.4.6.5 Peak Detection

CURRY 8 will automatically select the maximum positive and/or negative peaks within the Timerange. The results may be saved to a text file.

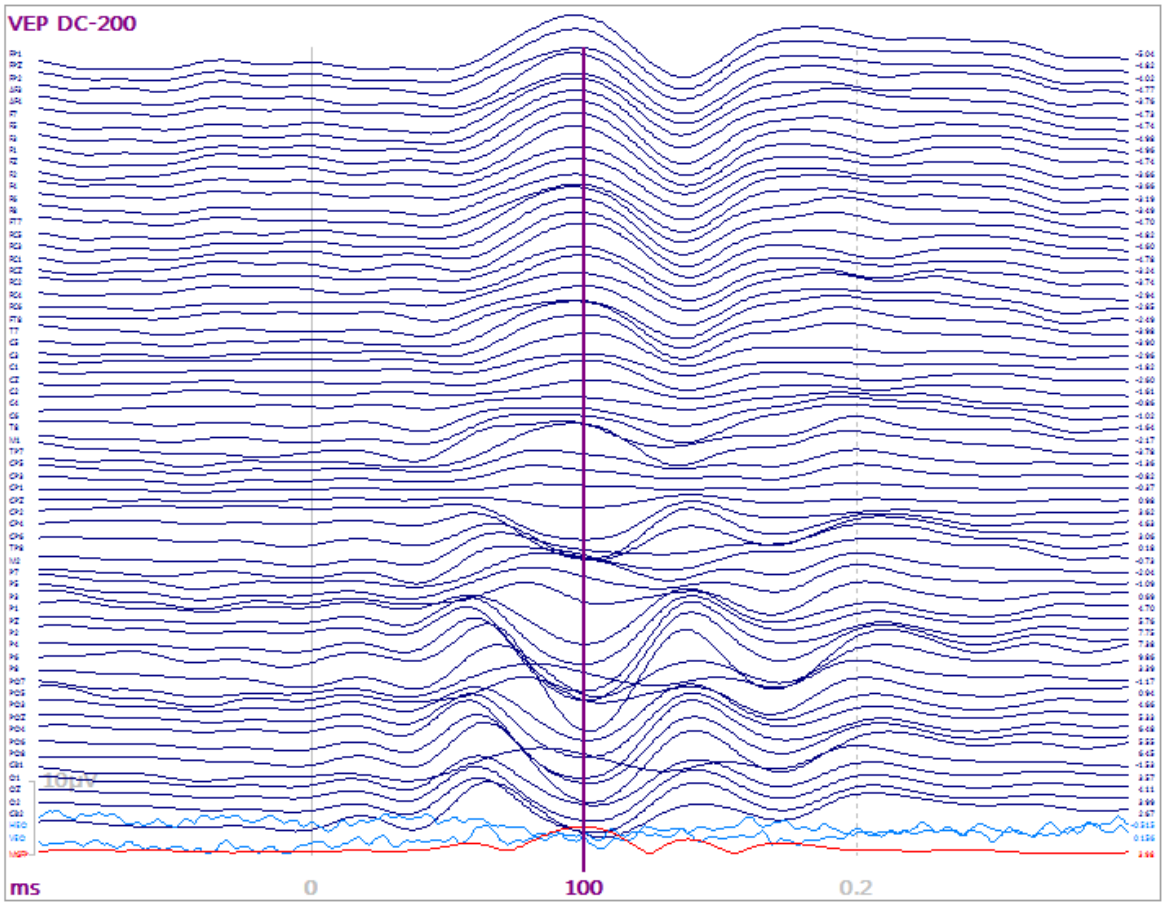
For this example, we will use the *VEP DC-200.cnt* file as shown below.



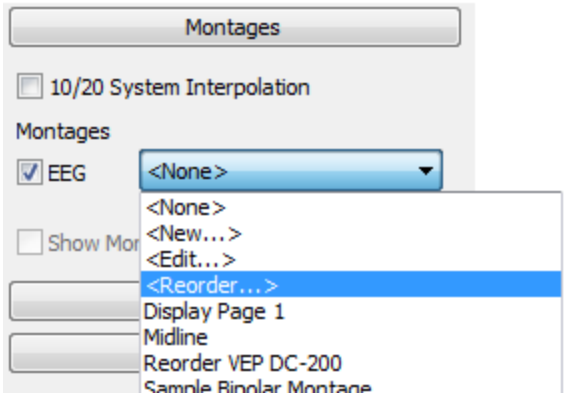
1. In this example, we will not be too concerned with artifact reduction - we just want the averaged VEP to work with. After opening the Study, select **Plus is Up** , set the **Reference** to **Off** (if needed), set the **Baseline Correction** to **Constant**, and set the **Bandpass Filter** to **User Defined (Auto)**. Rescale the data as desired. (See previous tutorials if you do not know how to set these parameters).

2. In the **Event List**, select **1** for **Type**, and set the **Pre** and **Post [ms]** times to **-100** and **300**. Then click the 

button. Now we see the averaged VEP for all channels.

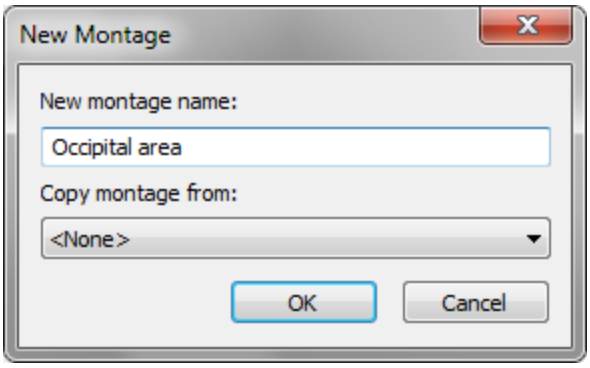


3. Let's say we wish to measure the amplitude and latency for the N1, P1, N2, and P2 components, and that were are only interested in the occipital area channels. First, we will create a new montage that contains only the channels we want. From the **Montages** panel, select the **<Reorder...>** option. The Montage Editor will appear.

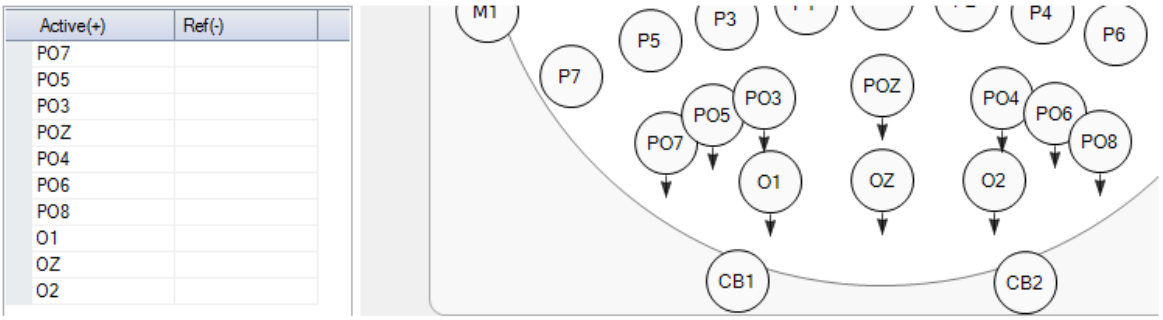


Click the **Create a new montage button** . Enter a name for the new montage and click OK. Make sure you have the **Current Study Placement** selected for **Placement**

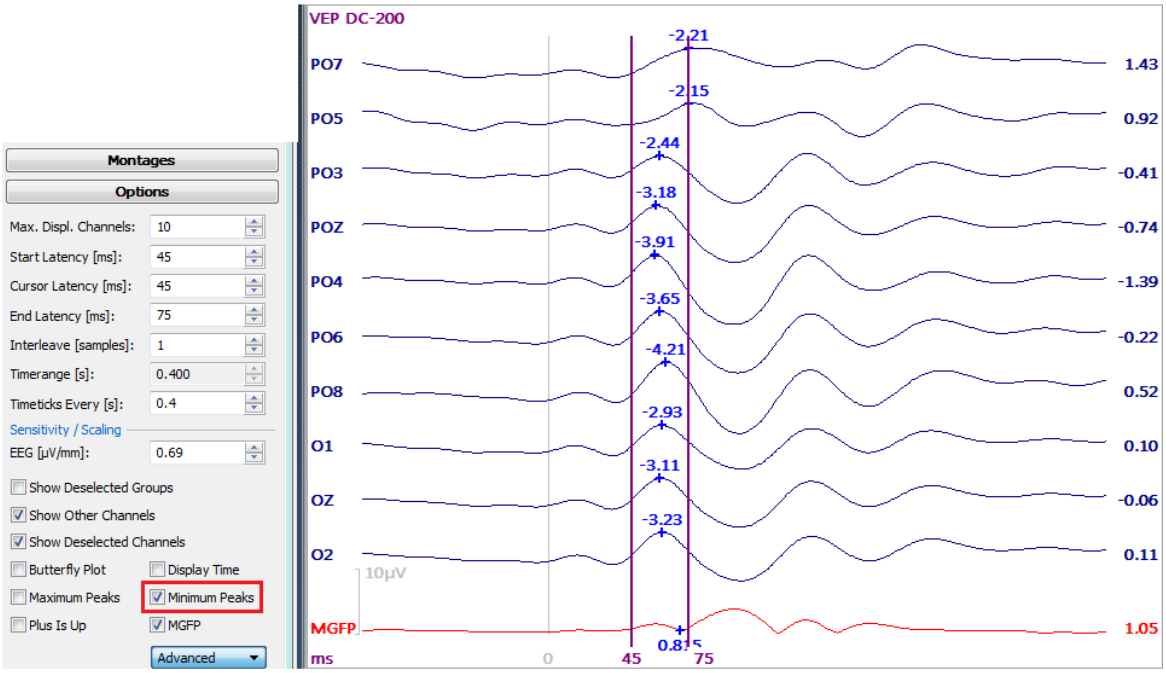
.



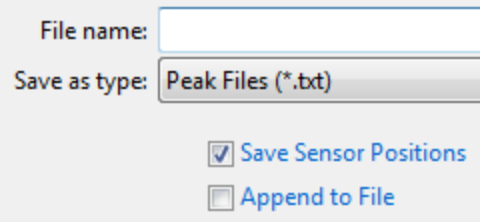
Now select (*double-click*) the channels in the order in which you wish them to appear. Then click **OK**.



4. Now you will see only the channels of interest. If you have 10 or fewer channels, you will see the amplitude values. If you have more than 10 channels, you will see the plus marks only. Set the Timerange for the first interval of interest - the N1 component (45-75 ms). Then select **Minimum Peaks** from the **Options** panel.



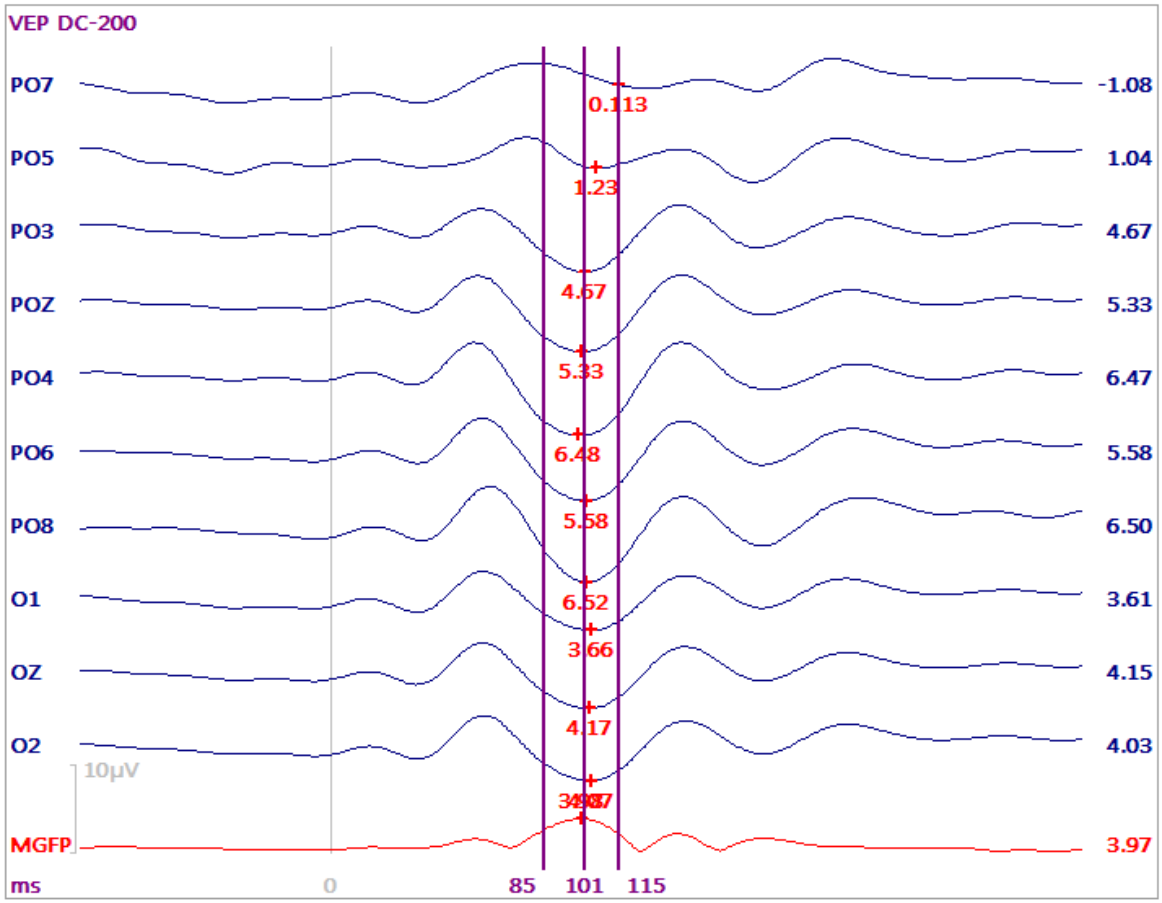
5. To save the information in a text file, either select Save Peak Detection from the **Workflow**, or go to **Functional Data → Save → Save Peaks**. On the Save As dialog, you have the option to include the XYZ coordinates, and the option to append the current results to an existing folder that has prior peak information (in case you want multiple peaks in the same file).



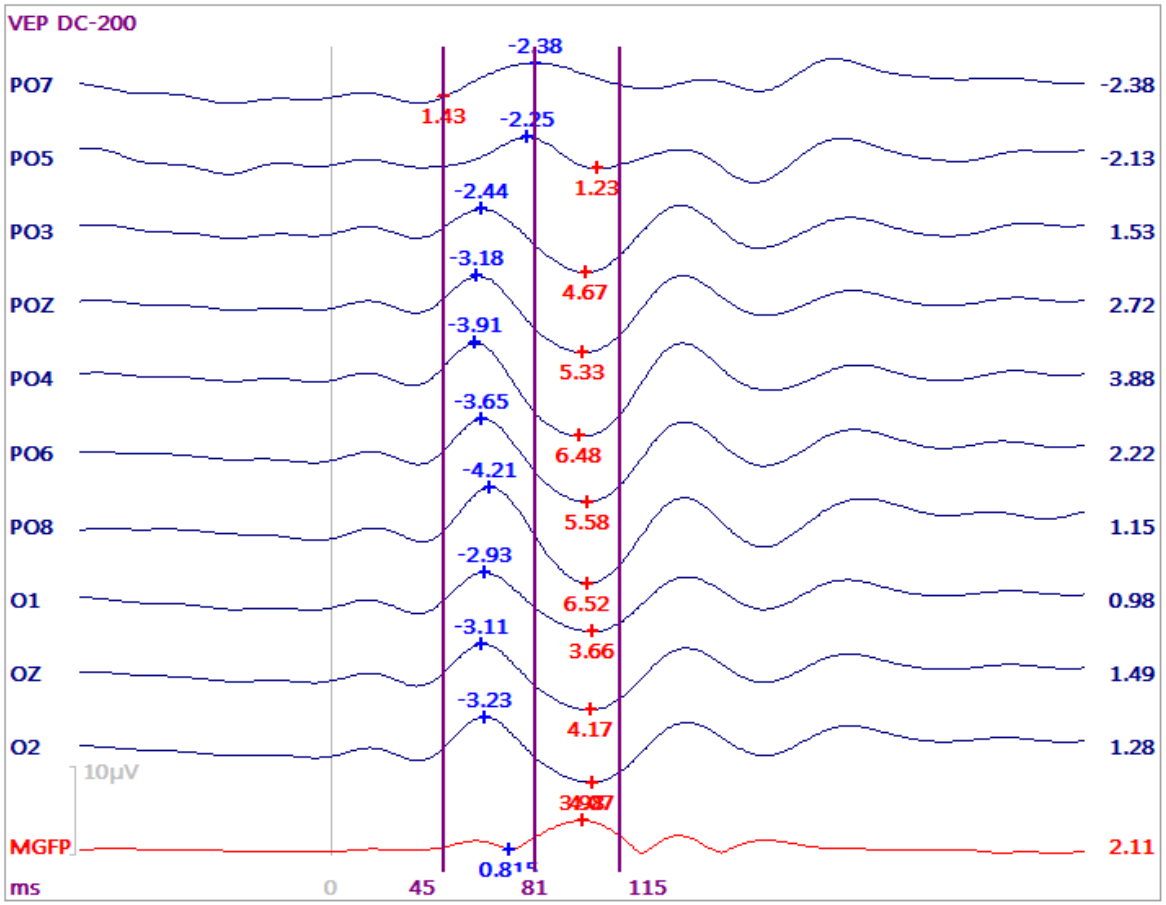
The text file contains information as shown below.

```
# time domain
# channels, tested samples
   10    30
# 45.0 ... 75.0 ms
# channel labels, min[µV], latencies[ms]
PO7    -3.423    75.000
PO5    -2.669    75.000
PO3    -2.494    60.000
POZ    -3.259    58.000
PO4    -3.745    57.000
PO6    -4.080    60.000
PO8    -4.923    63.000
O1    -3.527    61.000
OZ    -3.603    60.000
O2    -3.820    61.000
```

6. Now it is just a matter of selecting a Timerange for P1, selecting Maximum Peaks, and deselecting Minimum Peaks. Then Append those results to the same or other text file.

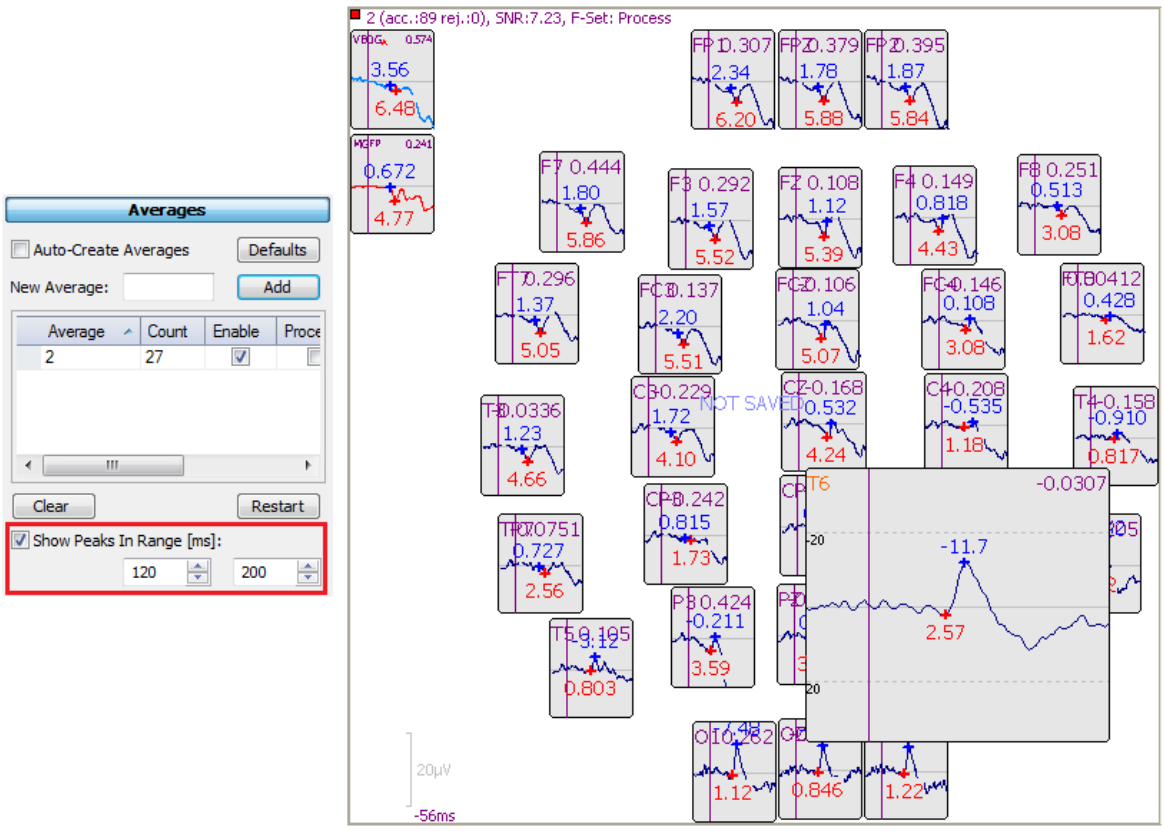


7. Continue the process until all desired peaks are chosen. In some cases you may be able to select the positive and negative peaks at the same time by using a wider Timerange and enabling **Maximum Peaks** and **Minimum Peaks**. Just be careful that the largest maximum peak does not occur outside of the interval you are interested in. In this file, for example, the largest positive value for "P1" occurs at 45 ms. Also, the negative values for N1 now occur at different latencies for PO7 and PO5 (compare to N1 results above). It is generally safer to define a Timerange for the component of interest only. CURRY does not perform peak/trough computations, but rather exports the values so that you can do the additions/subtractions in Excel or a statistics program.

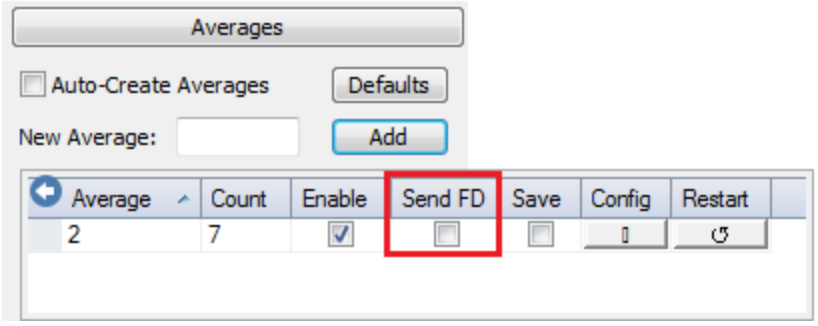


Online Peak Detection
Performing peak detection during acquisition is accomplished in either of two ways.

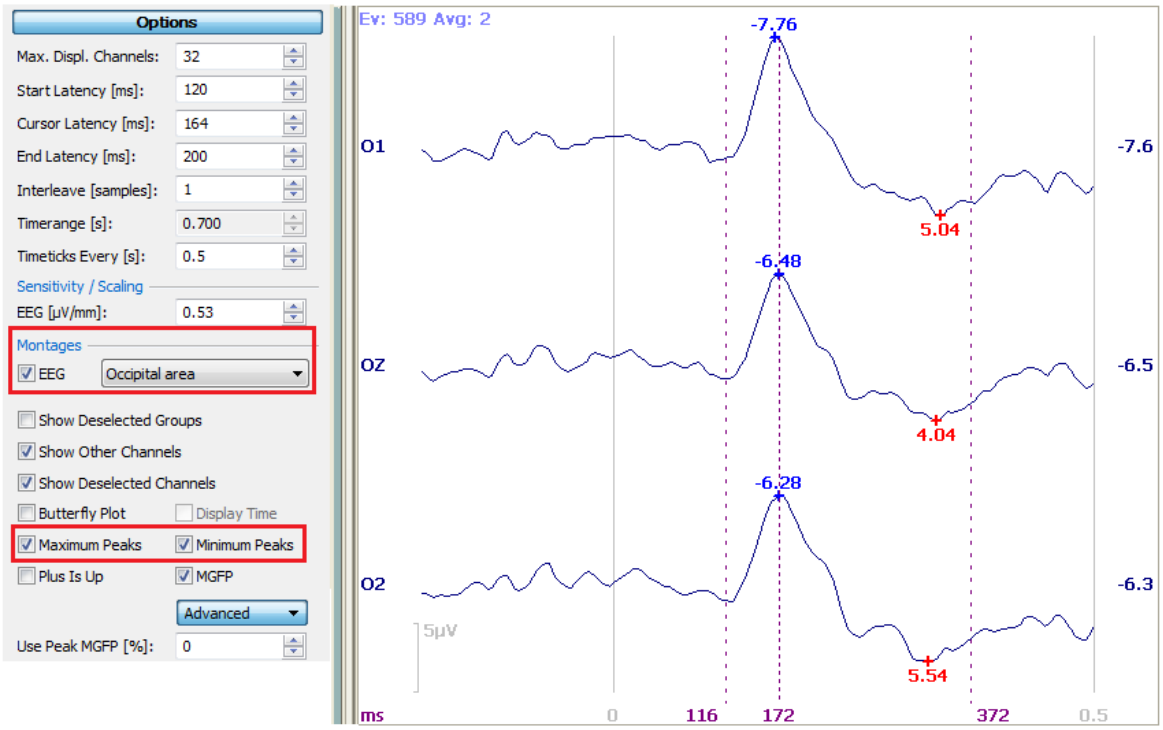
1. The first and simpler way is to create an online average, here shown as a **Position Plot**, where you enable **Show Peaks in Range**. These values are not saved, but can easily be recomputed offline.



2. The second way is essentially the same as the offline method. You need to first enable the **Send FD** option for the online average file of interest. The Send FD option gives access to most of the functionality that is available offline. It is also possible to use "Send Average to Functional Data" from the Average view toolbar (or from the context menu) to only submit the current state of the average to Functional Data.



After enabling Process, select the display. You can now use the Functional Data parameter panels just as you did above, and you can save the peak detection results using **Functional Data → Save → Save Peaks**.

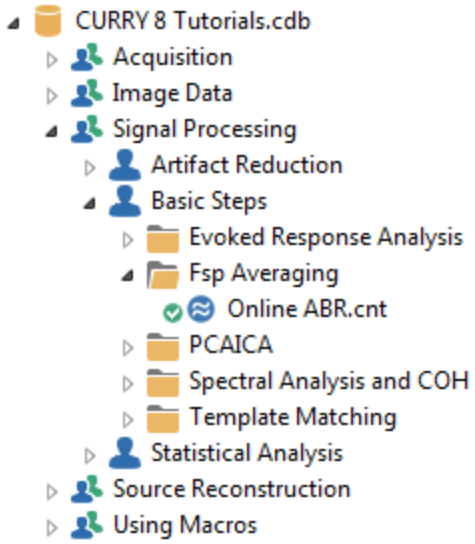


2.4.6.6 Fsp Averaging

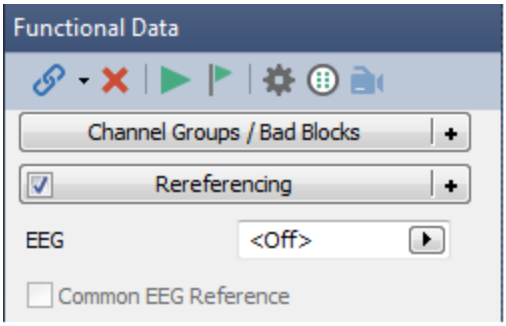
If the brain potential you are interested in has a particularly low signal-to-noise ratio (SNR), then you will need to collect a large number of epochs. For example, extraction of the auditory brainstem response (ABR) usually requires thousands of epochs. This situation presents two related problems: (1) the SNR can vary considerably between recording sessions, so that the same number of epochs may yield averages of different quality; and (2) the SNR can vary considerably within a recording session so that a "bad" block of epochs 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.

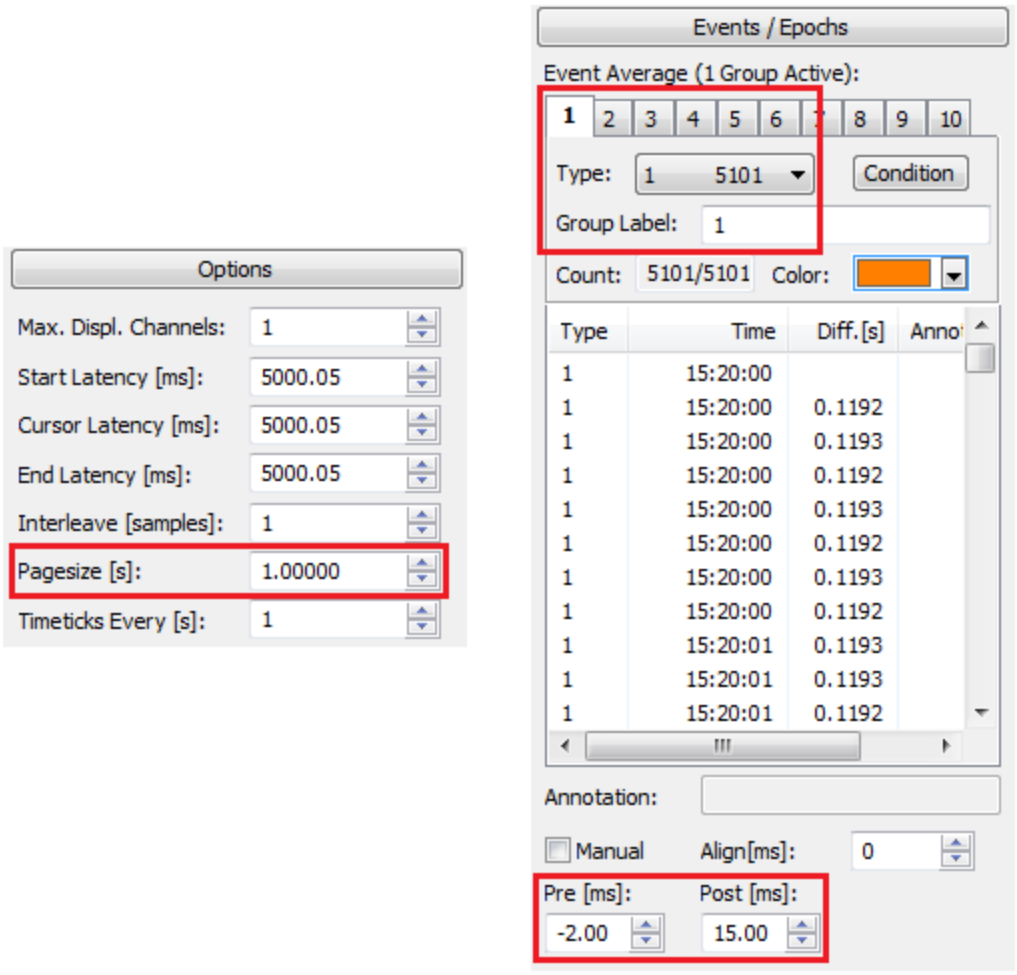
Fsp can be used online, where you can save both the continuous data and the averaged data. If desired, you can perform the same Fsp analysis offline. To use Fsp offline, you need to store a file containing the epochs first. We will start with the continuous data, found in the tutorial shown below.



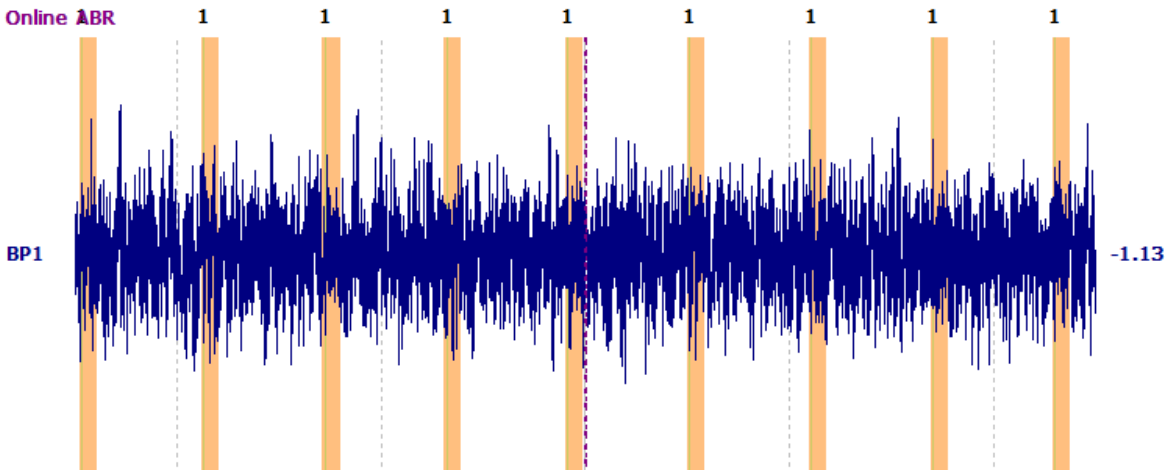
1. Open the Study containing the continuous data recording. There is a single channel of data, and if CAR is chosen for the Reference, you will see only a flat line. Go to Rereferencing and select **<Off>** for the **Reference** (if needed).



2. To better see the data, set the **Pagesize** to **1.0** secs (under Options), and in the Events / Epochs panel, set **Type** to **1**, and the **Pre** and **Post [ms]** fields to **-2** and **15**.

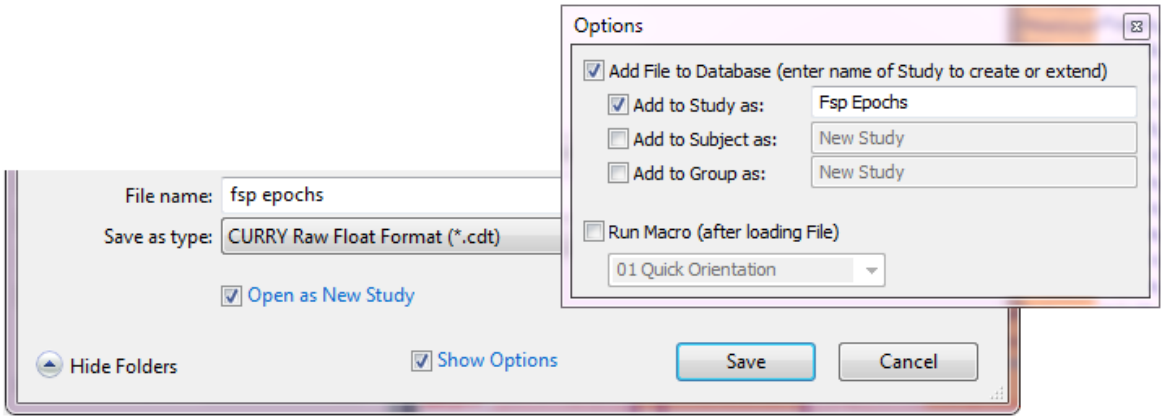


3. You should now see the EEG channel more clearly (rescale using the *mouse wheel*).



4. There are bursts of artifact in the file, so we will use epoch rejection methods to remove them. We will create an epoched file first, and then apply the rejection methods. Click the **Export Epochs** icon . Enter a file name and select a folder. In

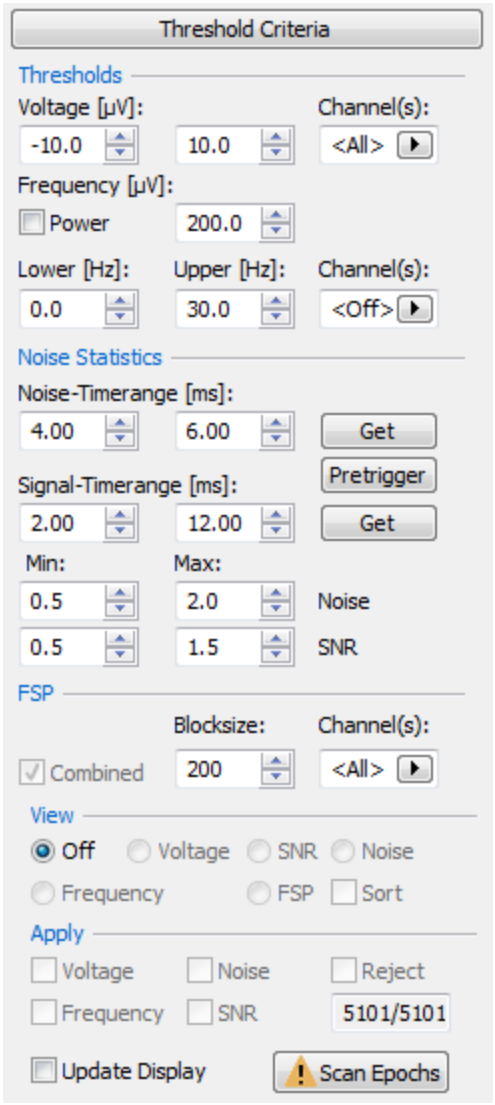
this case, we used *fsp epochs.cdt* for the file name, and created a subfolder called **Fsp Epochs**. Enable **Open File after saving**. Click **Save** - the process will take a little while.



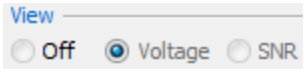
5. The epoched file will open automatically. The Threshold Criteria and Epochs panels have all the options for epoch rejection and **FSP** averaging.

6. We will delete the epochs that have voltages greater than +/-10μV. Enter the values as shown, select the BP1 channel (or **All**). Actually the Fsp algorithm is set up such that you do not really need to reject the epochs with higher voltages in them. The Fsp average is a Bayesian weighted average with computation of the Fsp statistic for each block, and blocks with lower noise are weighted higher than blocks with larger background noise. This recording has quite a bit of higher voltage activity, and so we decided to use epoch rejection. You can do it both ways - with and without epoch rejection - and see if there are any differences.

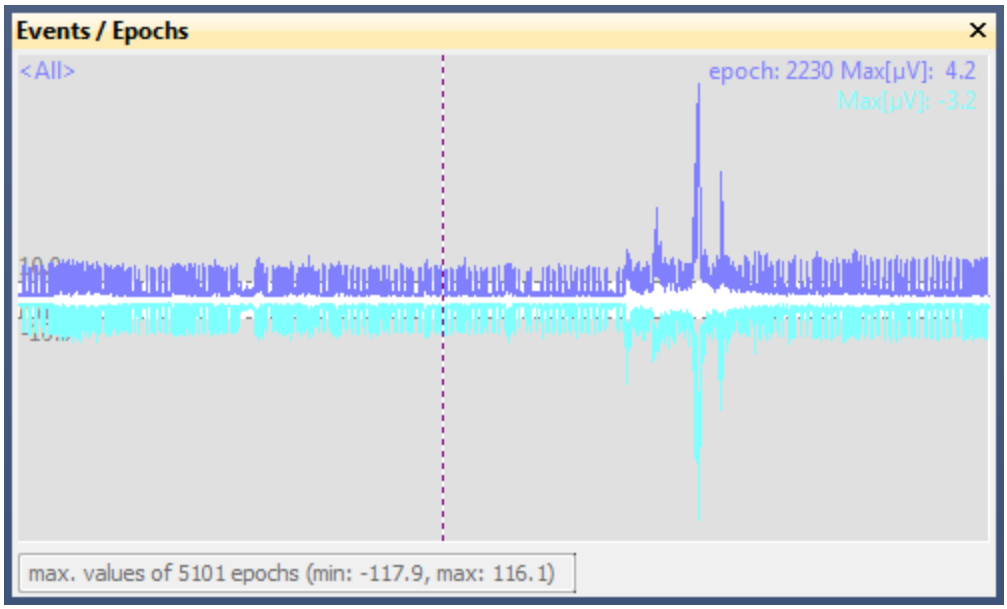
We can also set the parameters for Fsp at the same time. The **Noise Statistics** are used to select the single point for analysis (the **Noise Timerange**), and the interval for the signal (**Signal Timerange**). You can use an interval instead of the Single Point, if desired (4-6ms selected below). The Signal Timerange is typically 2-12ms. For **Blocksize**, enter **200**. For **Channel(s)**, select the single channel (or **All**). Click Scan Epochs after entering the parameters. (If you disable **Update Display**, the process will go faster).



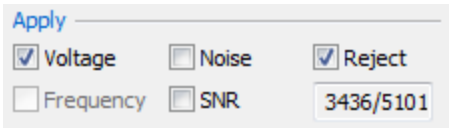
7. When the Scan has completed, select the **Voltage** option for **View**



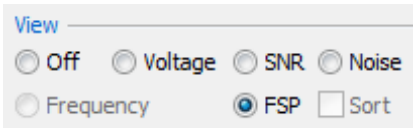
. Now you see all of the individual epochs, with the largest maximum and minimum voltages. The horizontal dotted lines show the positions of the thresholds. Only those epochs with voltages falling between the thresholds will be accepted.



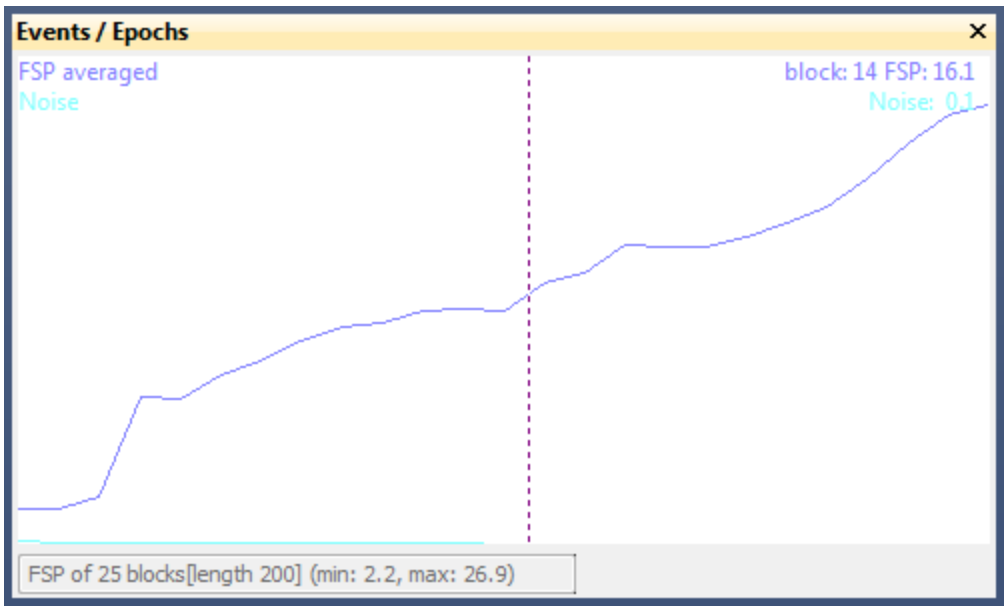
Select the **Voltage** and **Reject** options in the **Apply** section. We now see that about 3500 epochs remain.



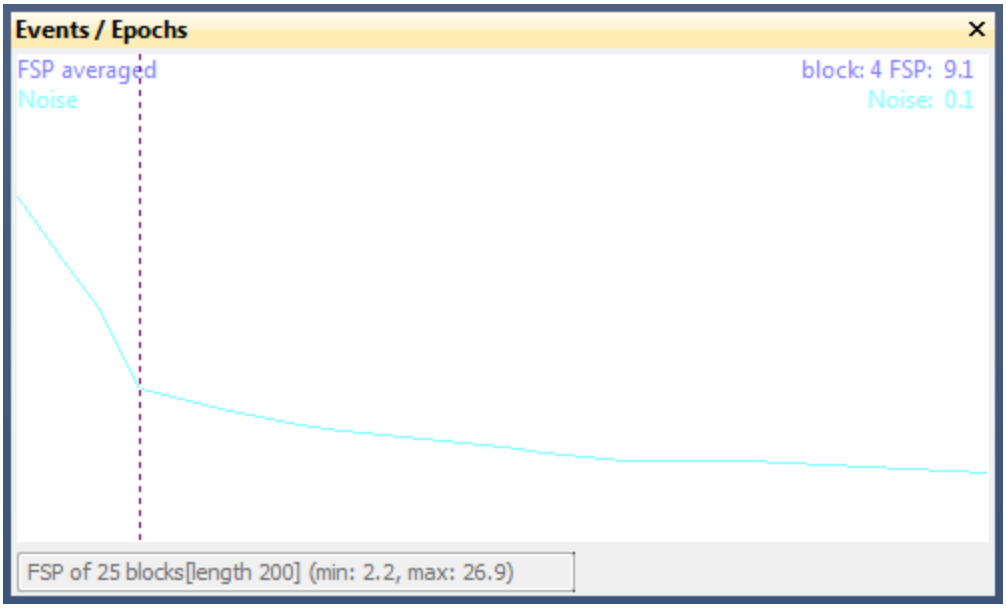
7. Now select the **Fsp**



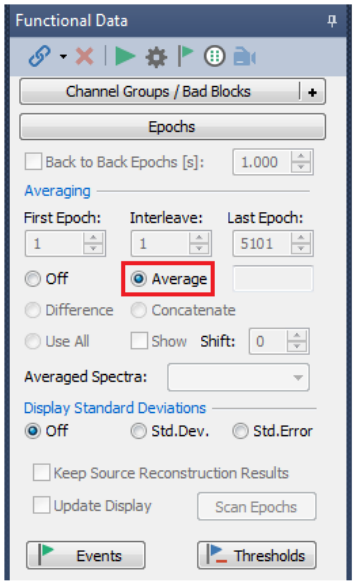
option under **View**. The F value and the Noise value are shown for each block. The top function shows the ascending values for F.

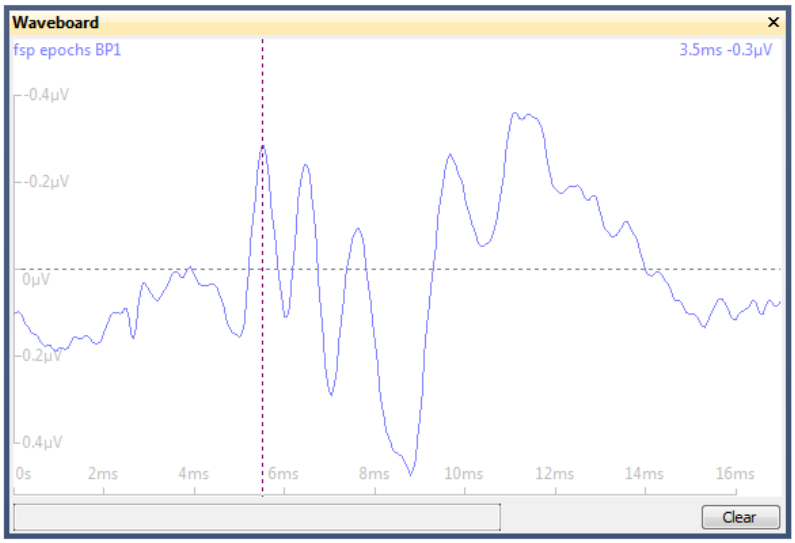


The lower function shows the descending values for Noise (rescaled using the *mouse wheel*).

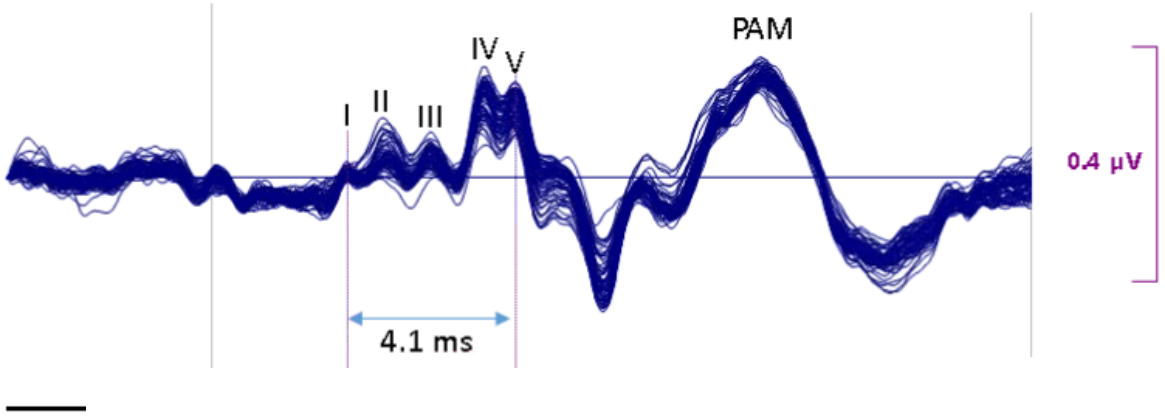


9. Close the **Events / Epochs** window and in the Epochs panel under **Functional Data**, select **Average**. Now you see the ABR (rescale as needed). *Right click* on the electrode label and select **Send to Waveboard 1**. Now you can measure the amplitude and latency of the peaks.



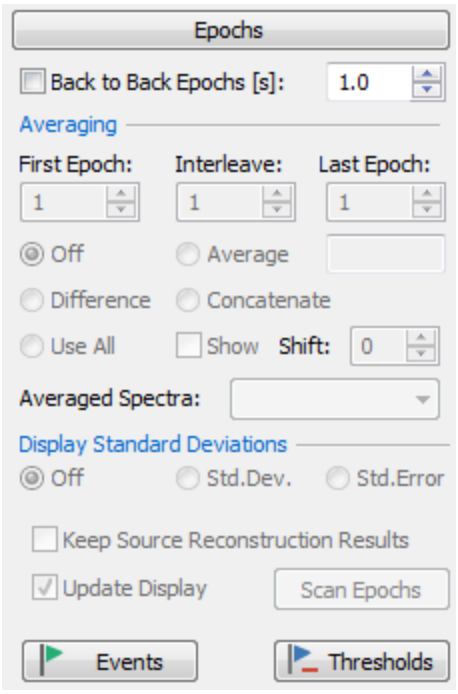


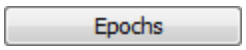
This is a typical ABR.



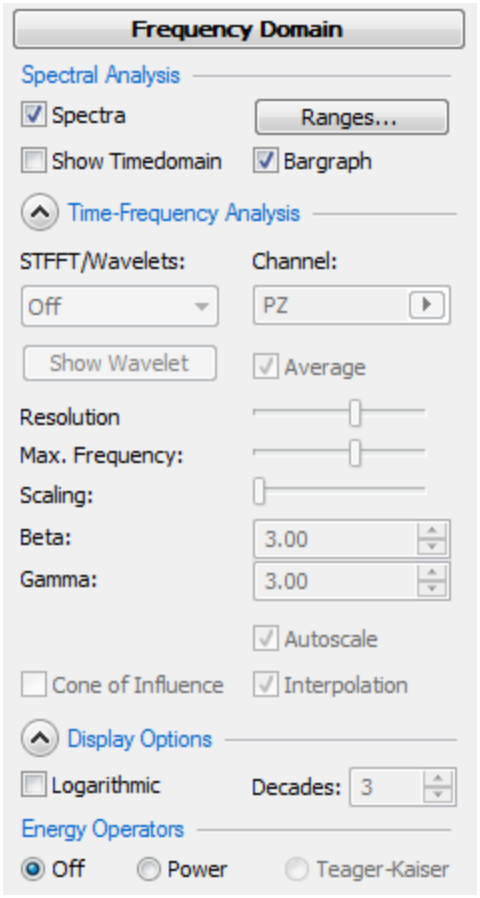
2.4.7 Spectral and Coherence Analyses

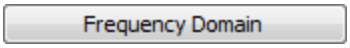
The relevant parts of the software for computing spectral and coherence analyses include:



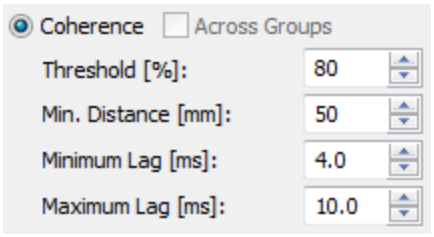
options in the 

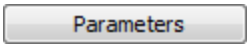
panel under **Functional Data**,



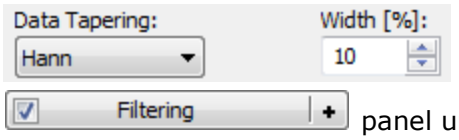
the 

panel under **Functional Data**,



Coherence options in the 

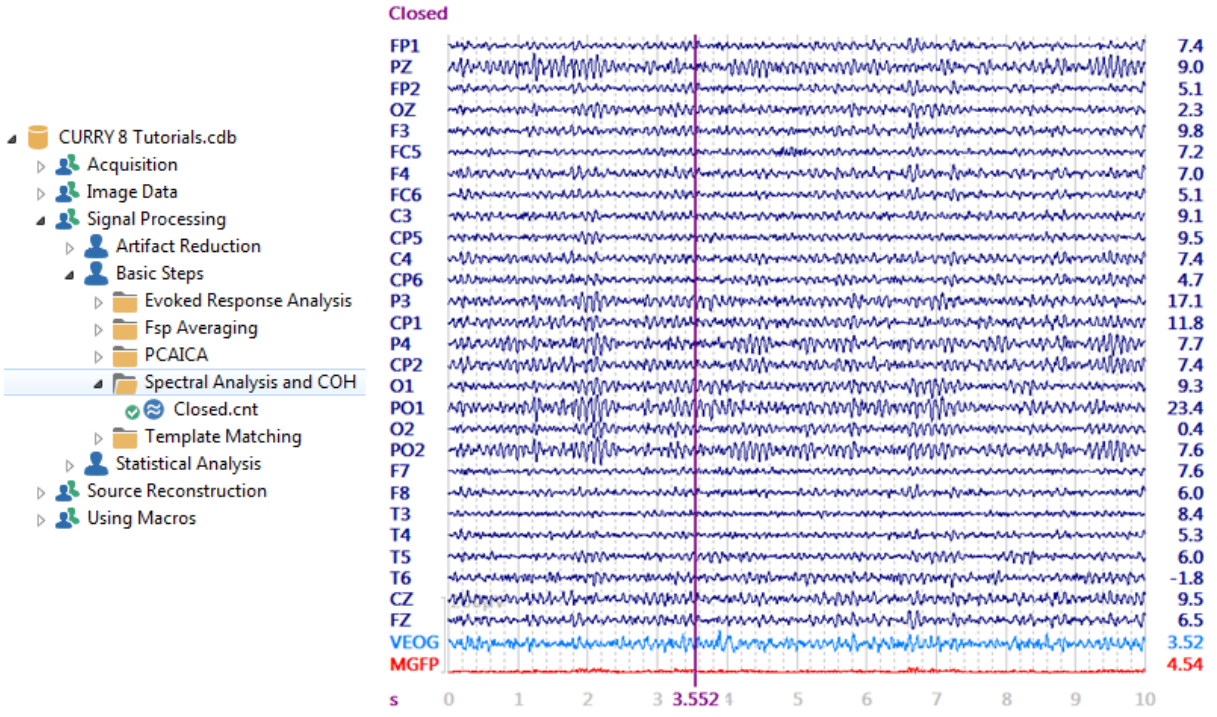
panel for **Maps**, and



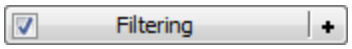
Data Tapering parameters in the

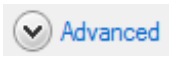
panel under **Functional Data.**

Spectral Analyses
We will start with a continuous data file of an eyes closed recording, with little or no artifact. This is found in the *Spectral Analysis and COH* study in the *CURRY 8 Tutorial* Database.



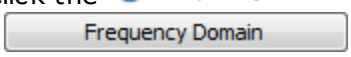
1. Open the Study. You can compute the power spectrum from the data that are displayed, or across epochs that have been created in a back-to-back fashion. You can also compute the power spectrum from the averaged data (the entire epoch interval is used, not a Timerange that has been selected). When computing the spectrum from the displayed data in a continuous data file, the program actually uses more than just the data that are displayed: additional data are added from before and after the displayed data in order to achieve a number of data samples that is the nearest power of 2. The FFT is computed irrespective of the cursor placements.

2. When performing an FFT it is typical to apply windowing at the ends of the sweep to avoid spurious increases at the edges of the interval. Go to the 

panel, expand the 

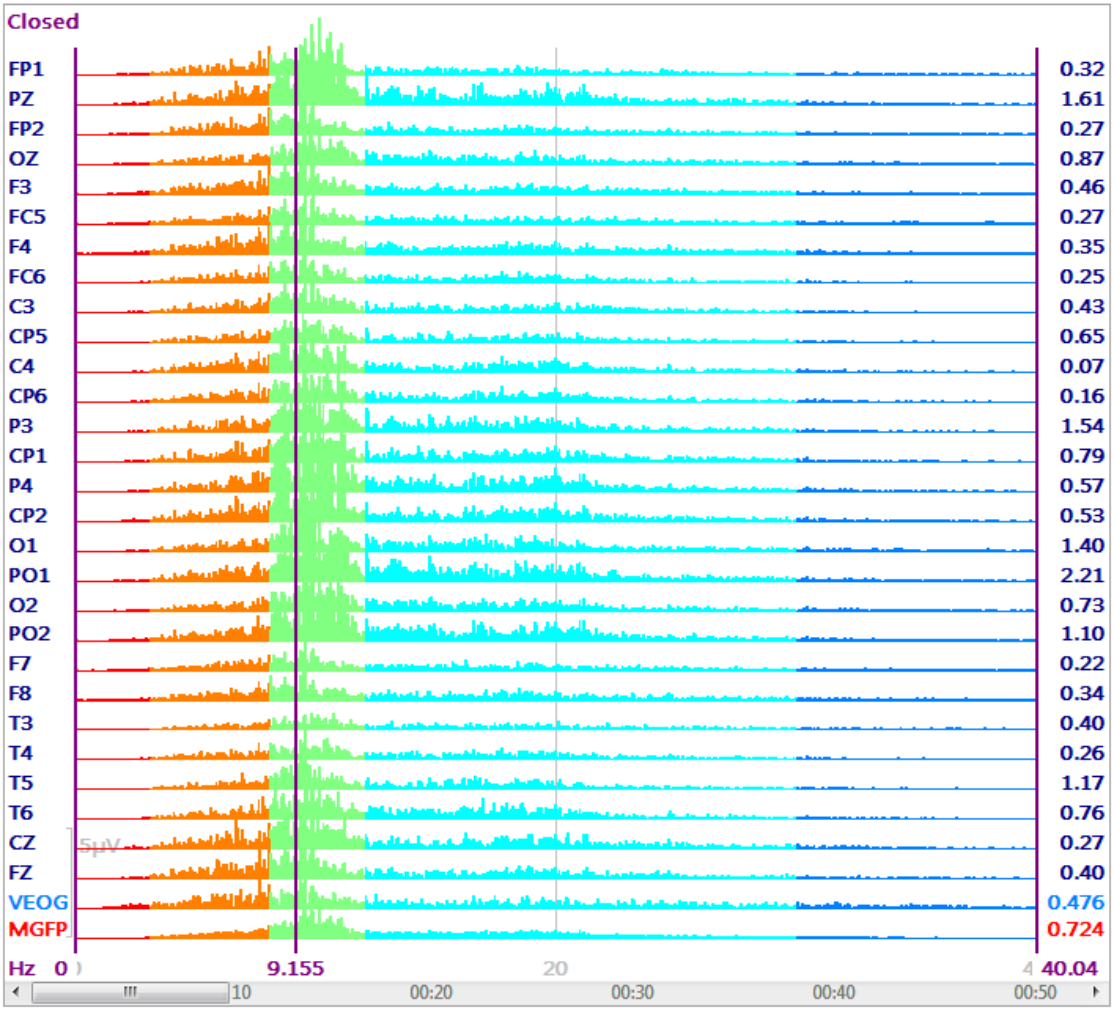
fields, and select (if needed) **Hann** for **Data Tapering** and a **Width** of **10%** (this means that 10% of each end of the interval will be tapered). These values are not cast in stone. Once the FFT has been computed, you can select different types and percentages to see the immediate effect on the results. We recommend the default Hann tapering with a 10% width.

3. Click the

line from the **Workflow**, or go to the 

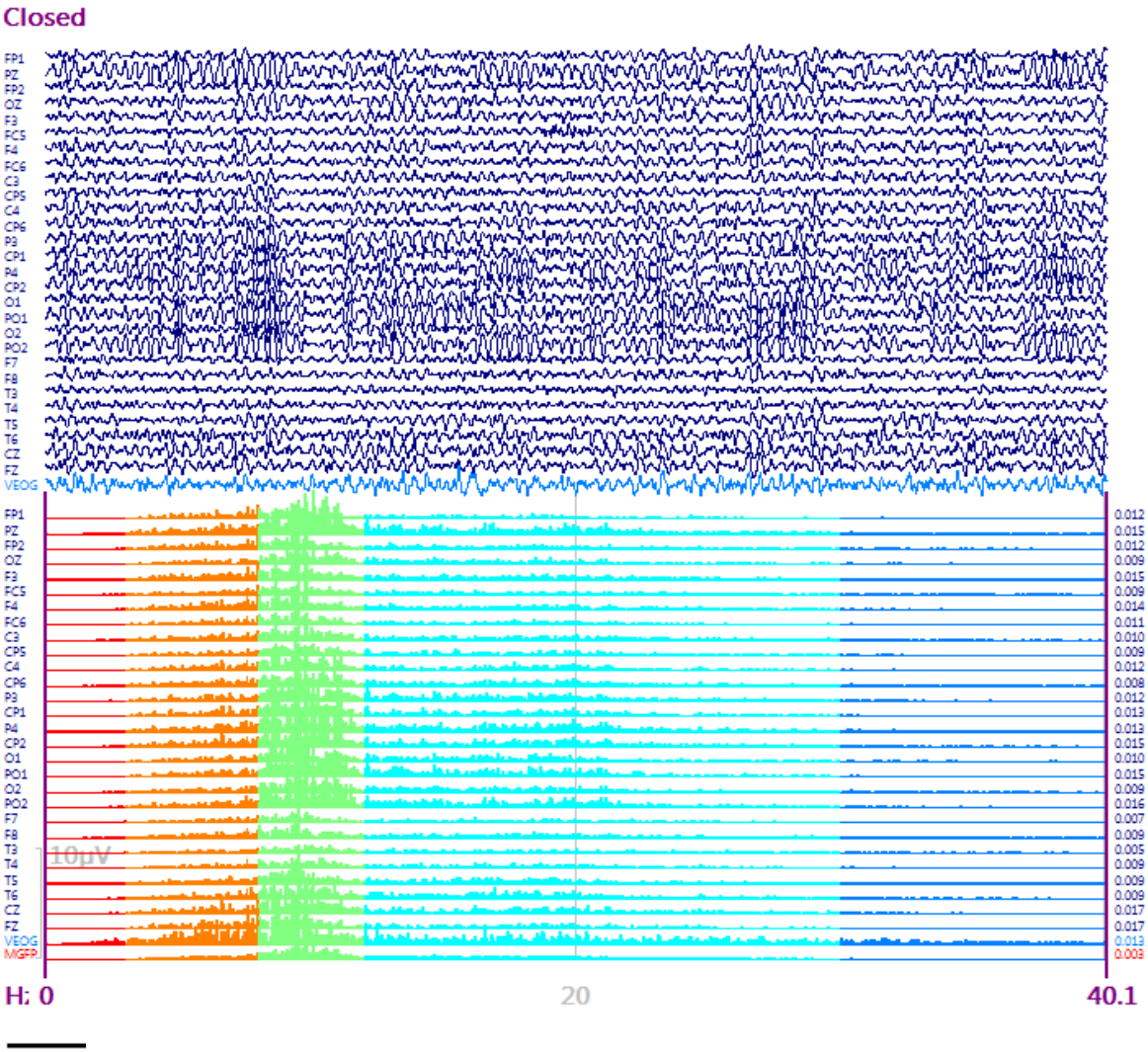
panel, and enable **Spectra**.

4. Position the two outer vertical cursors to select a frequency range of interest (such as, 0-40 Hz). *Right click* in the display and select **Zoom In** (*Alt+Z*). You can then see the spectral distribution for the frequency interval you selected. You can change the frequency range and color scheme for the frequency bands by clicking the Ranges... button, and making the desired changes.



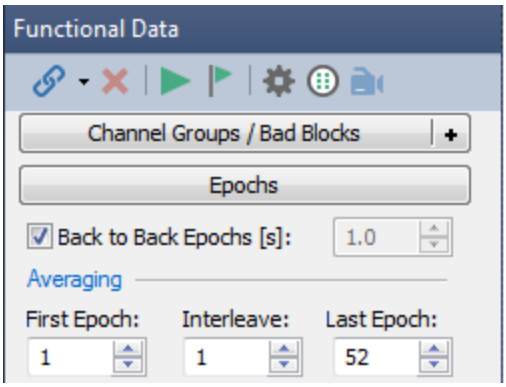
This gives you the FFT results for a selected section on the recording. By changing the data that are displayed (increasing or decreasing the number of seconds displayed), you can vary the section of the file that is being analyzed.

5. Enable the Show Timedomain option to see the waveform data as well. The spectral data are computed from the time domain data that are displayed (plus additional data before and after the displayed data to give a number of points that is a power of 2). As you move through the file, the time and frequency domain data will change together.



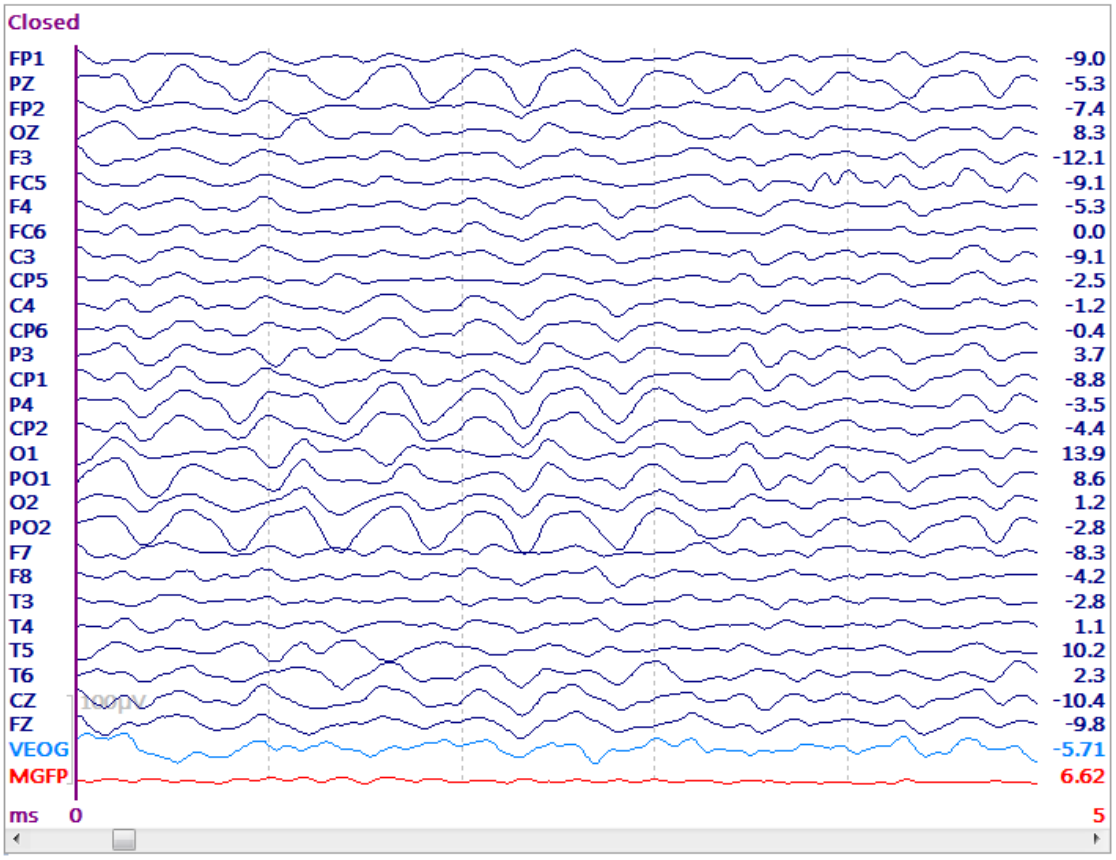
More typically, you may wish to create back to back epochs from the continuous data, compute the FFTs for the epochs, and average the results across epochs.

1. With the raw continuous data being displayed (disable **Show Timedomain** and **Spectra**), go to Epochs and enter the desired duration of the epochs (in seconds). The number of data samples does not need to a power of 2 - CURRY will accommodate any length (zero-padding). In this case, we entered **1.0** sec. Then enable the **Back to Back Epochs[s]** option.



2. You will see how many epochs were created (52). In the

display, you will see a sliding bar at the bottom that will let you look through the epochs (or use the *arrow* buttons or the icon buttons).

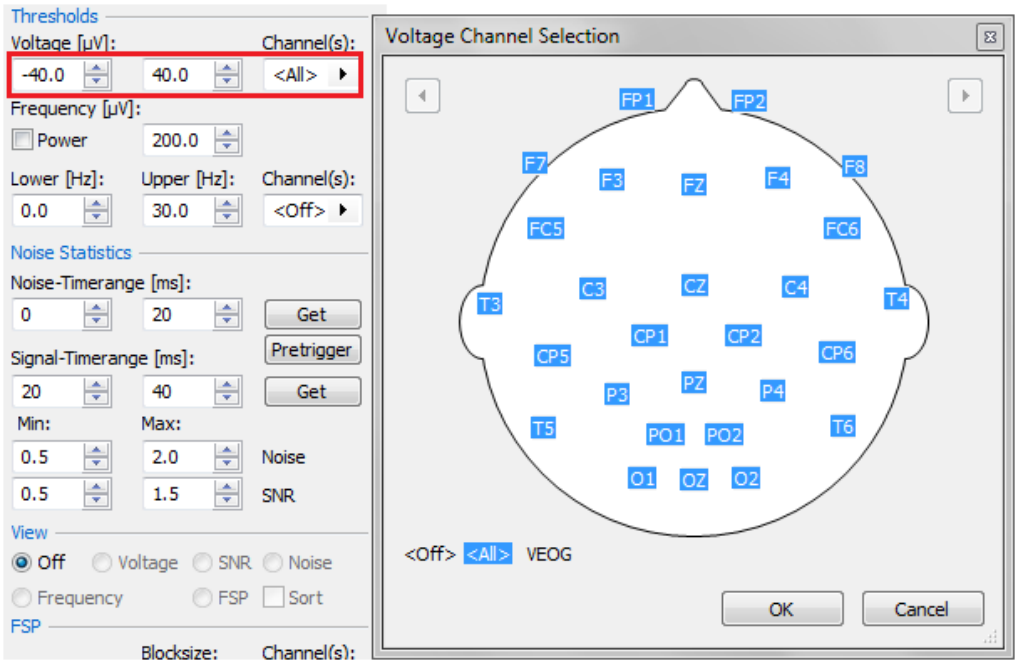


3. You then have several approaches for rejecting bad epochs: manual epoch rejection (step through the epochs and use the *spacebar* or the reject button to change the accept/reject state of the epoch), automatic epoch rejection using voltage threshold criteria, frequency threshold criteria, or SNR based rejection. Any or all methods can be used. With back to back averaging, where there is no "noise"

interval and no separate "signal" interval, the SNR based method may not always make sense, and it will not be demonstrated here. See the **Evoked Response Analysis** tutorial for a more realistic illustration of its use.

In this file, all epochs are good; however, we will illustrate the Thresholds method anyway.

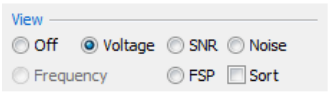
Automatic sweep rejection. Click the Thresholds button to display the Threshold Criteria panel. In the figure below, we set the program to reject any epoch where any data point from the selected channels is less than **-40μV** or greater than **40μV**. After clicking the **Channel(s)** button, click the **<All>** option. Note that all but the VEOG channel have been selected. VEOG is an "Other" channel (note the different color for it in the figure above), and will be excluded automatically.

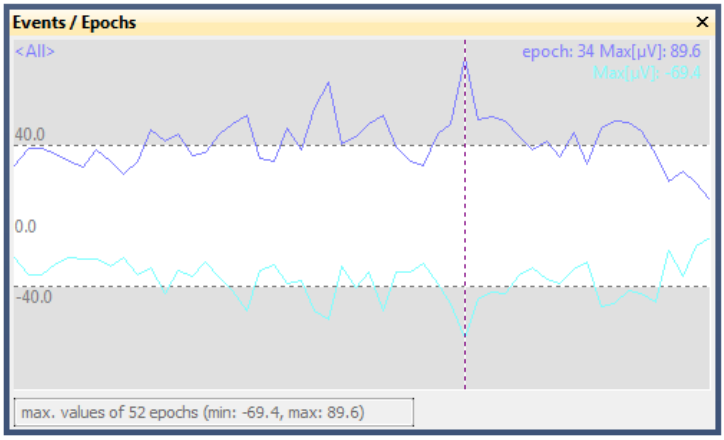


Click the Scan Epochs button to apply the criteria.

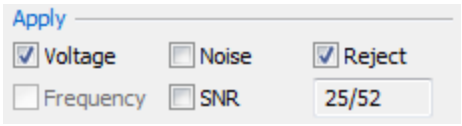
Click the Voltage option under **View** to see the Events / Epochs dialog. This is displaying the maximum and minimum voltages all selected channels across the 52 epochs. The horizontal dotted lines show the positions of the voltage thresholds, where the gray areas at the top and bottom are the rejection regions. The information in the upper right corner displays the epoch number and maximum voltage at the cursor position. The least and greatest voltages across epochs is shown at the bottom of the display. This information gives feedback about the criteria that were selected - were they too conservative, were they not conservative enough, etc. *Double-click* on any point, and you will see that sweep in the Functional Data display. Use the *spacebar* to change the accept/reject status of the sweep, as needed. (Again, this file has no bad

epochs - this is for demonstration purposes only). Close the Events / Epochs window.

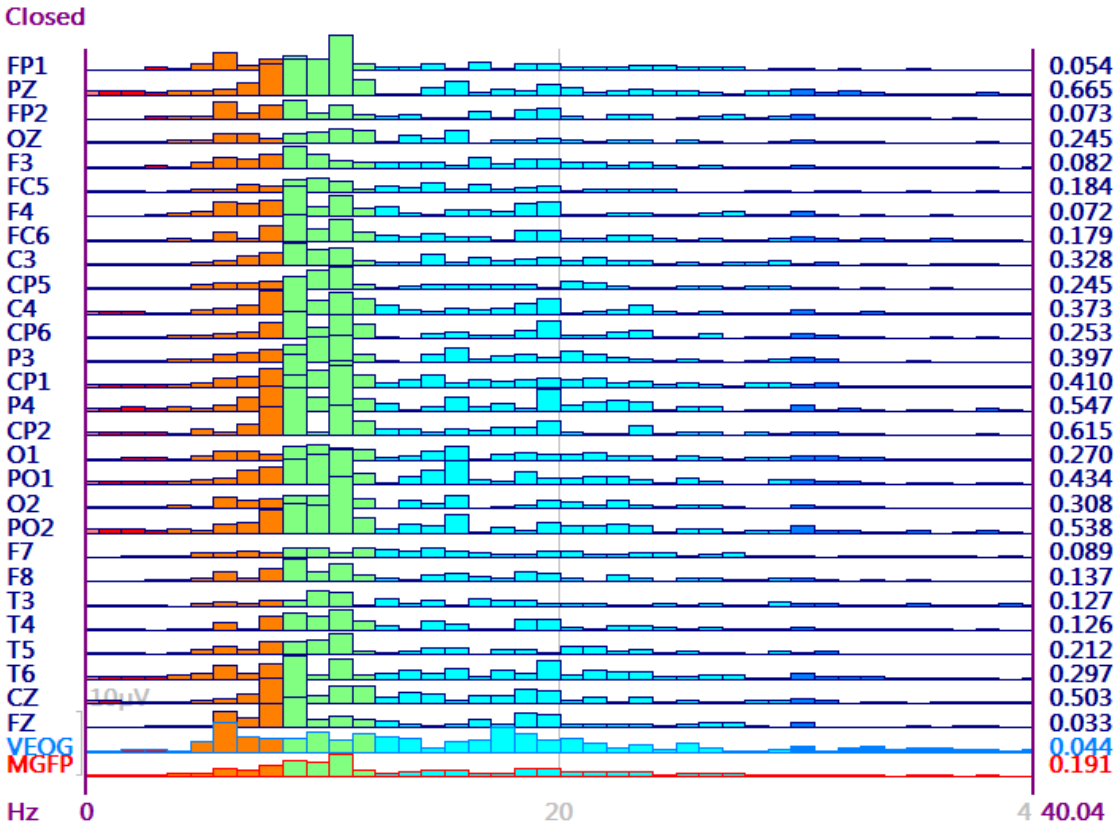




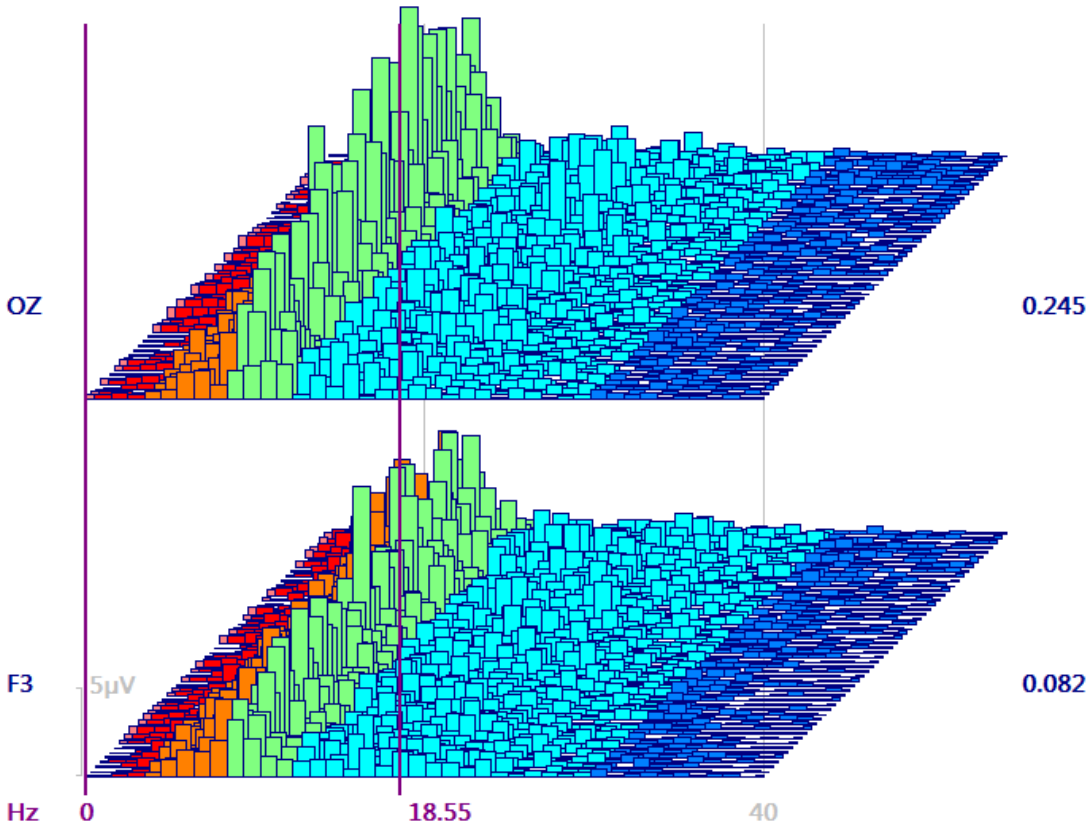
Then enable the Voltage option under **Apply** and click the Reject option. We see that 25/52 epochs have been accepted. Deselect the Reject option so that all epochs will be included.



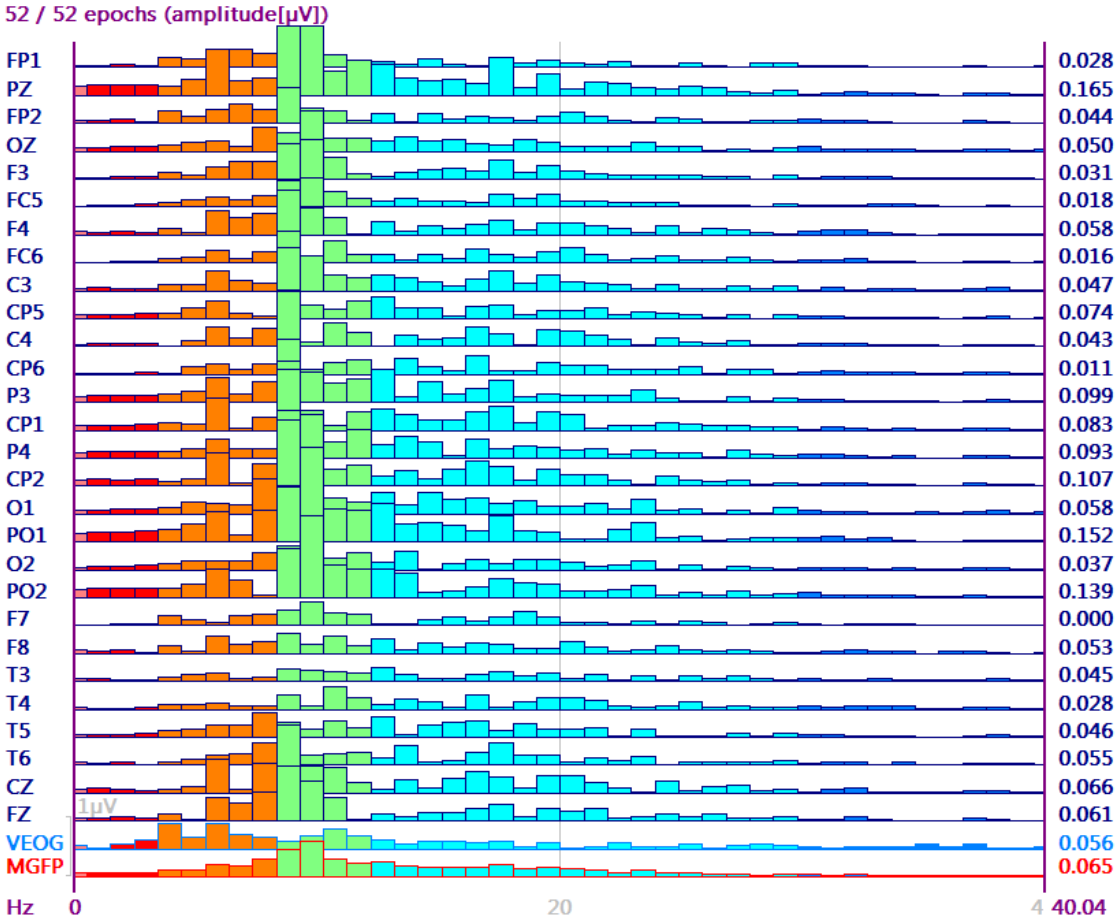
4. Now we wish to compute the FFTs for each sweep and then average the epochs. Enable the **Spectra** option under Frequency Domain to see the FFT results for each epoch. **Zoom In** to the frequency range of interest (such as 0-40 Hz; set the Timerange to the desired frequency interval first).



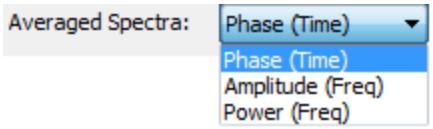
5. Reduce the **Max. Displ Channels** to, for example, **2** (under Options), disable **MGFP** (under Options), and then enable the **Use All** and **Show** options in the Epochs panel. Increase the **Shift** parameter to **3**. This will let you view the results in a landscape or cascading display across epochs. (Scroll down to see other channels).

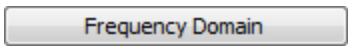


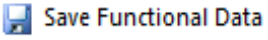
6. If you wish to average spectra across epochs, go to the Epochs panel and enable **Average** (all channels displayed). You will need to select the **Off** button first, then the **Average** option.



7. The **Averaged Spectra** option becomes active. The **Phase (Time)** option averages the raw waveforms first (time domain averaging), and then computes the FFT, thereby taking the phase relationships into account. The **Amplitude (Freq)** option computes the FFT on each epoch first, scaled in µV, and then averages the epochs (frequency domain averaging). The **Power (Freq)** option computes the FFT on each epoch first, scaled in μV^2, and then averages the epochs.

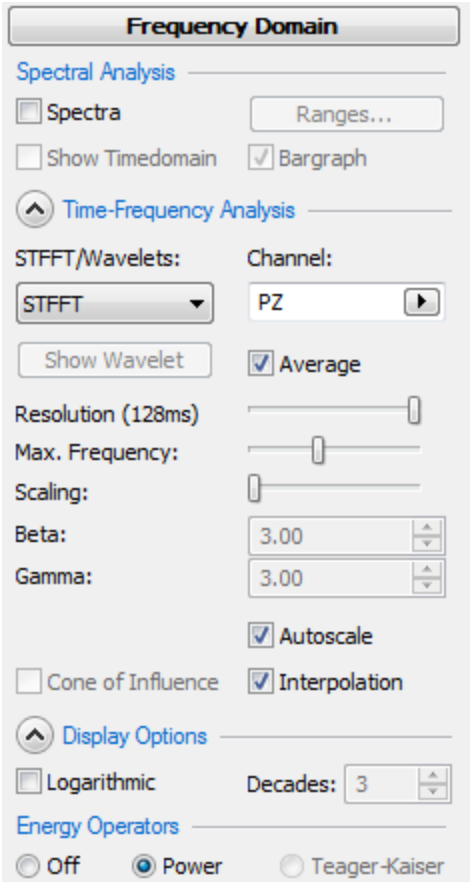


You can also use the option in the  panel to square the displayed results.

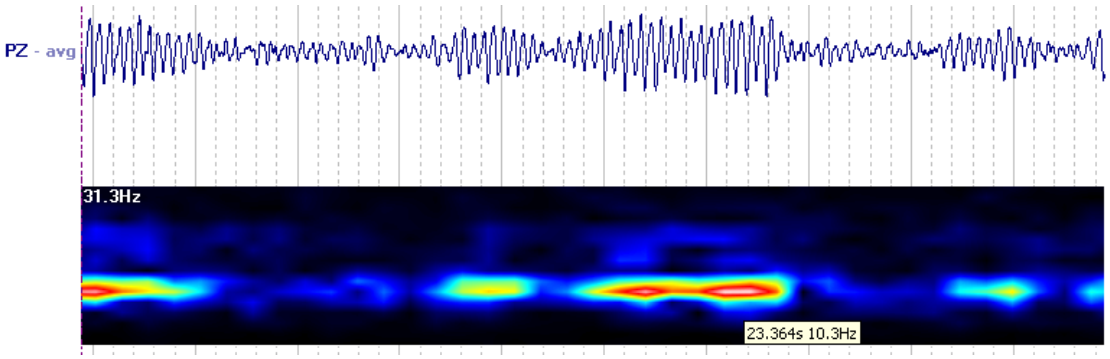
8. The spectral results may be saved by clicking  from the **Workflow**, or go to **Functional Data** → **Save** → **Save Data**, and selecting a path and entering a file name.

9. Disable **Spectra** to return to the original continuous data. Select the **STFFT** (Short Time FFT) option. STFFT is an alternative to wavelets. The spectra are averaged over all selected channels, or a single selected channel, and displayed

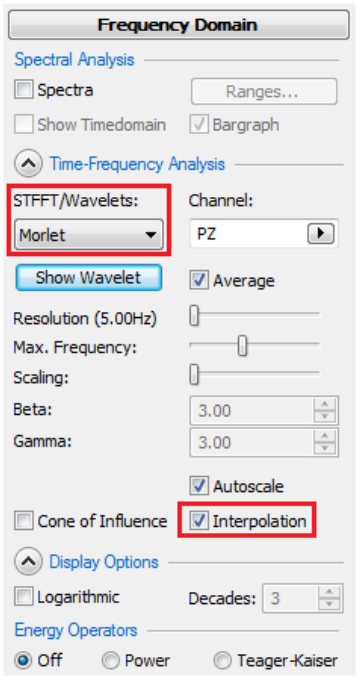
with color coding. In all of the STFFT and Wavelet displays, the y-axis is frequency, and the x-axis is time, corresponding to the waveform data being displayed. It is generally helpful to reduce the number of channels being displayed in order to see the wavelet display more clearly. If you have "Other" channels, such as artifact channels, these will not be included in the wavelet displays. In this case, we have selected the **PZ** channel only. Adjust the sliders as shown, and note the changes in the display as you do so. If you have multiple channels selected, you will see the STFFT results for each channel. Select **Average** to see the average of the selected channels.

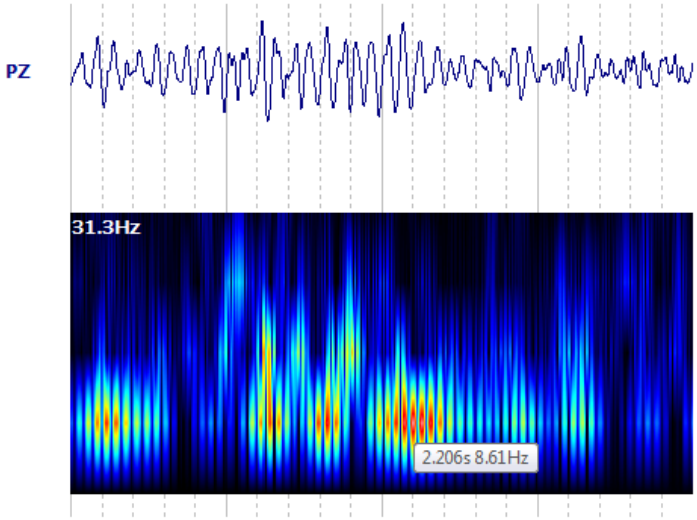


The STFFT results are seen at the bottom of the data display. Position the mouse cursor on a point in the display to see a tooltip showing those particular time and frequency values. (See the *CURRY 8 User Guide* for more information).



Now select some of the wavelets. See the difference that linear **Interpolation** makes. Generally speaking, STFFT is more effective with ongoing EEG, while wavelets are better for transient phenomena, such as spikes. If you have selected more than one Channel, and have enabled the **Average** option, you will see the average of all the channels. If you disable Average, you will see individual displays for each channel.



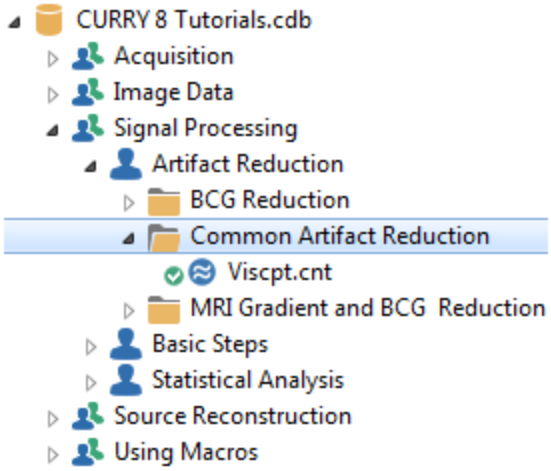


Close the Study when finished.

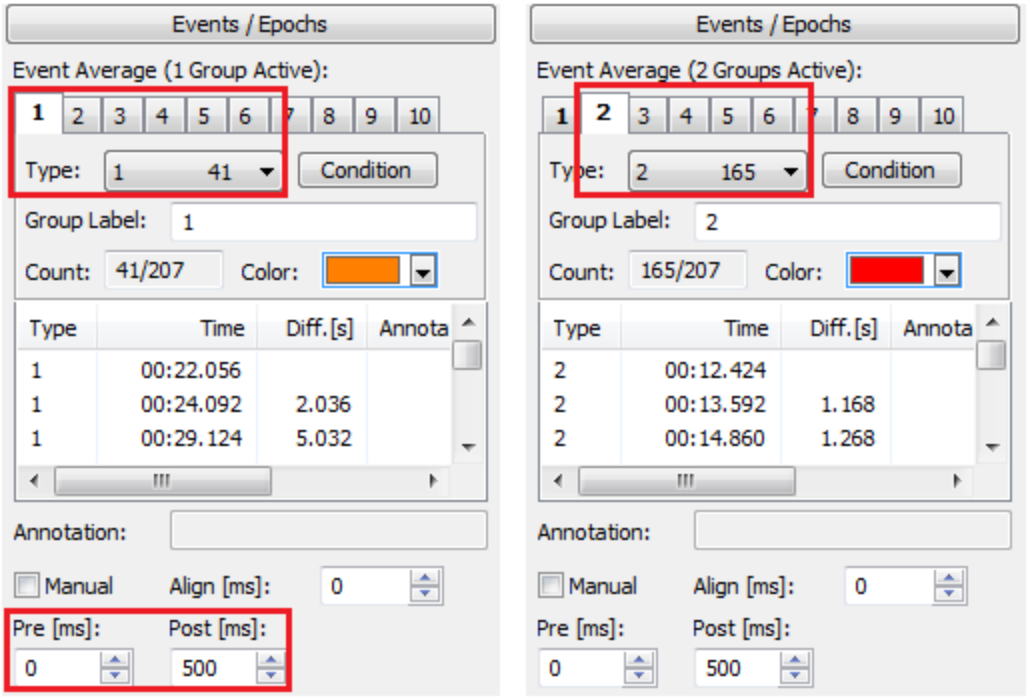
Creating Spectral Averages from Epoched Data

In some cases you may want to perform FFTs on evoked potential data, where you have more than one type code. The process is similar, with a couple of important differences.

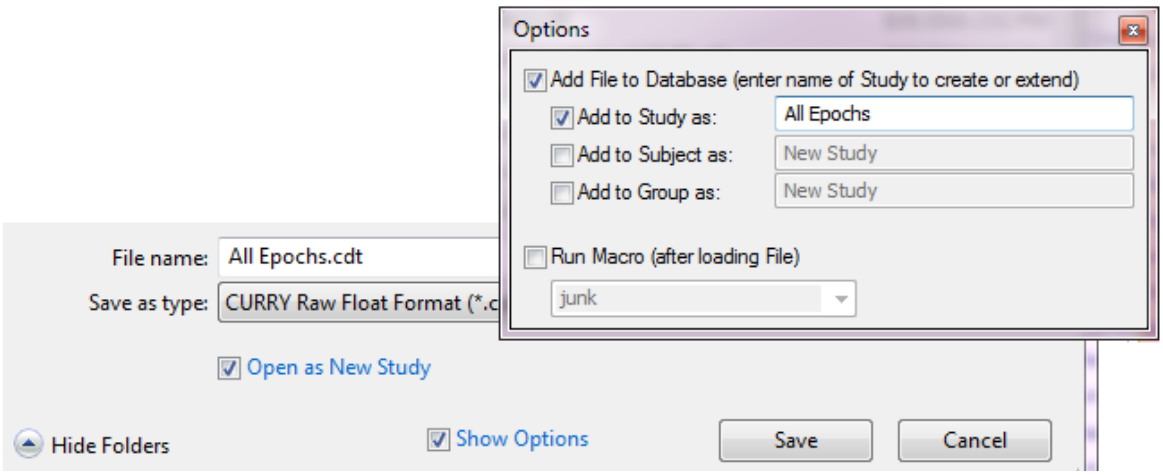
1. Start by opening the Study shown below, which we have used several times before. There are Type1 and Type 2 stimuli, similar to a P300 recording, where the 1's are the targets.



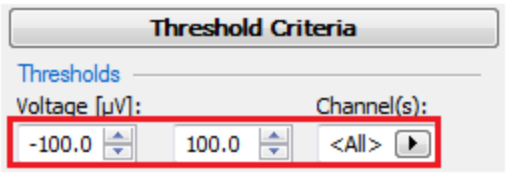
2. Let's say we are only interested in the first 500 ms post-stimulus. Select Type 1 for Group 1 and Type 2 for Group 2, and set the **Pre** and **Post** times for **0** ms and **500** ms.

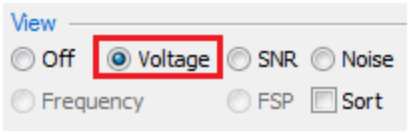


3. Click the **Export Epochs** icon , and enter a file name (*All Epochs.cdt*). Create a Study called *All Epochs* and enable **Open as New Study**. Click **Save**.

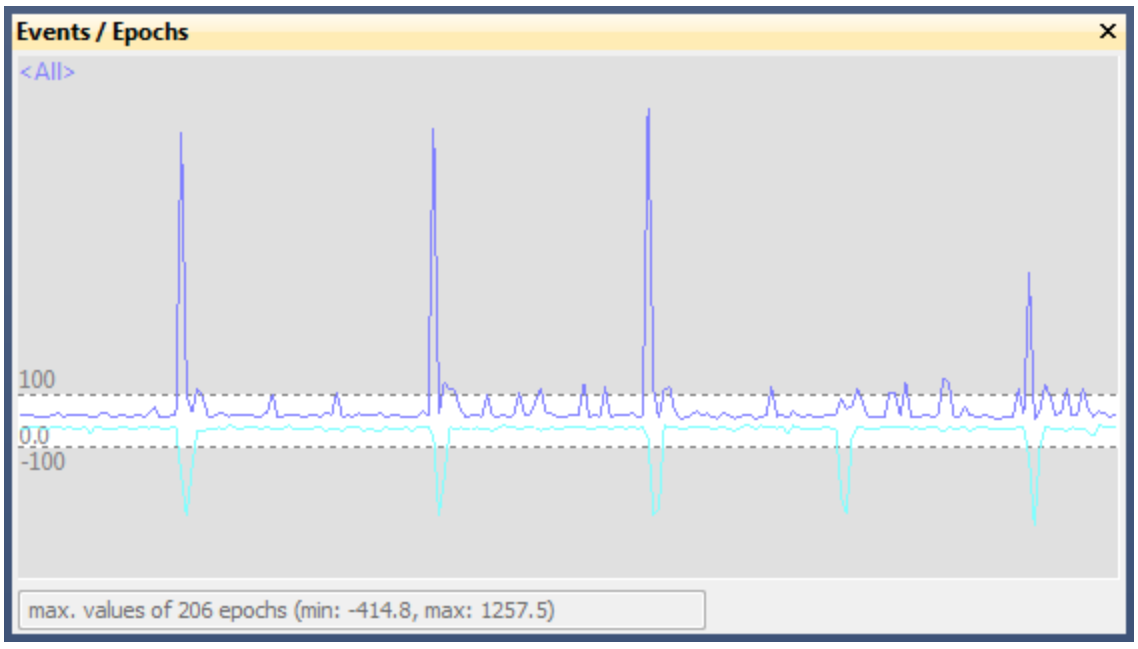


4. Now we see all 208 epochs, including those with artifacts. We will reject bad epochs using Voltage Thresholds. Expand the Threshold Criteria panel, under **Events / Epochs**. Set the Threshold **Voltages** to **-100** and **100** μVs, using **All** channels. Click Scan Epochs. When the scan has finished, click **Voltage** in the **View** area.

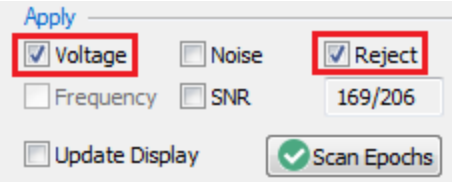


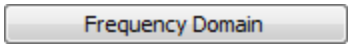


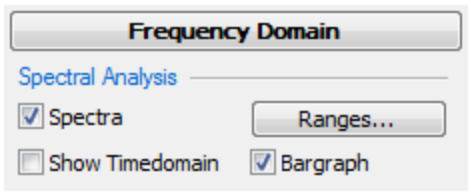
You will see the Waveboard where the epochs to be rejected are in the gray regions. The thresholds look appropriate.

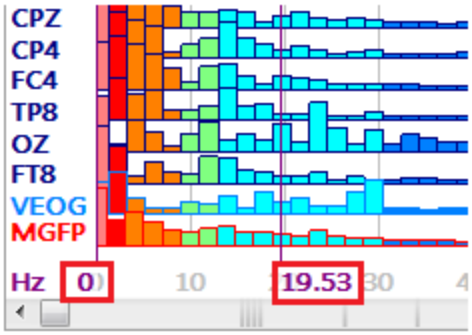


Finally, click **Voltage** in the **Apply** field, and enable the **Reject** option. 169 epochs will be accepted.

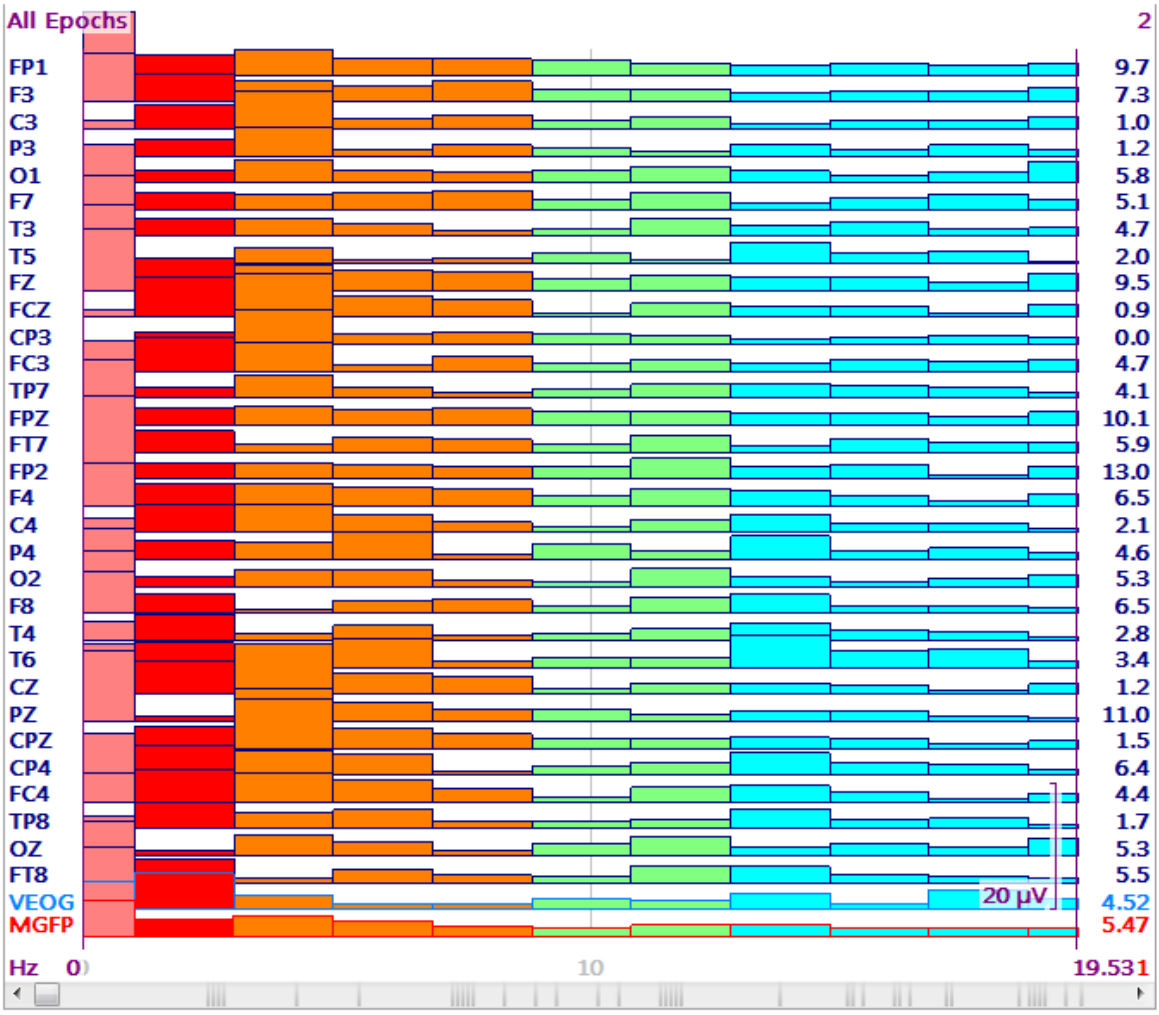


5. Expand the  panel and enable **Spectra**. In the data display, position the two outer cursors to define a frequency range of interest, such as, 0-20 Hz.

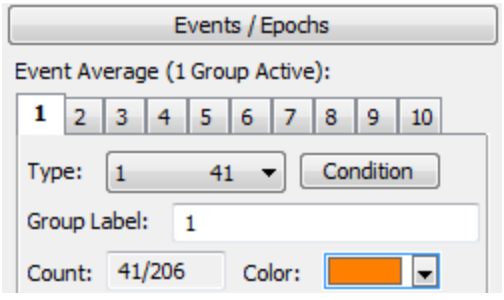




Then *right click* in the data display and select **Zoom In**. These are the FFT spectra for each channel for the first epoch. Drag the sliding cursor to see all of the epochs. The gray bars on the slider are the rejected epochs.

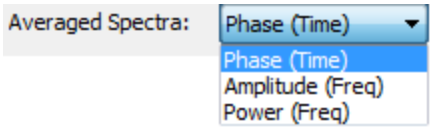


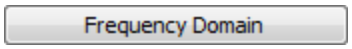
6. Since we are using the **Average** option under Epochs, we will need to average the type code groups one at a time. Select Type 1 for Group 1 under **Events / Epochs**.



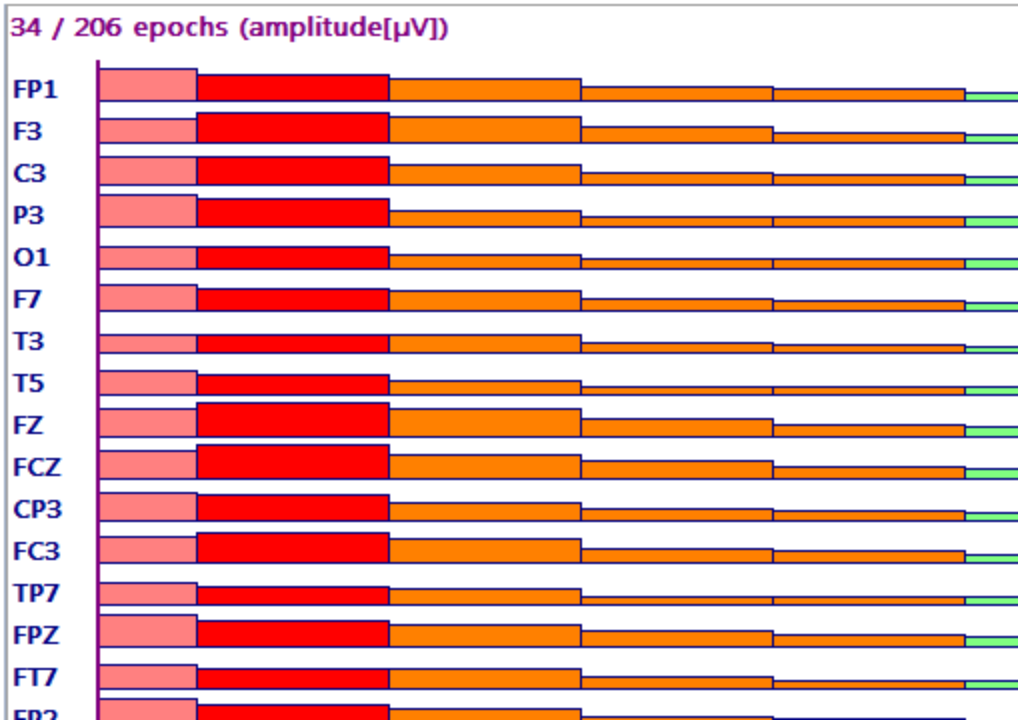
Select the **Average** option under **Epochs**. Note the options under **Averaged Spectra**. As described above, the **Phase (Time)** option averages the raw waveforms first (time domain averaging), and then computes the FFT, thereby taking the phase relationships into account. The **Amplitude (Freq)** option computes the FFT on each epoch first, scaled in µV, and then averages the epochs

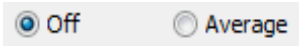
(frequency domain averaging). The **Power (Freq)** option computes the FFT on each epoch first, scaled in μV^2, and then averages the epochs.

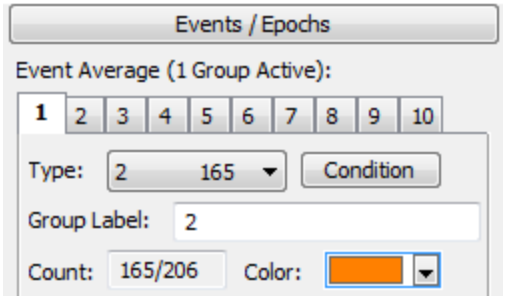


You can also use the option in the  panel to square the displayed results.

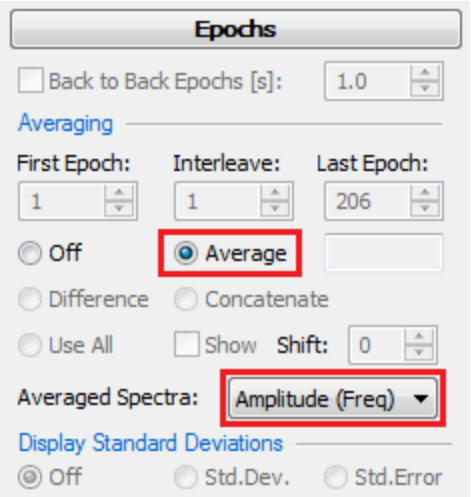
For this example, select **Amplitude (Freq)**. You now see the average of the remaining 34 epochs, scaled in μV. Save the results if desired.



7. To average the Type 2 epochs, turn Average Off  , and select Type 2 for Group 1.



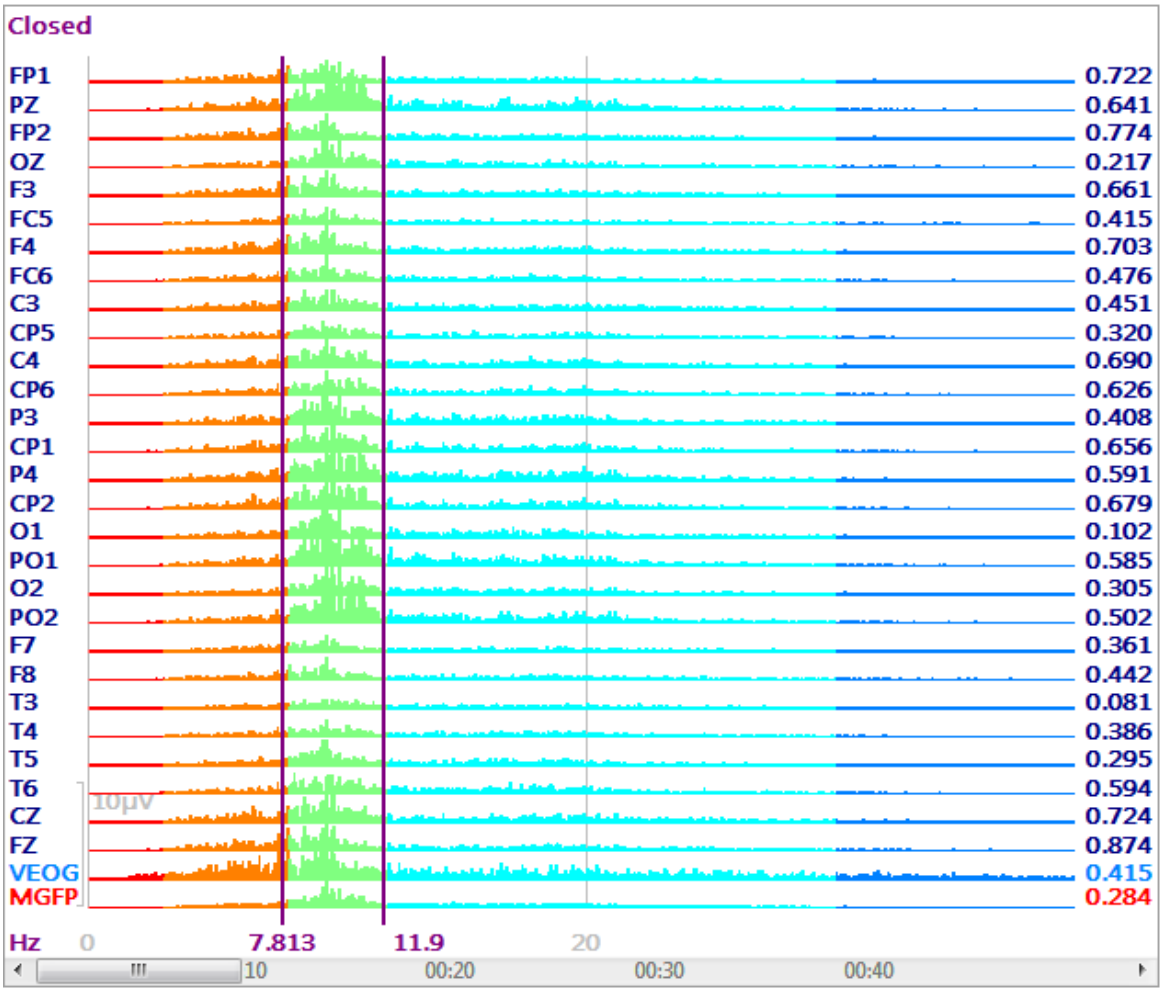
The select Average and Amplitude (Freq), saving the results if desired.



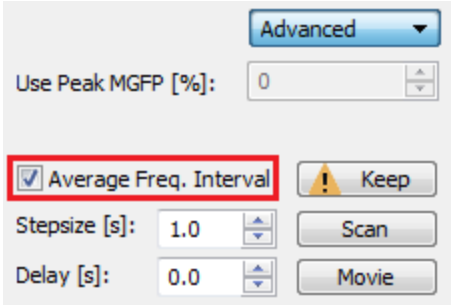
Close all open Studies.

Creating an Average Across Frequency Bins

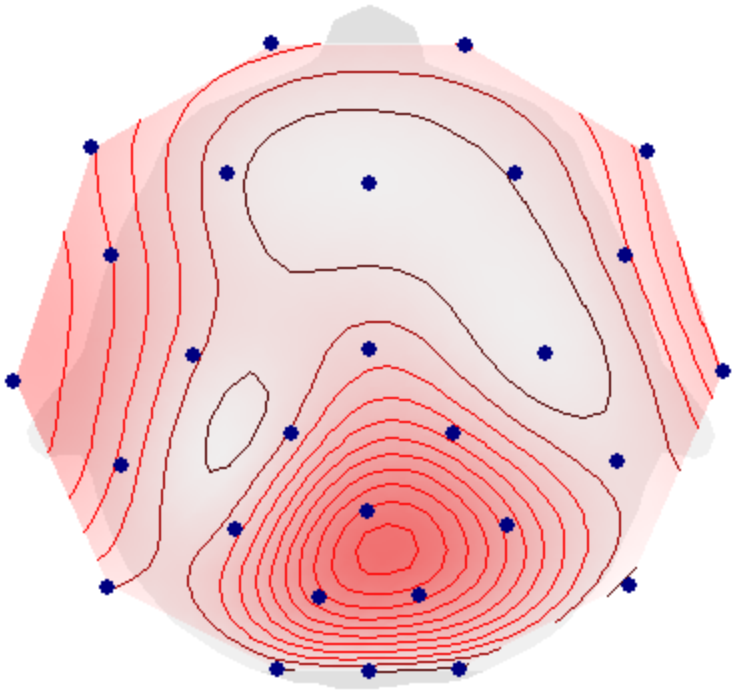
To create an average across several frequency bins, you first need to define the frequency range of interest using the outer cursors.



Then, in the lower part of the **Options** panel, enable **Average Freq. Interval**.



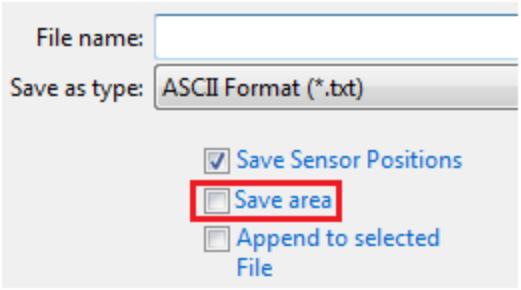
The 2D map that you see will be the average of that interval.



Once you select Average Freq. Interval, the column on the far right in the data display will list the averaged values for each channel. If you want to save these values, go to **Functional Data → Save → Save Averaged Interval**. From there you can save a text file with the results per frequency band (delta, theta, etc.) as well as the average defined by the outer cursors. The numbers in brackets in the header are the number of frequency bins per band and over the designated frequency range.

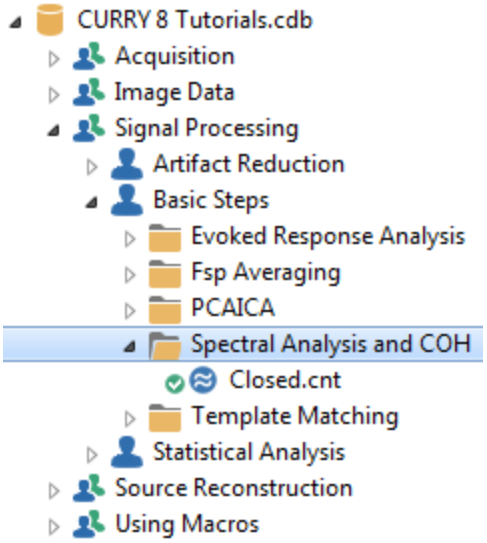
```
# frequency domain
# channels: 28
# averaged frequency ranges [bins]:
# 0.000...3.000 Hz [50]
# 3.000...8.000 Hz [83]
# 8.000...12.000 Hz [67]
# 12.000...30.000 Hz [296]
# 30.000...70.000 Hz [656]
# 59.000...61.000 Hz [33]
# averaged frequencies (cursors):
# 0.000...70.374 Hz [1154]

# 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
```

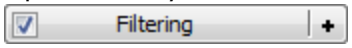
If you want the area within the Timerange, enable **Average Freq. Interval** and save the results using **Functional Data → Save → Save Averaged Interval**. In the save dialog, enable **Save area**. A new column will appear on the far right that contains the area for each electrode.



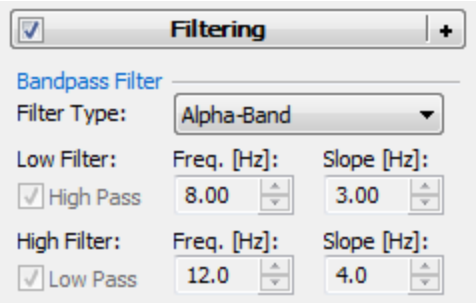
Sensor Coherence
You may compute Sensor Coherence from the raw time domain data (continuous, epochs, or averaged files). Complex demodulation is used in place of the FFT. Coherence is computed across all frequencies. If you wish to focus in on a specific frequency range, use the filter options to pass only that frequency range. (**Source Coherence** is described in a later tutorial).

For this tutorial we use the same Study used above. Open the Study.

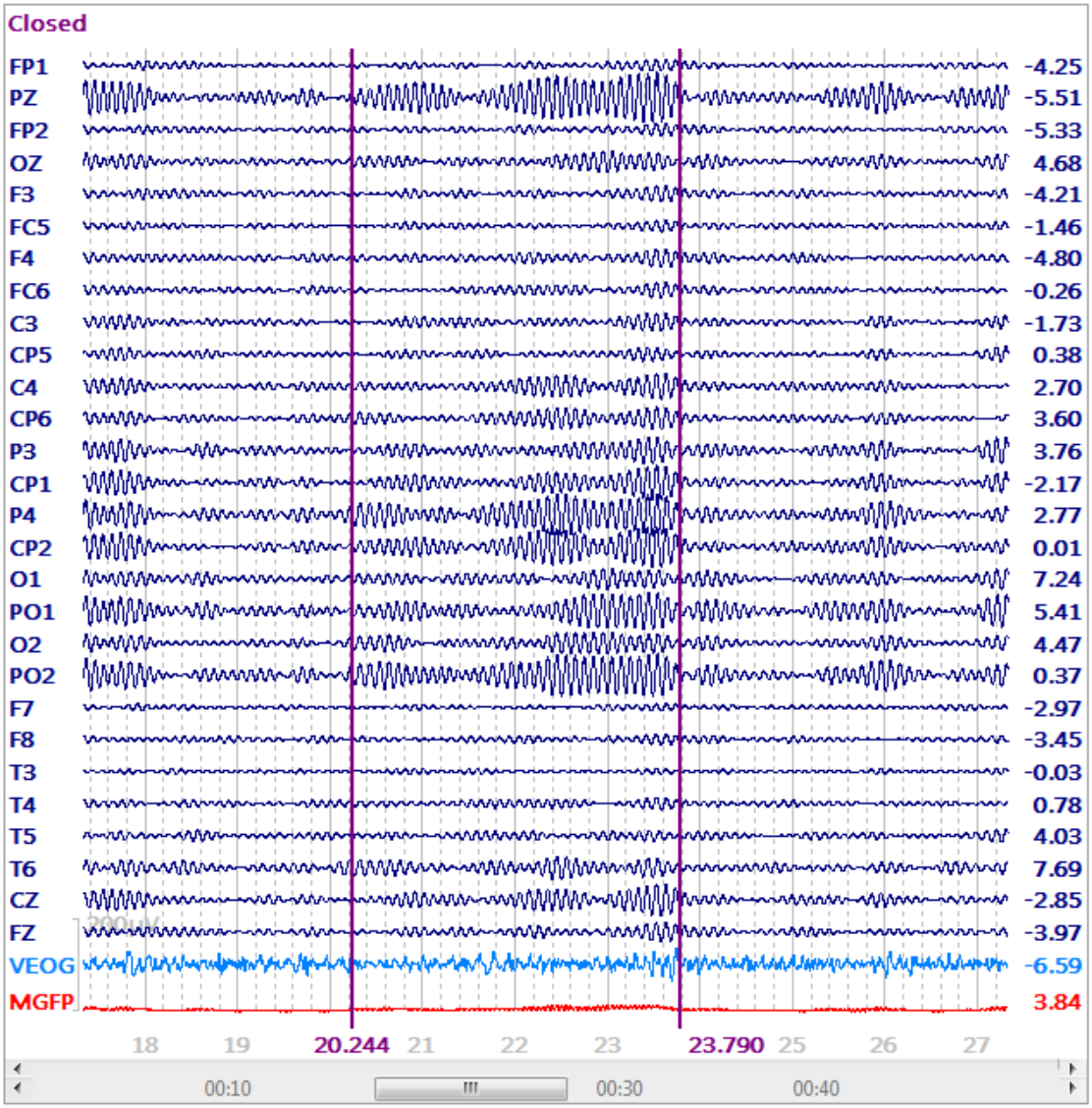


1. As mentioned above, Coherence is computed across all frequency ranges. Since this is an eyes-closed recording with abundant alpha, we will focus only on the alpha activity. This can be accomplished by filtering for alpha only. Expand the 

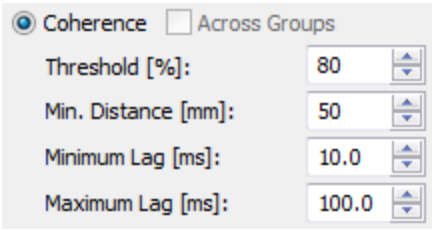
panel and select **Alpha-Band** for the **Filter Type**.



Now we see primarily alpha in the recording. Select a section with prominent alpha by positioning the two outer cursors. Unlike the FFT computations, which ignore the cursor positions, Coherence uses the Timerange you have defined (two outer cursors).



2. Select the FD, Maps display. Enable **Coherence** and enter the parameters shown below from the Parameters panel for Maps.

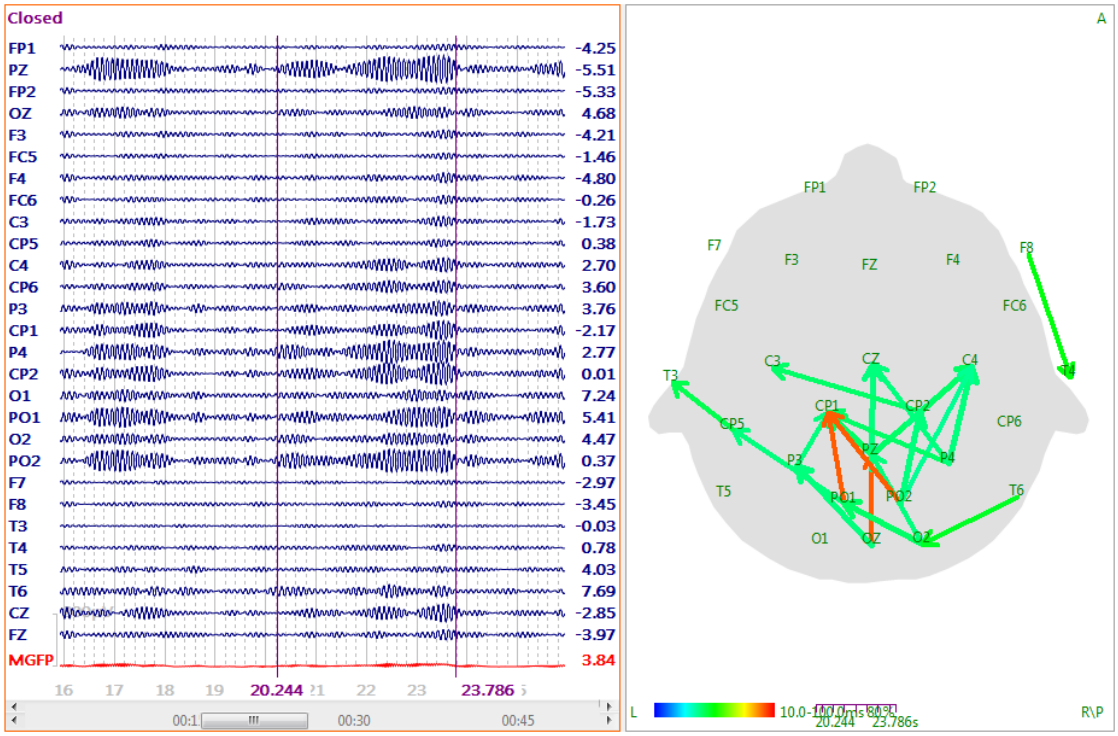


Coherence is computed between pairs of channels (similar to a correlation). All possible pairs are computed. Traditional Coherence values range between 0 and 1, where larger values mean that the signals are more coherent. Threshold is the coherence value x 100. The links between the pairs are seen when the coherence value exceeds the threshold you set. The **Minimum** and **Maximum Lag [ms]** settings take phase relationships into account. Minimum and Maximum Lag define the range in which links will be displayed, based upon the phase relationships. A range from 4 to 10, for example, displays only those links where there is a phase lag between 4-10 ms (depending on the AD Rate, you may see rounding to every other second [500 Hz], or every 4ms [250 Hz], etc.). When **Minimum** is set to **0**, and **Maximum** is set to a large enough value, all links will be seen regardless of any phase lags.

The arrows that are frequently seen at one end of a link indicate the direction of the lag. Coherence is phase-independent, meaning, for example, that you could have high coherence between two EEG channels at 10 Hz, and the 10 Hz activity could be perfectly in phase, perfectly out of phase, or anywhere in between. The arrows appear when there is a phase shift within the range of values entered for **Minimum** and **Maximum Lag [ms]**, meaning there is a delay between the two connected channels. The origin of the arrow indicates the leading electrode. When two electrodes are connected by just a line, the phase shift between the electrodes at maximum (absolute) correlation is less than **Minimum Lag [ms]**. **Minimum Distance [mm]** sets the minimum distance between electrodes; the closer two electrodes are to each other, the greater the Coherence (which may be attributed to volume conduction as well as functional connectivity). The colors are determined the by the

line in the **Colors** panel for **Maps**.

If you see few or no links, decrease **Threshold** or the **Minimum Lag** (or **Distance**).

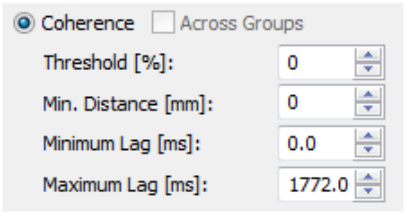


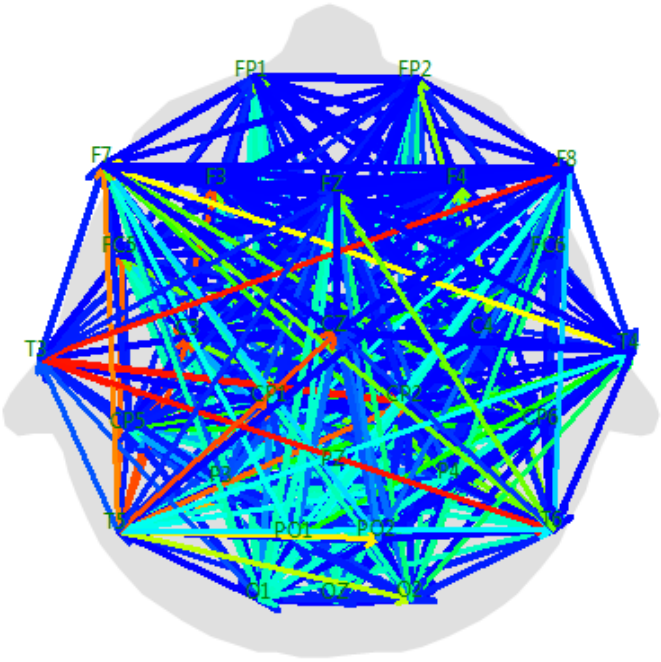
Now look at the information below the coherence display

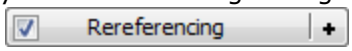
. **10.0-100.0 ms** are the lag times. The colors are distributed throughout that span. **80**% is the **Threshold** we selected.

Change the lag times to **0 ms** and **1772.0 ms**. This is the **Maximum Lag** that can be computed (which is half of the duration of the Timerange we selected). Now all of the links are blue, indicating the span in which the lags exist (0 ms to about 90 ms). Change the Lags back to **10** and **100**ms.

3. While looking at the Coherence display, vary the coherence level by changing the **Threshold** value. You can do this most easily by positioning the cursor in the Maps display and rotating the *mouse wheel*. To see all possible links, set the **Threshold** to **0**, **Minimum Distance** to **0**, **Minimum Lag** to **0**, and **Maximum Lag** to **1772** (in this example).

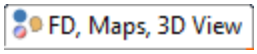




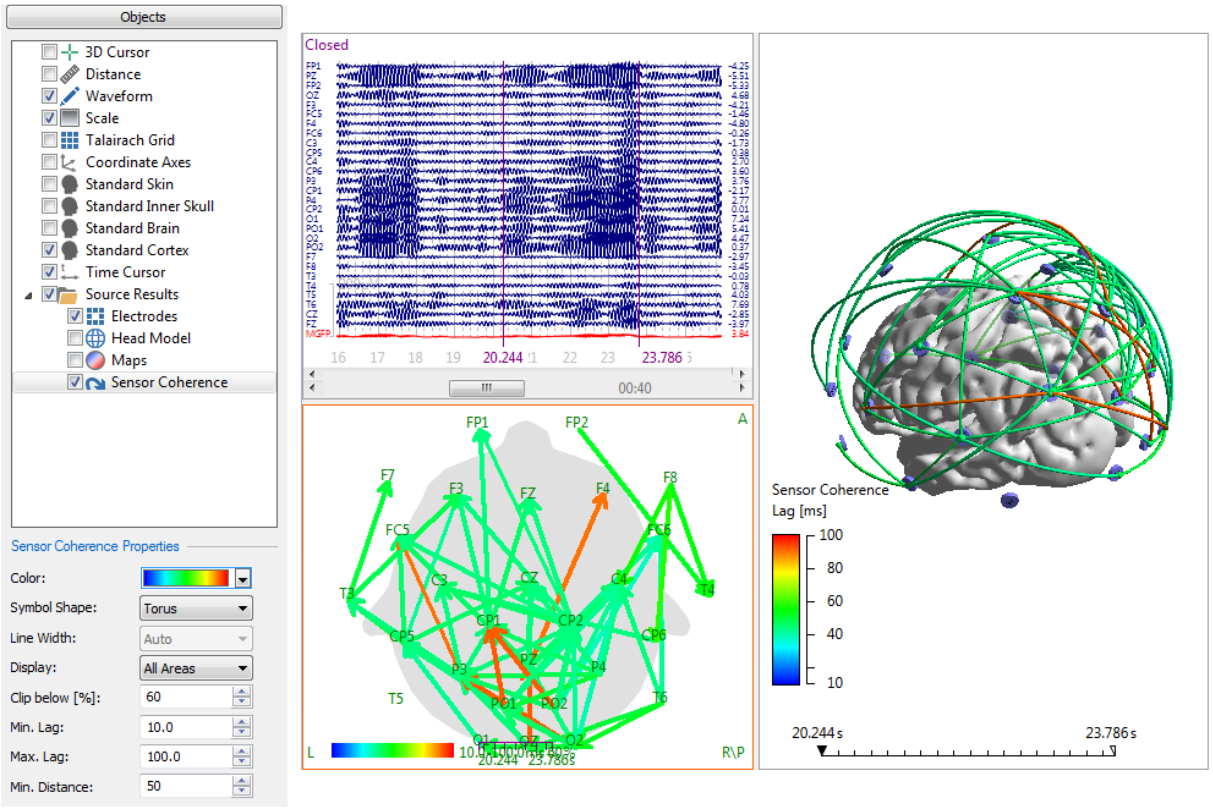
4. To select a different frequency, select a different **Filter Type**, and the new results are displayed instantly. If the pre-selected filter parameters do not fit your needs, select **User Defined** and enter the desired parameters. The Coherence results are updated immediately with the filtering changes. Similarly, if you want to change the reference, expand 

and select the channels(s) to use.

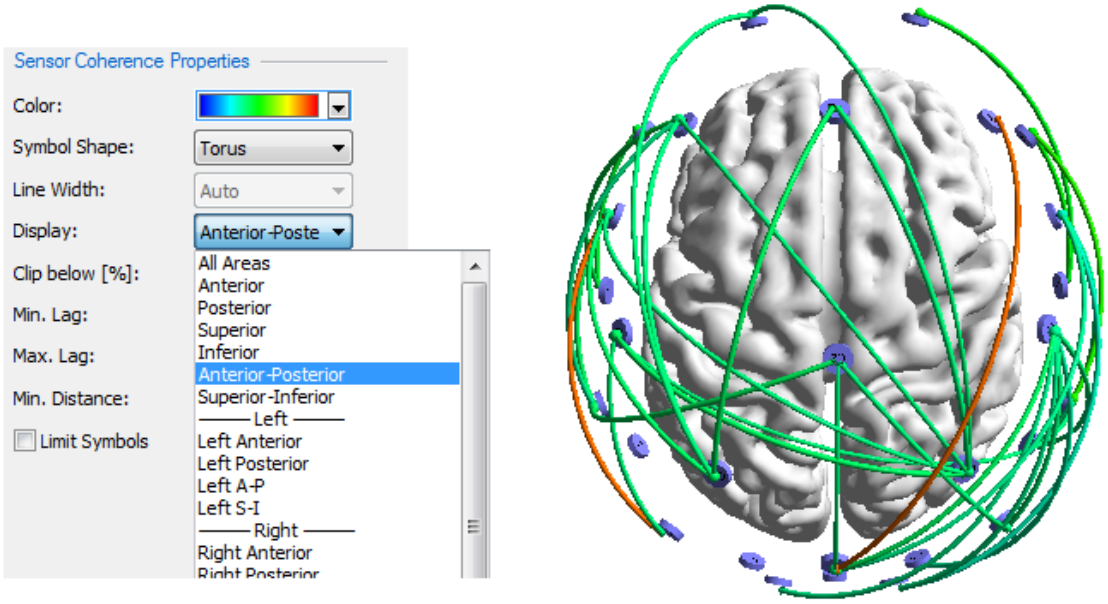
5. Coherence results may also be displayed in the

; select 

to see all three. In this case, we have no image data but we can use the **Standard Cortex** in the **Objects** list. The **Torus** option in the **Display As** field for **Sensor Coherence Properties** displays the coherence links as arcs. Note also that **Clip below** (Threshold), **Min. Lag.**, **Max. Lag.**, and **Min. Distance** are repeated here. These affect the **3D View** display, but not the **Maps** display. The same option in the **Parameters** panel for **Maps** will affect both the **Maps** display and the **3D View** display.



6. Note in the above figure that **Display** is set for **All Areas**. From its menu you can choose to limit the display a wide variety of options. The figure on the right shows only the Anterior-Posterior links (links that cross the central sulcus, approximately).



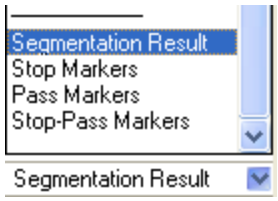
A summary of the results is seen in the **Output** display.

Sensor Coherence analysis: No. of arcs (lags from 10.0..100.0ms, min. distance 50.0mm, clipped at 0.6)

Brain Area	Total	Anterior	Posterior	Anterior-Posterior	Superior-Inferior
Both Hemispheres	61	1	28	32	27
Left Hemisphere	16	0	7	9	8
Right Hemisphere	14	1	3	10	9
Midline	2	0	1	1	1
Intra-Hemispheric	30	1	10	19	17
Inter-Hemispheric	18	0	11	7	6

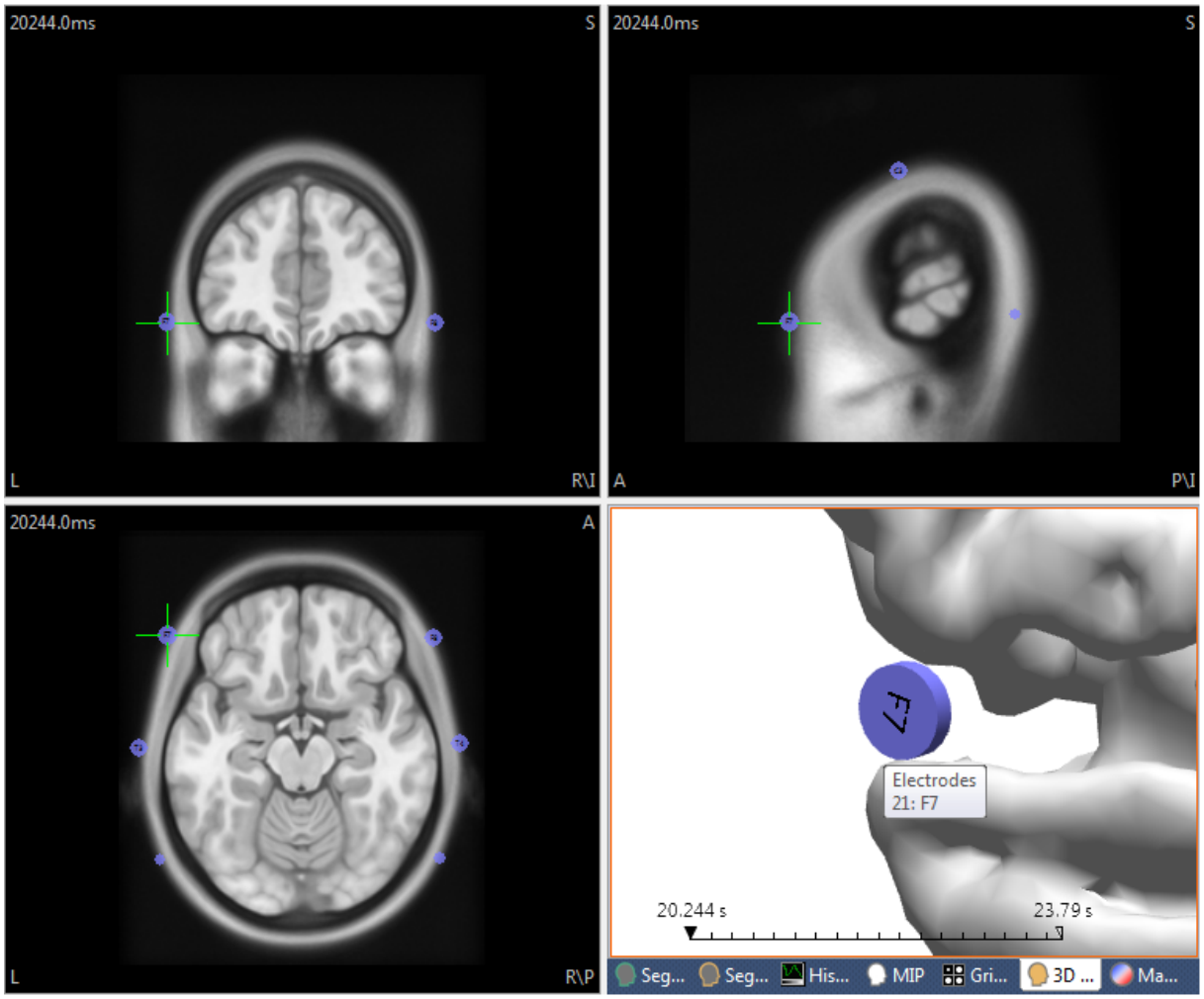
Sensor Coherence (Anterior-Posterior): 32 arcs, lags from 10.0..100.0ms, min. distance 50.0mm, clipped at 0.6

7. It is also possible to constrain the coherence links to the **Segmentation Results**, or to the **Stop Markers**, **Pass Markers**, or **Both**, using options in the same menu.

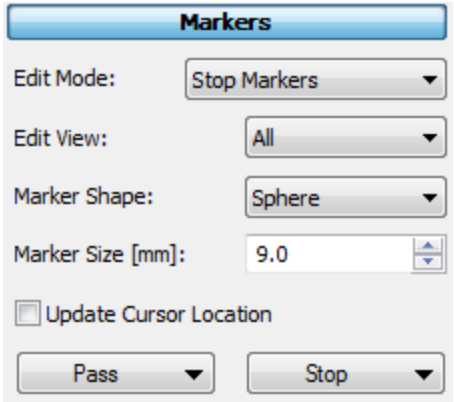


With sensor coherence, as opposed to source coherence, it may make most sense to use Pass or Stop Markers to select only those electrodes you wish to see. Using the same results as in Step 6 above, let's say we were interested only in F7, F3, T5 and P3 on the left, and F8, F4, T6 and P4 on the right. We want to look at just the left or right sides. We can use Stop and Pass Markers to select the electrodes.

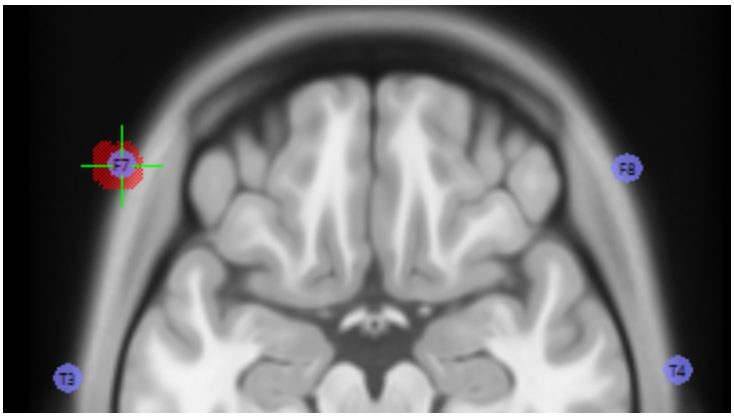
In the **Image Data** display, set the lower right pane to show the **3D View**. Enlarge and orient it as needed. Clicking on an electrode, F7, displays that electrode in the other three views. Disable the **Sensor Coherence** display to make it easier to see the electrode labels, if desired.



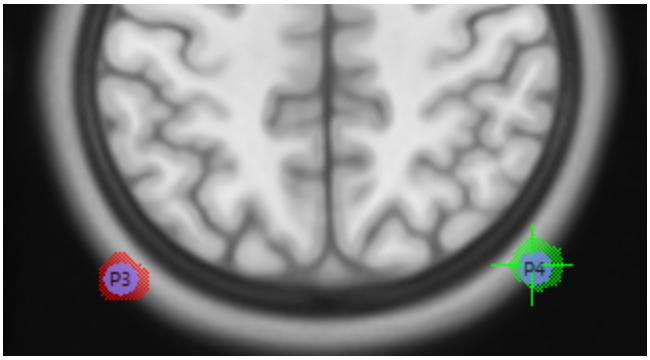
Set **Markers** for **Stop** markers.



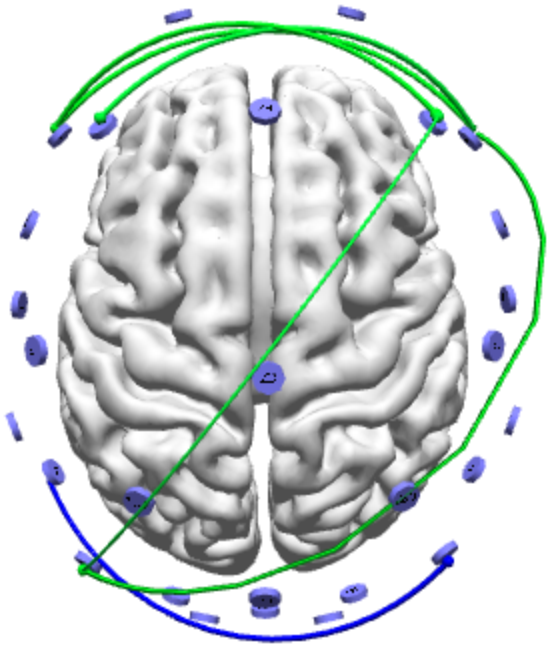
"Paint" the F7 electrode with Stop Markers.

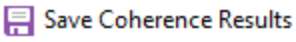


Repeat the process for F3, T5 and P3. Then switch to Pass Markers, and repeat the process on the right side.



When you are finished, select the **3D View**. Enable **Sensor Coherence** again. In its **Properties**, in the **Display** field, select **Stop Markers**. You will need to reduce **Clip below** to about **50%** to see anything. Then you will see whatever links there are among those 4 electrodes. Select **Pass Markers** to see the links on the right. If you select Stop-Pass Markers, you will see not only the left and right side links, but any links among all of the electrodes.



8. Save the coherence results by selecting 

from the **Workflow**, or select **Maps → Save → Save Coherence Results** (from the Main Menu Bar). The .coh file will be saved to a folder and with the file name of your choice. A text file is created that contains header information, the coherence matrix, and the maximum lag times. (While the extension is the same as that used with Coherence files in Scan's Edit program, the .coh files cannot be read in Edit). If you want to save the Coherence results for display in CURRY at a later time, save the **Study Parameters**.

The process for computing coherence with epoched and averaged files is basically the same.

2.4.8 Epileptic Spike Detection

There are two ways you may approach epileptic spike detection. The first uses Template Matching to detect the spikes automatically. Up to 5 different spike patterns may be detected at a time. This is described in the *Template Matching and Dipole Clusters* tutorial below. The alternative is to mark selected spikes manually, and it is described in the *Manual Spike Detection and Dipoles Clusters* tutorial.

Both methods allow you to display all dipole solutions at once, to see the scatter, as well as the dipole solution for the average of the spikes.

2.4.8.1 Template Matching and Dipole Clusters

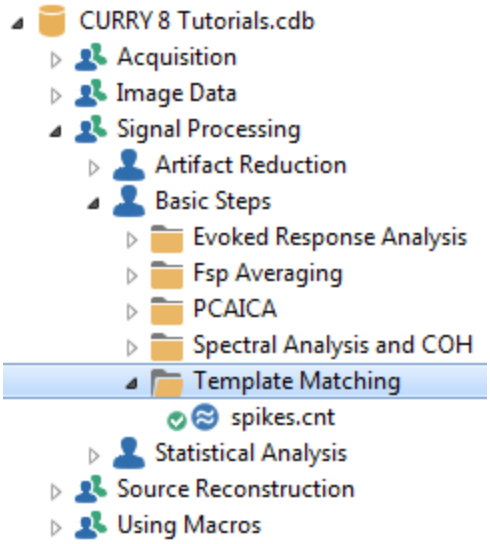
The

options allow you to identify recurring features in the continuous data recordings, such as artifacts or epileptic spikes. In one case, you want to identify the artifacts that you want to reduce. In the other case (spikes), you want to identify spike activity that you can then average (to reduce the background

noise and improve source reconstruction), or to view the dipole clusters. Template Matching can be used online, as described in the online **Template Matching** tutorial above.

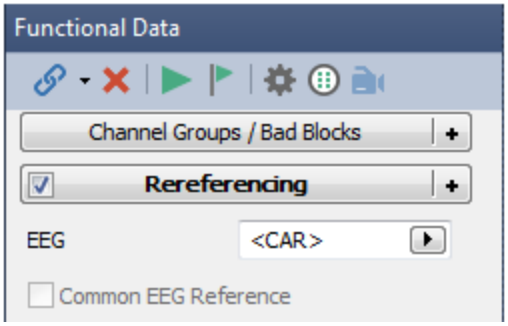
You select a Timerange that is used as a template. Events that match the template will be detected automatically, and those epochs can be averaged immediately, or retrieved as individual sweeps in a new Study.

The **Common Artifact Reduction** tutorial and the **Removing Pulse Artifact** tutorials both contain sections that illustrate how to use template matching to identify artifacts that you want to reduce. In this example, we will use Template Matching to identify spikes that we wish to analyze further. The file we are using is found in the *Template Matching* study. This has a single right hemisphere localization. In the example just after this one, we will demonstrate how to do multiple classes (localizations) of spikes.

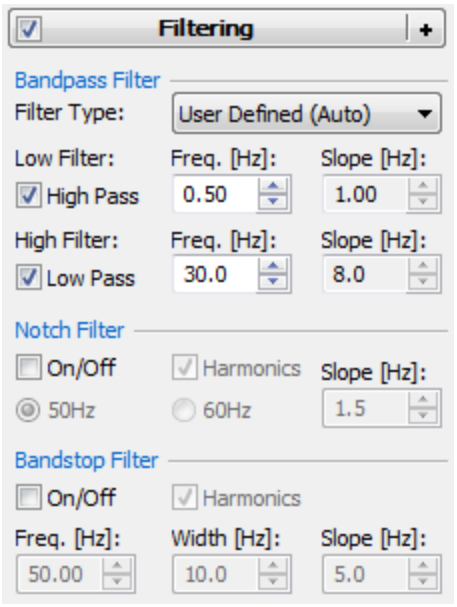


1. Open the Study. Since we will be computing dipole solutions, which require a Common Average Reference (CAR), add a **Rereferencing** panel and select **CAR**.

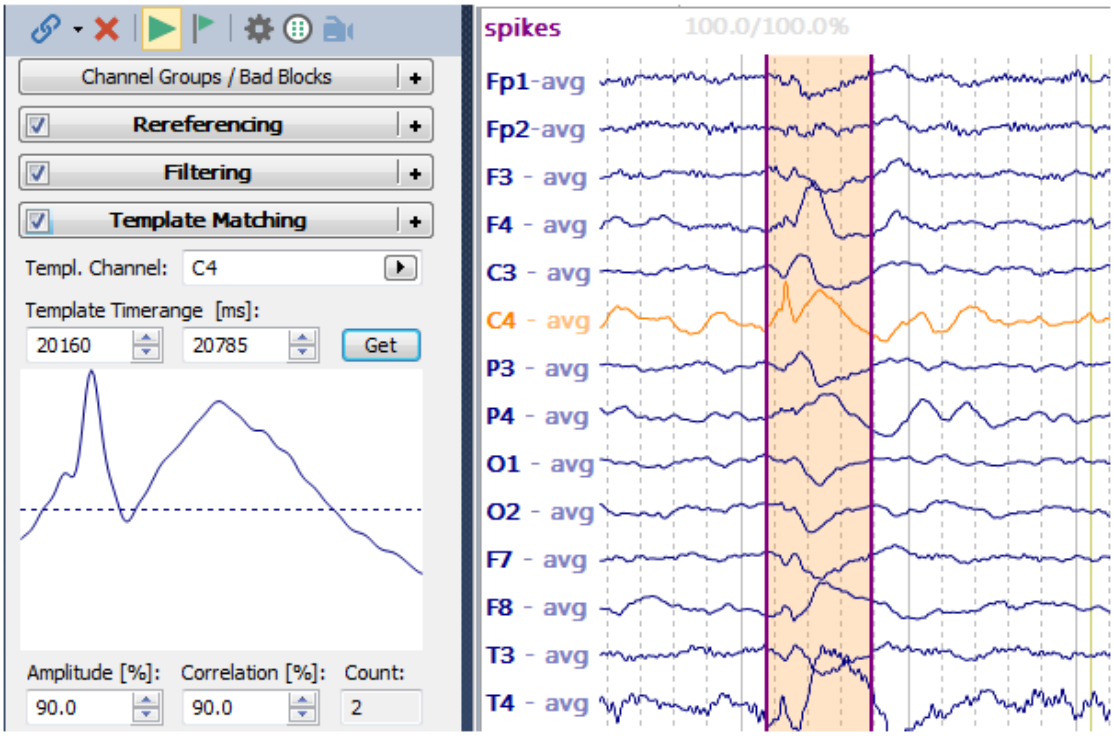
From the **Workflow** select Rereferencing . (Source Reconstruction will use the CAR whether you select it explicitly or not. Selecting it will let you see the data that are being analyzed).



2. We see that there is increased EMG activity from some channels, and this could make it a little harder to detect matches to the template. Add the **Filtering** panel and select **User Defined (Auto)**. Reduce the **High Pass** limit to **0.5 Hz**. From the **Workflow** select Filtering (Off) .

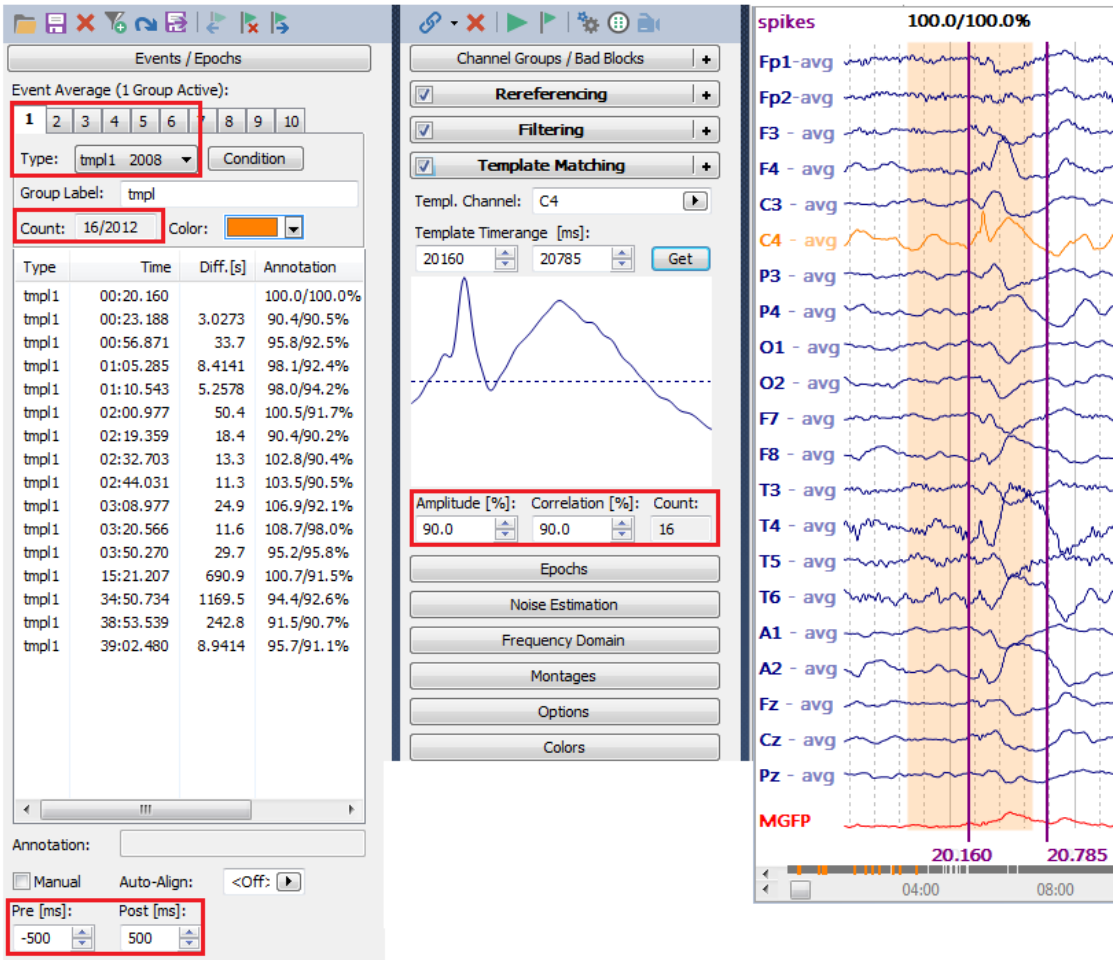


3. Add the Template Matching panel, or click Template Matching (Off) from the **Workflow**. Looking through the file, we see that the spike and slow waves are seen most easily in the C4 channel, so we select that as the **Template Channel**. The two outer cursors are set to define the span of the waveform (and the **Get** button is clicked). The waveform is then seen in the template display.

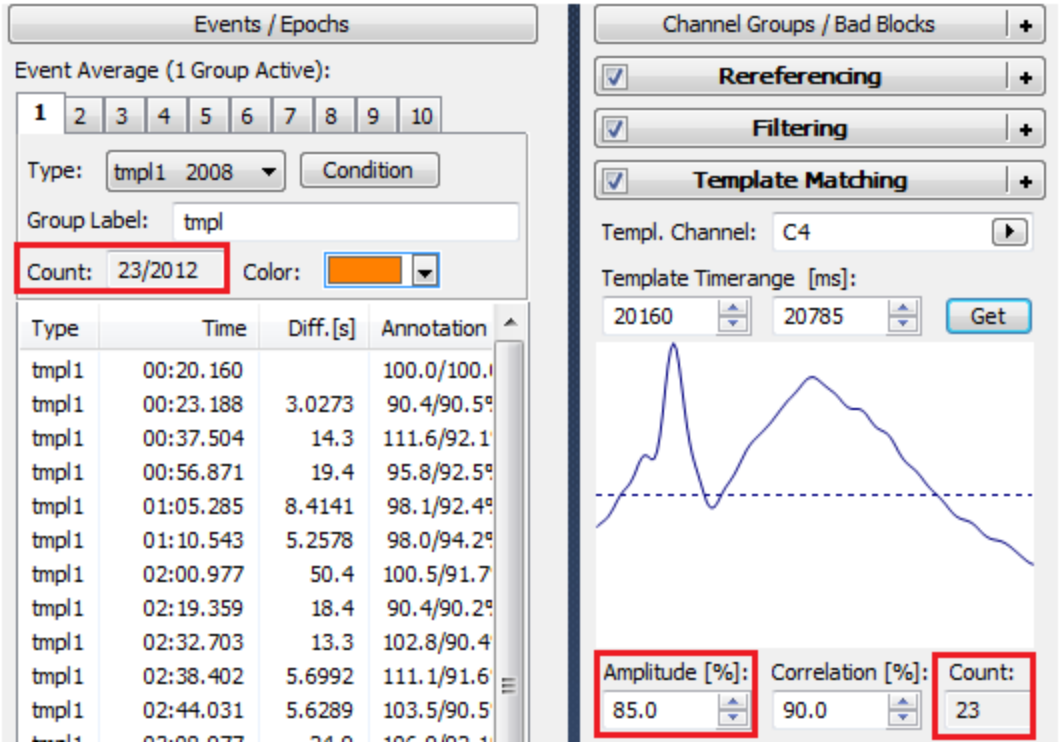


4. At this point, we do not know what combination of Amplitude and Correlation criteria will result in reasonable matches to the template. Leave the criteria set to 90% and click the flashing button at the top of the **Functional Data**. When the Scan has been completed, go to the Events / Epochs panel, and select "tmpl1" for the **Type**. Enter **-500** and **500** for the **Pre[ms]** and **Post[ms]** times, for later averaging.

We see that 16 matches have been found with the current Amplitude and Correlation settings (in the **Count** field for the **Event List** as well as under **Template Matching**). When you are just experimenting with different criteria, the Count field for Template Matching may be all you need. There are 2008 total matches with Amplitude set to its minimum of 30% and Correlation set to its minimum of 50% (these are counted automatically). Your counts may vary slightly. The 2012 means that there are that many total events in the file (4 were not related to the templates).

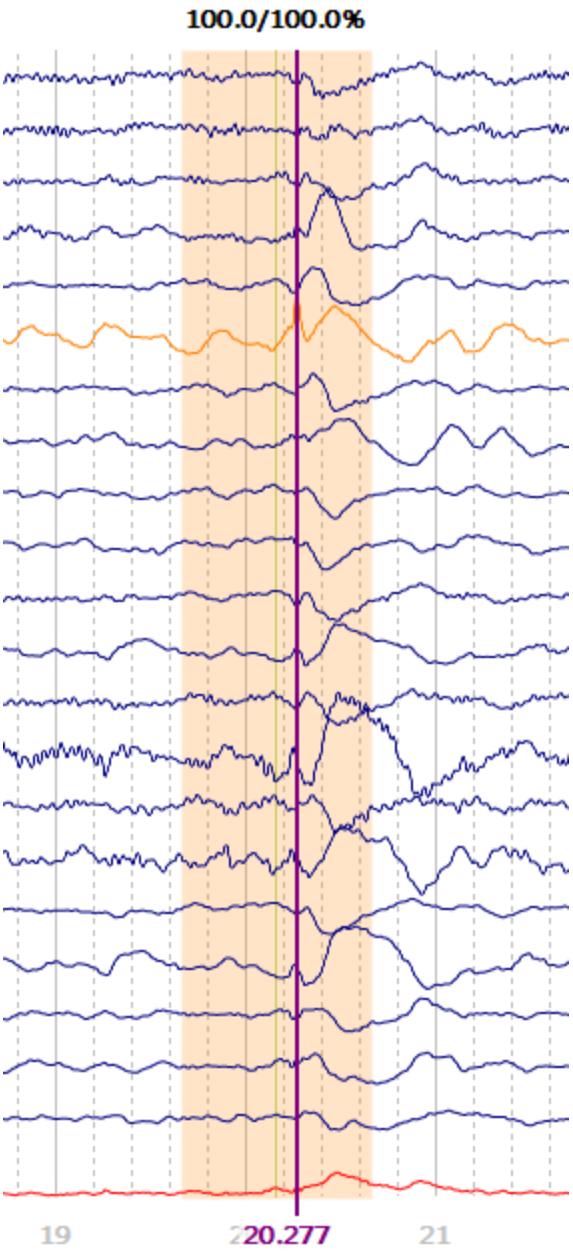


5. You can use the buttons on the Toolbar to step through the events that have been detected. Or, it is easier to click one of the lines in the list and use the *up* and *down arrow* keys on the keyboard to go through the **tmpl1**'s. Now that the file has been scanned, you can change the Amplitude and Correlation criteria and see the effects on the number of events that have been detected. Decrease **Amplitude** to **85%**. Now there are **23** events.

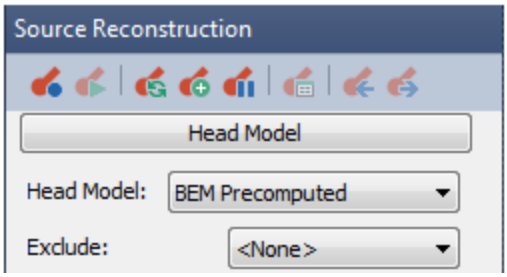


6. Step through the events using the Toolbar buttons and exclude any that are not good matches . In this particular file, most of the matches were good - we kept 19, which is enough to continue. You can continue varying the criteria and inspecting the results until you have satisfactory matches.

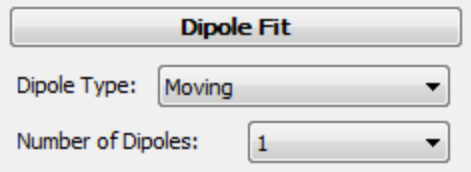
7. Now we want to compute simple dipole source solutions for the spikes. First, if needed, *double-click* in the Functional Data display to enable **Tracking Mode** (you now see a single vertical cursor). Position the cursor at the peak of a spike, such as the Template (100%/100%). (The time point is 20.277s).



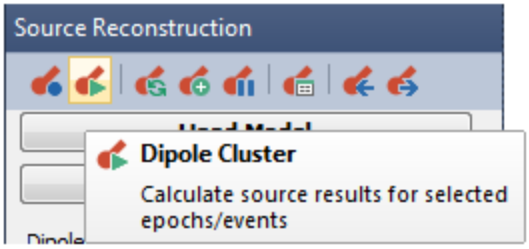
Now select a **Head Model** (under **Source Reconstruction**), such as the **BEM Precomputed** head model.



Then select a **Moving Dipole** (under **Dipole Fit**).

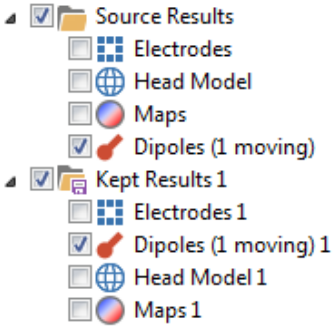


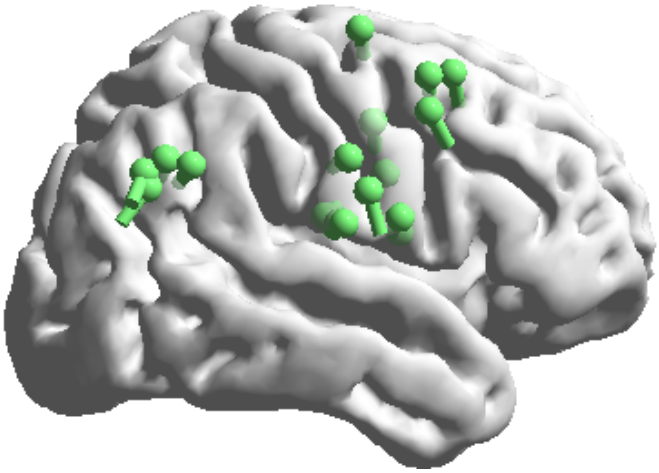
8. To compute and display dipole results for all epochs, click the **Dipole Cluster** icon .



9. Select the FD, 3D View display. Select the **Right View**, and in the **3D View Objects** list, deselect the display of the **Electrodes**, and select the display of the **Standard Cortex**. Turn the **Confidence Ellipsoids** off .

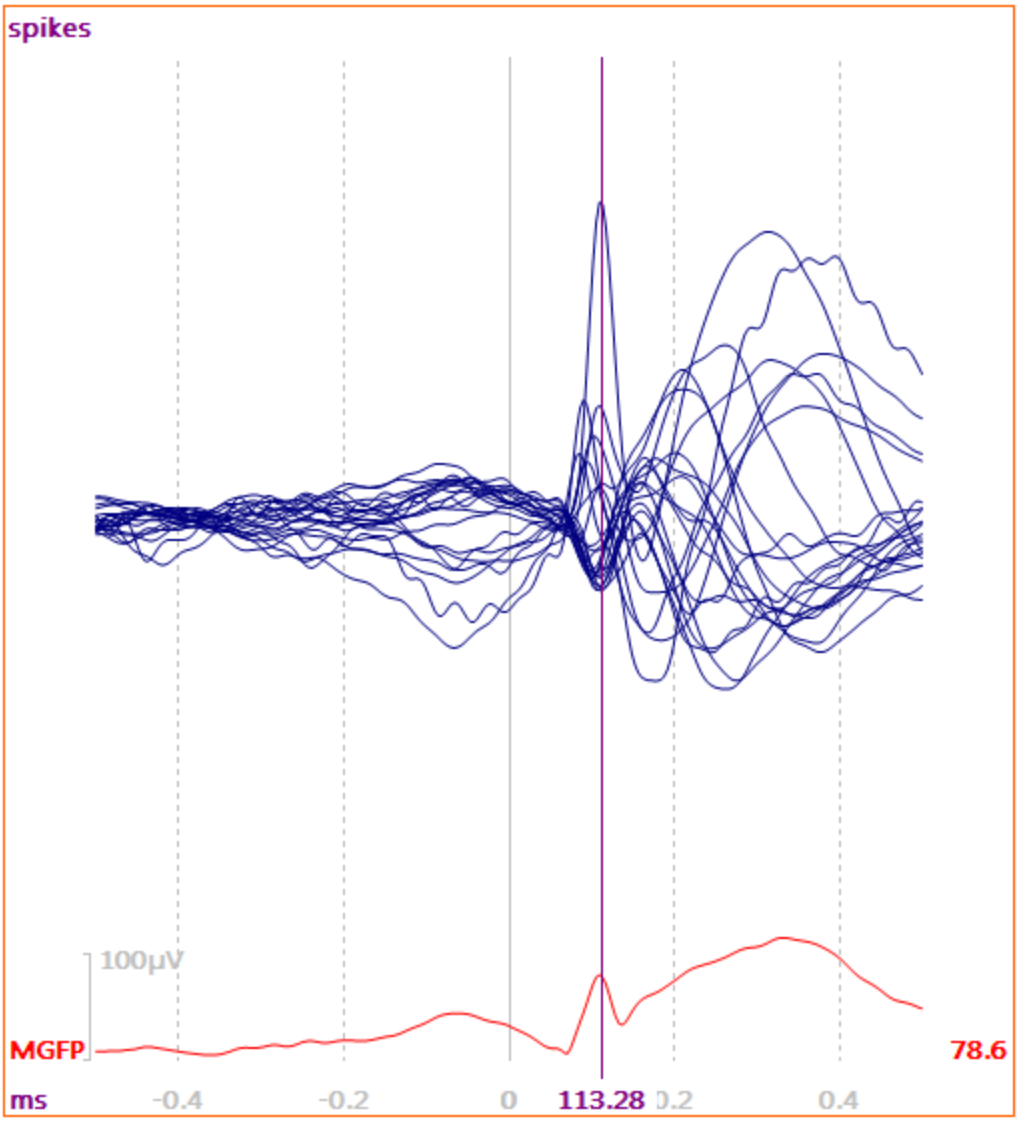
Now you see the cluster of dipole solutions at the selected latency. The **Kept Results** have been created automatically. The Kept Results contain the individual dipole solutions for each of the spikes in the epochs.



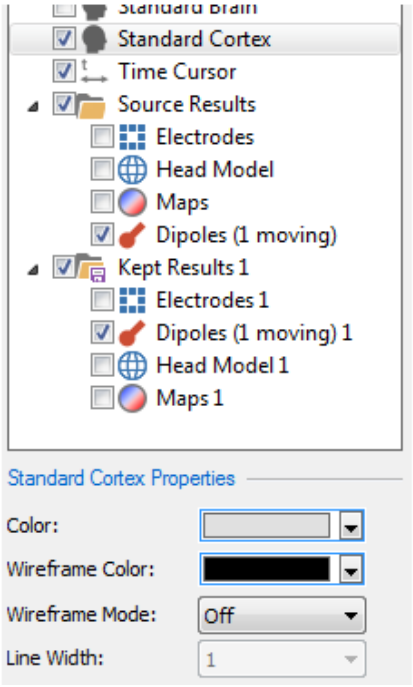


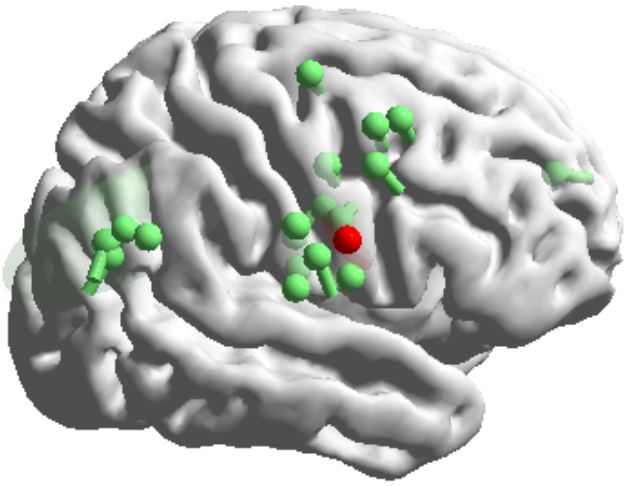
Last, at the bottom of the **Event / Epochs** panel, click the In-Place Averaging button. In the **Functional Data** display, select the **Butterfly Plot** and position the cursor at the peak of the spike.

The Functional Data display now shows the average of all spikes.



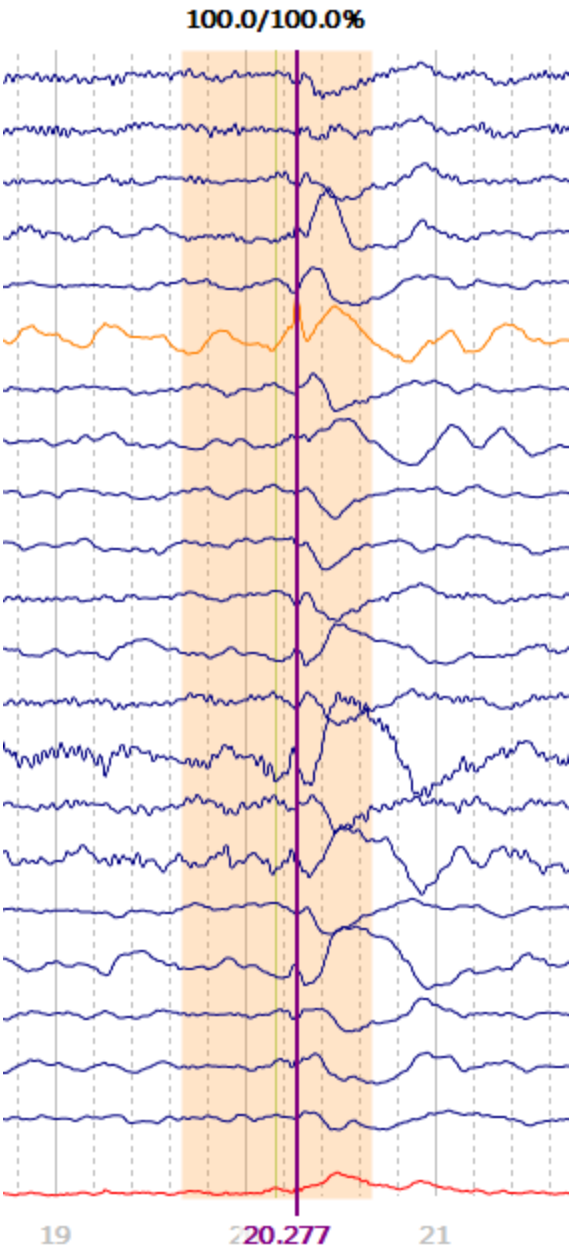
The **3D View Objects** list (left) shows that the **Standard Cortex** is being displayed. The red dipole is showing the current **Source Results**, which is the dipole computed from the average of the spikes.



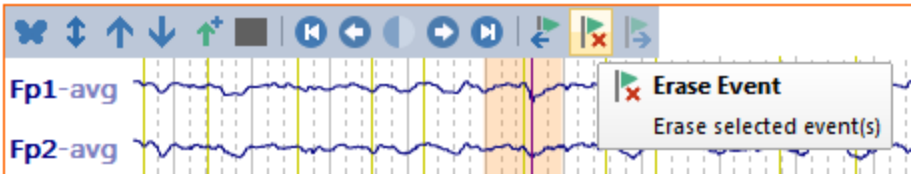


This particular file is showing a lot of scatter across dipoles. You can remove the dipoles that are incorrectly located. First, go back to the **Event List** and click the

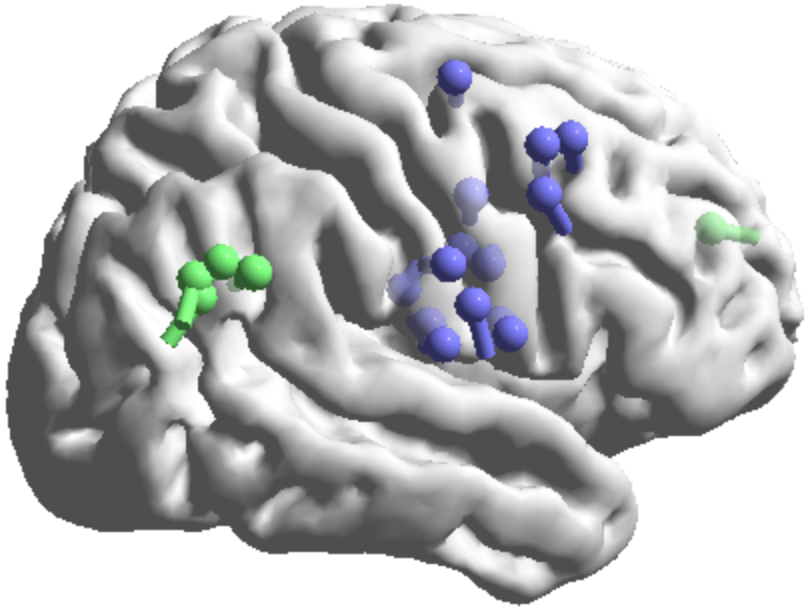
button. This returns you to the continuous data.



In the **3D View**, disable the display of the Standard Cortex to make it easier to select the bad solutions. Now use *Shift+click* on a bad dipole. This will take you to that spike in the continuous data file. Use the **Erase Event** icon to remove that event. Repeat the process until all questionable dipoles have been removed.



Then reselect the **Moving Dipole**, and again click the **Dipole Cluster** icon . Now you see only the good dipoles remaining (in blue). The new Kept Results contains these solutions.



The results are also seen in the **Event List**.

Events / Epochs

Event Average (1 Group Active):

1 2 3 4 5 6 7 8 9 10

Type: tmpl1 1999 Condition

Group Label: tmpl

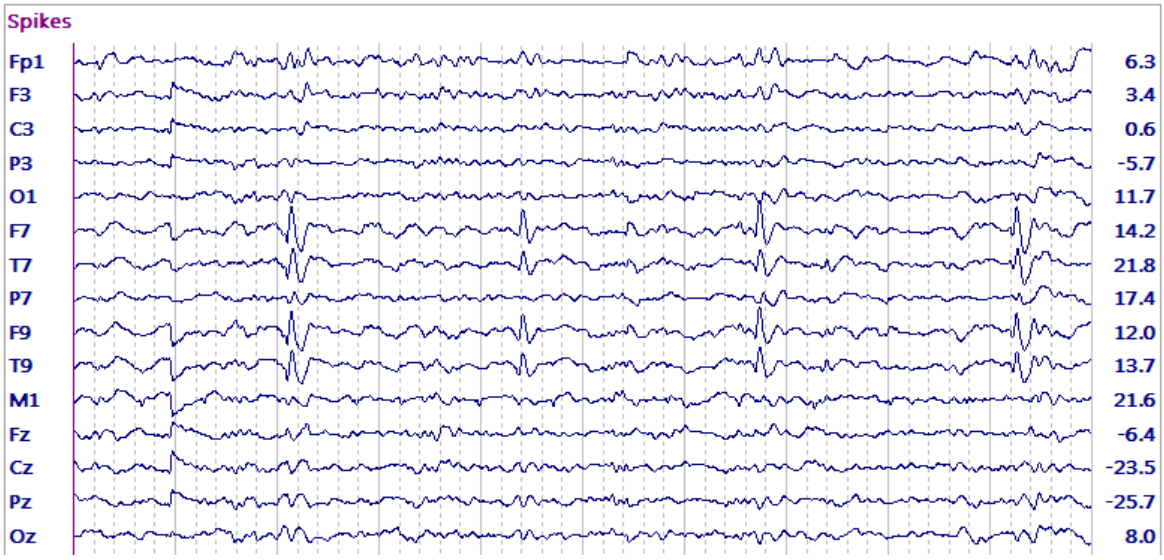
Count: 14/2003 Color:

Type	Time	Diff.[s]	Annotation
tmpl1	00:20.160		100.0/100.0%
tmpl1	00:37.504	17.3	111.6/92.1%
tmpl1	01:05.285	27.8	98.1/92.4%
tmpl1	01:10.543	5.2578	98.0/94.2%
tmpl1	02:00.977	50.4	100.5/91.7%
tmpl1	02:19.359	18.4	90.4/90.2%
tmpl1	02:32.703	13.3	102.8/90.4%
tmpl1	02:44.031	11.3	103.5/90.5%
tmpl1	03:20.566	36.5	108.7/98.0%
tmpl1	03:50.270	29.7	95.2/95.8%
tmpl1	04:20.598	30.3	113.6/98.2%
tmpl1	15:21.207	660.6	100.7/91.5%
tmpl1	15:24.043	2.8359	87.0/92.1%
tmpl1	34:50.734	1166.7	94.4/92.6%

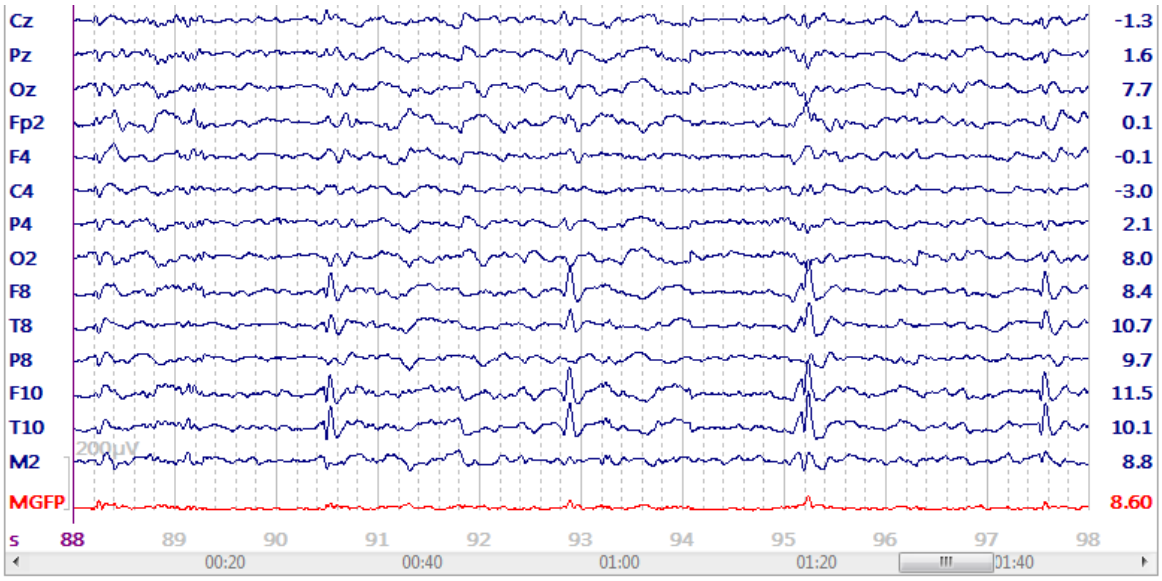
Using Multiple Templates

CURRY 8 allows you to create multiple templates and scan for all of them. The most common example is where there are more than one type of epileptic spike, due either to morphology or spatial distribution.

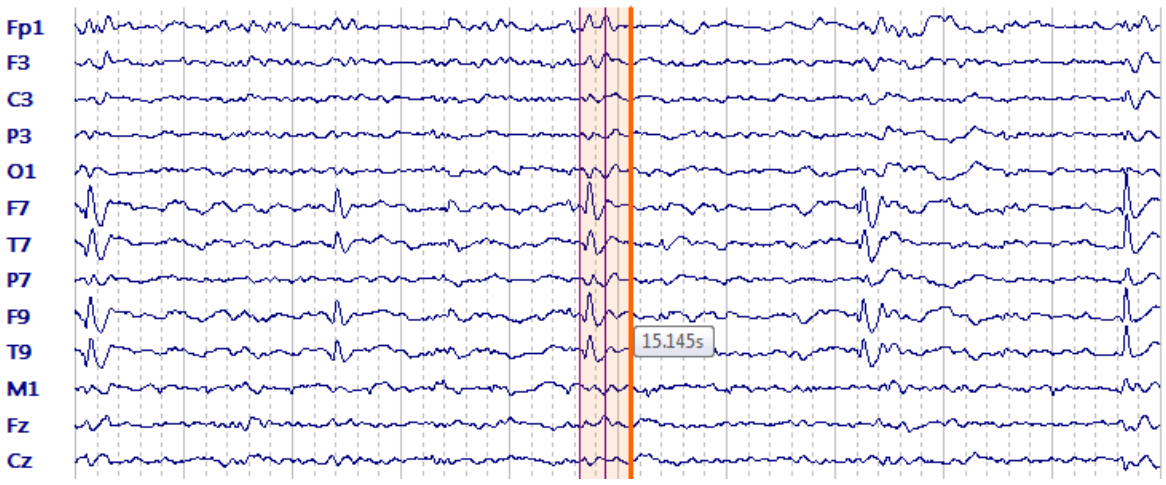
In this case, there were spikes from the left fronto-temporal area,



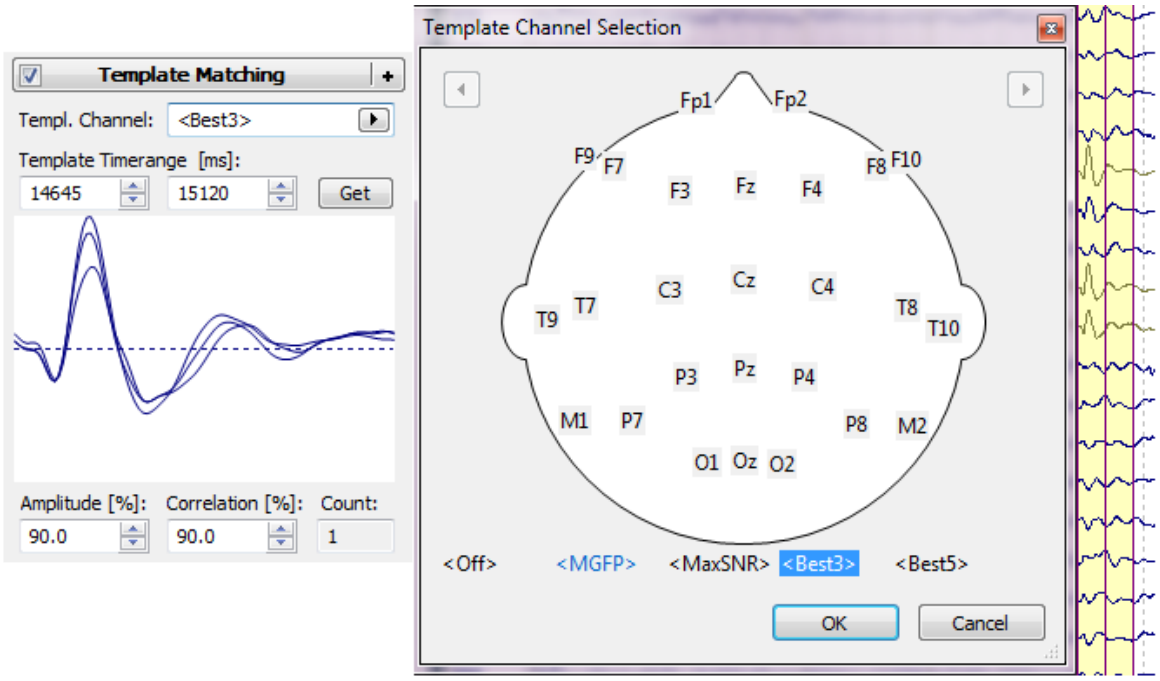
as well as from the right frontal area. This file is not included in the tutorial Database files, but the steps will be very similar with your data files.



1. Begin by using *Ctrl+drag* to create a Timerange that encompasses a spike and slow wave complex for the first class of spikes.

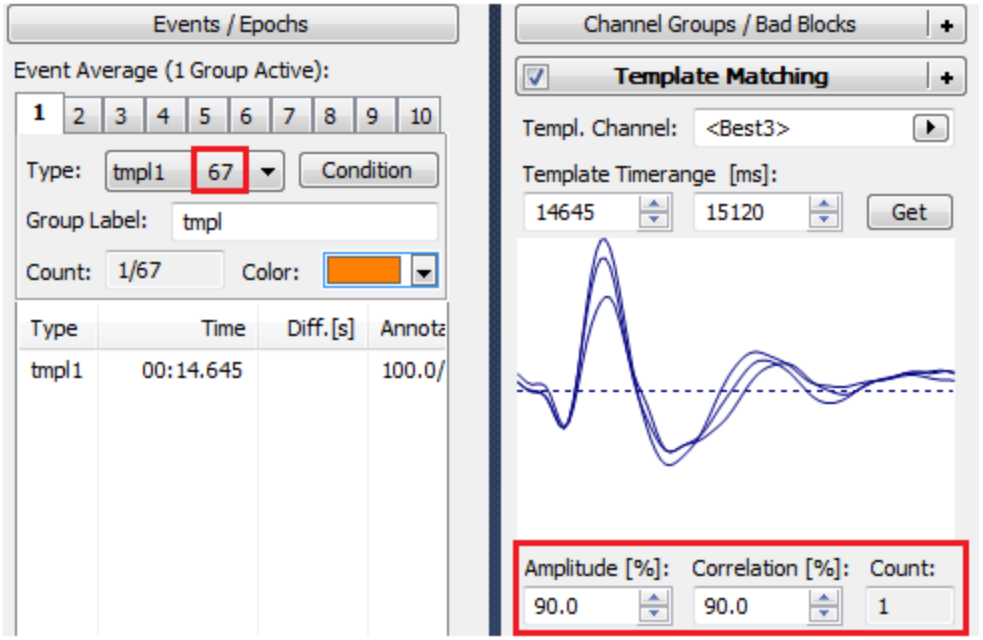


2. Add a **Template Matching** panel, and select **<Best3>** for the channels. You will see the selected channels (F7, F9, and T9 in this case) in a different color in the **Functional Data** display.

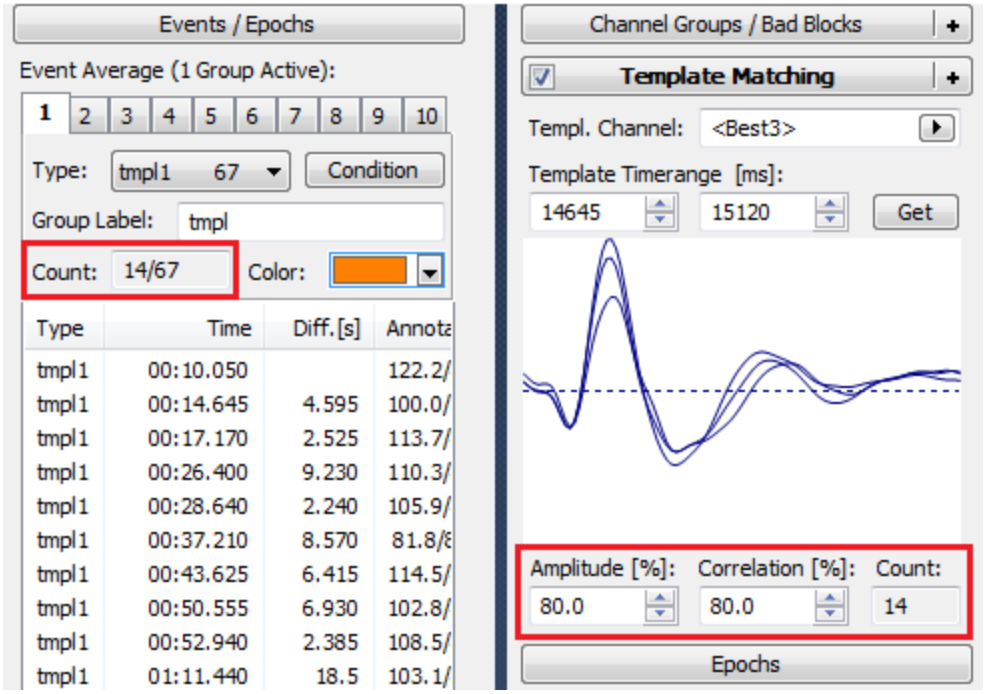


3. Then click the flashing **Scan Templates** icon .

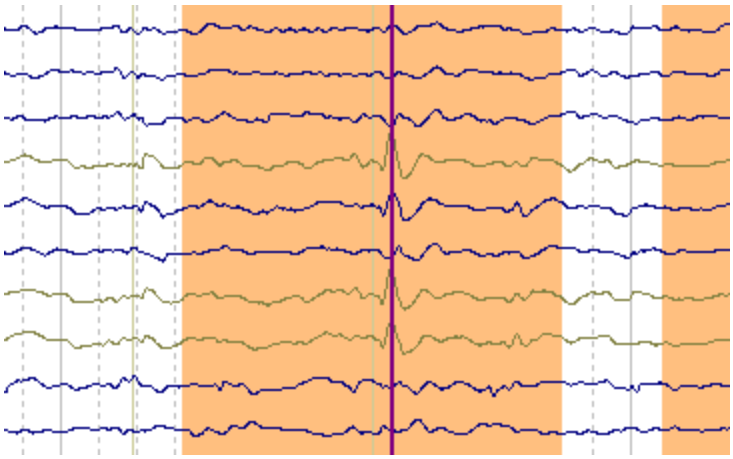
4. Click the **Open Events** icon to go to the **Events / Epochs** panel. Select "tmpl1" for **Type**. In this case, there are 67 matches, but none using the default **90% Amplitude** and **90% Correlation** criteria (just the template itself).



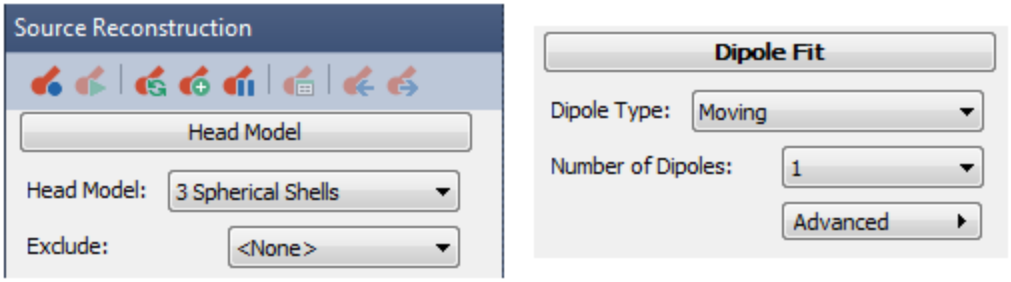
We therefore reduce the criteria to 80% for both Amplitude and Correlation. We now see there are 14 matches, enough to continue.



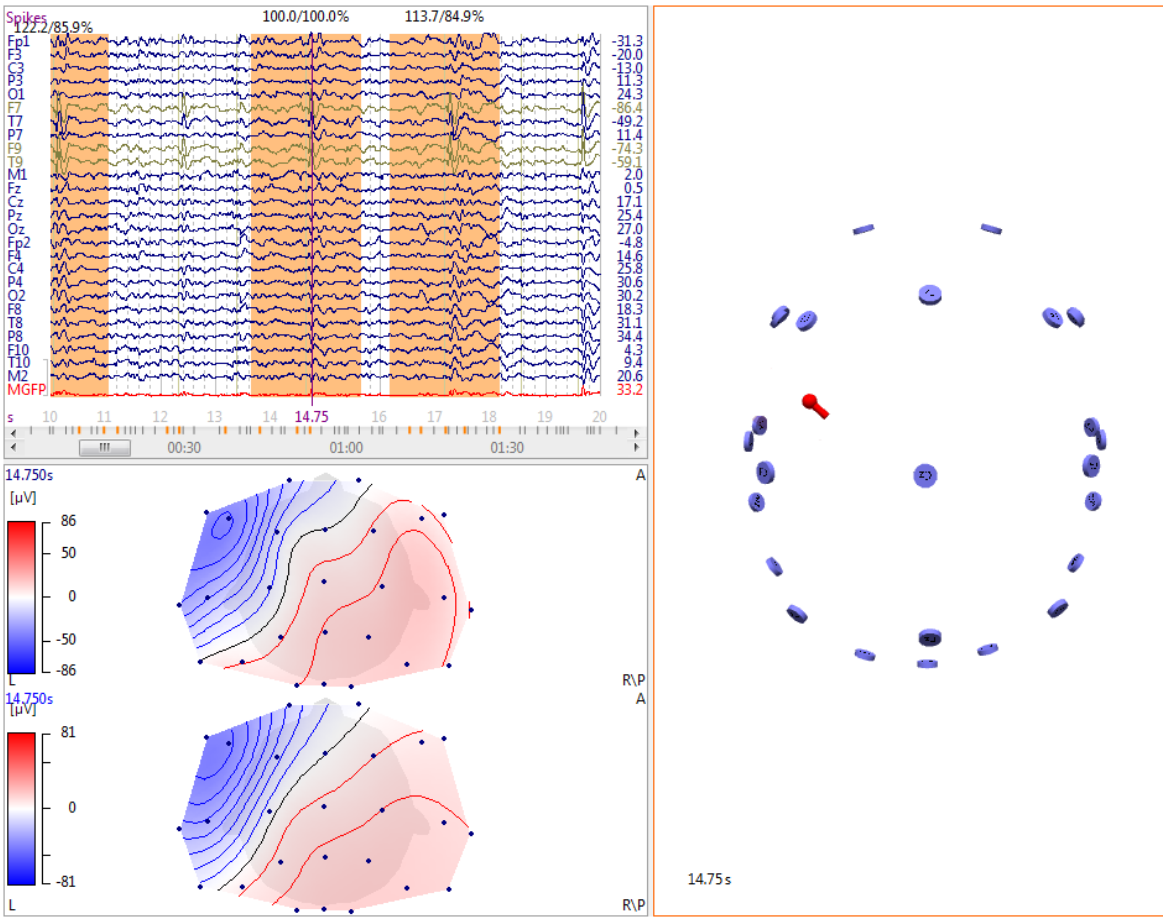
5. Select the FD, Maps, 3D View view (if there were MRI data, we would select the **All** view). In the Functional Data display, double-click to superimpose all three vertical cursors. This is to allow us to select a single time point. Then position the cursor at the peak of a spike.



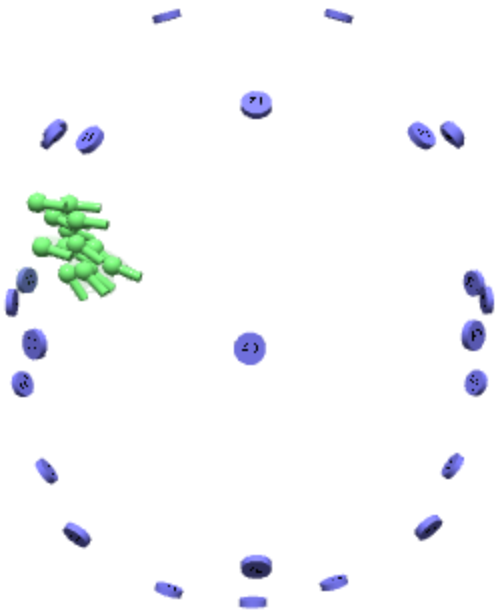
6. Since we do not have MRI data, and since this is more of an exploratory analysis, we will use the **3 Spherical Shells** Head Model (faster). Select **Moving** for **Dipole Fit**.

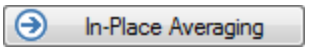


7. The dipole results are seen in the **3D View**, with the **Confidence Ellipsoids Off**. In the **Maps** display, we also enabled the **Fitted** option, so we can see the original Measured data, as well as the distribution with source reconstruction, and the two are very similar.

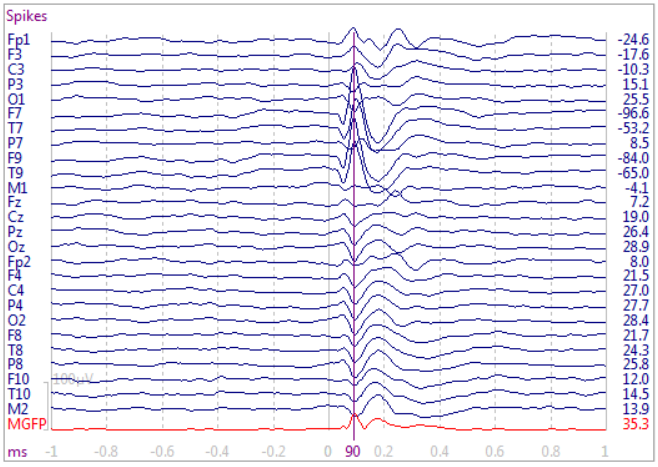


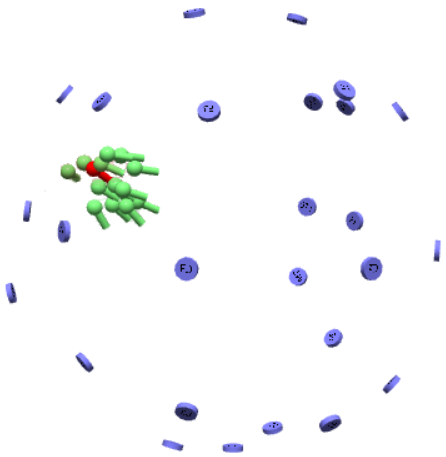
8. To see the cluster of dipoles for all detected events, click the **Dipole Cluster** icon . The cluster is seen in the **3D View**, and in this case it is a fairly tight grouping.



9. To see the average of these dipoles, click 

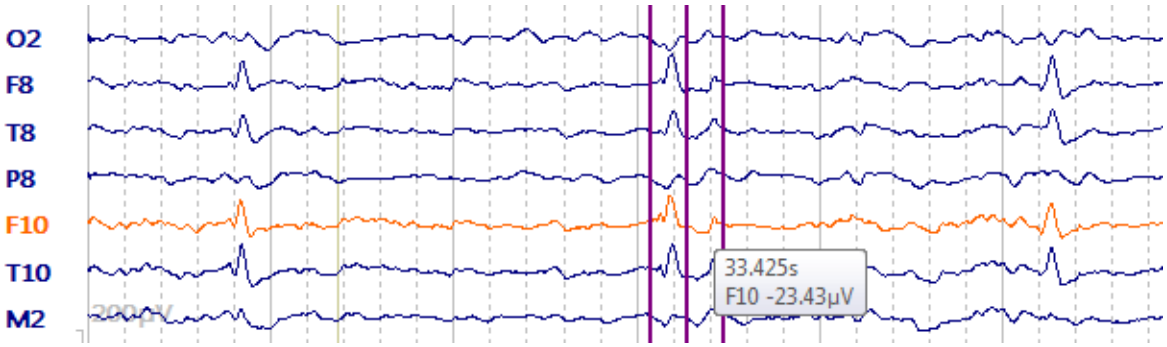
(at the bottom of **Events / Epochs**). Position the cursor at the peak. The dipole solution for the averaged waveforms is seen in red. Note that its Confidence Ellipsoid is smaller, likely due to the increased SNR.



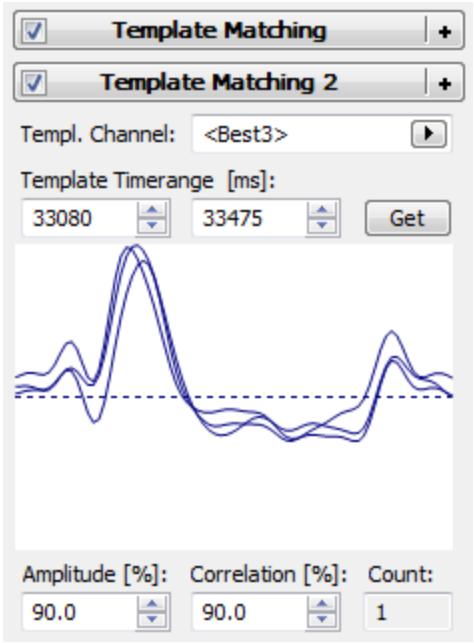


10. Return to the original continuous data by clicking

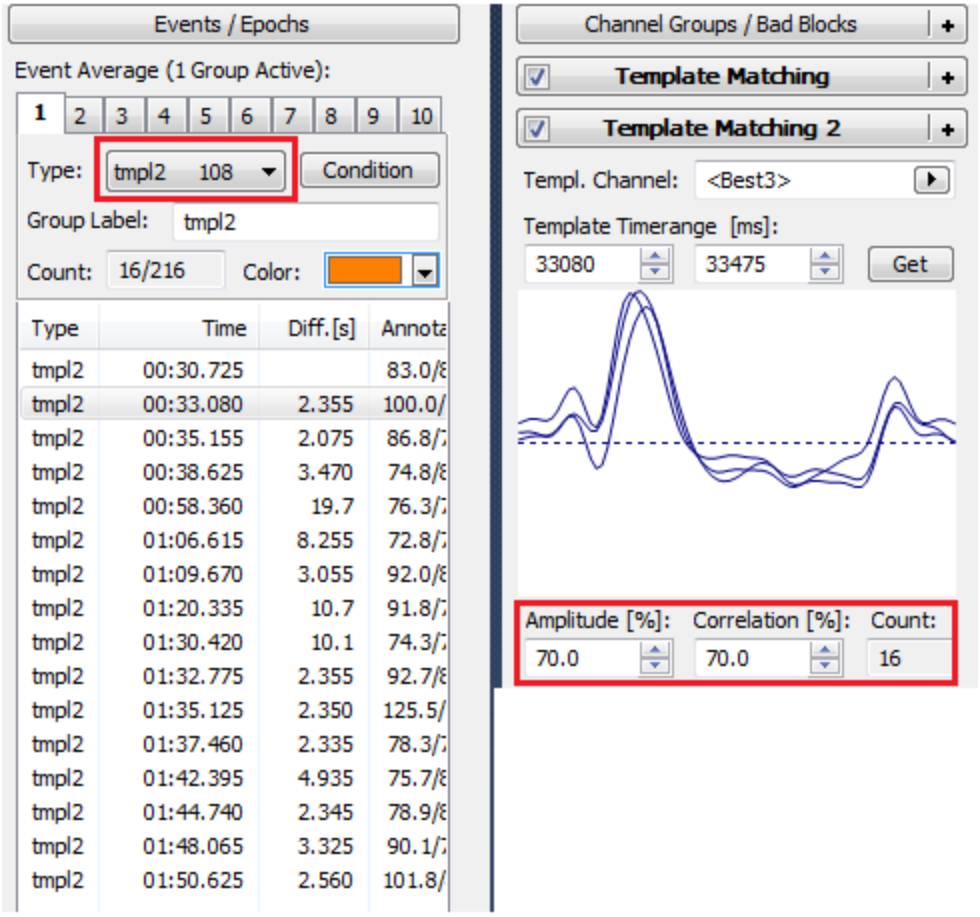
(at the bottom of **Events / Epochs**). Select a spike from a different brain area. In this case, there are also spikes from the right fronto-temporal area. Set a Timerange to encompass a spike and slow wave complex, as we did above.



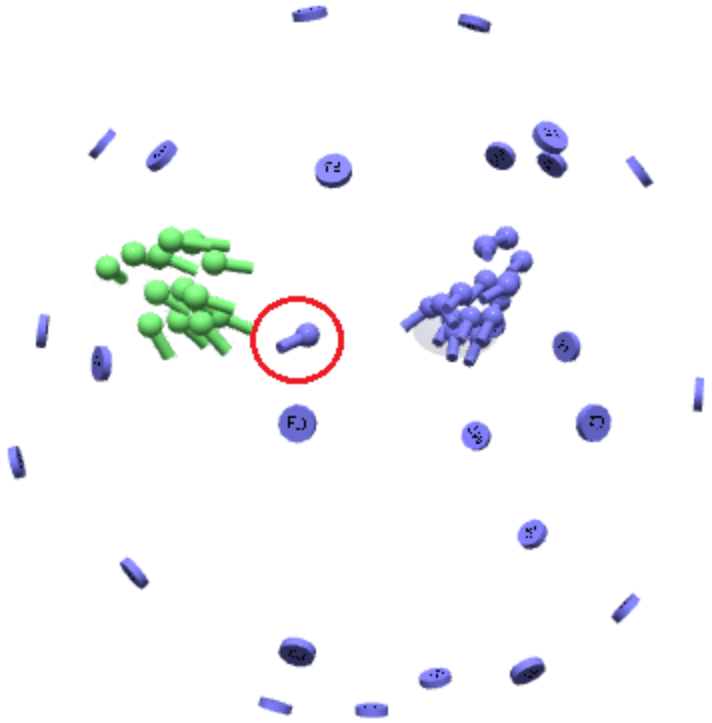
11. Add a second **Template Matching** panel, select **<Best3>**, and **Scan** again.



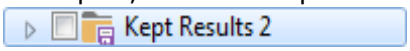
12. In the **Events / Epochs** panel, select "tmpl2", and reset the **Amplitude** and **Correlation** criteria to **70%**. Now we see there are 16 events.



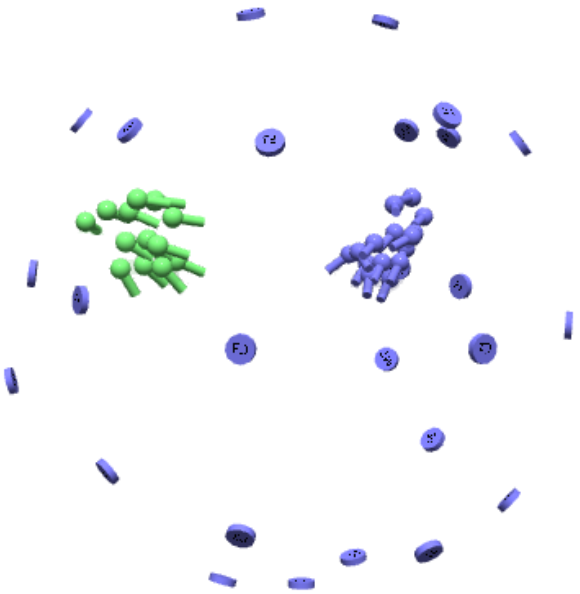
13. Again select a single time point at the peak of the spike, reselect **Moving** for the **Dipole Fit**, and click the **Dipole Cluster** icon. The results are see in the **3D View**.

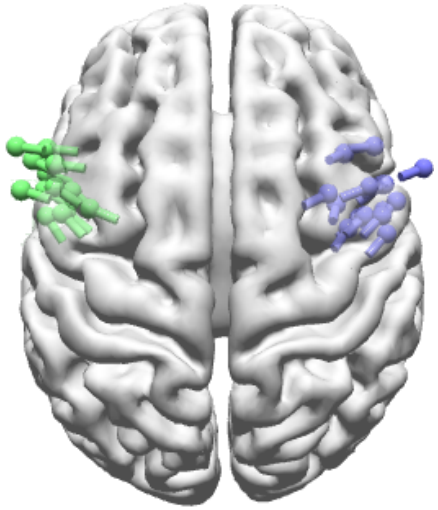


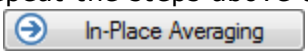
In this case there is an outlier. Use **Shift+click** to go to that spike in the continuous data. In this case, there was an artifact in that epoch and we need to delete it. This particular event is highlighted the Event list, and pressing the *Del* key will remove it.

14. We then need to reselect the peak of the spike, and click Dipole Cluster again. It is also necessary to deselect the display of 

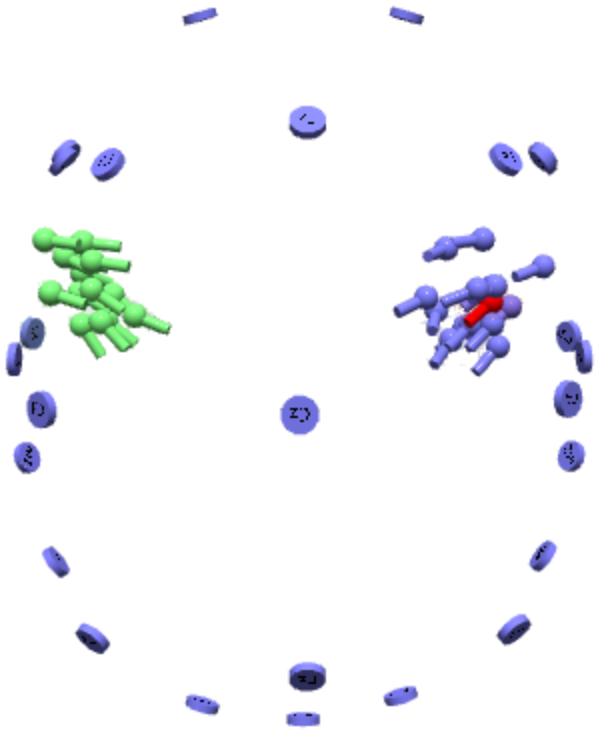
in the **3D View Objects** list. Then we see just the two sets of dipole solutions. The Standard Cortex was added for orientation.





15. Repeat the steps above to see the dipole solution for the average of the spike (click 

and set cursor).



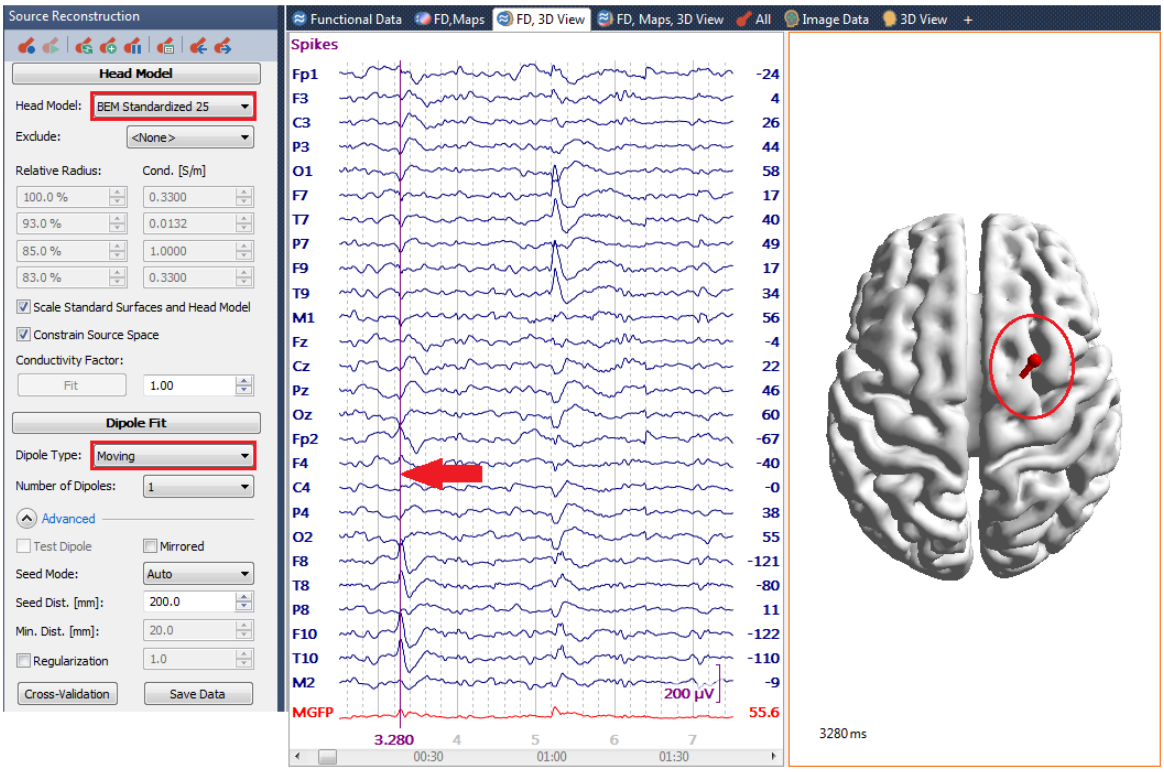
2.4.8.2 Manual Spike Detection and Dipole Clusters

There are two ways to detect epileptic spikes. One is to detect them automatically using **Template Matching**, as is described in the **Template Matching and Dipole Clusters** tutorial. The other is to manually insert events in the continuous data (which should be done by physicians only). In either case you will be able to see the distribution of the individual spikes, or the average of all spikes.

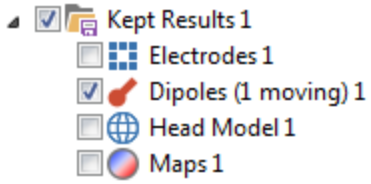
There are also two ways to perform manual spike detection. The first one gives a quick view of dipole clusters. The second way is more involved, but also provides some additional flexibility.

The data file we will be using is not included in the Tutorials data base, so you can simply view the steps.

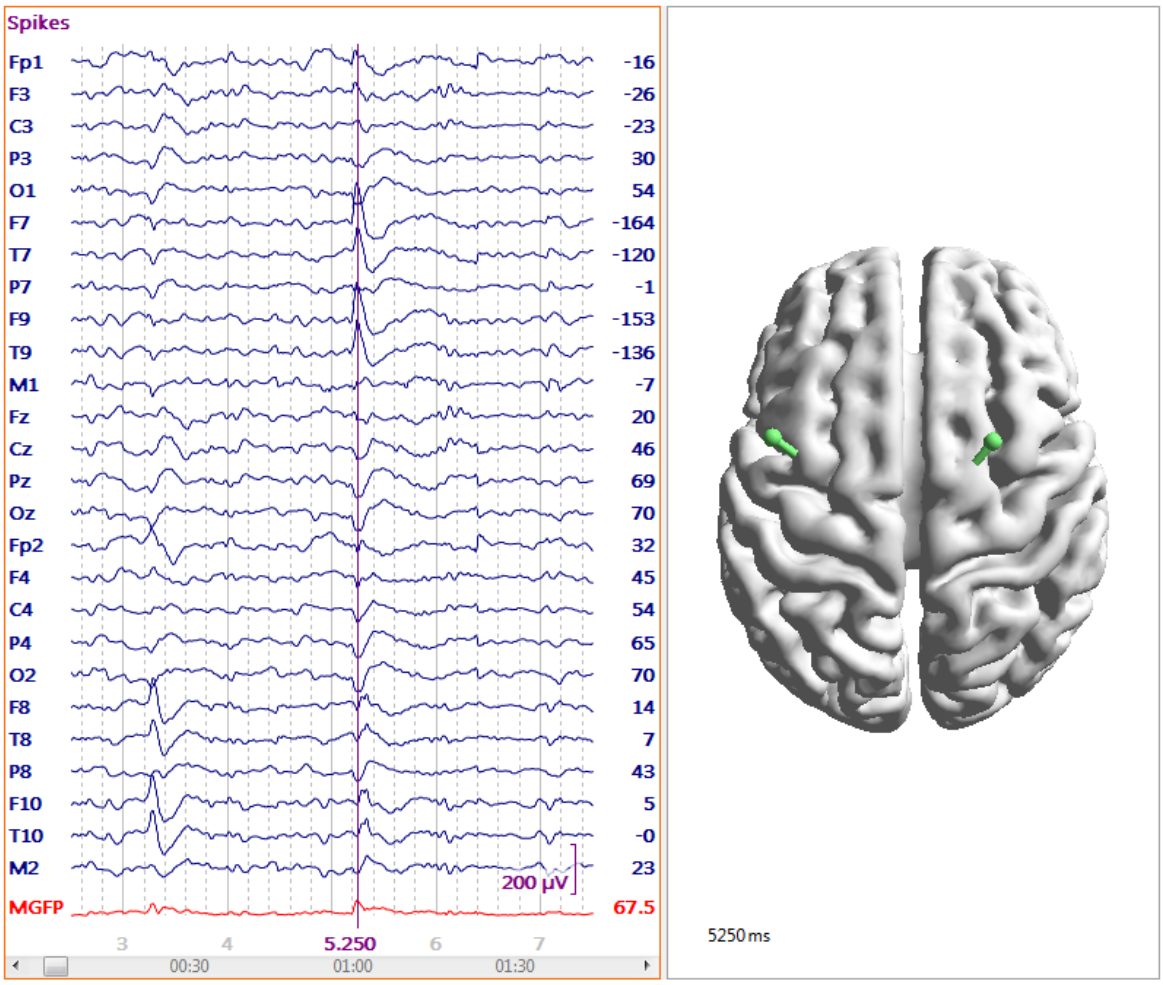
1. In this file, there are clusters of spikes in the left and right fronto-temporal areas. In this case we do not have the MRI data, so we are using the **Standard Cortex** ion the **3D View** display. A **Head Model** was selected, along with the **Moving Dipole** where we are using the single cursor (Tracking Mode) at or just before the peak of the spike. The dipole result is seen.



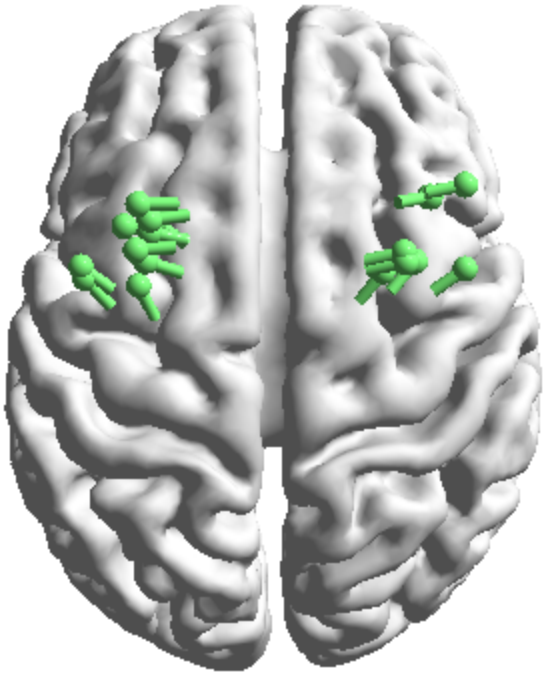
2. Click the **Keep Results** button and enable the **Append to Keep Results** Mode . You will see the **Kept Results** in the **Objects** list.



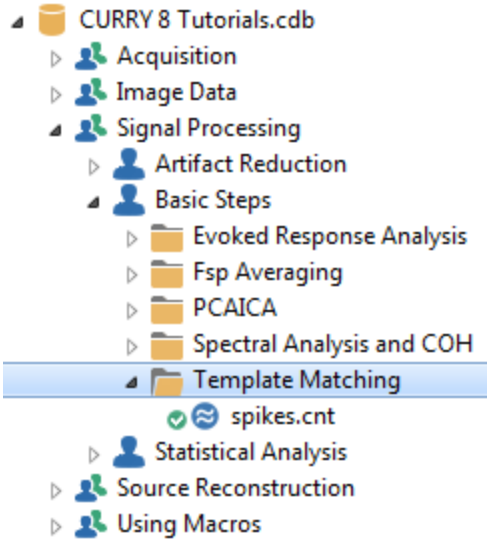
Click on the next spike, and again click the **Keep Results** button. The second dipole appears. Continue through the file to see the clusters of dipoles. If you don't like one you have just added, remove it using **Source Results** → **Remove Last Results**.



At the end you will have dipole cluster(s) for the spikes you select. The results can be saved, printed, or copied to the Report.

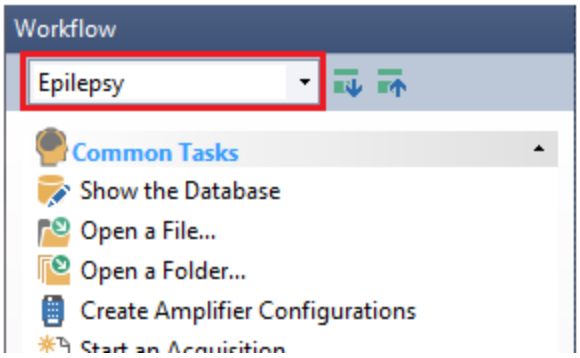


The other manual method is a little more involved, but gives you some additional flexibility. We will use the same data file as in the **Template Matching** tutorial.

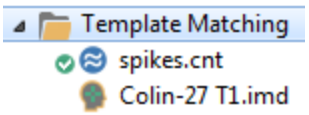


This is not an ideal file to use, primarily because it does not have enough channels to compute really stable dipoles, and the noise levels are a bit high. It will work for demonstration purposes.

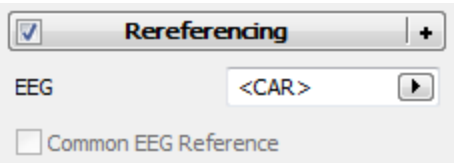
1. This is a good example for when to use **Scope Parameters**. At the top of the **Workflow** display, select **Epilepsy** from the drop down list. The presets a number of parameters for you. Then switch back to the **Database**.



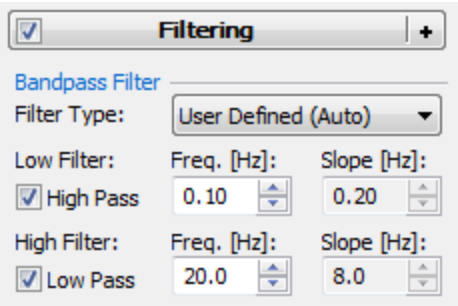
2. Since there are no MR data, we will use a hi-res MR data set, rather than the averaged MR data. *Right click* on the Template Matching study and select **Insert Built-In Image Data → Colin**. You will see the MNI27T1.imd file added.



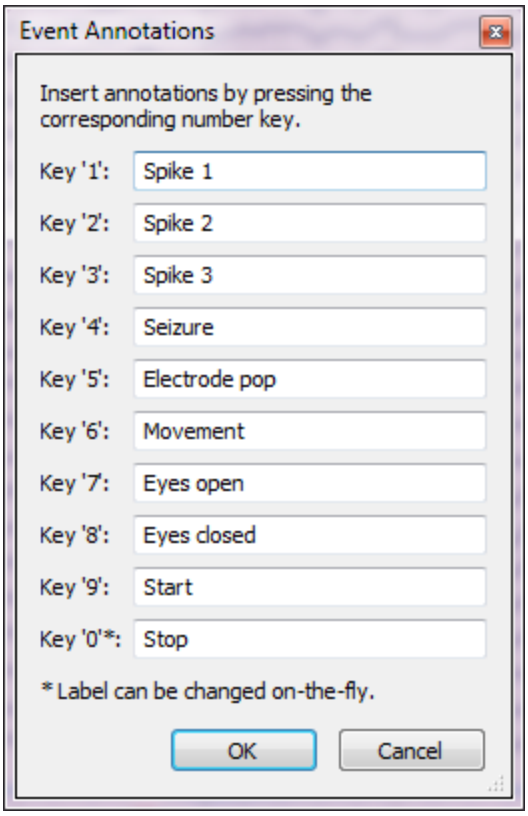
3. Open the Study. Add a **Rereferencing** panel and select the **CAR**. We will be calculating dipole sources, and that requires a CAR. Actually, CURRY will use the CAR whether you select it explicitly or not. Selecting it let you see the data that will be used in the reconstructions.



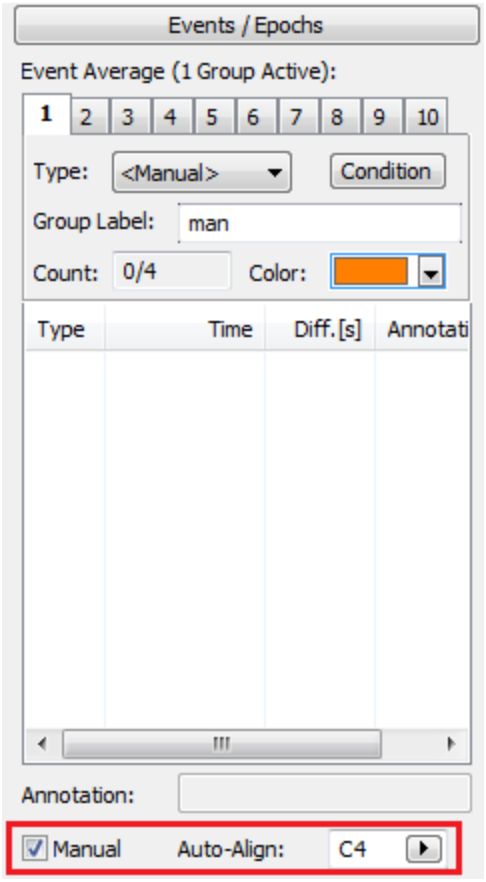
There is also some prominent anterior EMG activity that we will filter out - use the values shown. Use care not to select filter parameters that will affect the spike and slow wave complexes.



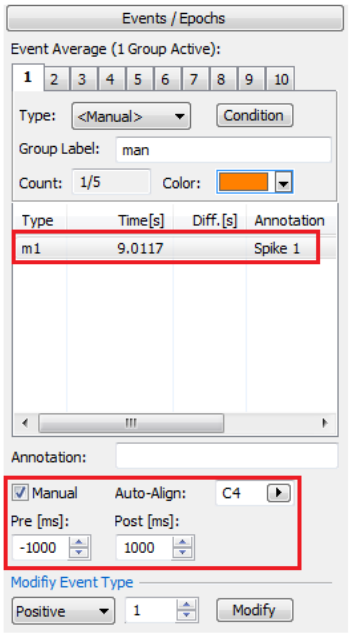
4. We will insert events manually in this file (the **Template Matching** tutorial demonstrates how to do this automatically). Go to **Functional Data → Edit Event Annotations** and verify that *Key 1* will display *Spike 1*. (In practice, you may encounter more than one type of spike, and you can use additional keys to mark them and analyze them separately).

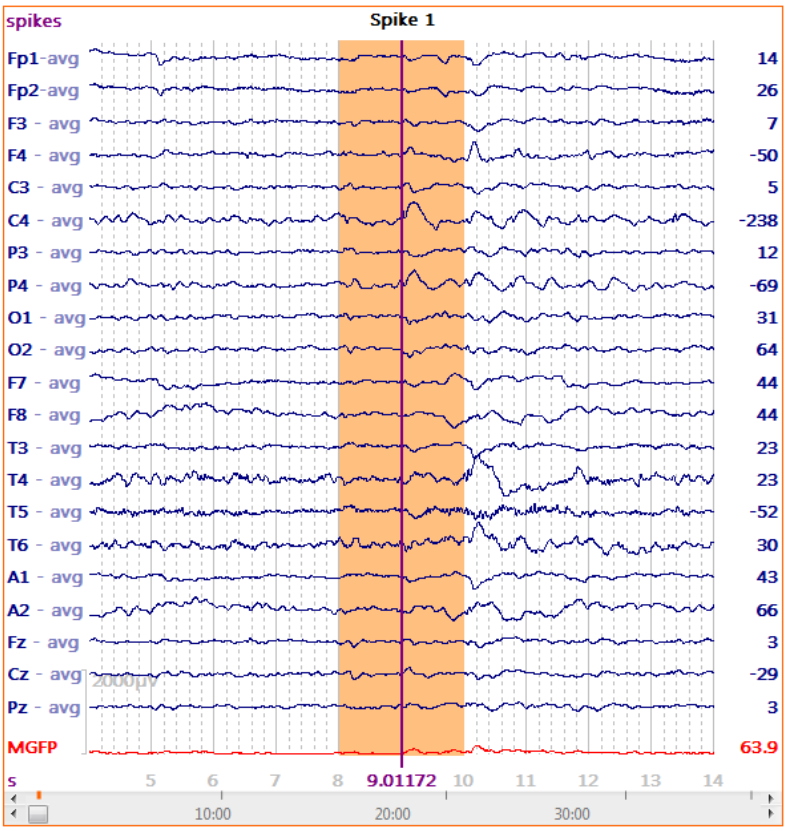


5. Go to Events / Epochs and enable the **Manual** option. Select **C4** as the channel for **Auto-Align**. The spikes are seen most clearly from C4. Auto-align will use the peak within ±50 ms of where you click - you do not have to obsess over clicking exactly on the peak.

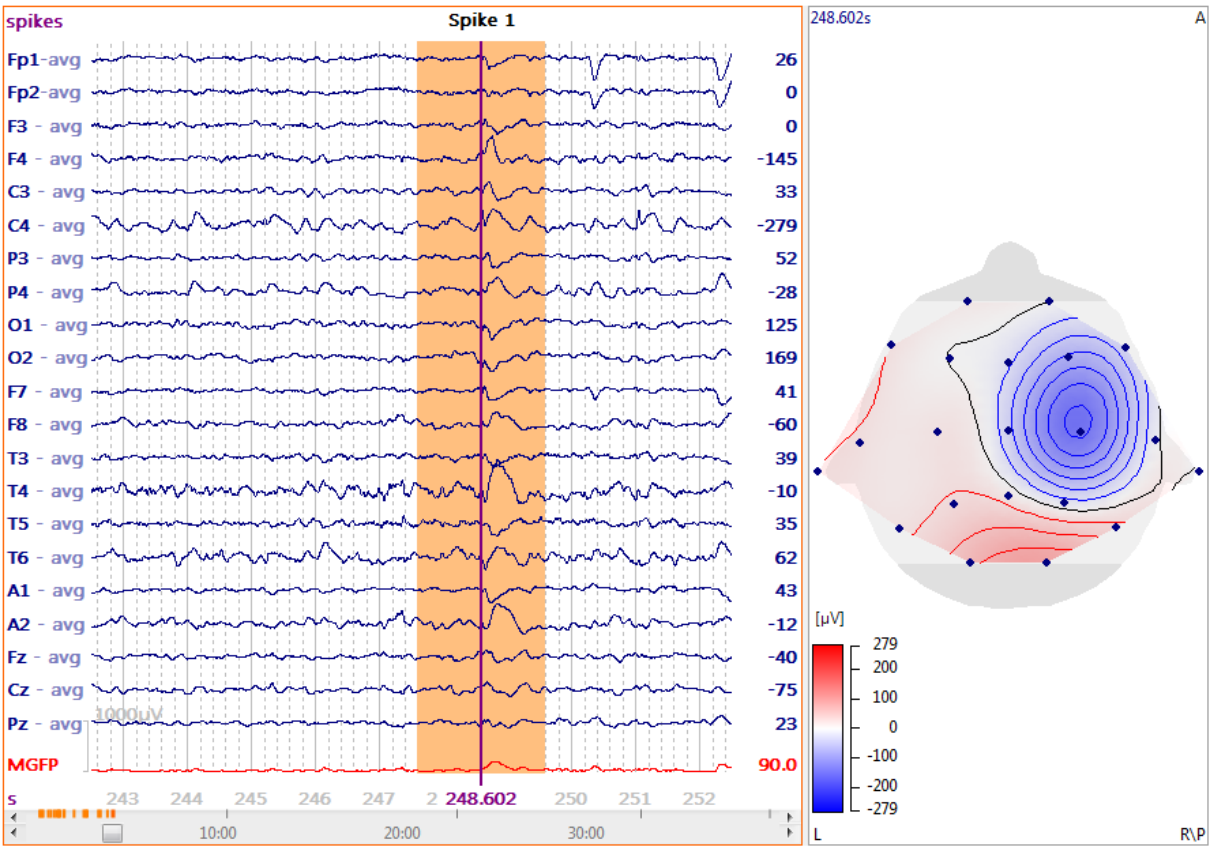


6. Click on a spike at C4 and press the *1 key* on the keyboard. The "m1" manual event is added to the list. The duration of the epoch interval was set automatically with the **Epilepsy Scope Parameters** at **-1000** to **1000 ms**.

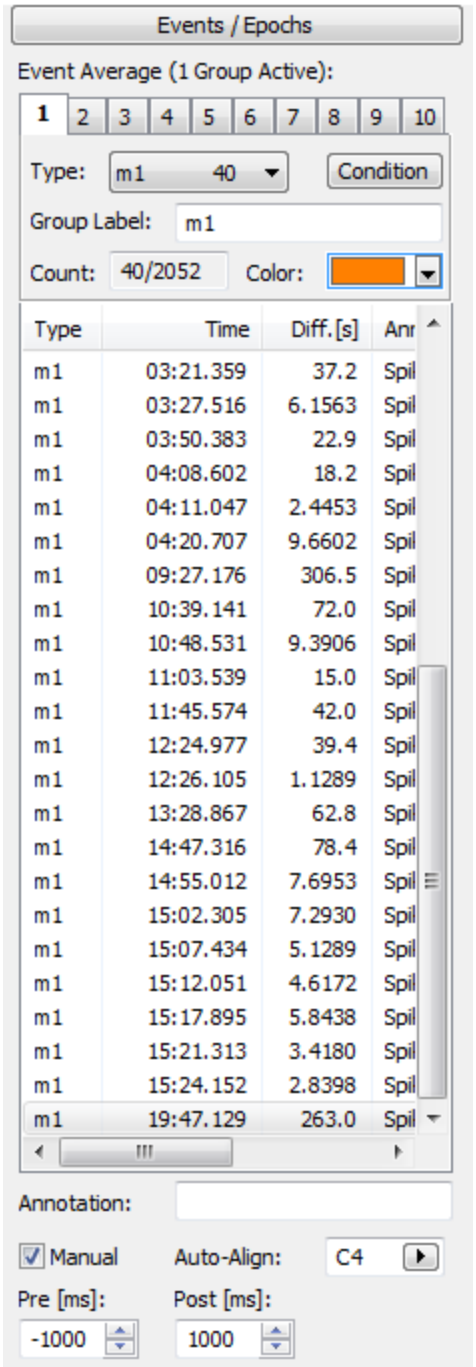




7. Now we will go through the file and select the spike peaks at C4. Select only the best matches. You can facilitate the process by selecting the FD, Maps display. Select the examples that have the most consistent maps. There are some seizure and post-seizure sections that you may skip through. We marked about 40 spikes.



8. You will see the spike events appear in the event list.

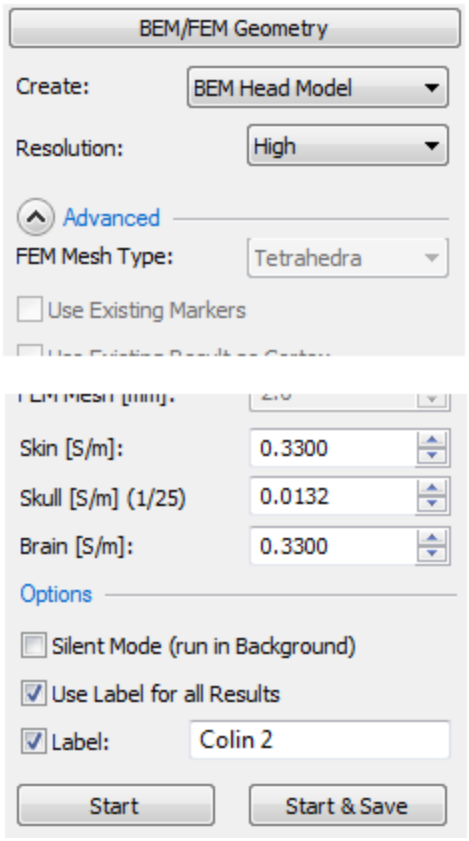


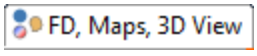
Now you have the option to save the spikes out in a separate file containing epochs with the individual spikes, or you can take a shortcut and create a Dipole Cluster at this point. You can also create a dipole cluster from the epoched data file. We will create the cluster first using the more simple, direct method, after completing the next steps first.

9. Since we do not have the MRI data for this subject, we previously loaded the "Colin" MRI data. We need to create a BEM model using that MRI data set. Select the

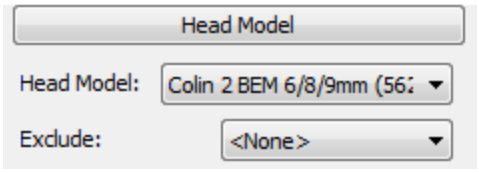
display. In the **BEM/FEM Geometry** panel, select the **BEM Head**

Model (if needed), enable **Use Label for all Results** (in the **Advanced** section) and **Label**. Enter a name, such as "Colin". Use all other default settings. Then click **Start** (or **Start & Save** if you want to save the results).

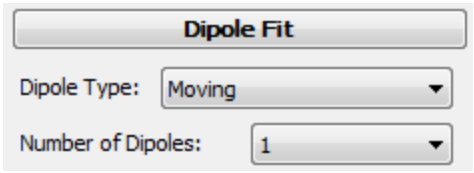


10. When finished, click the 

display. For **Head Model**, select the *Colin* model you just created.

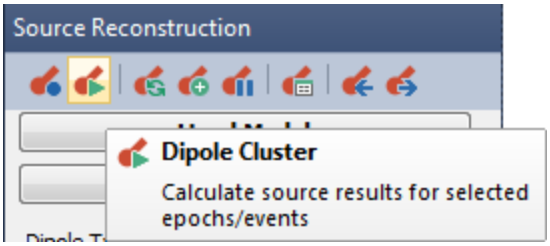


11. For **Dipole Fit**, select a **Moving Dipole**.

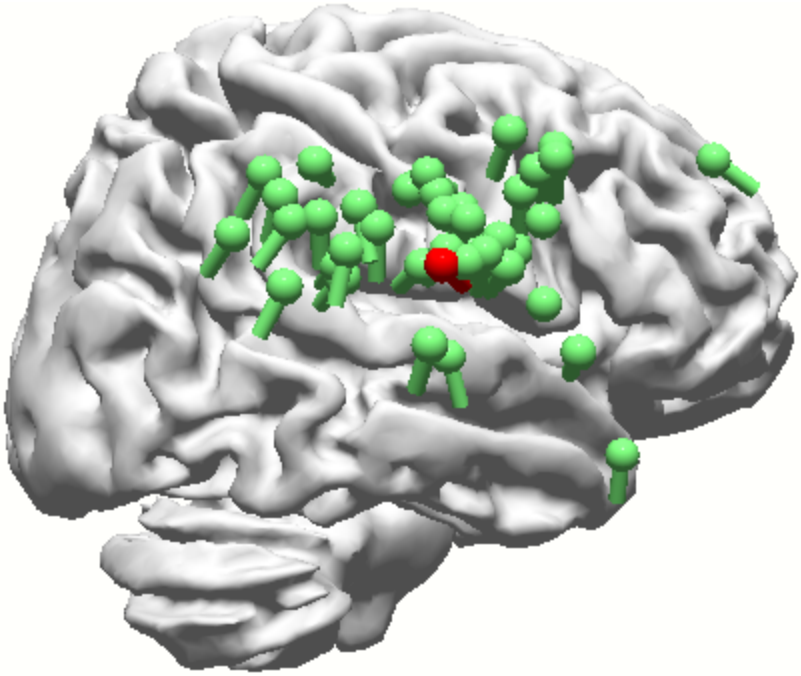


12. In the **Objects** list for **3D View**, enable the **Colin Cortex** and disable the **Electrodes**. Set the Cortex **Transparency** to **100%**. Select a **Right View** for the display. The **Confidence Ellipsoids** were turned off.

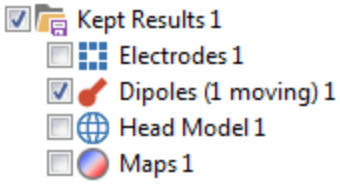
13. Click the **Dipole Cluster** icon at the top of the **Source Reconstruction** panel (this bypasses the creation of an epoched file).



CURRY will go through all of the manually selected spikes in the list and superimpose the results.



These are seen as Kept Results in the **Objects** list.



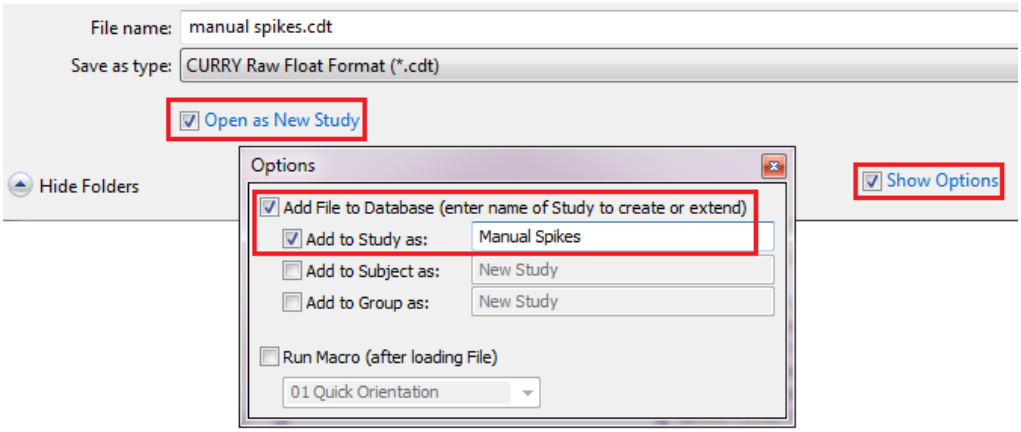
With this method there is no immediate way to compute the average of all dipoles and then compute the dipole source. You would just need to click

and then compute the dipole source using the averaged data.

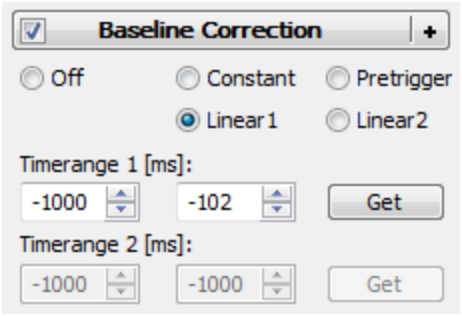
14. The alternate method is to create an epoched file containing the spikes. Return to the

panel. Make sure the **Pre** and **Post [ms]** times are **-1000**

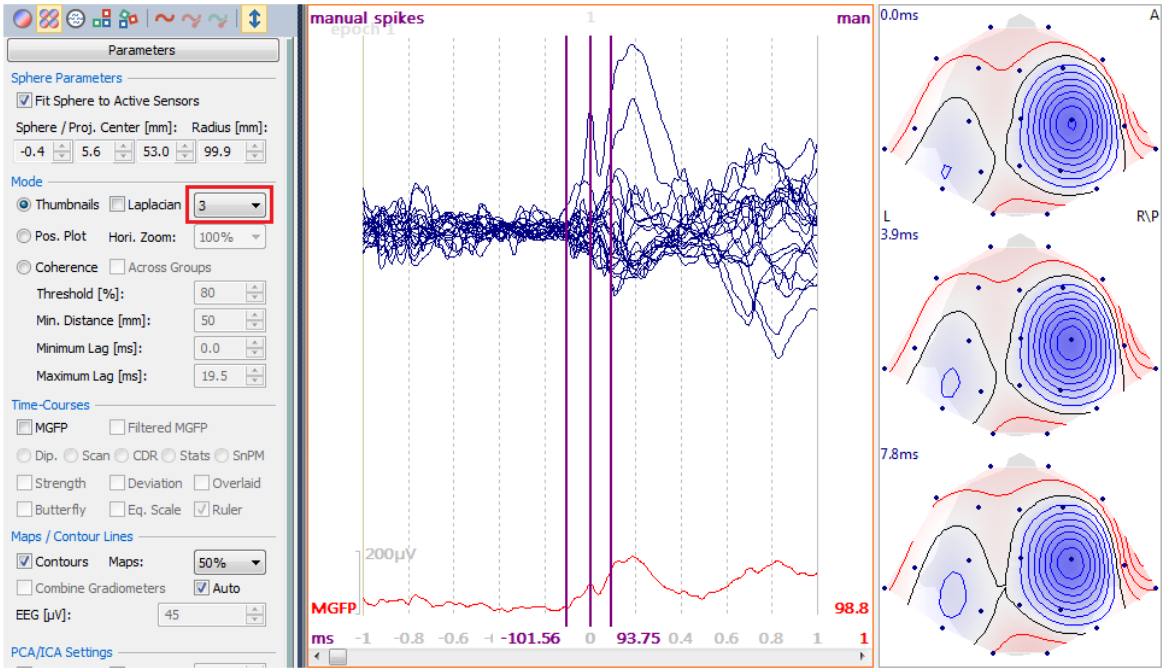
and **1000**ms. Click the **Export Epochs** icon at the top of the panel. Click **Use <Manual>** to the message. Enter a file name - *manual spikes.cdt*. Enable the **Show Options** field and **Add File to the Database**, in a Study folder called *Manual Spikes*. Select **Open as New Study**. Then click **Save**.



15. Now we see the epochs, each containing a spike at 0 ms. Select the **Butterfly Plot** display. For **Baseline Correction**, select **Linear 1**, and enter **-1000** and **-102** for the correction interval.

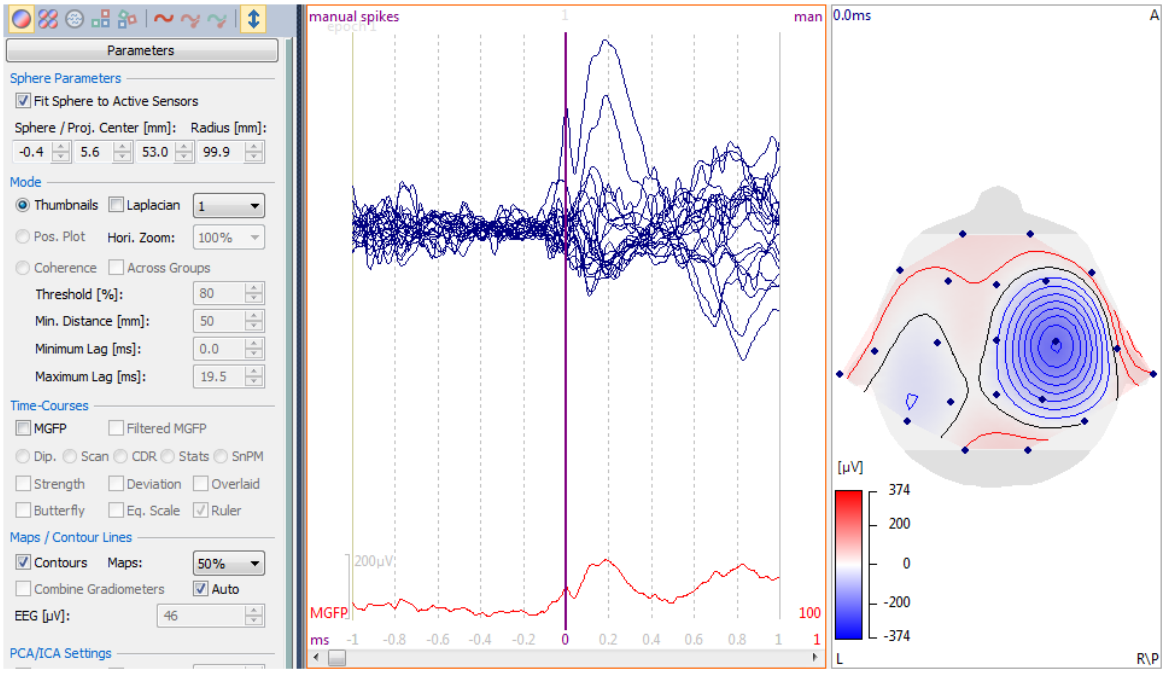


16. With spikes you typically use a **Moving Dipole** with a single point for the Timerange. A single point means that all three vertical cursors are at the same time point. There are different ways to do this. The easiest is as follows. In this example, note that the three vertical cursors are separated and there are three maps displayed (about the center cursor). A **3** is selected for the Thumbnail number.



In the **Maps** Toolbar, click the **Contour Map** icon (if needed), and *double-click* the mouse in the Functional Data display.

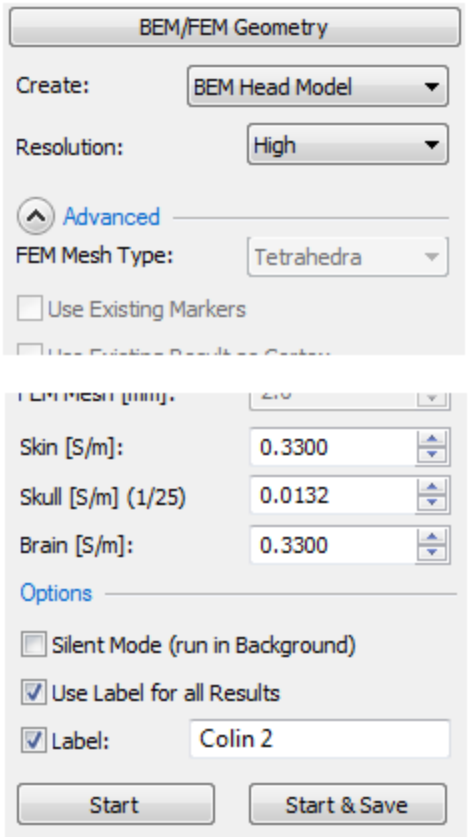
Position the mouse at the peak of the spike, at 0 ms. Now there is a single map and a single cursor.

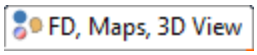


17. Use the Toolbar arrow buttons to step through the epochs. Deselect the ones that do not have consistent looking waveforms or maps (use the *spacebar* or the Toggle Epoch icon to deselect an epoch). This is somewhat of an arbitrary process the develops with practice. The point here is to eliminate any obviously inconsistent spikes, just to reduce the number of dipoles later. You will have other chances to eliminate bad epochs. (Return to the first epoch when finished).

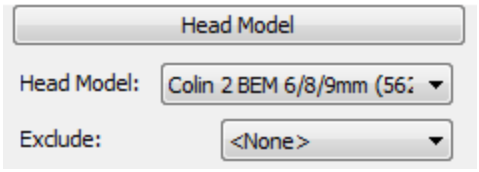
18. Since we do not have the MRI data for this subject, we previously loaded the "Colin" MRI data. We need to create a BEM model using that MRI data set, as we did above. Select the

display. In the **BEM/FEM Geometry** panel, select the **BEM Head Model** (if needed), enable **Use Label for all Results** (in the **Advanced** section) and **Label**. Enter a name, such as "Colin 2". Then click **Start** (or **Start & Save** if you want to save the results).

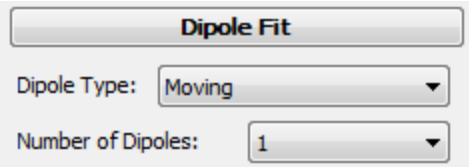


19. When finished, click the 

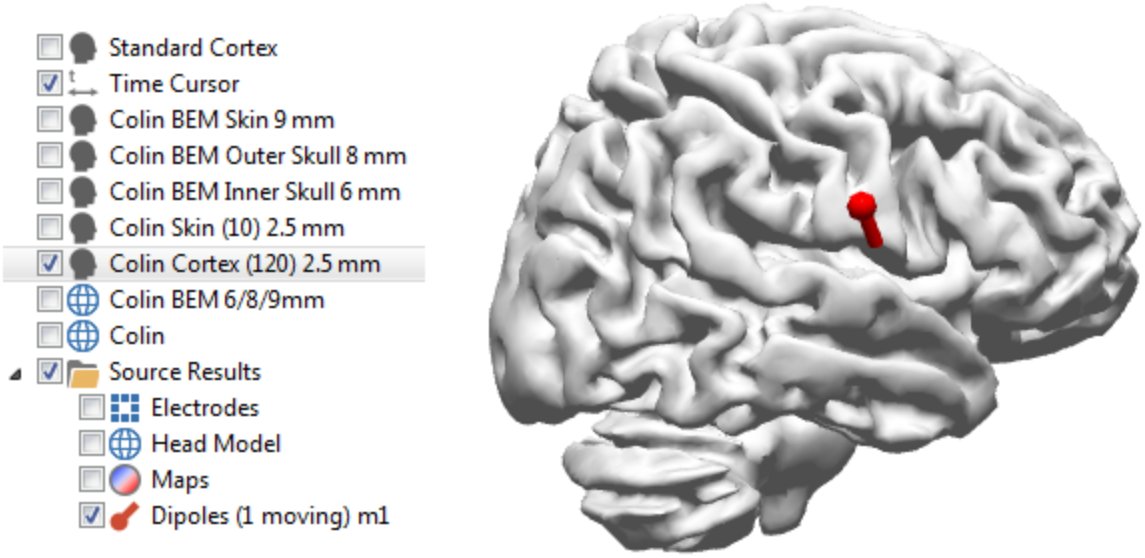
display. For **Head Model**, select the *Colin 2* model you just created.



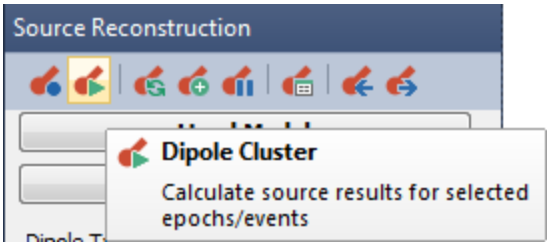
20. For **Dipole Fit**, select a **Moving Dipole**.



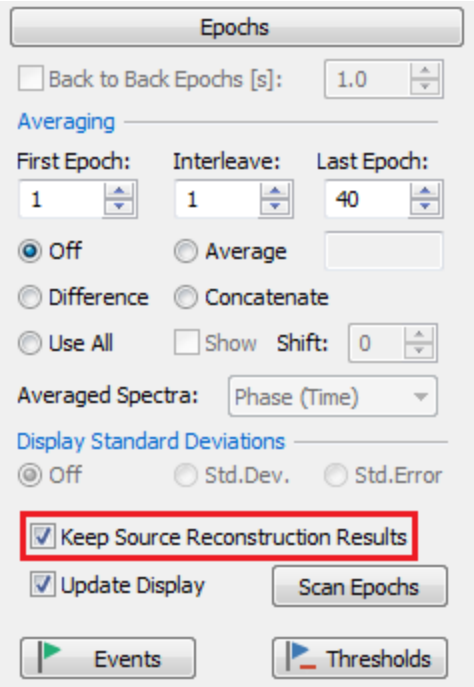
21. In the **Objects** list for **3D View**, enable the **Colin 2 Cortex** and disable the **Electrodes**. Set the Cortex **Transparency** to **100%**. Select a **Right View** for the display. The **Confidence Ellipsoids** were turned off. If you move the cursor in the Functional Data you will see the single solution for each time point.



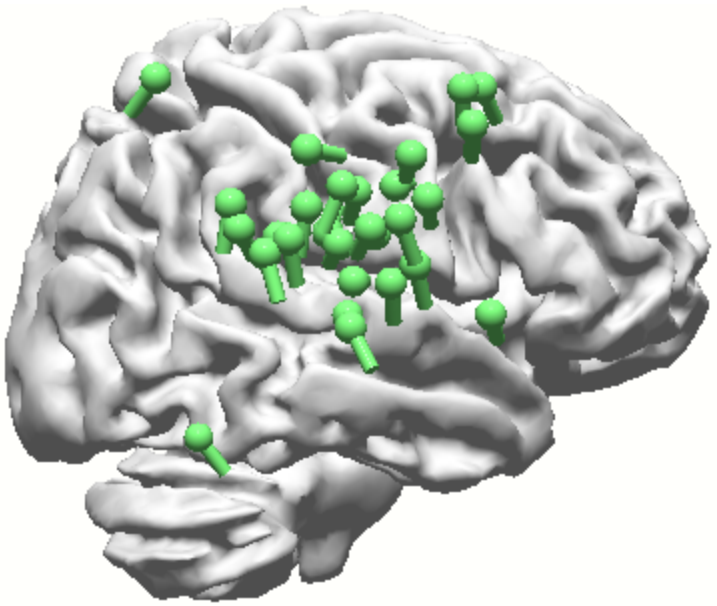
22. What we want to do now is to go through the selected epochs, compute the dipole solution for each, and superimpose the results. This is accomplished by clicking the **Dipole Cluster** icon at the top of the **Source Reconstruction** panel.



In CURRY 7 the same process was accomplished by using the **Keep Source Reconstruction Results** option and clicking the Scan Epochs button, in the Epochs panel under **Functional Data**. This alternative will still work.



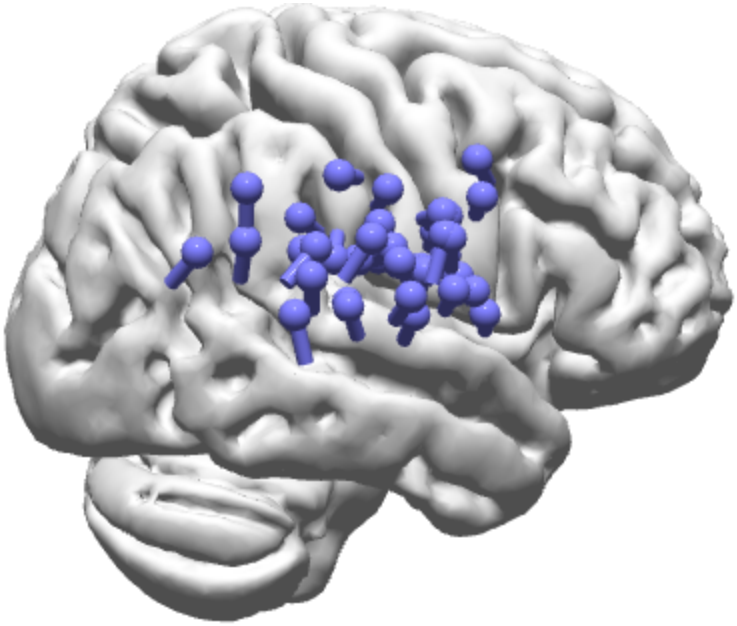
23. As the epochs are scanned, you will see the dipole solution for each epoch, where the last one is in red (hidden in the figure below). In the **Objects** list for the **3D View**, you will see a new section called **Kept Results 1**.



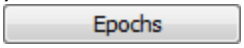
If you should need to make the dipole sizes uniform, you can use **Source Results** → **Uni Size for Kept Results**, or highlight the **Dipoles** in the **Kept Results** and, in the **Properties** section, set the **Scale Mode** to **Uni**. You may vary the size of the dipole symbol using **Symbol Size [mm]**.

24. If there are aberrant looking dipoles, *Shift+click* on a dipole symbol and you will see the originating epoch in the Functional Data. Here you can decide if you want to

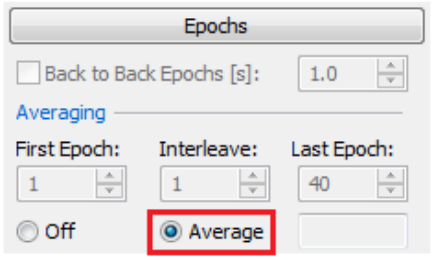
include or exclude that dipole. To exclude it, just press the *spacebar* (with the cursor in the Functional Data display; the display will turn gray). Repeat for all questionable dipole results. When you are finished, click the **Scan Epochs** button again, and the revised set of dipoles will appear as new Kept Results. If you cannot click on a bad solution because it is inside the cortex, disable the display of the cortex. If you want to look at a different type of dipole (Rotating), select it and click the **Dipole Cluster** icon again. And so on.

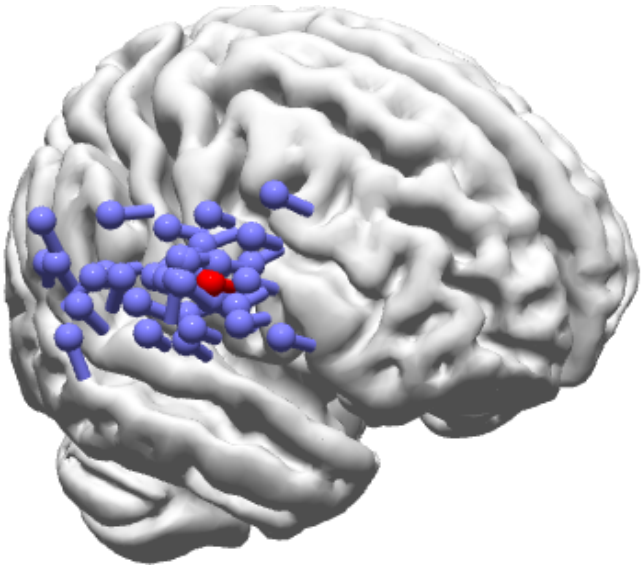


Incidentally, you can rename the Kept Results as desired. Highlight the Kept Results line and press *F2*. You can then rename them. Note the various "Results" options under **Source Results**. For example, use **Remove Last Results** or **Remove All Results** before running the final **Scan Epochs**.

25. Lastly, if you want the average of all selected epochs, just click the **Average** option under 

. The red dipole is based on the average of all spikes. (Make sure the most recent Source Results are enabled).





Again, this is not an ideal data set - too few electrodes, no MRI data, no measured sensor positions, etc., so the results are somewhat more scattered than what we typically see.

2.4.9 PCA and ICA Analysis

Principle Component Analysis (PCA) and Independent Component Analysis (ICA) are statistical techniques akin to factor analysis that are used (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 (first order decorrelation).

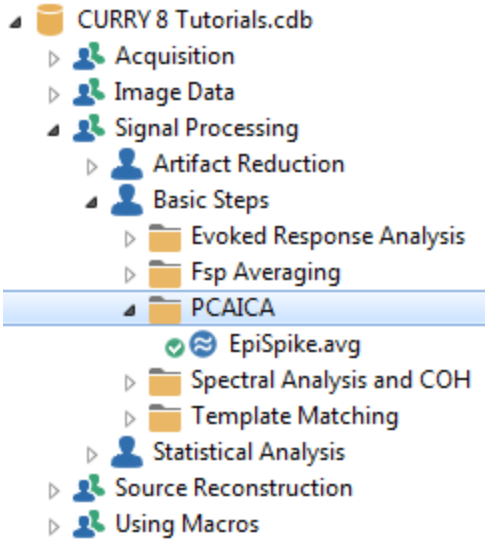
ICA generates patterns and loadings use statistical independence (requires that all second order and higher correlations are zero). The generality of ICA lies in the simple principle that different physical processes tend to generate statistically independent signals. Given that scalp-recorded EEG is 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.

PCA can used to determine the number of valid components for use in the ICA program. The ICA results are more appropriate for filtering unwanted components from the signals prior to source analysis (although you may filter the PCA components also).

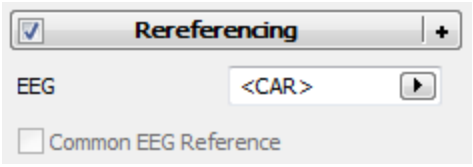
Although the ICA algorithm leads to a unique set of patterns, strengths and time courses, it should not be forgotten that it is only a mathematical tool for analyzing the data, and it lacks all knowledge of the properties of the underlying sources which shall be reconstructed from the measurements. Therefore, it is not possible to identify each ICA pattern, for example, with a pattern generated by an individual

dipole. Nevertheless, the method does yield the number of different (independent) patterns that are significant, i.e., the number of patterns that rise above the noise level that was estimated. Evidently, this number corresponds to the minimum number of independent source configurations that are required to account for or explain the data in the selected Timerange. In addition, the ICA can also be used to filter the data in a spatio-temporal fashion by identifying and suppressing insignificant patterns which are dominated by noise, as described in the *CURRY 8 User Guide*.

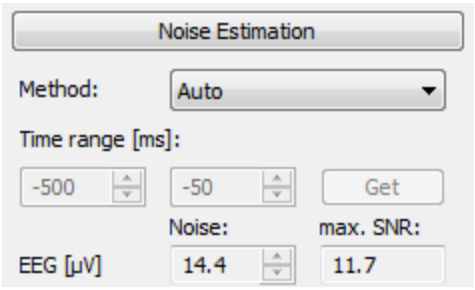
For this example we use the *epispike.avg* file, a single filtered epileptic spike. This is found in the Study shown below. Open the Study.



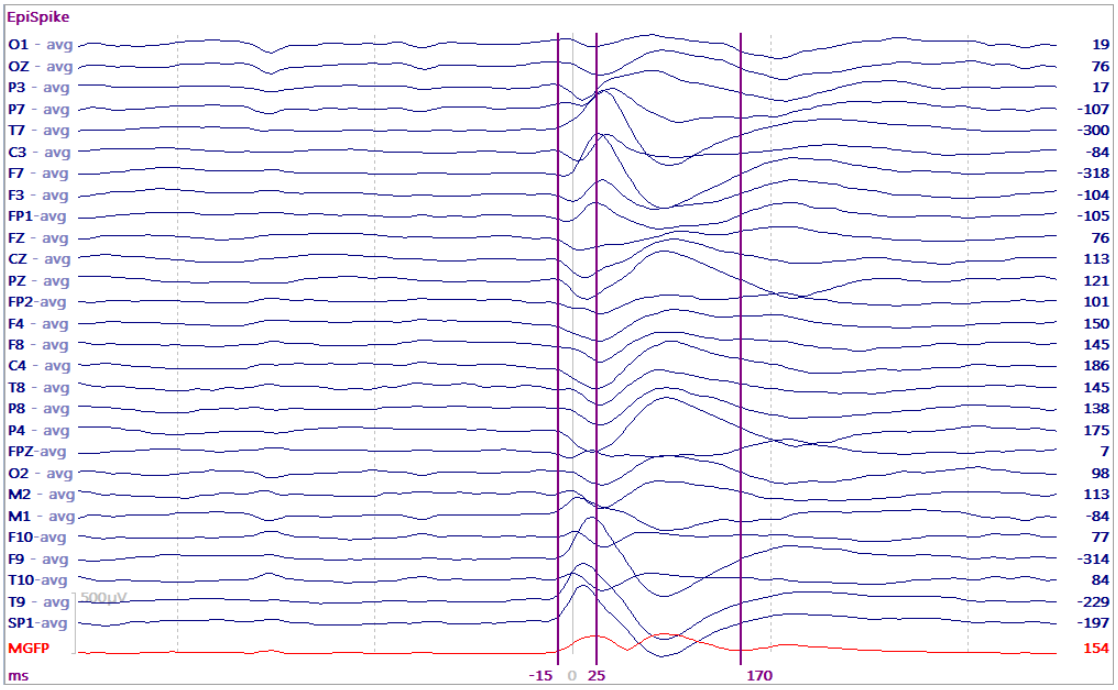
1. There are a couple of preliminary steps that need to be performed. Select the **CAR**. Add the **Referencing** panel and select **CAR**. (For PCA and ICA, CURRY will use the CAR whether you explicitly select it or not - you should select it anyway to see the data as they are being used).



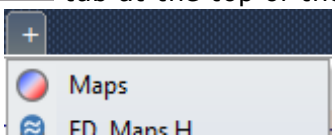
Select Noise Estimation (Auto) from the **Workflow**, or go to the Noise Estimation panel under **Functional Data**. By default, the Method is set to **Auto**. Auto, in cases like this, will automatically select the range from the start of the epoch interval (-500 ms) to -50 ms, giving the Timerange in this case of -500 to -50 ms. This is because in many cases epileptic spikes will be selected based on the peak of the spike. Noise should be estimated from the pre-spike interval, and so the -50 ms time point is used to exclude the start of the start of the spike. These values may be modified, as needed. In most cases, you may not even need to check Noise Estimation; we did it here to illustrate what it is doing.



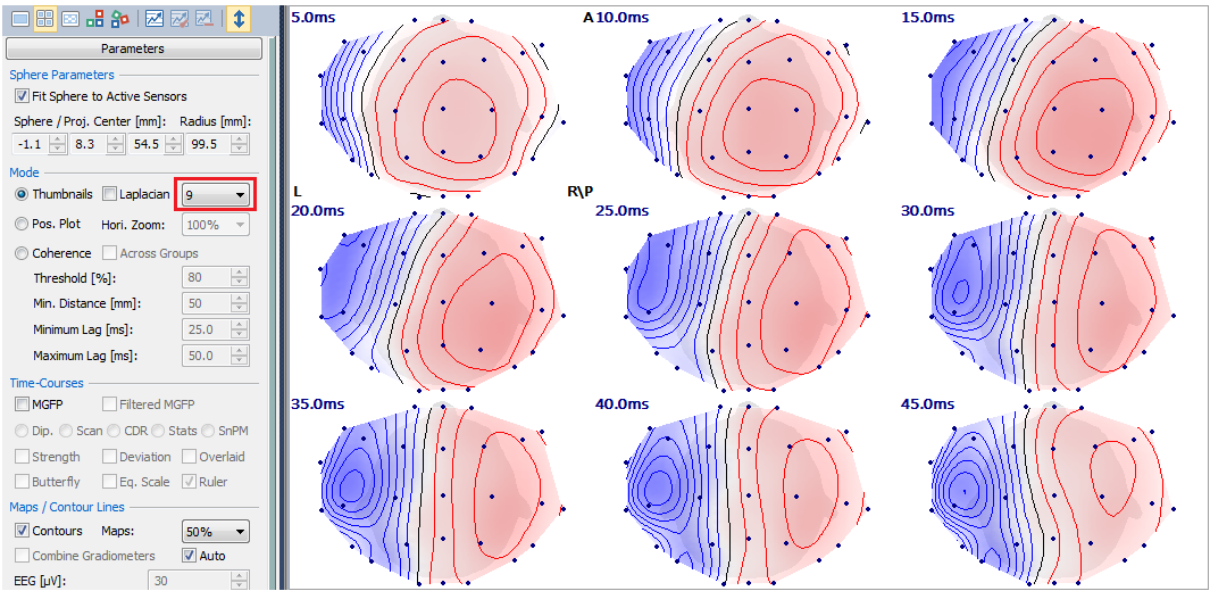
2. Position the two outer vertical cursors at **-15**ms and **170**ms (if need be, *right click* in the data display and deselect **Tracking Mode** in order to place the cursors independently). Position the middle cursor at 25 ms.



3. Click the

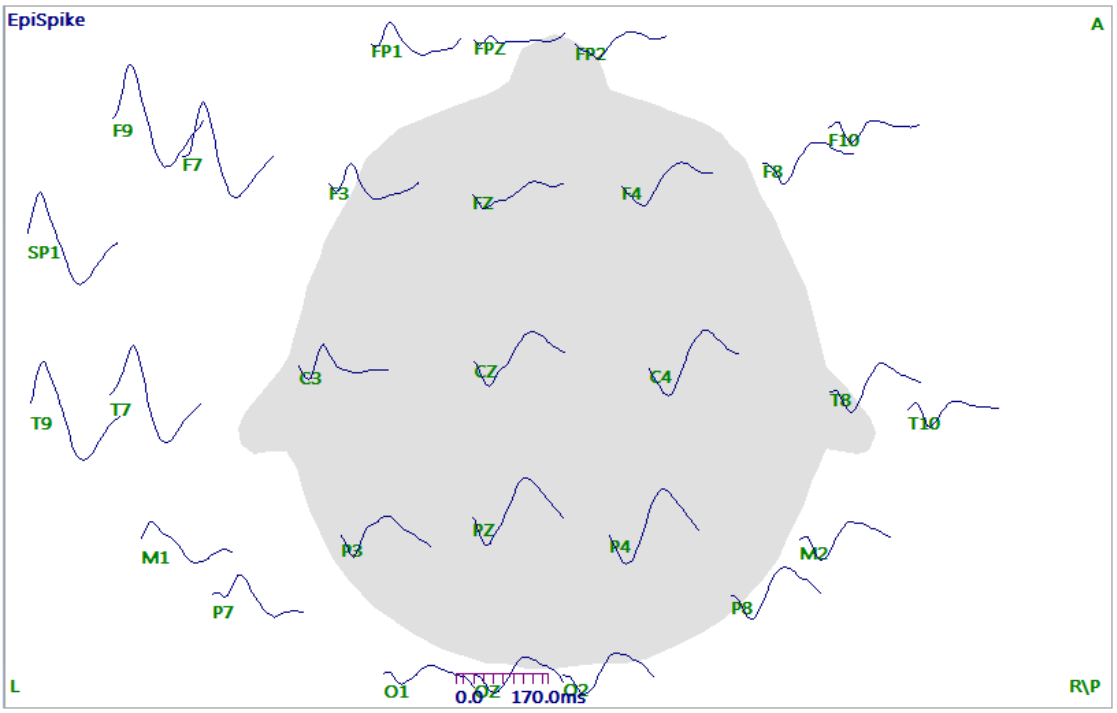
tab at the top of the Data Display window (select it if needed from the + list 

). This brings up the window shown below, as well as the **Parameters** options on the left. Set the number of maps to **9**.

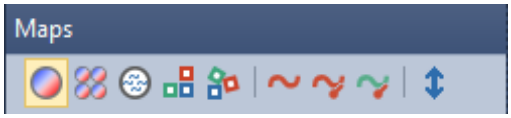


The 9 maps are those around the position of the middle cursor in the Functional Data display (set at 25 ms above). All of the maps in that range can be displayed by selecting All.

4. Select **Position Plot** (Pos. Plot) to see the data in their topographic positions (demonstration purposes only). Scale as desired using the *mouse wheel* or *up* and *down arrows* on the *keyboard*. Use the **Horizontal Zoom** field to adjust the width of the displays Hori. Zoom: 50%



Note that the there are icons on the **Maps Toolbar**

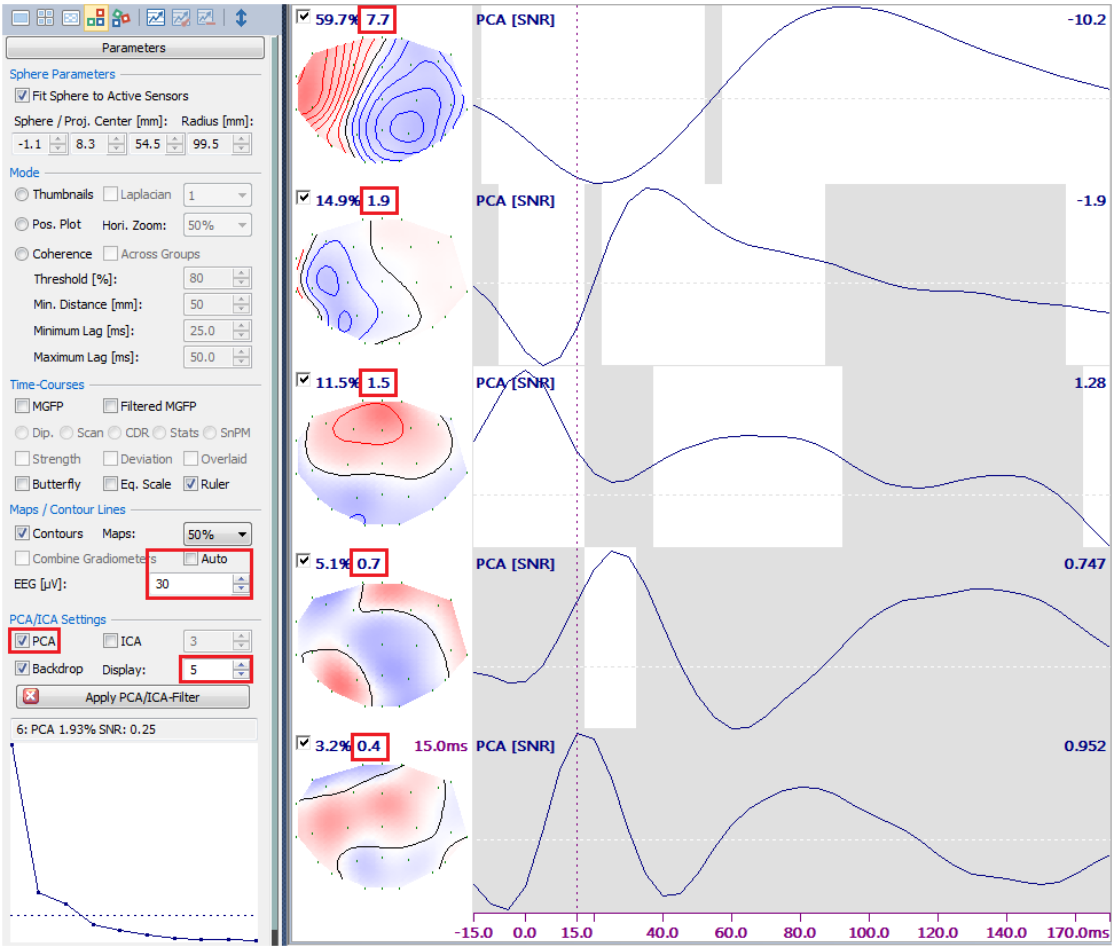


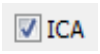
that let you select the **Contour Maps** (*Alt+C*), **Thumbnails** (*Alt+T*) and **Position Plots** (*Alt+P*) very easily.

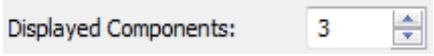
Click the **Contour Maps** icon to see a single contour map corresponding to the position of the middle cursor in the Functional Data display, then click the **Show Movie** icon on the **Standard** Toolbar (or use *Alt+M*). This will display the maps in succession (demonstration purposes only). The movie can be saved as an .avi file (*right click* and select **Save Movie As**), and replayed outside of CURRY.

5. Select PCA for the **Mode** (or *Ctrl+A*), deselect Auto (in the **Parameters** panel), and enter a scaling value of **30** 30. Increase the number of **Displayed Components** to **5** Displayed Components: 5.

The Maps display now shows the first 5 PCA components (with a fixed scale value). One purpose of PCA is to determine the number of valid components in the decomposition. As a general rule of thumb, the average SNR should be $\geq$1.0 for the component to be considered valid. The average SNR values are shown in the red boxes below. They will decrease in value across components, as shown in the "scree" graph in the Parameters panel. In this case, there are 3 valid components (where the first one is relatively much stronger than the other two: 7.7 versus 1.9 and 1.5). The gray regions are where the SNRs are $\leq$ |1.0|.

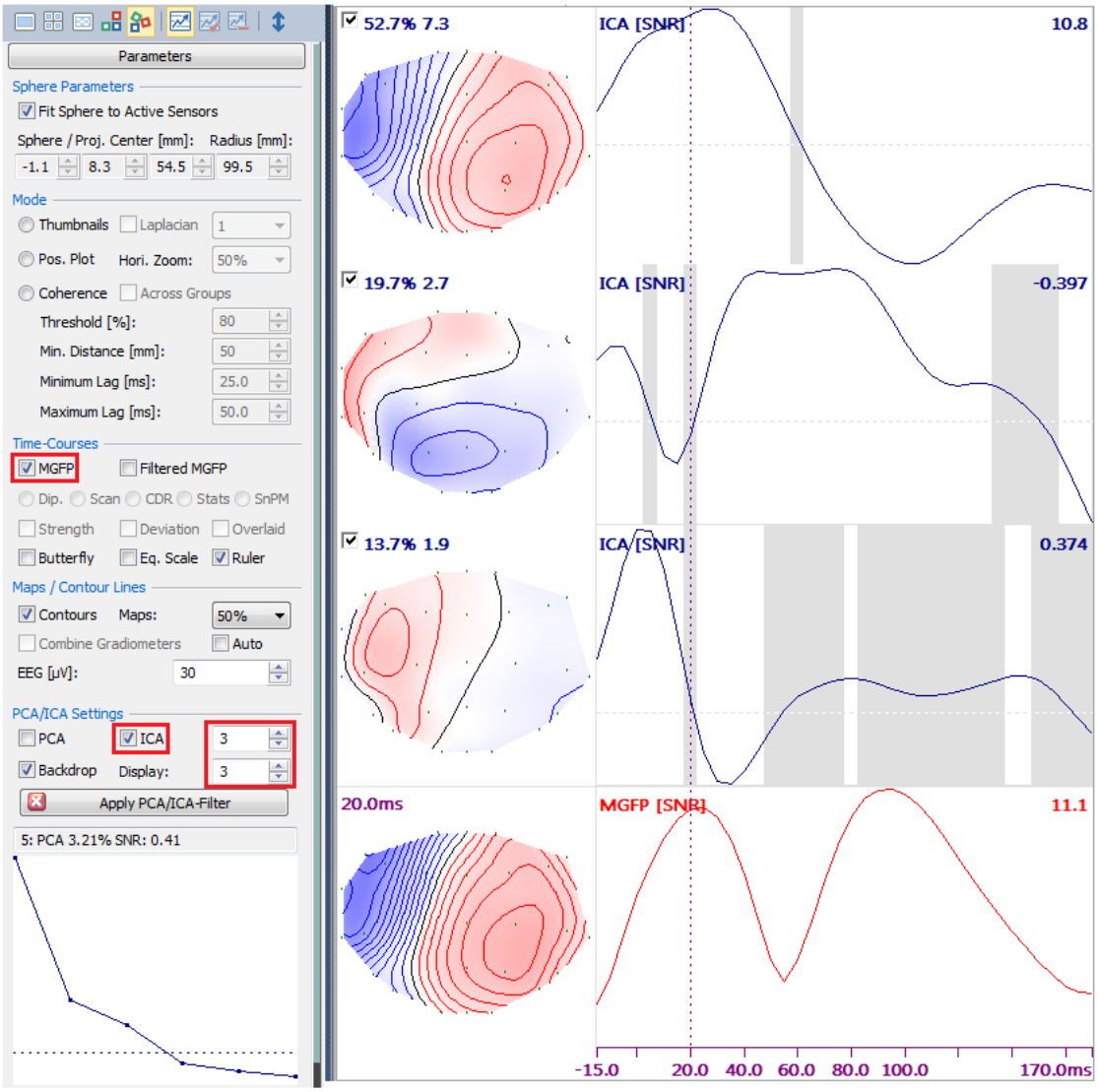


6. Having determined there are 3 components from the PCA, select 

for the **Mode**, set ICA Components to **3**, and 

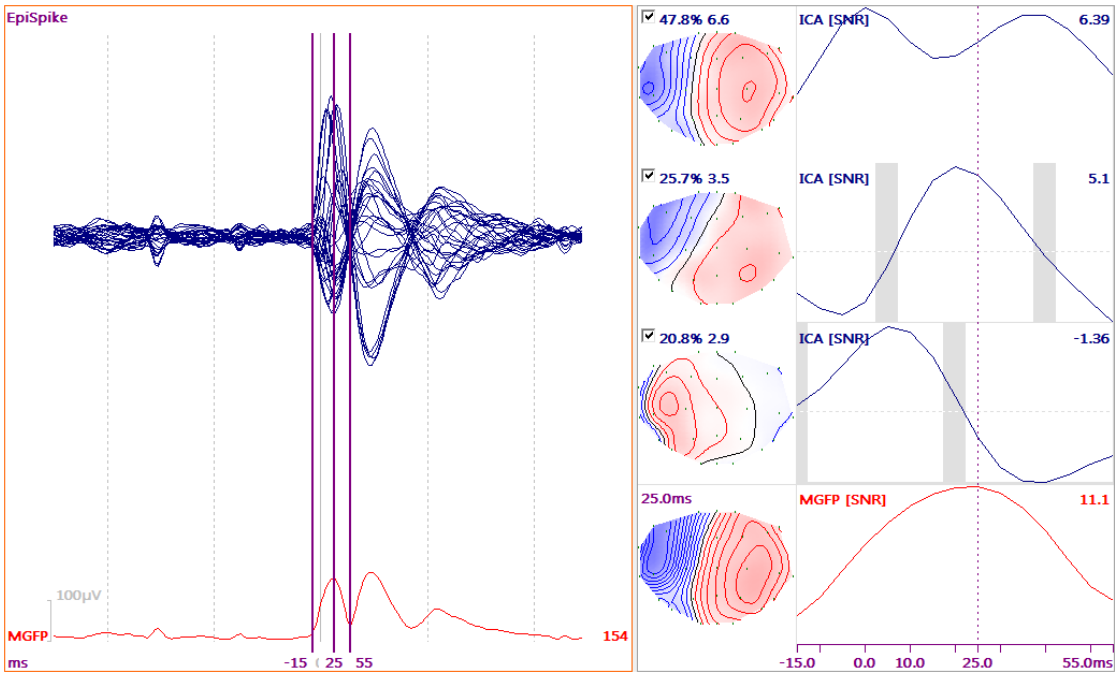
to see the 3 valid ICA components. Enable the

option. The display will appear as shown.



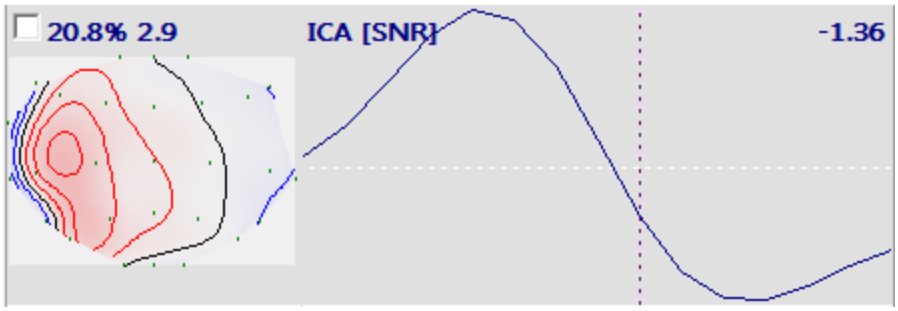
The EEG data in the Timerange from -15 ms to 170 ms are decomposed into 3 non-orthogonal, independent patterns (one would expect multiple components for a moving dipole for spikes). The distributions, explained field percentages of the components, and overall SNRs are shown to the left of each component. Position the vertical cursor at an MGFP peak to see the SNR values for each time point (the *left* and *right arrow* keys will move the cursor, or use the mouse).

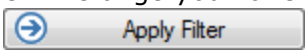
7. Select the FD, Maps display, and reposition the right vertical cursor to **55**ms. This sets the Timerange for source reconstruction to the initial MGFP peak. (The data are displayed in a **Butterfly Plot**).

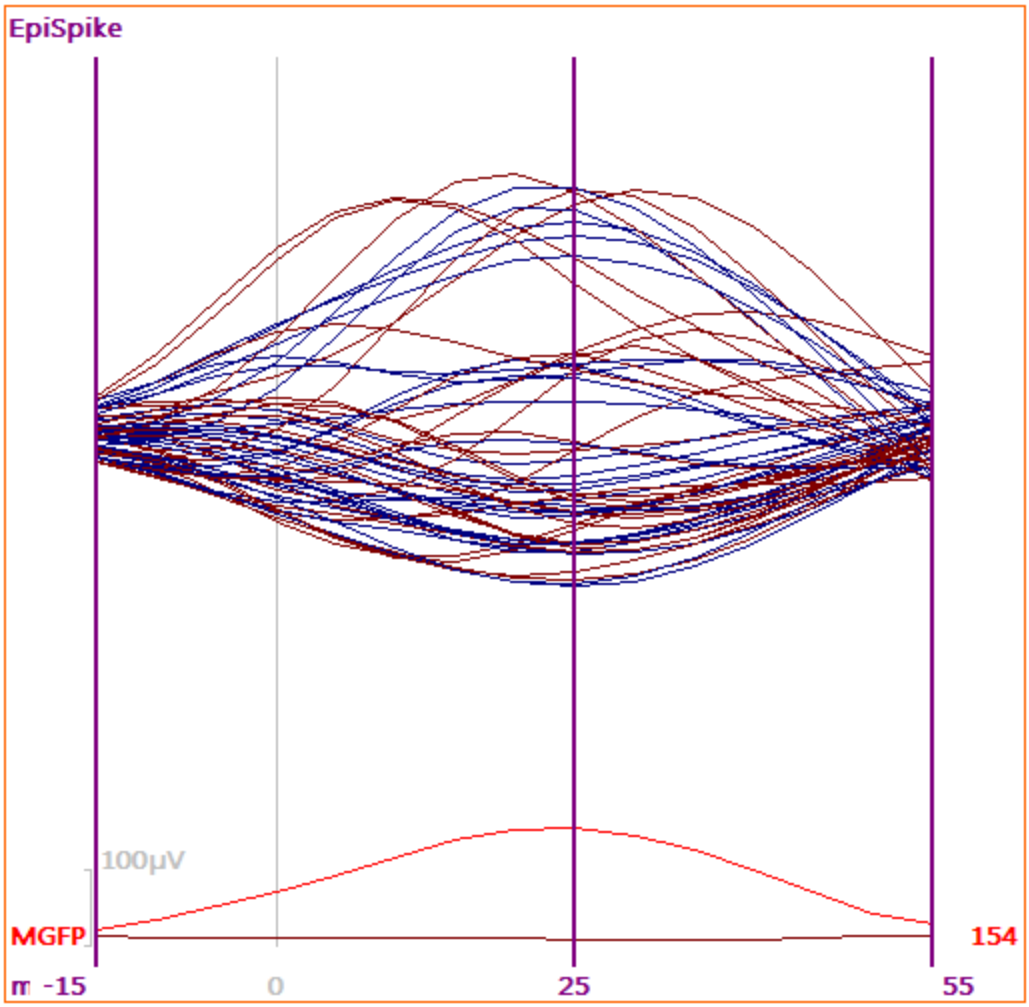


8. The recomputed ICA results over the modified Timerange are displayed.

9. In practice, you might wish to exclude one or more independent components from the source reconstruction (if one were, for example, clearly blink artifact). For demonstration purposes, *deselect* the third component (so that the check disappears and the component turns gray):



Watch the Timerange you have selected and the MGFP in the same interval as you click the  button. The additional lines that appear are the filtered waveforms (zoomed in the figure below). These are the values that would then be used in source reconstruction (rather than the original waveforms).



Click the button to remove the Filter, and reselect the third component.

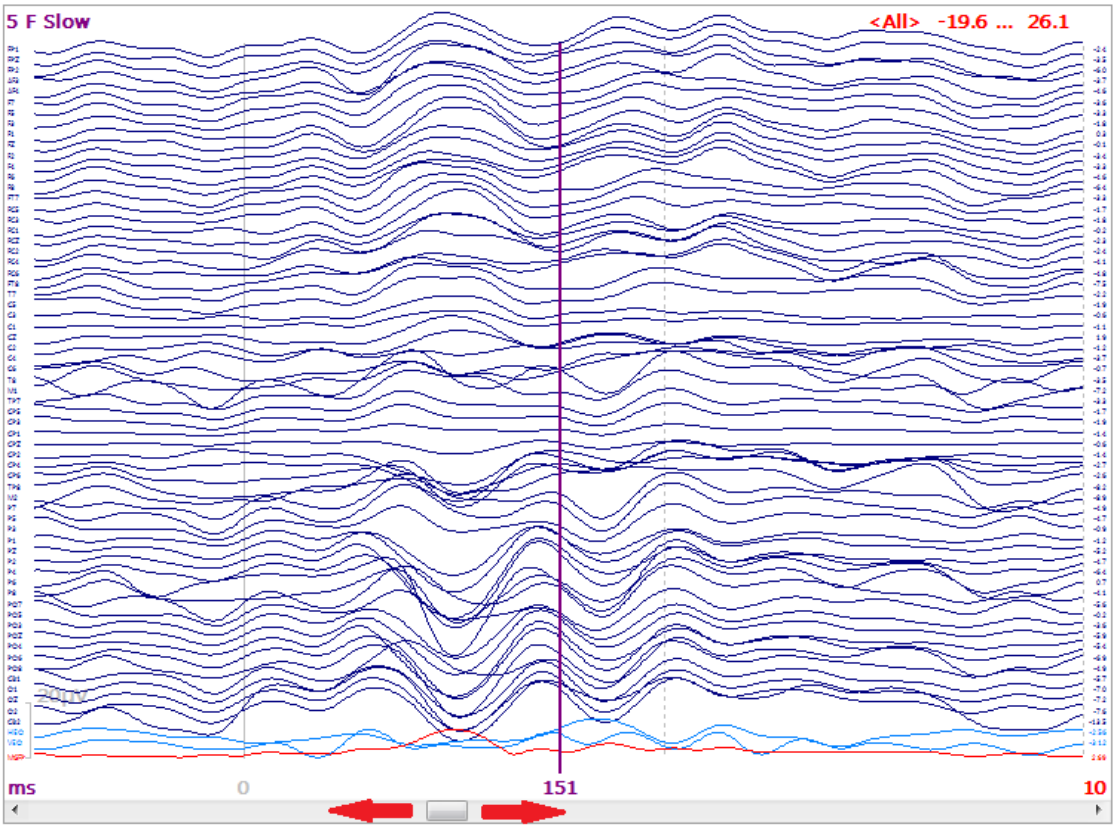
Please see also the **Simulated Data** tutorial for an example that combines PCA/ICA with source reconstruction, using simulated data.

2.4.10 Group Averaging

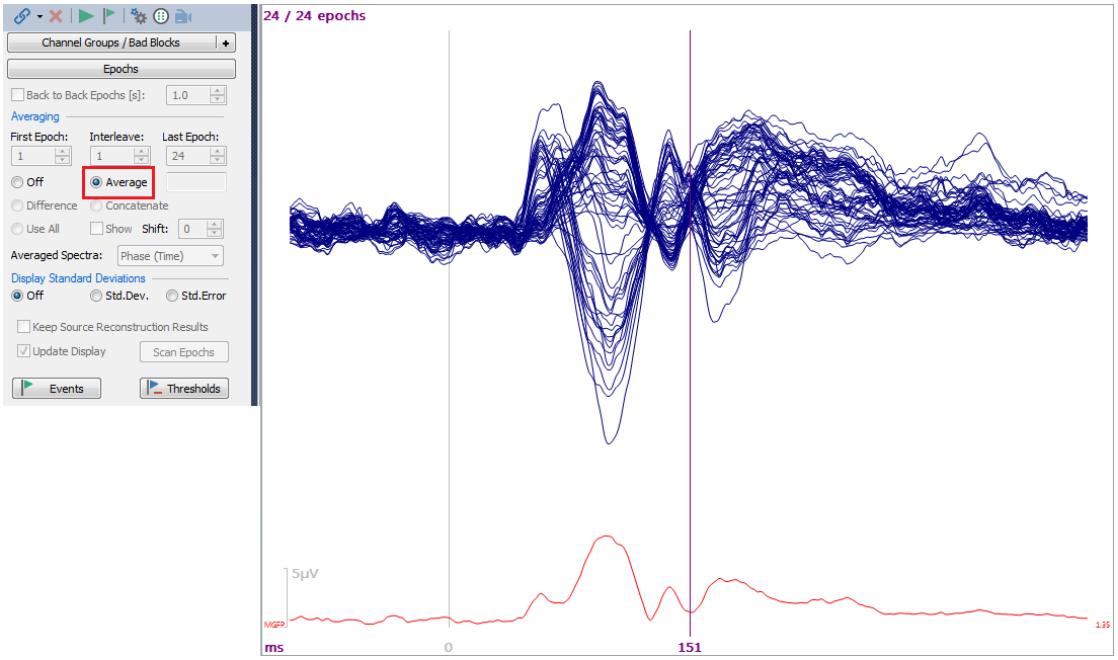
It is a simple operation to create an average of a group of averages, or the grand average. The main thing you need to know is that all files should be placed in the same folder, and the files should be compatible (same start and end times of the epoch interval, same number of points, same number of channels, same channel order, and so on). The parameter files that are created for first file are used for the remaining files.

1. For this example, there are 12 subjects - 6 male and 6 female. Each were presented stimuli in sort ISI (Fast) or long ISI (Slow) sessions. The averages for each subject/condition have been computed. (The files were created from simulated data for illustration purposes).

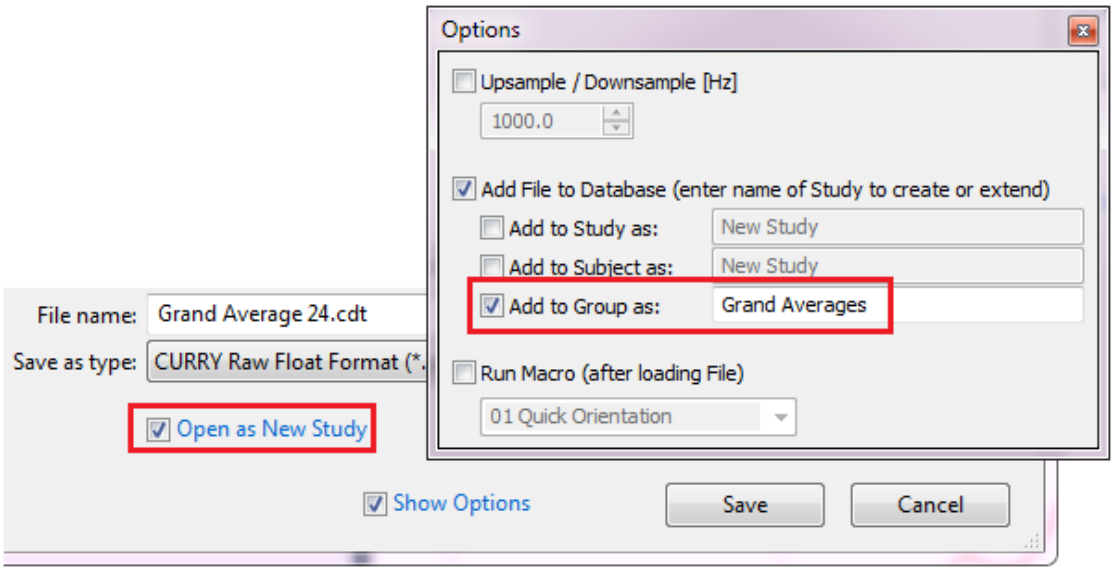
Open the Study and the averaged files will be seen as individual "epochs". Drag the sliding bar below the data display to look through the files.



If you want to average them altogether, expand the Epochs panel and select the **Average** option. 24 of 24 files were averaged to obtain the grand average for all subjects and conditions.



To save the average file, select Save Functional Data from the **Workflow**, or go to **Functional Data → Save → Save Data**. Enter a file name. In this case, we want to add the file to the Database, at the Group level, in a folder called *Grand Averages*, and we want to open that Study after saving it.



2. There are a few considerations that should be kept in mind when creating grand averages. All of the files to be averaged must have the same AD Rate, the same number of channels, and the same channel order. While this seems simple enough, it can sometimes require some preliminary planning.

For example, in the original continuous data file, if you click on a channel label to deselect it, the averages you create from that file will not include the deselected channels. If you deselect a channel(s) in one subject, you will need to deselect the same channel(s) in all subjects. Or, you can leave all channels selected until you get to the point of averaging, and deselect the channels then. When you deselect a channel on one subject's average, the same channels will be deselected in all subject averages (the averages are treated as if they were epochs from a single subject, even though each "epoch" is from a different subject).

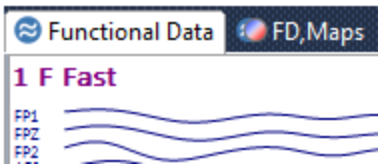
If you have a bad channel in one subject, you have the option to replace that channel with the interpolated data from surrounding channels. You can interpolate channels in the original continuous data or in the averaged data, but you cannot interpolate channels once you open the Study containing all of the averages (interpolating a channel in one subject would be applied to all subjects, regardless of whether the channels were bad or not). Perform the interpolation and save the file(s) (**Functional Data → Save → Save Data**...) before you combine the files in a grand average. 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.

3. Let's say you have multiple subject averages in a single Study, but you decide you only wish to average some of them. You have three choices.

a. You can create a new Study in the Database and drag-and-drop the selected files into that Study, then average those files as we did above.

b. You can open the Study containing all of the subjects, and deselect the subjects you want to exclude (by clicking the *spacebar* to deselect the "epochs").

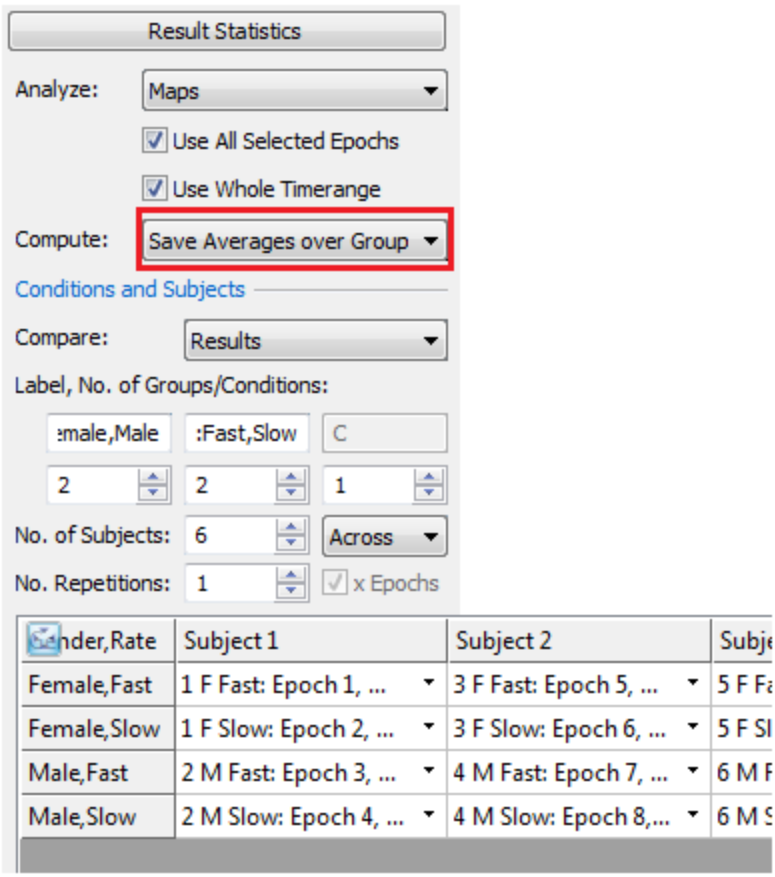
In this Study, let's say we wanted to average only the Females in the Fast condition. Start by right clicking in the data display and selecting **Deselect All Epochs**. All epochs will be tinted gray. Then step through the file and select only the Females in the Fast condition (using the *spacebar* or the **Toggle Epoch** button on the Toolbar). Use the file name as seen in the upper left corner to verify your selections. Then average and save the file as above.



Note that you have the option to apply the Threshold and Noise Statistics methods to multiple average files that you have opened. Outliers can be identified on the basis of quantifiable criteria.

c. The third option is a bit more involved. For this you need to understand how to use

, which is demonstrated in the **Statistical Comparisons - Maps** tutorial. Briefly, select the **Save Averages over Groups/Conditions** option for **Compute**. Set up the 2x2 design as shown (refer to the *Tutorials* and *User Guide* for more details). When you click the **Start** button, you will be asked for a folder/file name. The averages for all female, all male, all fast, all slow, all female fast, all female slow, all male fast, and all male slow groups will be computed automatically, which you can then load selectively into a new Study.



You therefore have considerable flexibility in the ways to create averages.

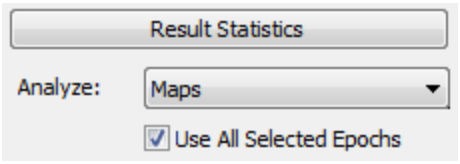
2.4.11 Statistical Comparisons - Maps

CURRY uses two non-parametric approaches for analyzing data. The first is topographic ANOVA (TANOVA) computed by randomization statistics. The second is a similar method developed by Compumedics Neuroscan, which provides statistical values for each time point and each electrode (Maps SnPM). See the *CURRY User Guide* for more details about both. Which should you use? The Topographic ANOVA method was developed elsewhere and has been in use for many years. It has a history and a familiarity. The SnPM method was developed by us, and has the advantage of being able to display statistical values (F's) for each electrodes, rather than a contribution of each electrode expressed as a percentage.

There are some fundamental points to understand in order to use the methods easily and effectively.

In the Result Statistics panel under **Results**, you will create an analysis matrix, based on the experimental groups and conditions.

The files that you are using will be seen as epochs in the Functional Data display (unless you are using dipoles or CDRs). To use statistics, it is necessary to enable the Use All Selected Epochs option. This is the same as the **Use All** option found in Epochs.



The cells in the matrix are filled with individual data files, or with source results that have been computed and "Kept" in the **Objects** list for **3D View** ("Kept" using **Source Results → Keep Results**). The order in which these appear determines the order in which the matrix cells are filled.

If you are analyzing, for example, averaged evoked responses, you will have multiple data files. The cells in the matrix can be filled automatically based on the order in which these files appear in the **Functional Data**. That order is determined by how the files are listed in the **Study** in the **Database**. Therefore, you should first determine how the data matrix should appear, how the cells should be filled, and then load the files in the order that will fill the cells correctly. The cells can be filled in either a **Columnwise** fashion (down column 1, then down column 2, and so on), or in a **Rowwise** fashion (across row 1, then across row 2, and so on).

If you are analyzing dipole results or CDR results, the cells in the matrix are filled from the **Kept Results** that are seen in the **Objects** list for **3D View**. The cells are filled in the order of the **Kept Results**, therefore, you should create the **Kept Results** in an order that will result in the cells being filled correctly.

Having said that, it is also possible to 1) reorder (drag and drop) the files in the **Study** to place them in a desired order, and 2) select the files/results manually to fill the cells in the matrix. The important thing is to ensure that the results in the cells are in the correct order for the analysis you wish to perform.

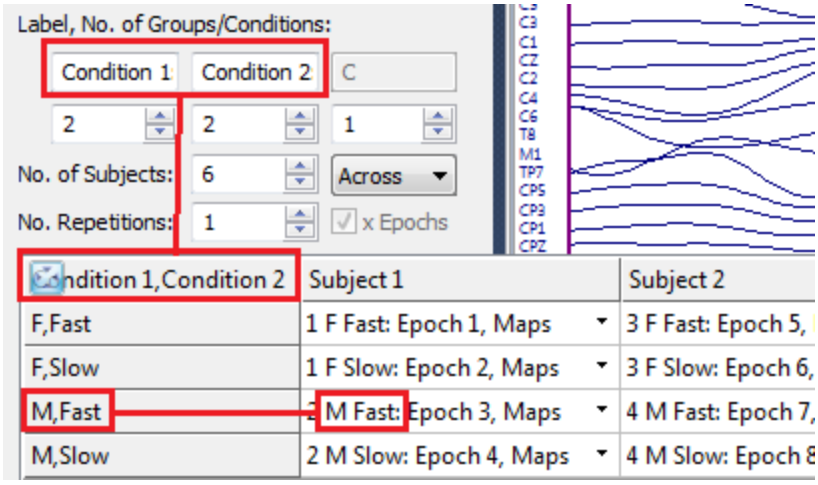
Example
In the following example, we have created files to illustrate a basic 2x2 design. There are two different experimental groups (female and male, F and M), and two conditions (stimuli presented rapidly and slowly, Fast and Slow). There are 6 subjects per group. The VEP P100 component is the feature of interest.

If you are not familiar with how the matrix is set up, you should first examine it in detail (Result Statistics, under **Results**).

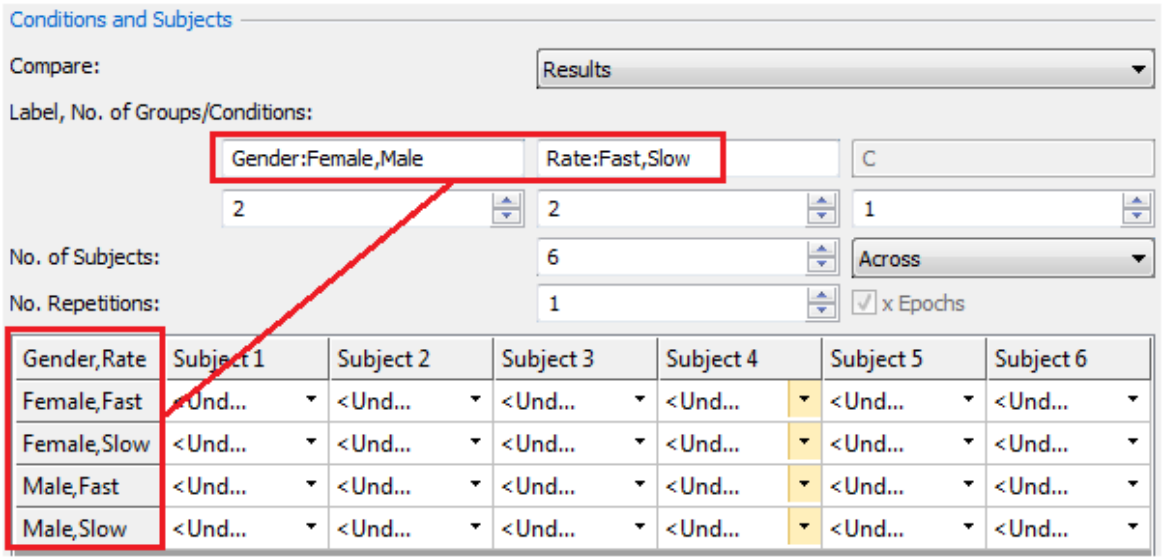
Groups and Conditions are treated the same way mathematically, and therefore they are interchangeable in CURRY. That is why they are referred to initially as A, B, and C, where A, B, and C can be Groups or Conditions.

CURRY will attempt to create Labels for the Conditions automatically, based on the file name. You may also create the Labels manually. In the automatic instance below, the beginning of the file names are subject number, gender (F or M), and rate (Fast or Slow). CURRY uses the information to label the fields as F,Fast,

F,Slow, etc. This will be illustrated shortly. Condition 1 and Condition 2 are entered automatically.

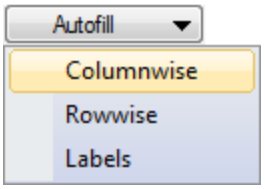


If you need or prefer to enter the labels manually, you need to enter the information using the following format. For the first group, Gender, enter "Gender:Female,Male". For the Condition, enter "Rate:Fast,Slow". What you enter will be transferred to the Labels for the cells.



You probably recognize that this is a repeated measures design, and therefore you might be tempted to set Repetitions to 2. Repetitions in this case does not mean repeated measures in an experimental sense, but rather to designate the specific instance in which you have multiple recordings from the same subjects that you want to combine in order to, for example, increase the SNRs. Repeated measure analyses are dealt with in a different way, as described shortly.

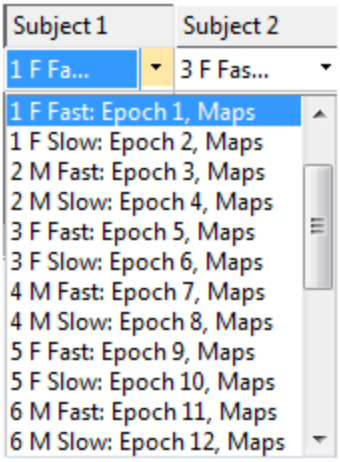
The next step is to decide whether to fill the cells by rows or by columns. **Autofill** provides the options.



For this example, we will use the **Columnwise** option, dictated by the order the files were listed in the Database, which is Subject 1, Female, Fast condition; Subject 1, Female, Slow condition; Subject 2, Male Fast condition, Subject 2, Male Slow condition, and so on. Knowing how the matrix is filled may affect how you list the subjects (files) in the Study. Having a file naming scheme, as shown below, can be very helpful.

hder,Rate	Subject 1	Subject 2	Subject 3	Subject 4	Subject 5	Subject 6
Female,Fast	1 F Fast: Epoch 1, ...	3 F Fast: Epoch 5, ...	5 F Fast: Epoch 9, ...	7 F Fast: Epoch 13, ...	9 F Fast: Epoch 17, ...	11 F Fast: Epoch 21...
Female,Slow	1 F Slow: Epoch 2, ...	3 F Slow: Epoch 6, ...	5 F Slow: Epoch 10,...	7 F Slow: Epoch 14,...	9 F Slow: Epoch 18,...	11 F Slow: Epoch 2...
Male,Fast	2 M Fast: Epoch 3, ...	4 M Fast: Epoch 7, ...	6 M Fast: Epoch 11,...	8 M Fast: Epoch 15,...	10 M Fast: Epoch 1...	12 M Fast: Epoch 2...
Male,Slow	2 M Slow: Epoch 4, ...	4 M Slow: Epoch 8,...	6 M Slow: Epoch 1...	8 M Slow: Epoch 1...	10 M Slow: Epoch ...	12 M Slow: Epoch ...

You can always select the files manually for each cell from the drop-down list. If you have bad or missing data for one or more cells, select the **<Skip>** option.



With that brief introduction to Result Statistics, we will proceed with the steps that are needed.

1. In this example, the study has been created for you, in the *Files for Statistics* study. This is manufactured data for illustration purposes. We will first use the **Topographic ANOVA** method, and then we will show the same results with the **Maps SnPM** method.

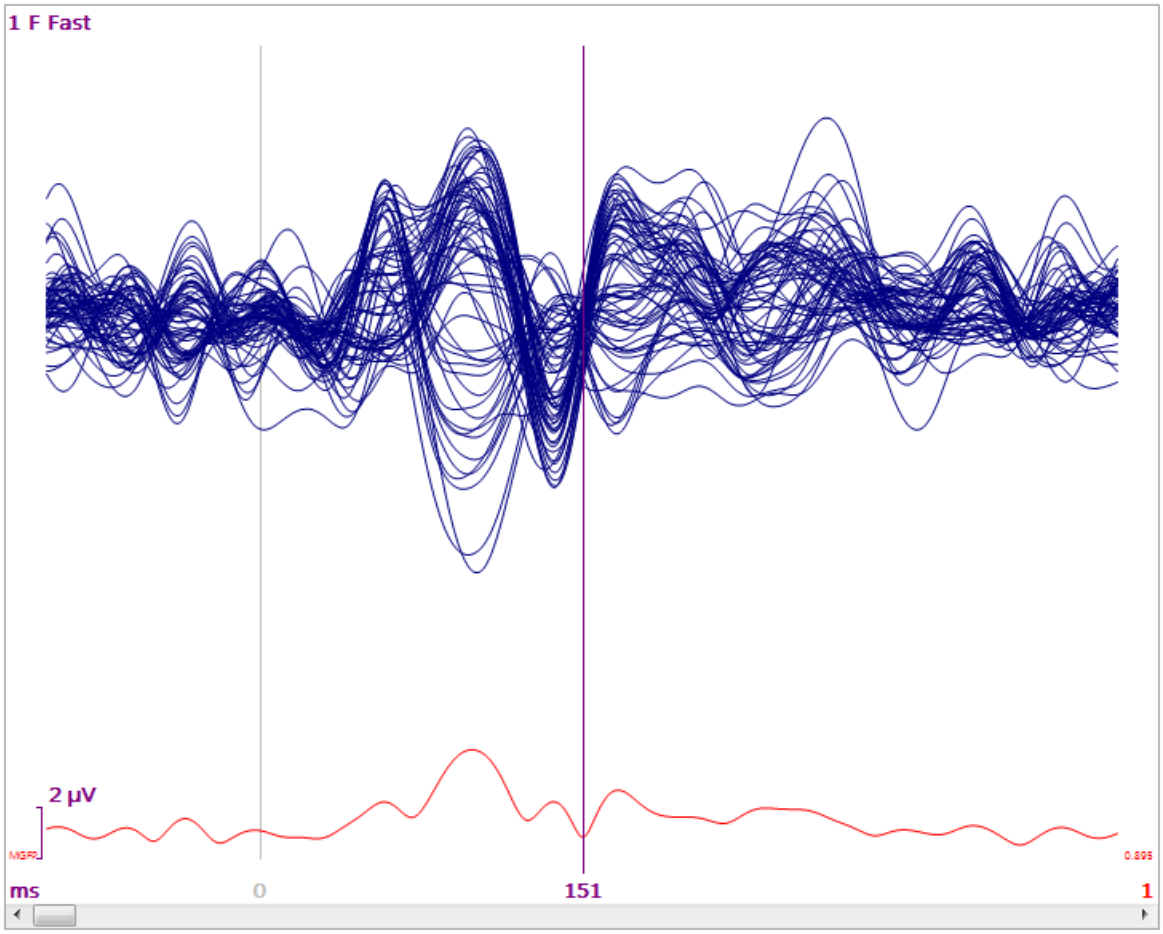
2. When creating your own Database, you can load the data files one at a time, in the desired order, or you can use *Ctrl+left mouse* to highlight the files and add them all at once (after selecting **Insert Functional Data File**, through any of the ways to access the Open File dialog).

If, after loading the data files, you find that one or more are in an incorrect position, you can simply drag the file to the desired location (you can also drag files across Studies).

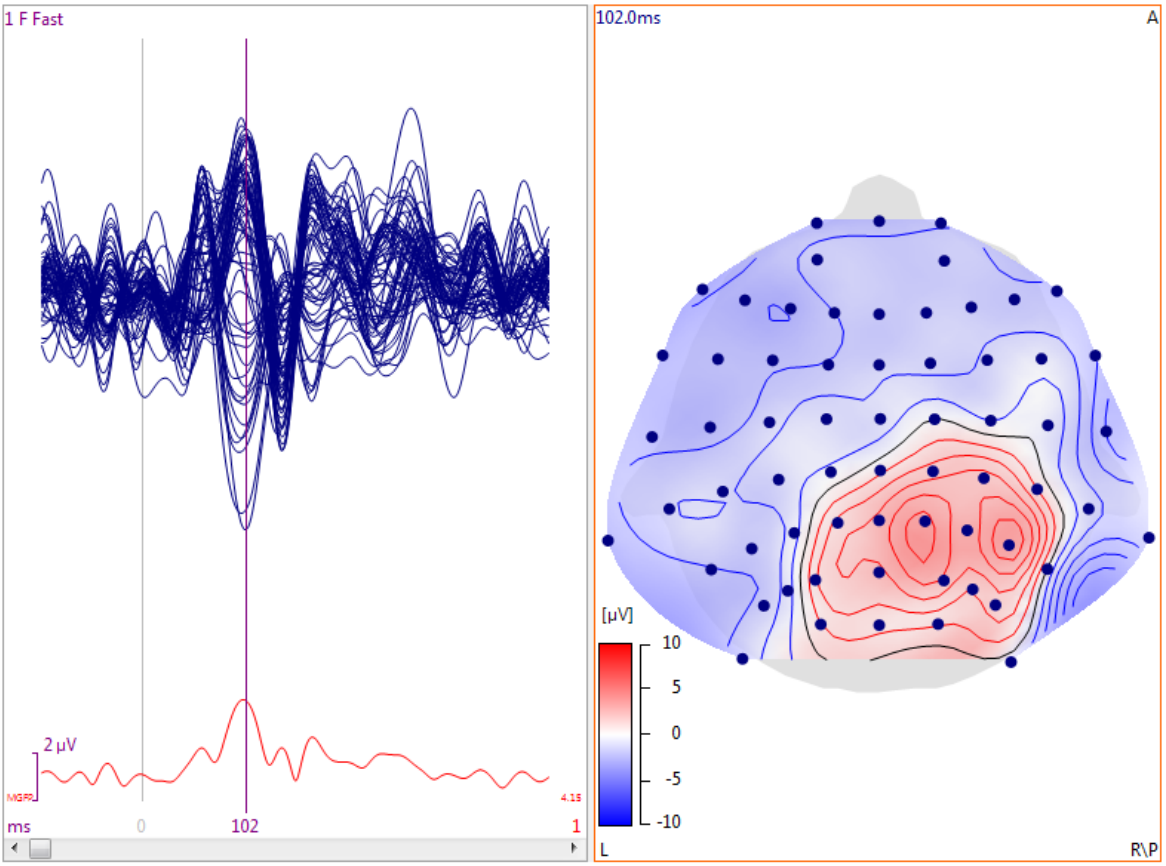
If these files had not been loaded before, the **Functional Data Import Wizard** would appear for the first file. Verify that the information is correct and go to the next screen, selecting Label Matching, if needed (or make whatever changes are needed for

the file). Then click **Finish**. The parameter file (.dpa) that is created for the first file will be applied for all of the files in the study, using the settings you made for the first one (but not actually created for all files). Internal consistency checks are made to be sure the files are compatible, and error messages will relate any significant inconsistencies (different numbers of sensors may be accommodated). If the files are all sufficiently similar, you would only need to go through the Wizard just the one time with the first file. If you remove the first file from the Study, you will see the Wizard again when you attempt to reopen the Study, and the new first file will be used for all remaining files. You may highlight any file in the Database list, and then click the **Functional Data Wizard** icon on the Toolbar to set and save the parameter files for that file.

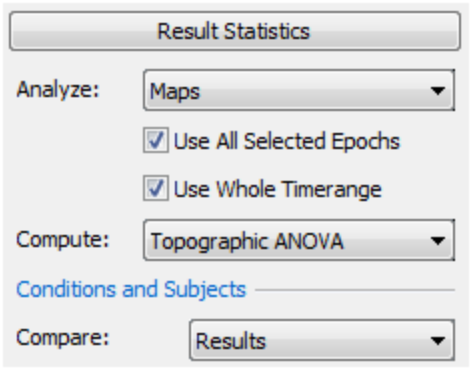
3. Open the Study and you will see the first data file in the Functional Data display. Drag the sliding bar at the bottom to see the individual data files (**Butterfly Plot** selected), or use the Toolbar icons .

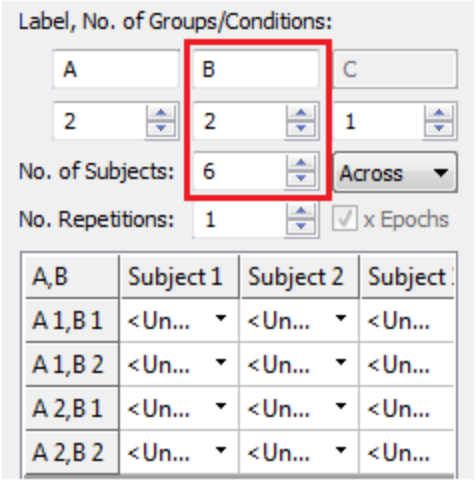


4. It is a good idea to check the **Maps** display FD, Maps to see if there are any unwanted channels. In these files, the HEO and VEO channels were designated as "Other" channels in the import Wizard. They are therefore excluded automatically from the Maps, and the maps look correct (VEP P100 component).

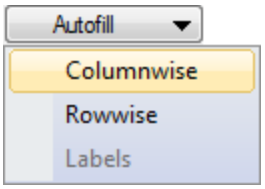


5. Click the Epoch Statistics line in the **Workflow**, or expand the Result Statistics panel, under **Results**. The parameters should be entered as shown for **Analyze**, **Compute**, and **Compare**. Next, we will illustrate how to let CURRY do the Labeling of the Conditions automatically. Increase the number of the second condition to 2, and the number of Subjects to 6 (per subgroup).

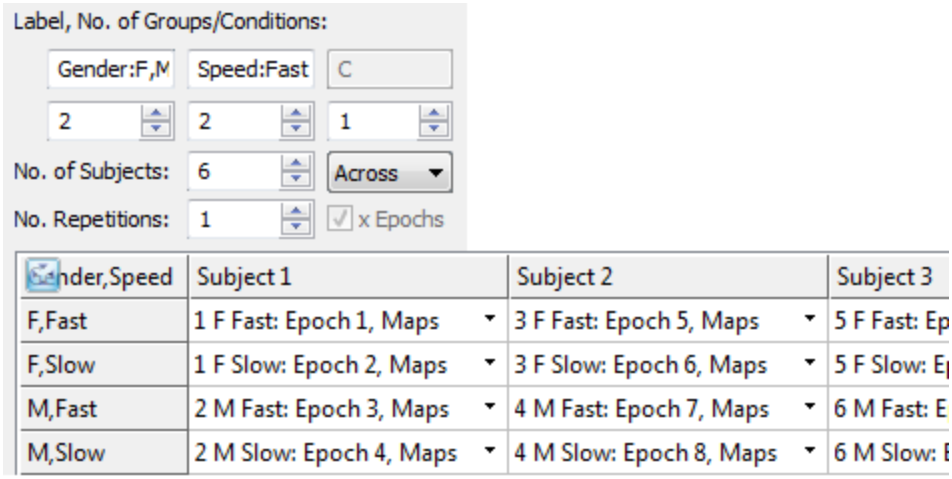




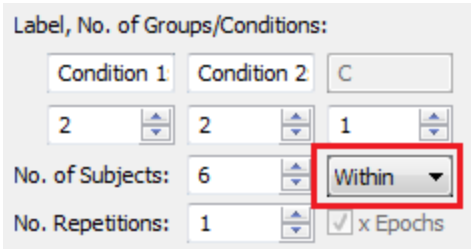
Under **Autofill**, select **Columnwise**.



The Labels have been added, and the cells in the matrix have been filled. If you look down the columns and then across columns, you will see the same order in which the files appear in the Database (thus, Columnwise).

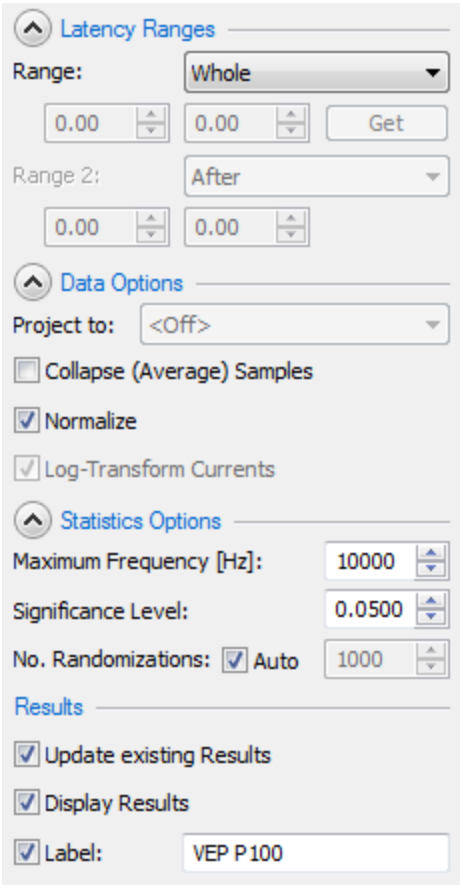


Select **Within** since we have Fast and Slow conditions for each subject (repeated measures).



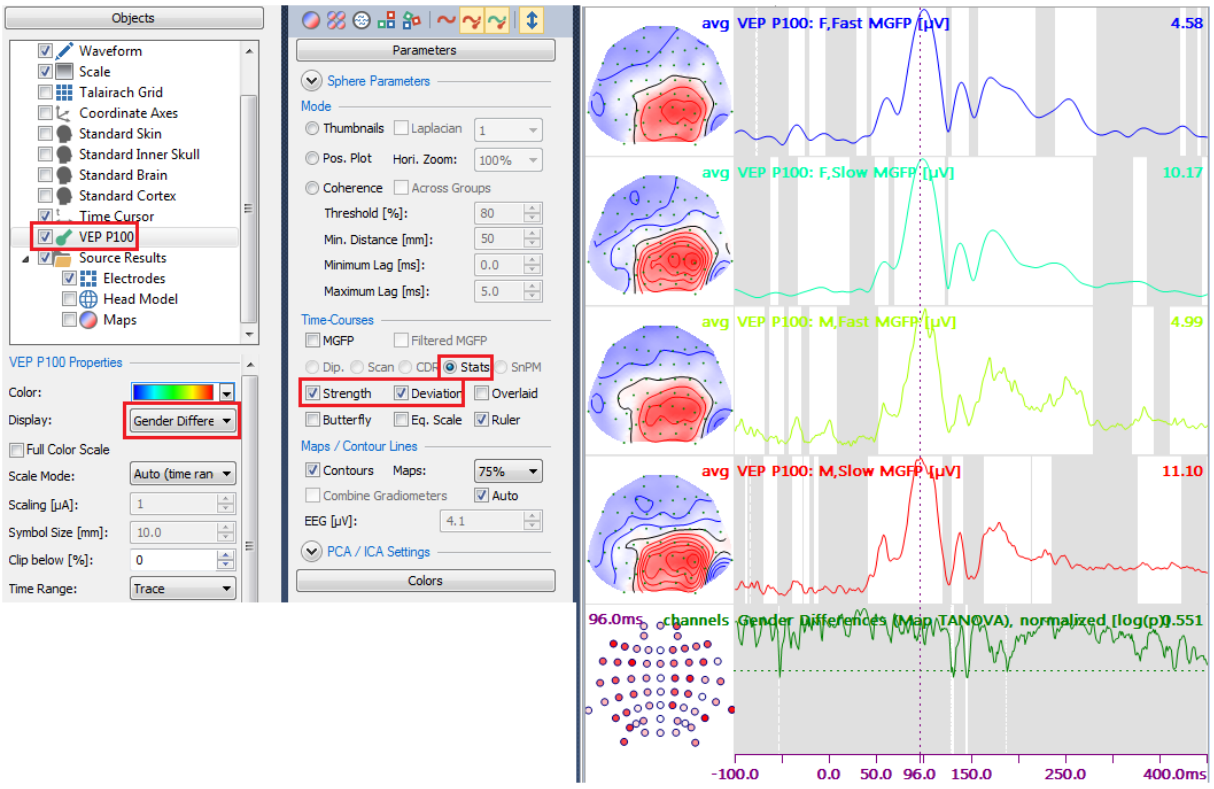
If after reviewing the file averages you find that the data for a particular file should be excluded, select **<Skip>** for that cell. If you have missing data for some cells, you will need to either include "dummy" epochs for those epochs, so that you can still use Autofill, or else select the files you want to use from the drop-down lists. In either case, you will need to use **<Skip>** to fill in the missing cells.

We will not be using the **Advanced** options, but you should note that this is where you select the **Significance Level** that you wish to use (p=0.05 is the default), and the **Number of Randomizations** (leave it at **Auto**; refer to the *CURRY 8 User Guide* for details). Leave **Normalize** enabled. Leave **Update Existing Results** enabled. This will overwrite any existing results that may be present. Enabling **Display Results** will automatically select the displays and parameters we will need to view the results. The only change here is to enter a Label, such as "VEP P100". Labeling the results will avoid confusion later on when you are looking at multiple results.

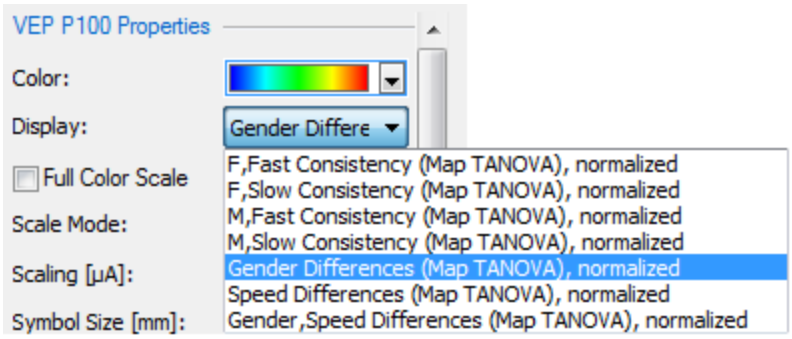


7. When all is ready, click the Start button. If you had not already filled the cells, clicking the Start button will fill them. Generally it is recommended that you fill the cells first to be sure they contain the correct data files. After clicking Start, you will not see anything happen, aside from the progress indicator on the Status Bar.

8. The results are seen in the in the **Maps** display, with selections made from the **Objects** list for **3D View** (if we had not selected **Display Results** in the previous step, we would need to make these selections manually). In the **Objects** list, there is the **Label** (*VEP P100*) for the results. Clicking on it displays its Properties. The main one of interest here is **Display**. In the **Maps Parameters**, the **Stats**, **Strength**, and **Deviation** options are selected automatically.



Note the options in the drop-down list for **Display**.

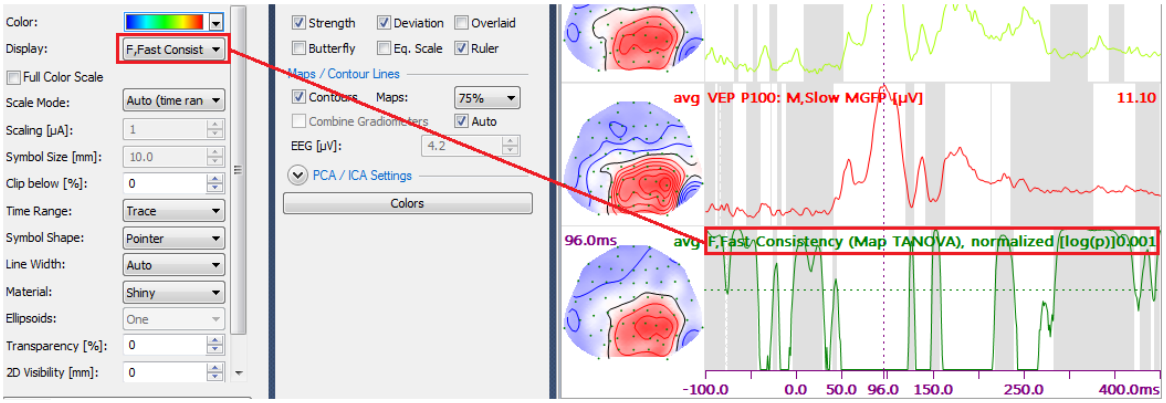


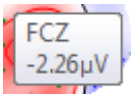
The statistics used in CURRY 8 compute a number of things automatically. First, there is a **Consistency** test that is performed for each group (similar to a homogeneity of variance test). The results should be significant throughout the epoch that was analyzed. This means, literally, that there is significant consistency across subjects in the group. Absence of significant differences, especially in the Timerange(s) of interest, indicates that there are inconsistencies across subjects in that group. Check for residual artifact, or to see if there are a few subjects with questionable data (where you can justify their exclusion). It is unlikely that you will obtain significant differences between groups if one or more groups do not have significant consistency. Should that happen, the between groups differences could be considered questionable.

Next are the **Differences** tests, where **Gender Differences (Map TANOVA)** tests the main effects for Group (Gender in this case), **Speed Differences (Map TANOVA)**

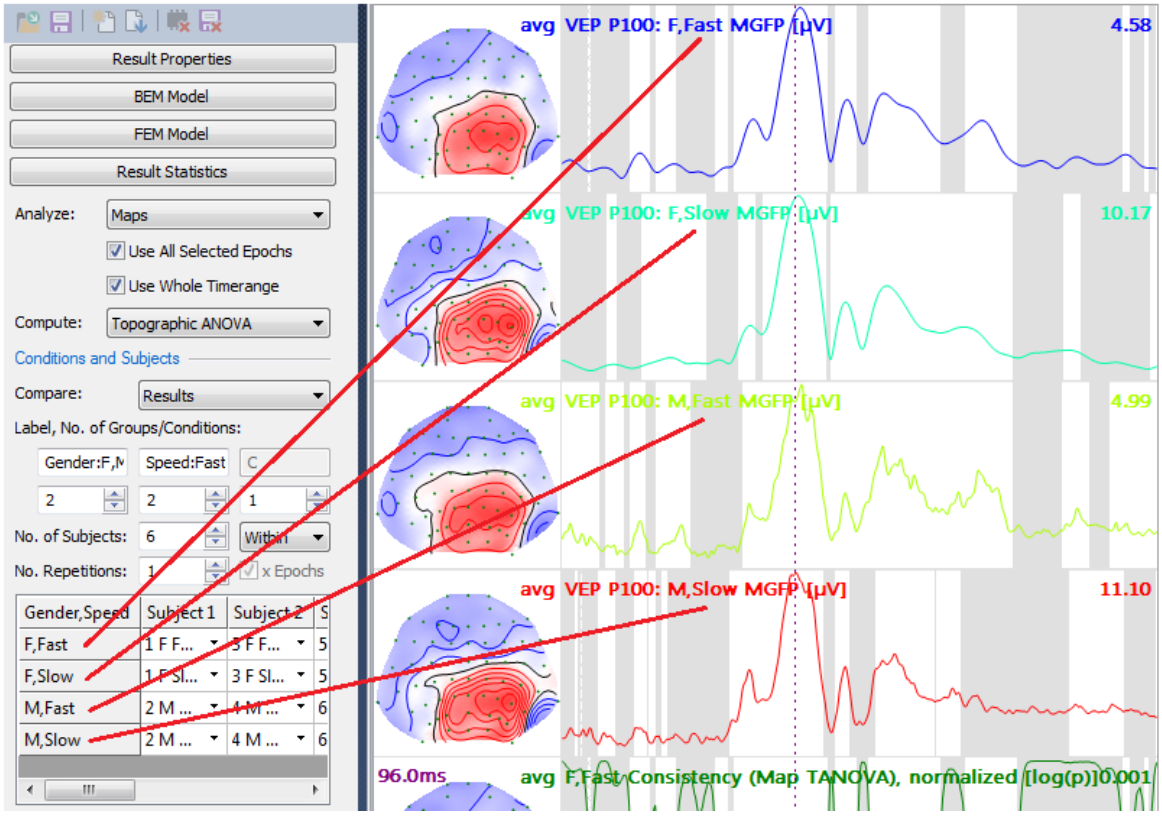
tests the main effects for Condition (Speed in this case), and **Gender,Speed Differences (Map TANOVA)** is the interaction of **Gender x Speed**.

The option you select for **Display** determines what is displayed in the lowermost field in the **Maps** display.

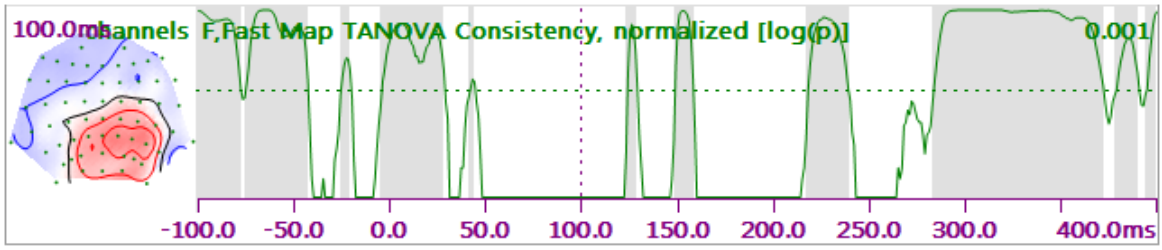


Looking at the **Maps** display, the four waveforms are the MGFPs for each group, in the order they were created in the analysis matrix.
The 2D Maps show the distribution of the averaged data. A Tooltip displays the voltage for each electrode 

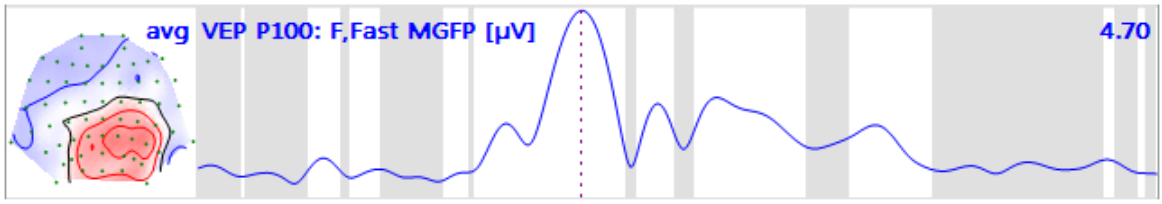
. The white background indicates the regions where the consistency was significantly consistent, and the gray regions show where the consistency was not significant.



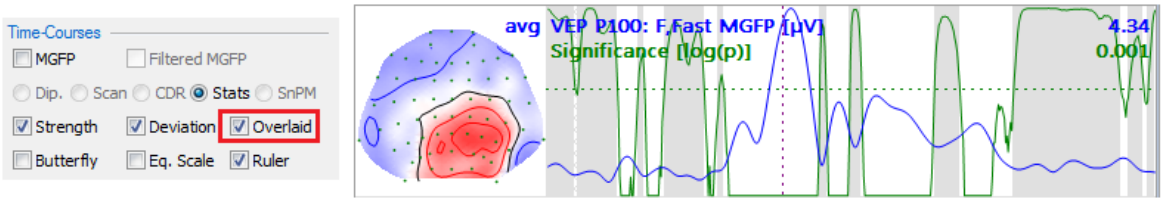
9. Lastly, examine the **Deviations** display (the lowermost one). These are the **p-Values**. The dotted line near the middle is the 0.05 level; values below that line are significant at the 0.05 level. The white regions are where the p-values are less than 0.05. This is the Consistency analysis for the first group. If the values are predominantly significant, especially in the Timerange of interest, as they are in this case where we are focusing on the P100 component, then we conclude that there is sufficient consistency across the subjects to continue. Had there not been consistency, we would try first to clean the data better, or look for outliers in the group that had bad data - some measure that would reduce the error variance.



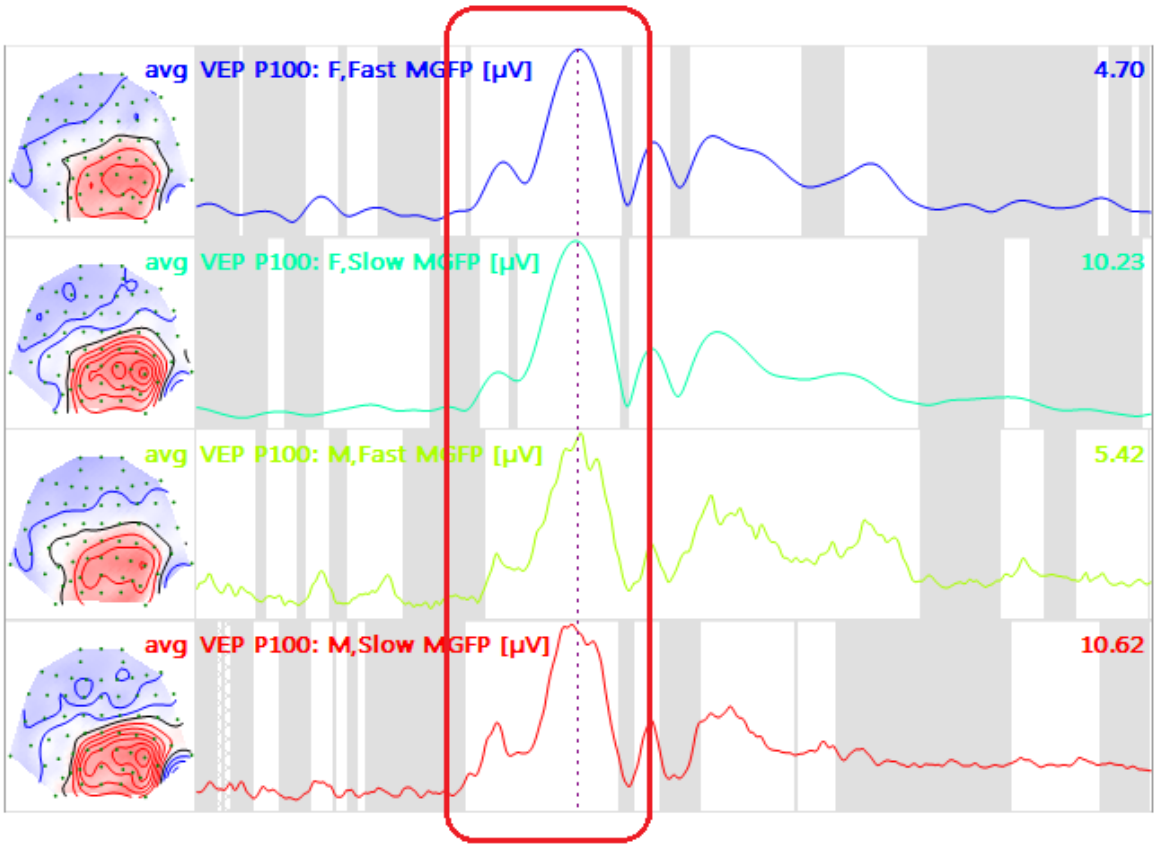
If you look at the sections that were *not* significant, in grey, you can see these generally align with lower MGFP values (see in the second row in the figure above).



If you enable the **Overlaid** option, in the **Maps Parameters** panel, you will see the p values superimposed on the MGFP values.

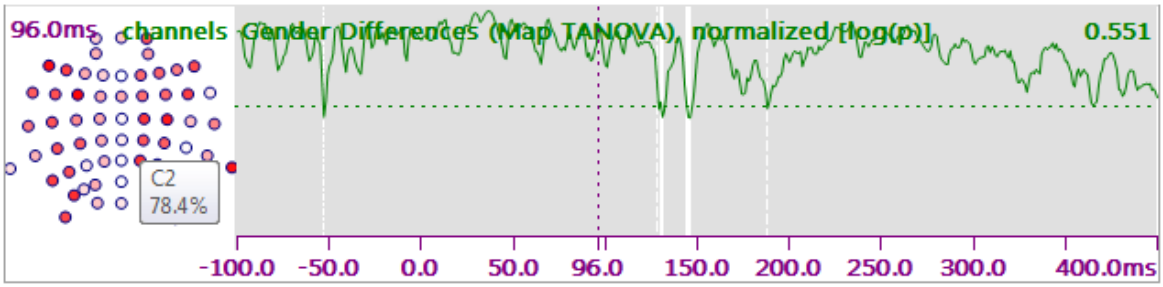


At a glance, you can see where the inconsistent segments were across all groups. In the Timerange we care about - that encompassing the P100 component - there is significant consistency in all groups.

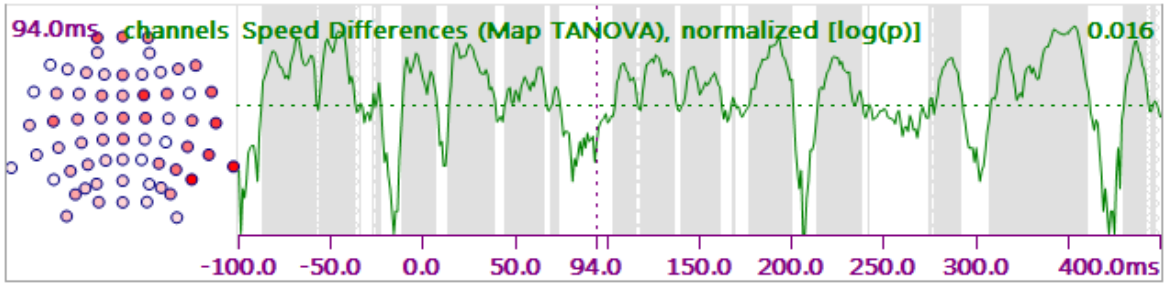


If we select **Gender Differences (Map TANOVA)** - the main effect for gender - we see there are some sporadic significant differences (the white intervals), although none in the region we are interested in. Here it is important to note that *the 2D map is not a significance probability map* - these are not p-values that are being displayed

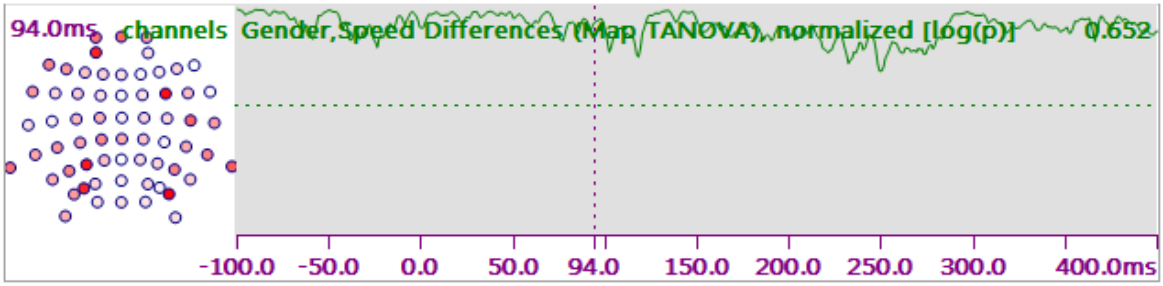
(they are "unitless" values from the SVD, displayed as percentages, where the site with 100% best represents the differences). I.e., you cannot look at the map and conclude that the colored electrodes are the regions where the *significant* differences occurred. The statistical results are computed across all sensors (electrodes). While there are composite differences, you cannot say anything about individual channels, other than the highlighted regions of the maps indicate where the significant effects may be best represented (without putting p-values on them). If you use the **Maps SnPM** method, you will see F values here instead.



If we select **Speed Differences (Map TANOVA)** - the main effect for presentation rate - we see there are some significant differences, including the span of interest (P100).



Lastly, the interaction between group and condition shows no significant differences.



The numerical results are seen in the **Output** display (shown in part below). The consistency results for the first group are shown. There were 260 samples below the 0.05 level, and there was 0 probability of this being random (24 would be expected due to chance randomization). Next comes a summary of where the differences were found.

VEP P100 Map TANOVA Consistency, normalized: testing if the total number of significant samples and the length of contiguous significant segments are significant...

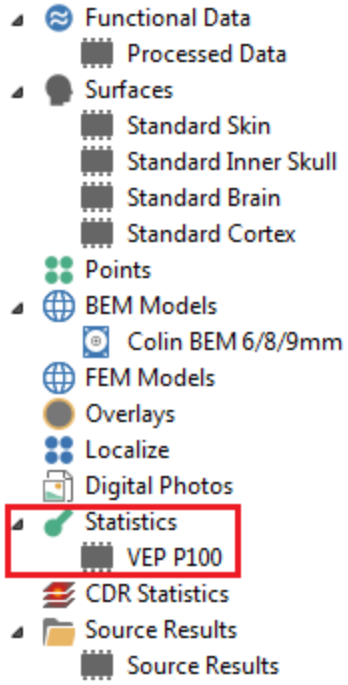
F,Fast: 260 samples with p < 0.05; this number of samples is significant (with p=0); 24 samples with p < 0.05 should be expected due to randomization
F,Fast: contiguous segment with p < 0.05 from 45.0 to 123.0ms (79 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from 159.0 to 217.0ms (59 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from 240.0 to 283.0ms (44 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from 129.0 to 148.0ms (20 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from -42.0 to -26.0ms (17 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from -20.0 to -5.0ms (16 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from 29.0 to 41.0ms (13 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from 373.0 to 378.0ms (6 samples); this segment length is significant (with p=0)
F,Fast: contiguous segment with p < 0.05 from 391.0 to 394.0ms (4 samples); this segment length is significant (with p=4.16e-005)
F,Fast: contiguous segment with p < 0.05 from -77.0 to -76.0ms (2 samples); this segment length is significant (with p=0.0497)
F,Fast: contiguous segments with p < 0.05 of 1 sample (1.0ms) are to be expected; this segment length is not significant (with p=1)

Further on in the results are the group differences for Gender. There were 5 samples below 0.05, and that number was not significant. A summary of the differences then follows.

VEP P100 Map TANOVA Differences, normalized: testing if the total number of significant samples and the length of contiguous significant segments are significant...

Gender: 5 samples with p < 0.05; this number of samples is not significant (with p=1); 23 samples with p < 0.05 should be expected due to randomization
Gender: contiguous segments with p < 0.05 of 2 samples and less (2.0ms) are to be expected; this segment length is not significant (with p=0.0522)

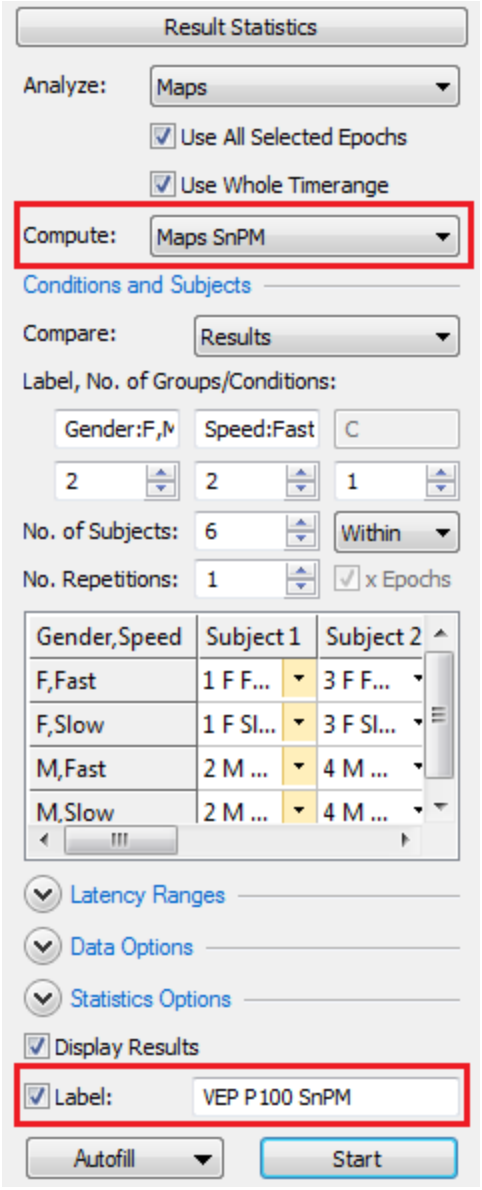
10. If you want to save the results, expand the Results panel. and see the results under **Statistics**. The symbol indicates that the results are loaded, but have not been saved. To save them, *right click* on VEP P100 and select **Save As**. In the dialog, select a folder and enter a file name (.std extension). You will then see that the results have been saved VEP P100 (with the addition of the hard drive symbol).



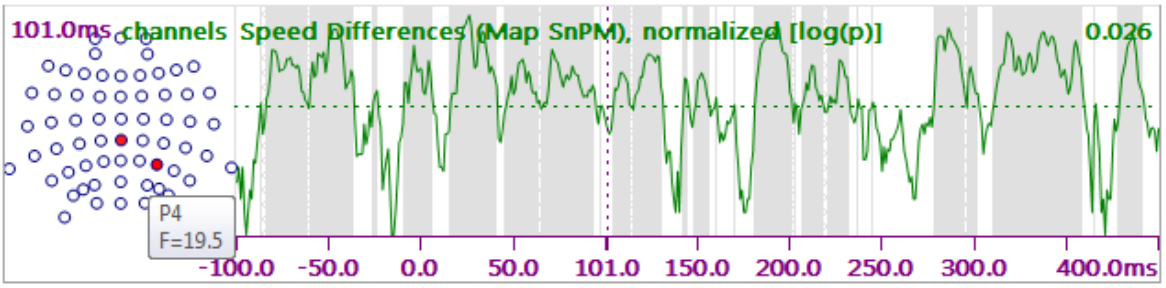
The next time you wish to see the results, open the Study and set the Timerange in Functional Data as you had it when the results were saved (this just makes it easier). Expand the Results panel. *Right click* on Statistics and select **Load From**

to select the results file. Select the Maps display and enable the desired options. Display also the 3D View **Objects** list to access the **Display Properties**.

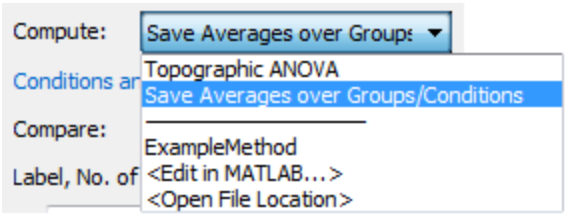
11. Now we will perform the same analyses using the **SnPM** method. Go to **Results Statistics** and set **Compute** to **Maps SnPM**. Change the **Label** to **VEP P100 SnPM**. Press **Start**. This will take a little longer than the TANOVA method. While the results look very similar, the mathematics are quite different.



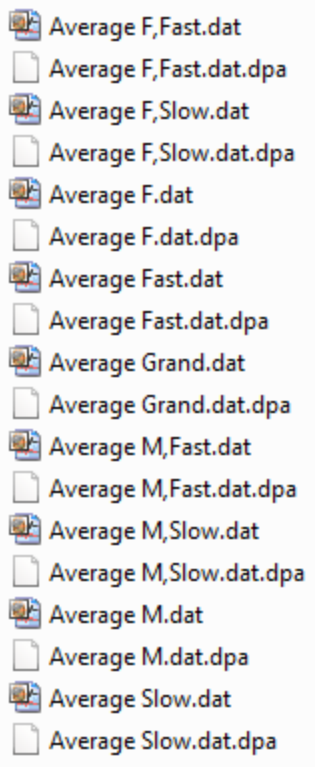
The main difference you will see is that the 2D map values in the **Deviations** display (the lower one showing the main effect for **Speed**, in this case) are F's rather than a percentage. Now you can say which electrodes had the significant differences (at each time point).



12. This illustrates the basic use of the Statistics feature. One more option should be mentioned. The other choice for **Compute** is **Save Averages over Groups/Conditions**. Select that option and click **Start**.

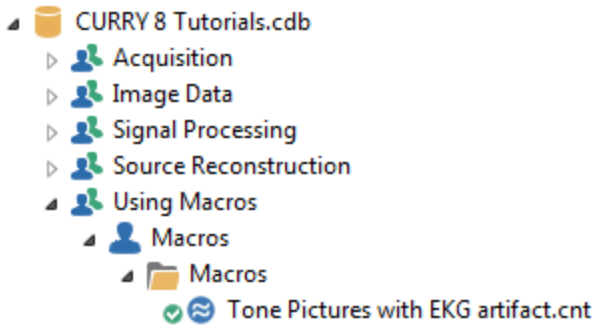


You will be asked for a folder name. In that folder will be the averages for main effect groups, the individual groups, and the grand average, along with the parameter files needed to open the files in CURRY. This saves you from having to create the averages manually.

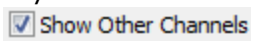


Single Subject Analyses
It is also possible to perform single subject statistics. For example, in a standard P300 recording, you may wish to know if there are significant differences between the rare and frequent responses - within the single subject.

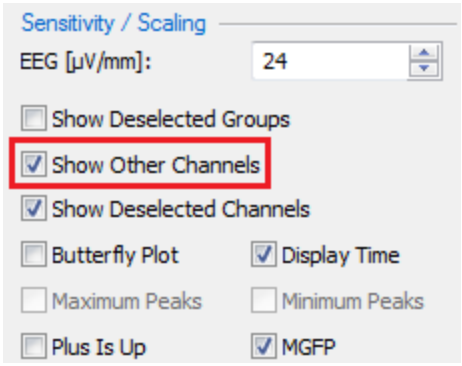
1. This tutorial uses the study shown below. It has alternating presentations of audio (type 1) and visual (type 2) stimuli. The main question is: are there differences between the responses to both kinds of stimuli in the single subject's recording.



2. Open the study. Glancing through the file, we see some fast activity due to anterior EMG, some unused channels at the bottom, heart beat artifact, occasional blink artifact, and the FC3 channel is floating. We want the statistical comparisons to be as "clean" as possible, so we will do the following preprocessing.

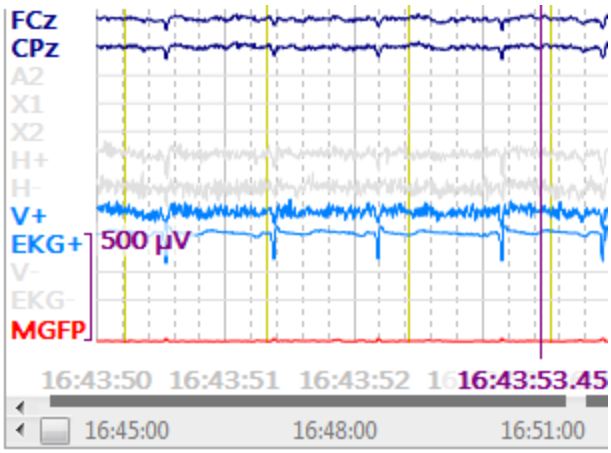
If you do not see the "Other" channels at the bottom, enable 

in the **Options** panel.

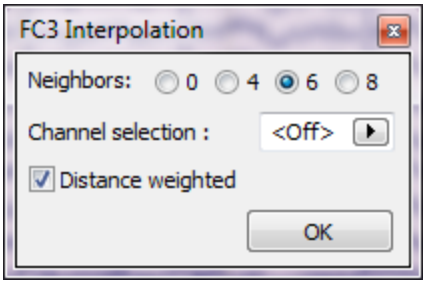


Deselect all of the "Other" channels except for the **V+** and **EKG+** channels (click on the labels). In the **Options** panel, deselect

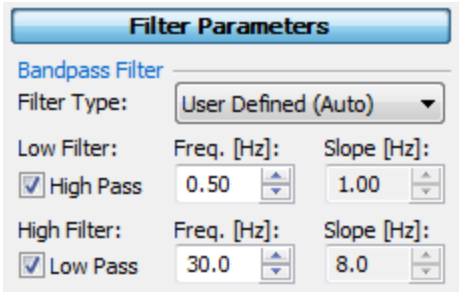
.



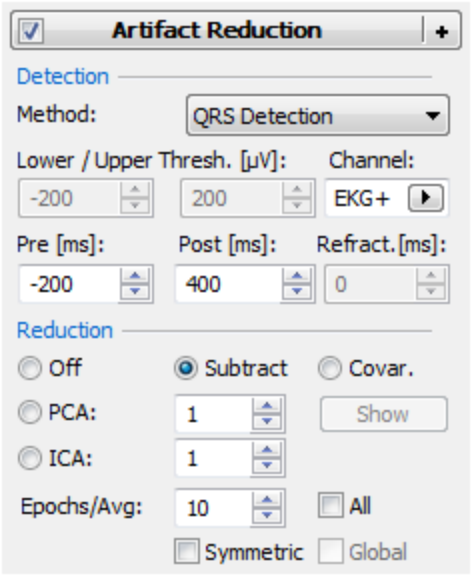
Right click on the **FC3** label and select **Interpolate**. Set **Neighbors** to **6** and enable **Distance weighted**.



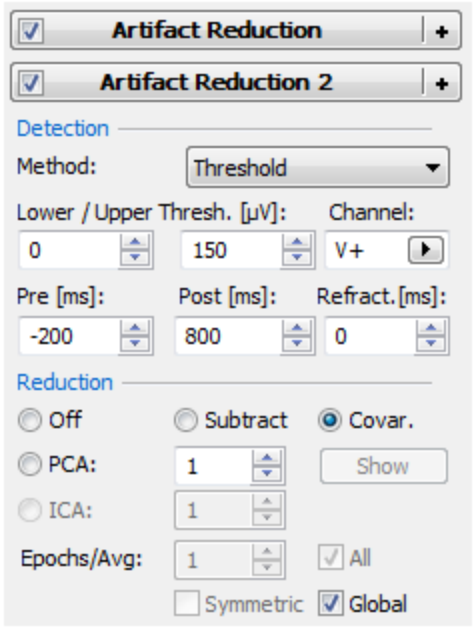
Filter the data as shown (add a **Filtering** panel).



Add an **Artifact Reduction** panel and set the parameters as shown to reduce the heart beat artifact. Setting the Reduction method and number of **Epochs/Avg** at this point shows how effective it will be, based on the artifacts that are displayed.

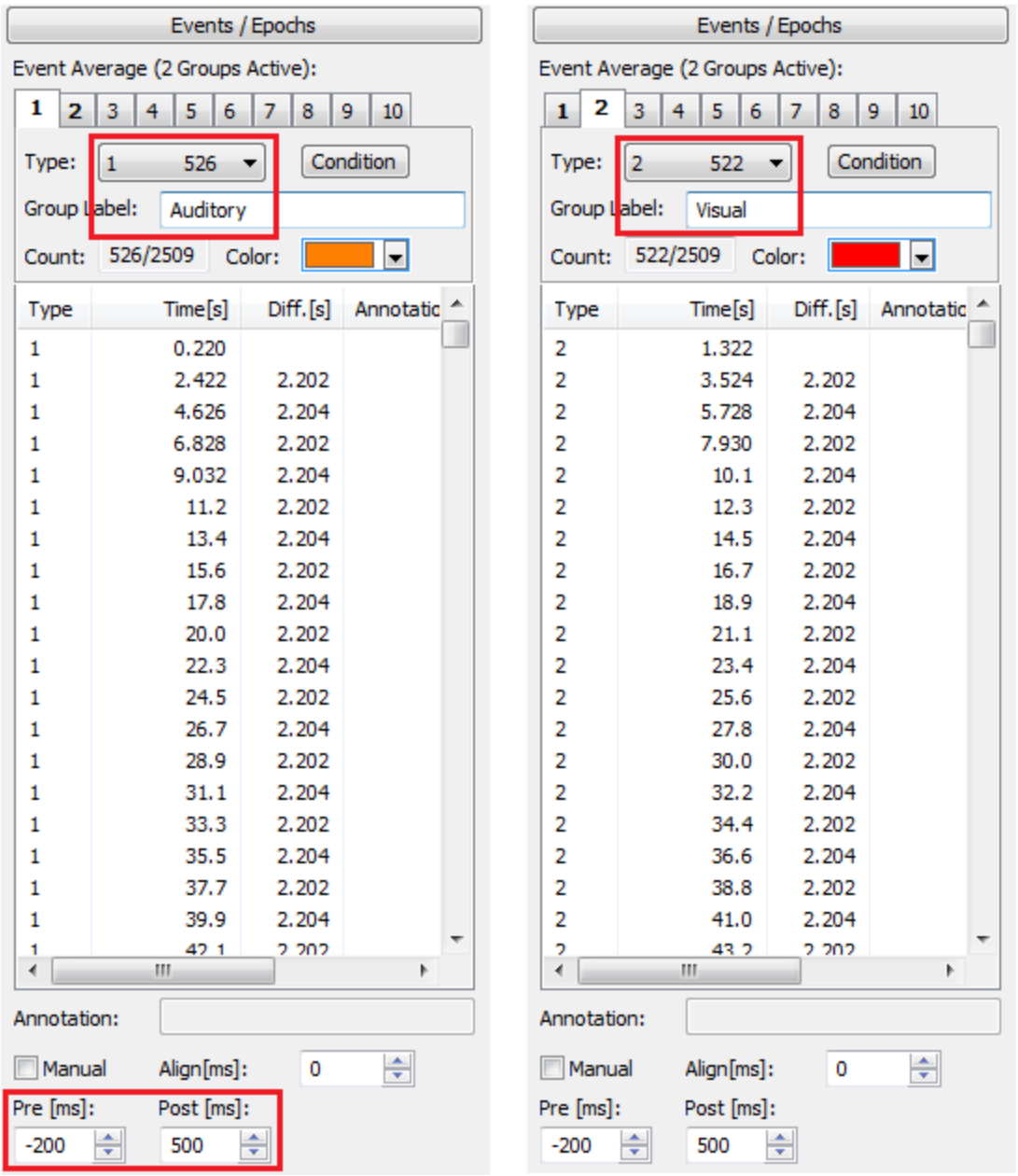


Add a second **Artifact Reduction** panel, as shown, to reduce the blink artifact. We determined the **Threshold** and **Pre** and **Post [ms]** times from measuring a few blinks. Then click the flashing button at the top. The file will be scanned twice, once for each artifact.



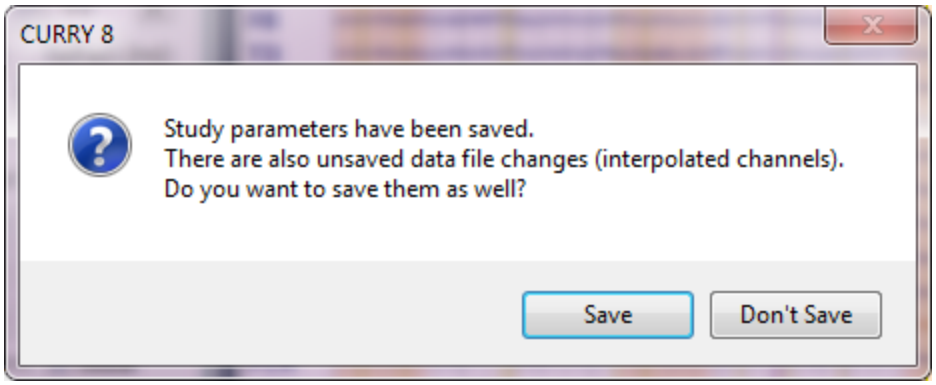
3. Display the

list . For Event Group 1 select **Type 1**, and for Event Group 2, select **Type 2**. Set **Pre** and **Post [ms]** to **-200** to **500**ms. If you type in a text string for the **Group Label**, the statistics section will use that to label the groups (shown below).

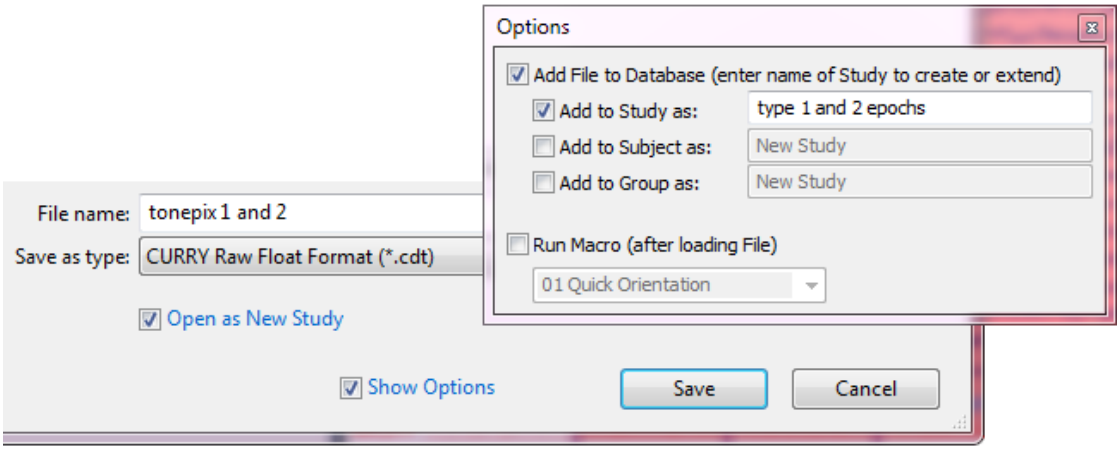


4. Save the **Study Parameters** at this point. In case we want to come back to this place, the parameter settings will still be in place. It would be necessary to rescan the data file for Artifact Reduction (reapplying the Reduction parameters for each).

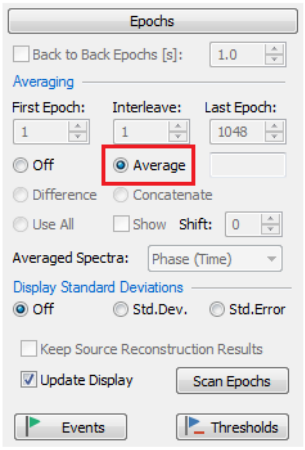
If you see the following message, click **Don't Save**.

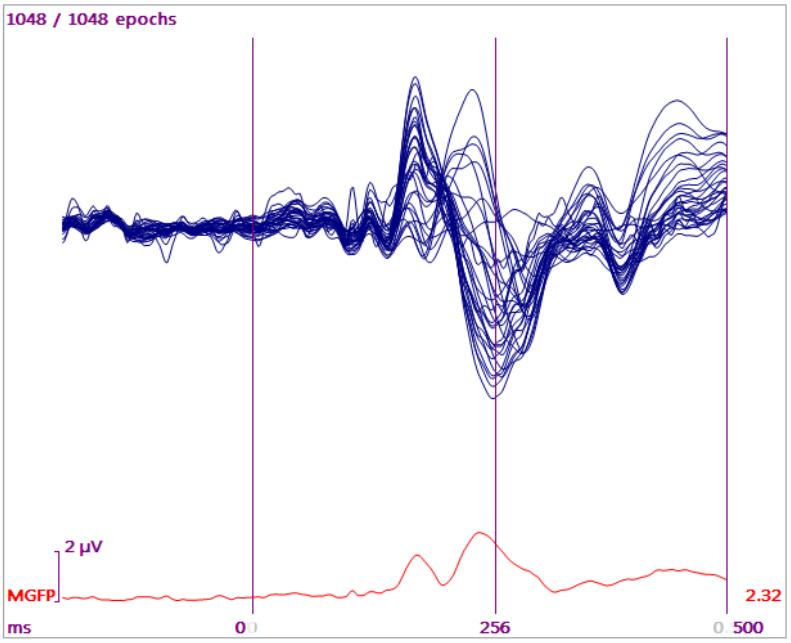


5. We need the epochs for the statistical analyses, so click the **Export Events** icon at the top. When prompted for a folder and file name, select a folder, use *tonepix 1 and 2.cdt* for the file name, and enable **Add to Study as**, which will in this case create a derived folder called *type 1 and 2 epochs*. Enable **Open as New Study**. Click **Save**. It will take a few moments to create the epoched file.



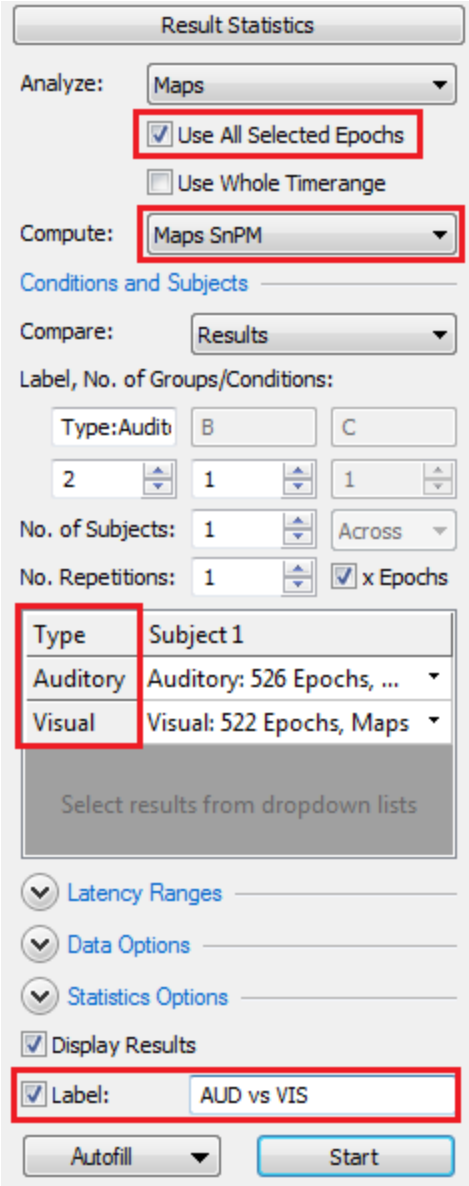
6. When the file opens, perform a **Baseline Correction** (**Pretrigger**). Set the Timerange in the Functional Data display to **0-500 ms**. The **Average** option was selected below to see the averaged waveforms. Deselect it after examining the waveforms.



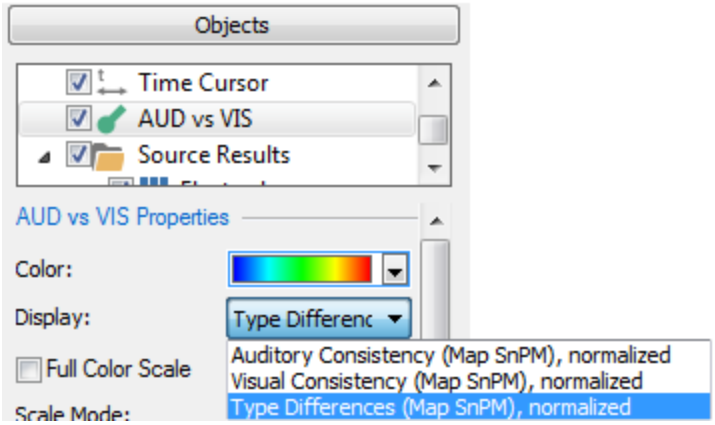


In the **Result Statistics** panel, set the parameters as shown, using **Autofill Columnwise** to fill in the table (or you can select them manually). The "Auditory" and "Visual" labels that we entered in the Events / Epochs list are entered here automatically. If you wish to enter them manually, the format is, Type:Auditory,Visual. Similarly, you could enter Event:Group 1,Group 2.

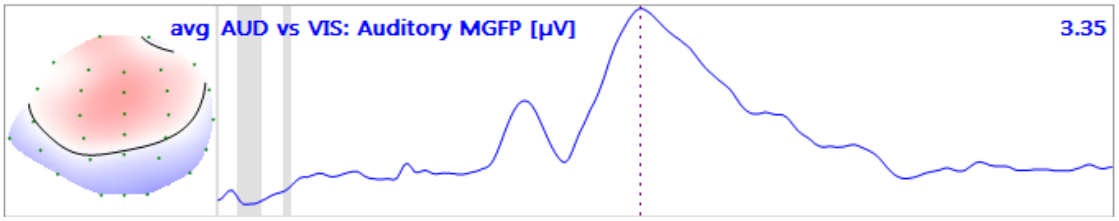
Enter a **Label**. Click **Start**. This will take a few moments.



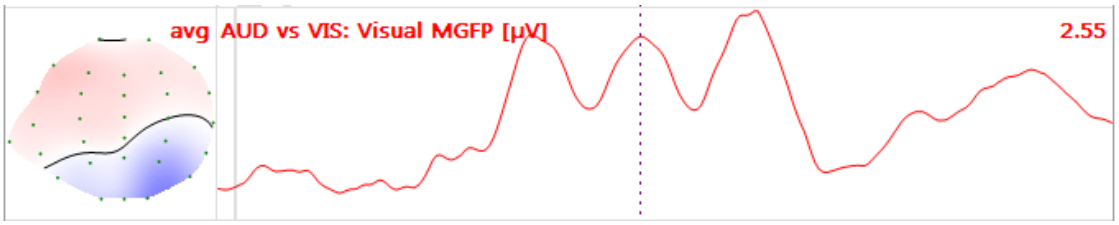
7. As above, you can select the results from the **Display** option under the statistics Properties. In this case you get the consistency for each group, and the difference between groups. The groups are consistent within, and the differences are significant throughout the selected timerange.



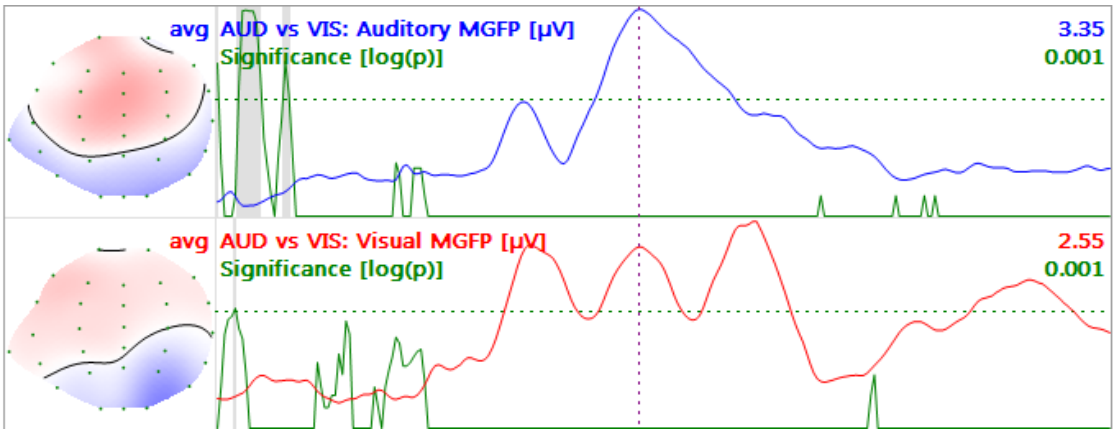
Consistency for Type 1:



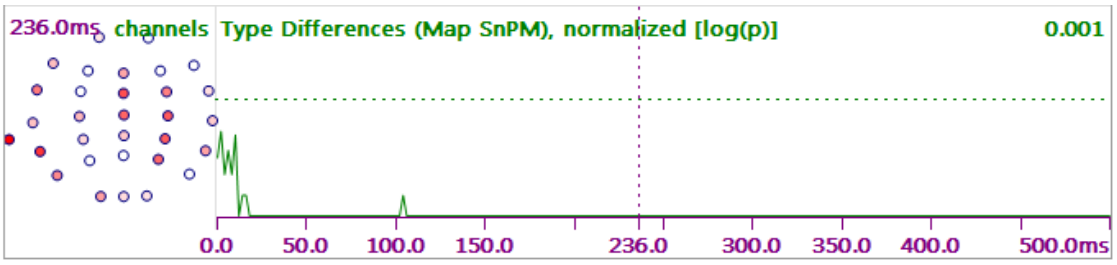
Consistency for Type 2:



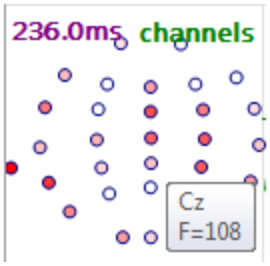
Enable under **Maps Parameters** to see the p-values as well.



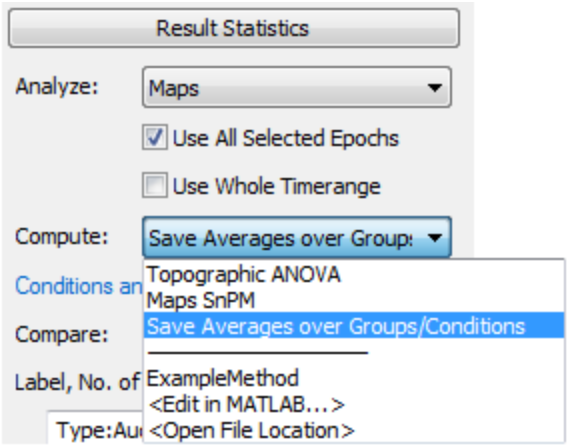
Differences between types 1 and 2:



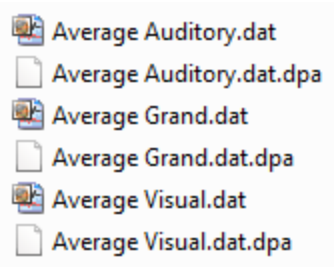
Since we selected **Maps SnPM**, we can see the F values for the significant electrodes.



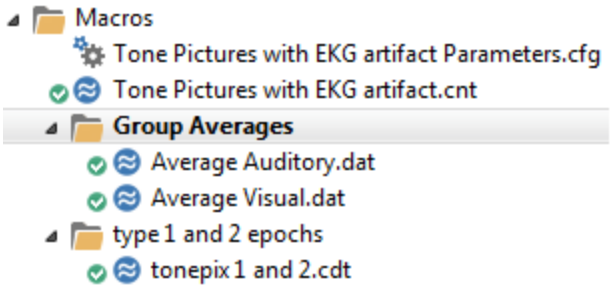
8. If you want to compare the statistics results along with the group averaged waveforms for Types 1 and 2, select **Save Averages over Groups/Conditions**.



After clicking **Start**, a Save As window will appear. This is asking you for a folder name; a new folder will be created below whatever folder you have selected. In it will appear the average data files, labeled *Average Auditory*, *Average Visual*, etc. - whatever type codes were used - as well as the grand average of all groups combined.



9. Create a new Study (e.g., a Derived Study - *Group Averages*) in the Database, and insert the files into it. Then open the Study.

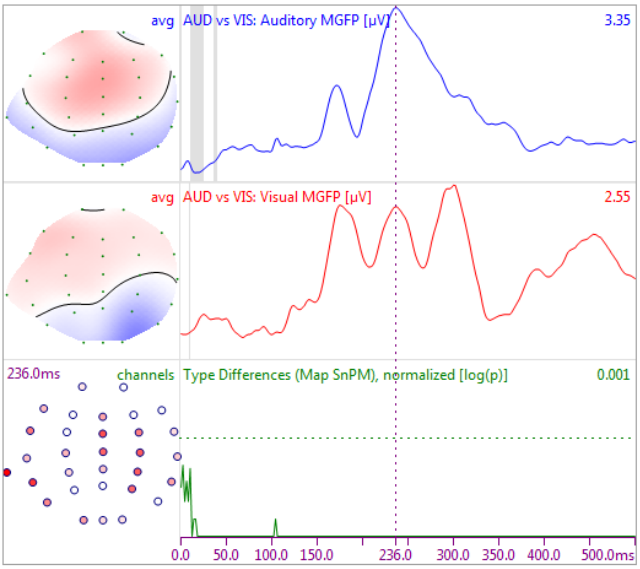


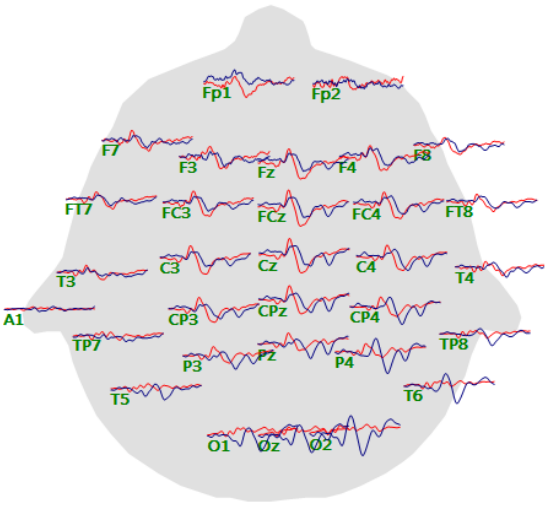
10. Select the FD, Maps display. In the Functional Data display, you will see two epochs, one for each average. Select the full Timerange (*Ctrl+double click*).

Select **Position Plot** Pos. Plot for the **Maps** display. *Right click* in the **Maps** display and select **Keep Waveforms**.

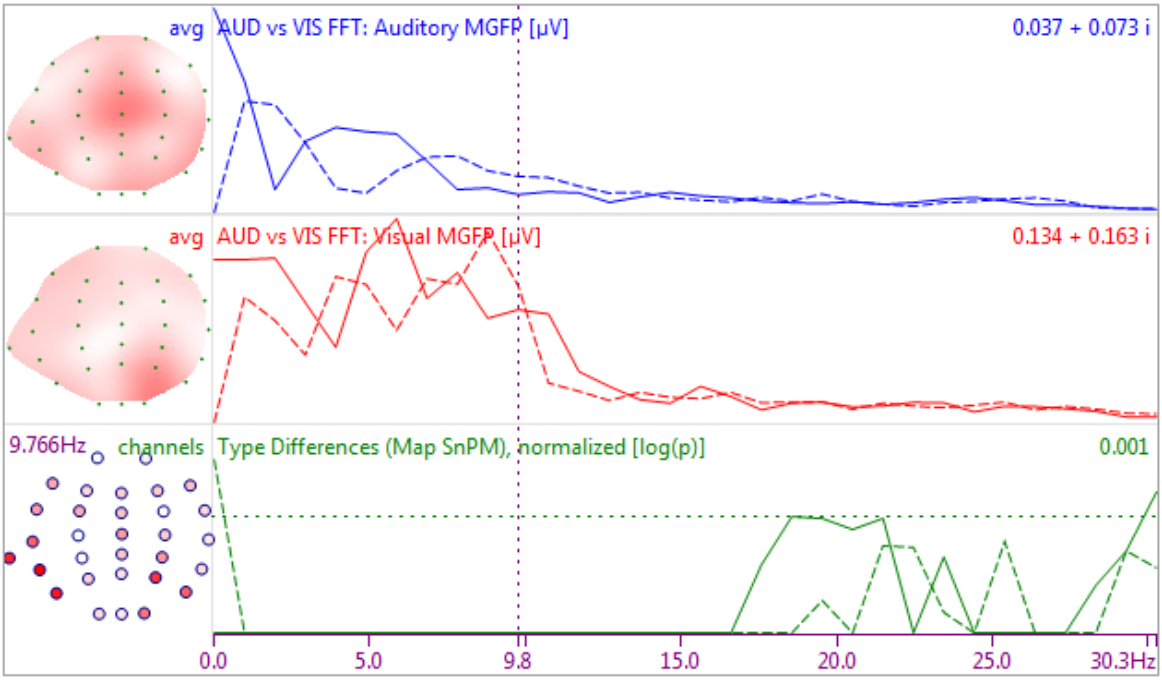
Then select the second averaged file (move the slider below the data to the right).

You will see the averaged data for both groups. By reducing the window sizes, you can position the **Maps** displays side by side, allowing you to see the averaged waveforms along with the statistics results. There are significant differences throughout the Timerange (0-500 ms). At the 232ms time point shown, the 2D Map indicates that the differences may most evident in left temporal and right vertex areas. The waveforms show what the differences may be attributed to. As above, the p-values are based on all EEG channels, and it is not possible to draw statistical conclusions regarding specific channels.



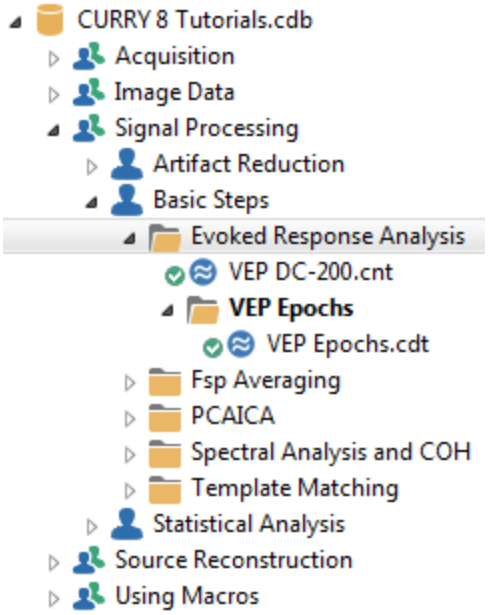


Statistics may be performed on frequency domain data as well (FFTs); the procedures are the same. In that case, you will see results for both the real and imaginary (dashed) data.

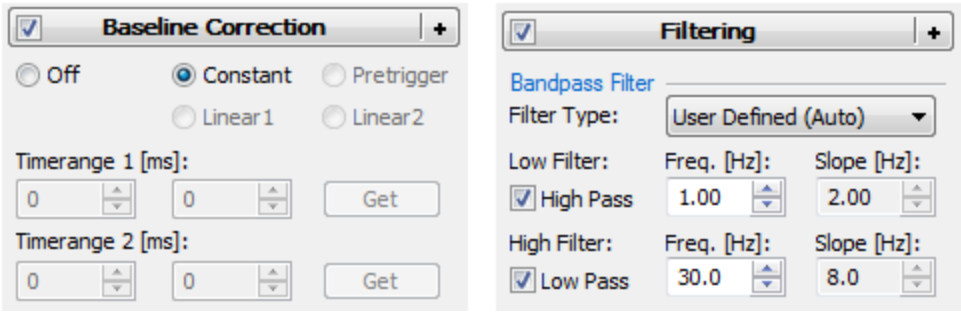


Single Event Type Analyses
These methods can also be used in a single subject file where there is only a single event type. In that case, the internal consistency is calculated as usual, then the event epochs are compared to noise epochs (where noise was created by randomly multiplying epochs by -1 and shuffling the results to obtain "noise" data). For this type of analysis you need only to set the number of **Conditions** to **1**. You may use either **Topographic ANOVA** or **Maps SnPM** methods.

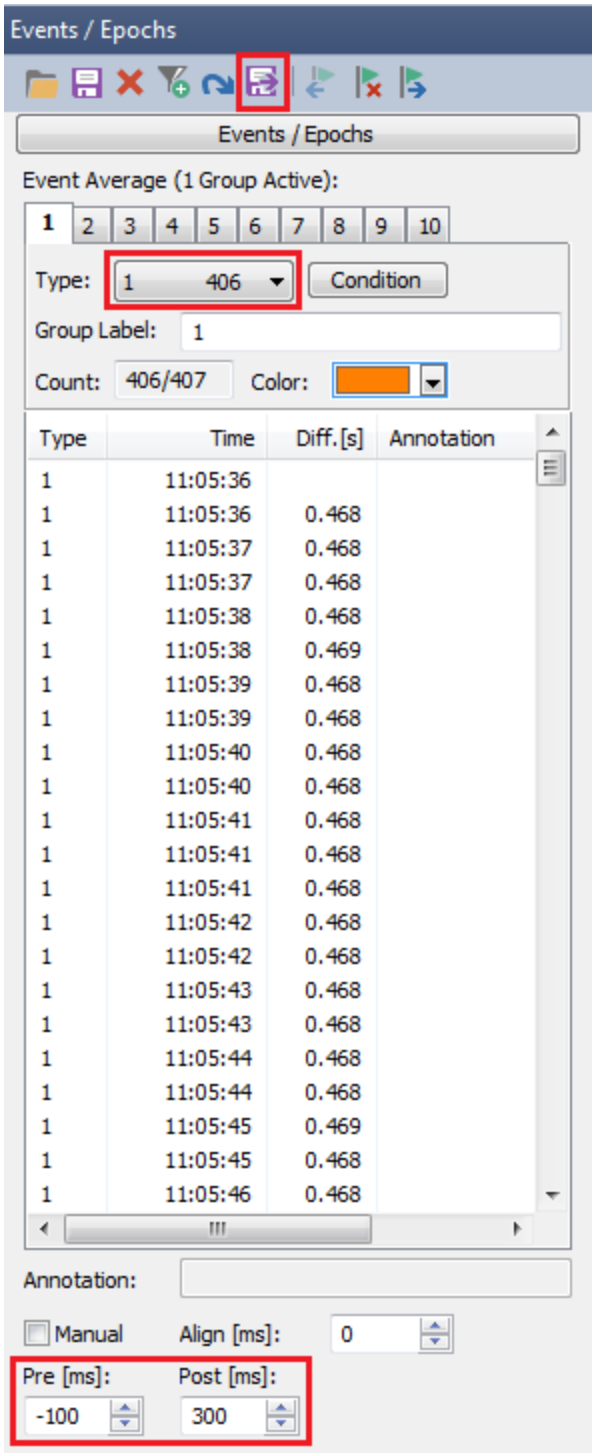
For this example, we used the following file.



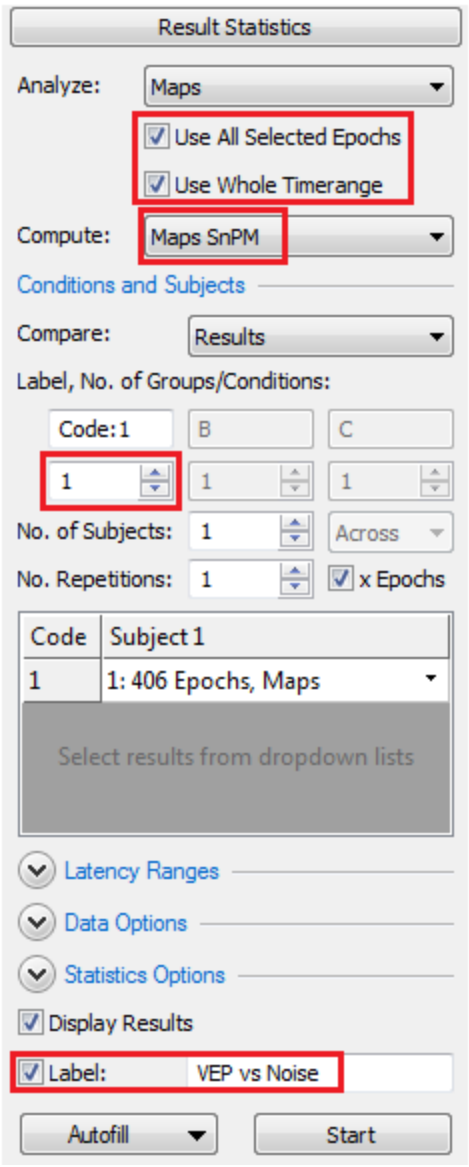
1. The preliminary steps have been described before and are very simple. **Baseline Correction**, and **Filtering** were performed.



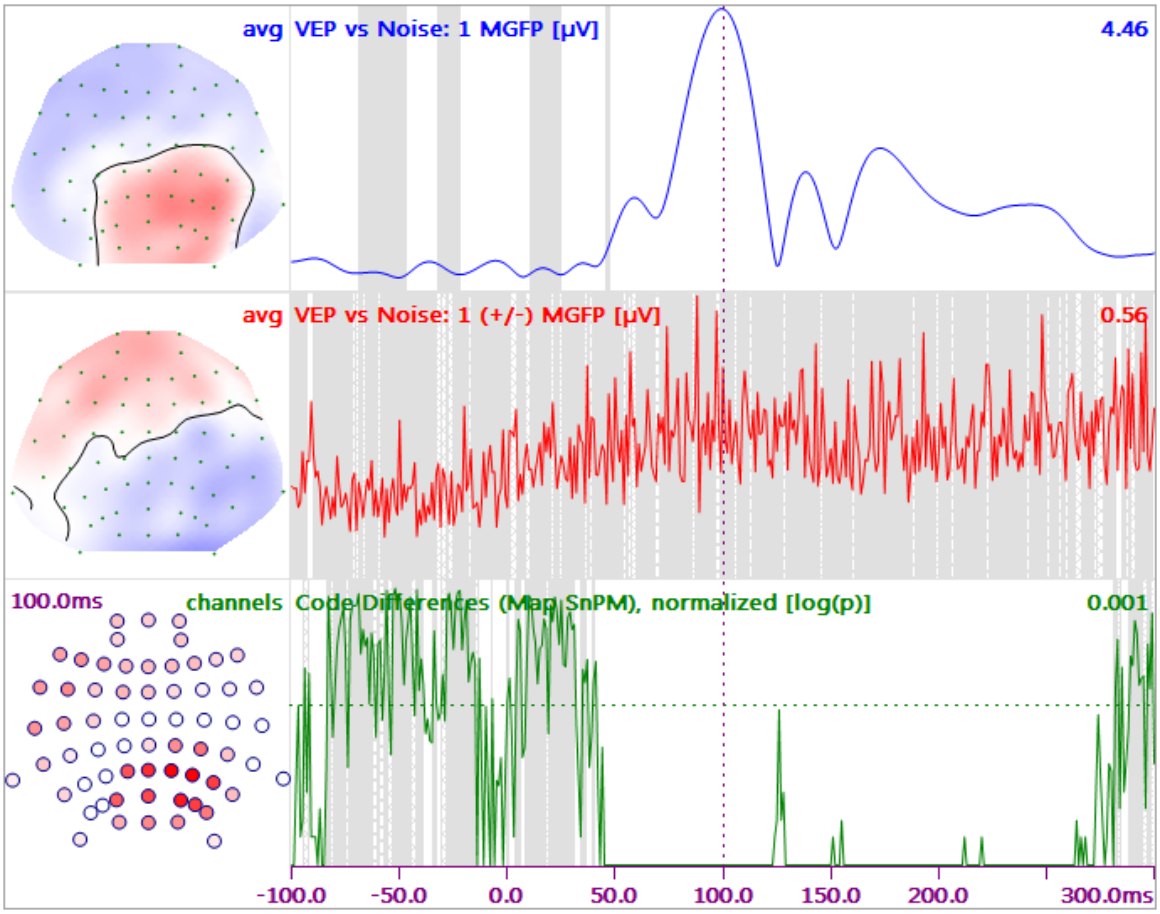
2. An epoched file was created using -100-300 ms for the interval.



3. **Prestimulus Baseline Correction** was performed, and a Timerange for the entire epoch was set. The following parameters were then used (**Autofill**, **Columnwise** filled the single cell). Click **Start**. This will take a few minutes.

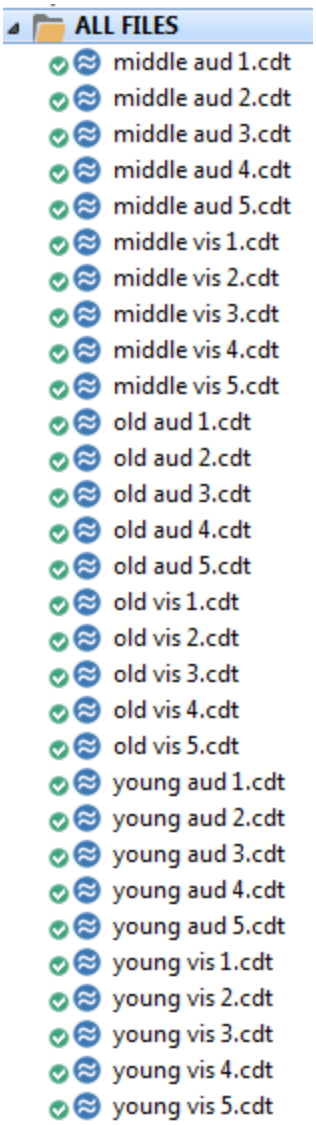


4. The results are seen below. The top line is the MGFP for the events. The gray areas again are where the consistency was not significant. The next line is the MGFP for Noise, and there are only sporadic time points were there was consistency, as expected. The bottom line shows where the differences occur in time, which are throughout the VEP components. Only sporadic differences are seen in the prestimulus interval. The lower left map shows where the differences occur (F values).

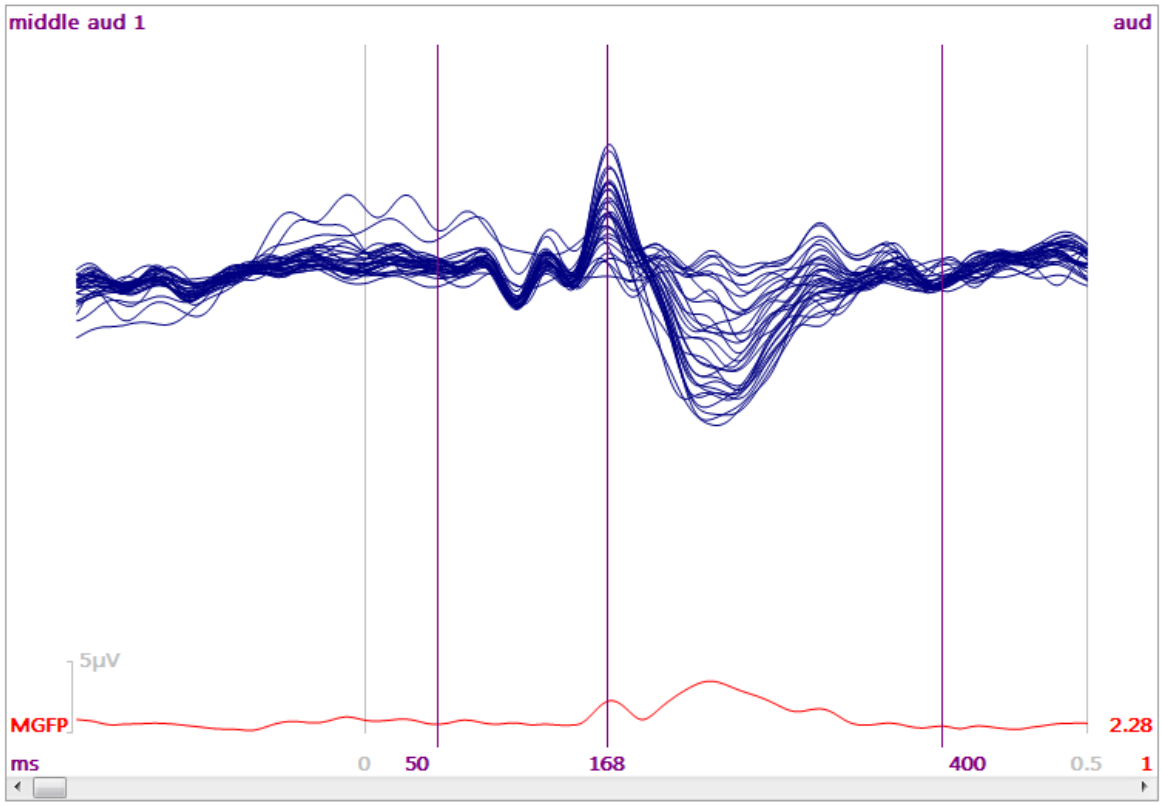


More Complex Designs
It is likely that you will have designs more complicated than the ones shown above. In the mock example below, there are 15 subjects, divided into 3 age groups: young, middle and old. For each there are averages for two types of stimuli: auditory and visual. This results in a 3x2 design with 5 subjects per cell.

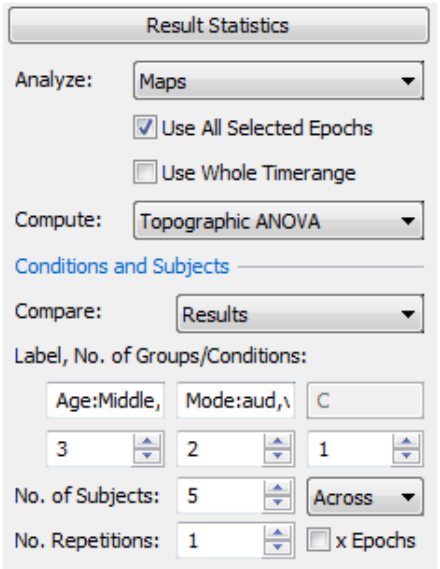
In the Database, enter the files in an order that will facilitate the filling of the matrix in **Result Statistics**. In this case the groups were entered as shown. This will permit a **Rowwise** filling of the cells.



A Timerange of 50-400 ms was selected.



In the **Result Statistics** panel, select 3 groups and 2 conditions. Enter labels for the groups: "Age:Middle,Old,Young", and conditions: "Mode:aud,vis". Enter the number of Subjects per cell (5). Looking at the options for the matrix cells, you see all of the epochs in the Study.

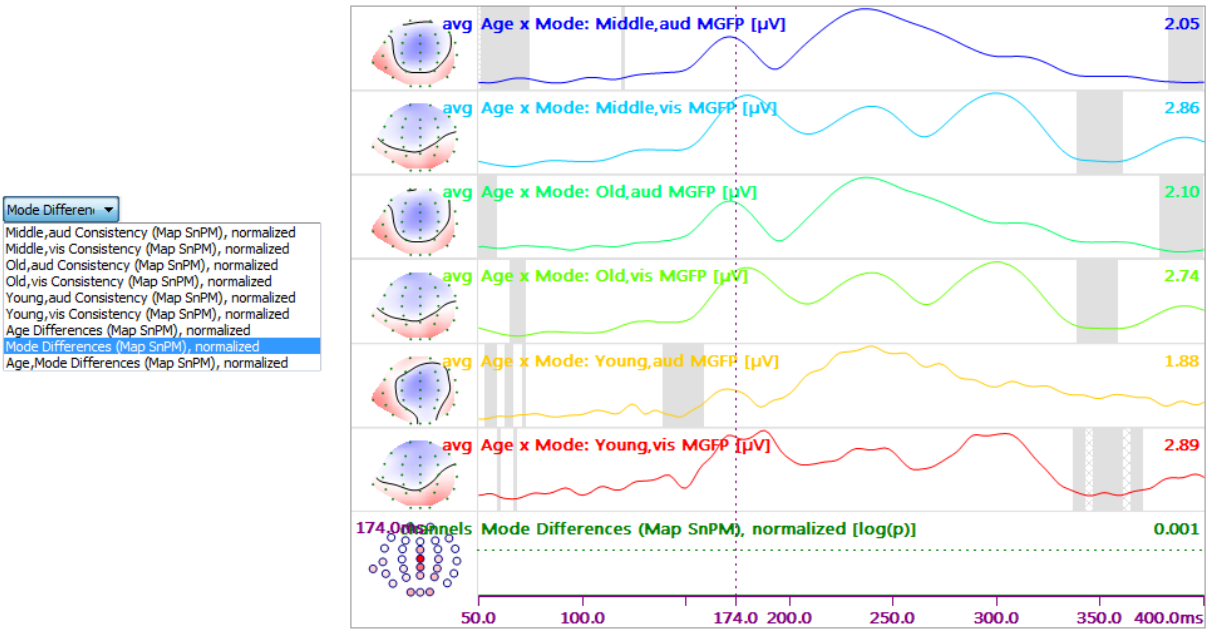


e,Mode	Use	Subject 1	Subject 2	Subject 3	Subject 4	Subject 5
Middle,aud	☑	<Undefined>	<Undefined>	<Undefined>	<Undefined>	<Undefined>
Middle,vis		<Undefined>	<Undefined>	<Undefined>	<Undefined>	<Undefined>
Old,aud	☑	<Undefined>	<Undefined>	<Undefined>	<Undefined>	<Undefined>
Old,vis		<Undefined>	<Undefined>	<Undefined>	<Undefined>	<Undefined>
Young,aud	☑	<Undefined>	<Undefined>	<Undefined>	<Undefined>	<Undefined>
Young,vis		<Undefined>	<Undefined>	<Undefined>	<Undefined>	<Undefined>

Clicking **Autofill -> Rowwise** will fill in the cells properly. Again, this is assuming you have set up the matrix to correspond to the order of the files in the Study.

e,Mode	Use	Subject 1	Subject 2	Subject 3	Subject 4	Subject 5
Middle,aud	☑	1: Epoch 1, Maps	1: Epoch 2, Maps	1: Epoch 3, Maps	1: Epoch 4, Maps	1: Epoch 5, Maps
Middle,vis		2: Epoch 6, Maps	2: Epoch 7, Maps	2: Epoch 8, Maps	2: Epoch 9, Maps	2: Epoch 10, Maps
Old,aud	☑	1: Epoch 11, Maps	1: Epoch 12, Maps	1: Epoch 13, Maps	1: Epoch 14, Maps	1: Epoch 15, Maps
Old,vis		2: Epoch 16, Maps	2: Epoch 17, Maps	2: Epoch 18, Maps	2: Epoch 19, Maps	2: Epoch 20, Maps
Young,aud	☑	1: Epoch 21, Maps	1: Epoch 22, Maps	1: Epoch 23, Maps	1: Epoch 24, Maps	1: Epoch 25, Maps
Young,vis		2: Epoch 26, Maps	2: Epoch 27, Maps	2: Epoch 28, Maps	2: Epoch 29, Maps	2: Epoch 30, Maps

After running the statistics, you will see the expected display of the results.



Statistics results can be exported to Excel from **Source Results → Export Results → Export Statistics to Excel**.

The purpose of this Tutorial was to demonstrate how the statistical part of the program works when using functional data. In the **Statistical Comparisons - Dipoles, CDRs** tutorial, we will continue on with the example using statistical analyses with dipole and CDR results.

2.5 Image Data Processing

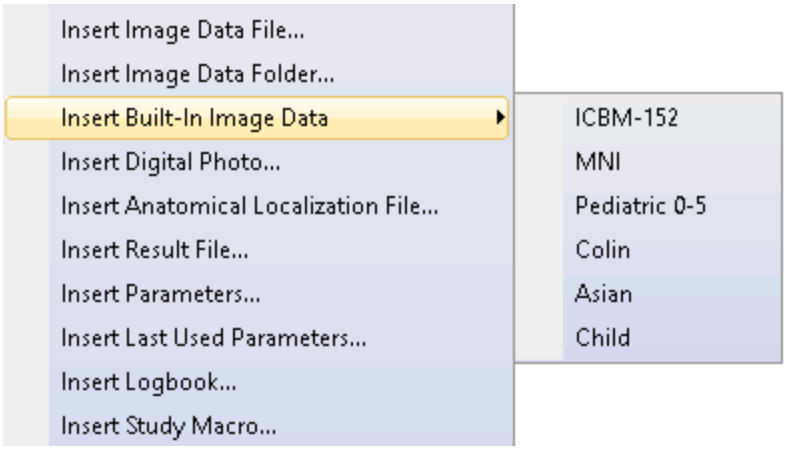
The tutorials in this section demonstrate much of the functionality that is available with image data files, including:

- A description of the supplied averaged MRI data sets,
- Performing manual and automated segmentation,
- Co-registration of MRI and CT data sets,
- Talairach coordinate system (used to identify anatomical and functional structures),
- The special case of fiber track imaging,
- Creating an average of MRI data files across subjects, and
- And the setup of ECoG grids or strips.

The actual importation of image data files is described in the **Image Data Parameters** windows tutorial above.

2.5.1 Averaged MR Data Sets

If you do not specify an image data set, one or more of several MR image data sets are available. These data sets can be used whenever individual image data are not (yet) available. If you do not select any image data set, the MNI adult averaged data set is inserted automatically. *Right click* on the Study folder and see the following options (any or all may be inserted):



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).

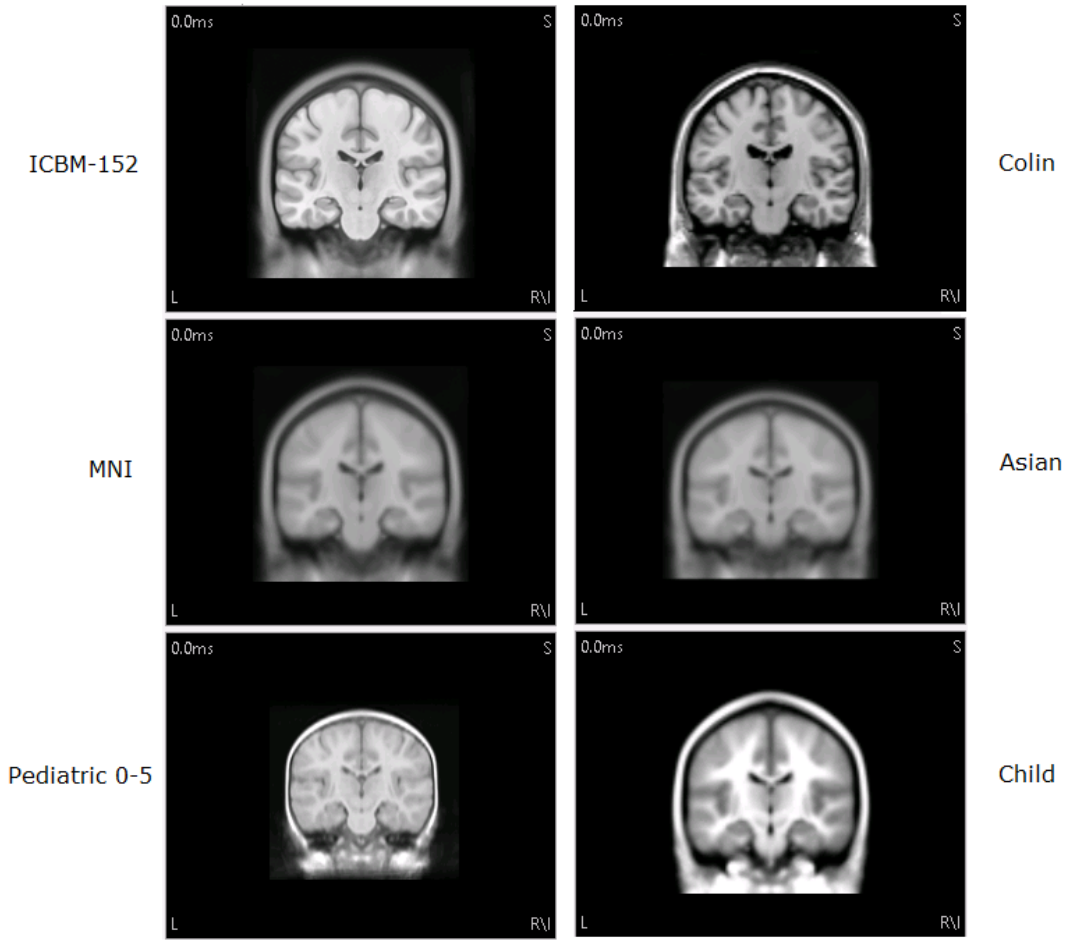
Pediatric 0-5. This is an unbiased magnetic resonance imaging template brain volume for pediatric data from birth to 4.5y age range. These volumes were created using 317 scans from 108 children.

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.



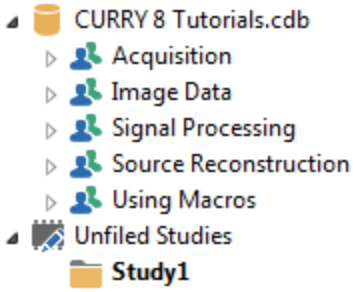
To find out more about the datasets, please see the McConnell Brain Imaging Center (McGill) web site *http://www.bic.mni.mcgill.ca/ServicesAtlases/HomePage*.

Note

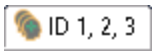
The unusual parameters for the standard image data set show some of the capabilities of the image data import in CURRY: A square sub-image starting at any pixel location may be loaded from the rectangular original image, and zoomed so that it will fill the Iso-Image cube.

The standard image data set shows only the upper part of the head, with the lowermost axial plane only approximately 18 mm below the left and right preauricular points.

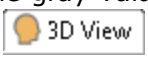
For this example, we will create a New Study - click on the **New** icon on the main Toolbar. An Unfiled Study will be created.



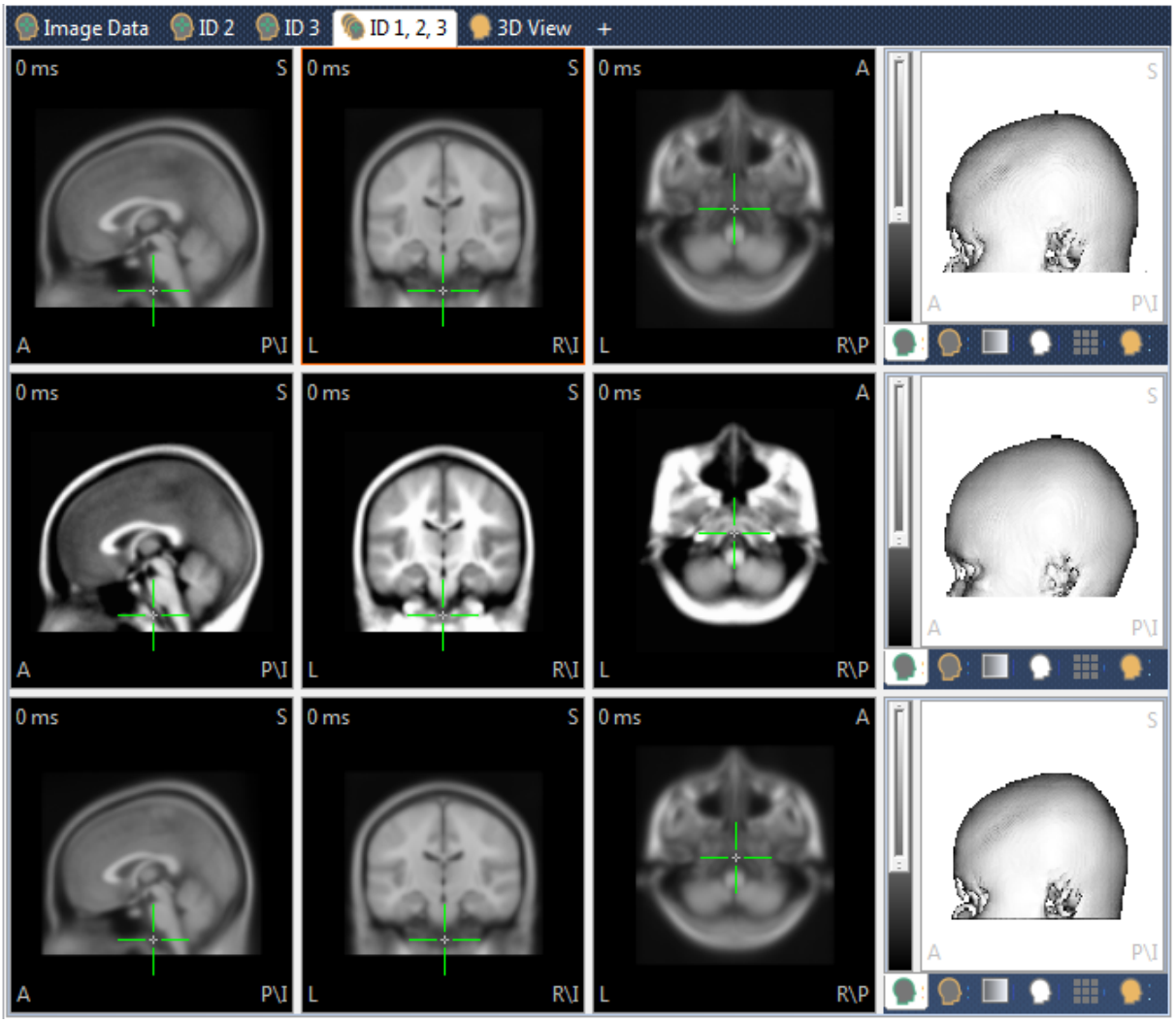
1. *Right click* on the **Study**, and select **Insert Built-In Image Data**, and select **MNI**. *Right click* again and select the **Child** dataset. *Right click* again and select the **Asian** dataset. Then open the Study.

2. The 

window displays three orthogonal views for each image data set in the sagittal, coronal, and axial display.

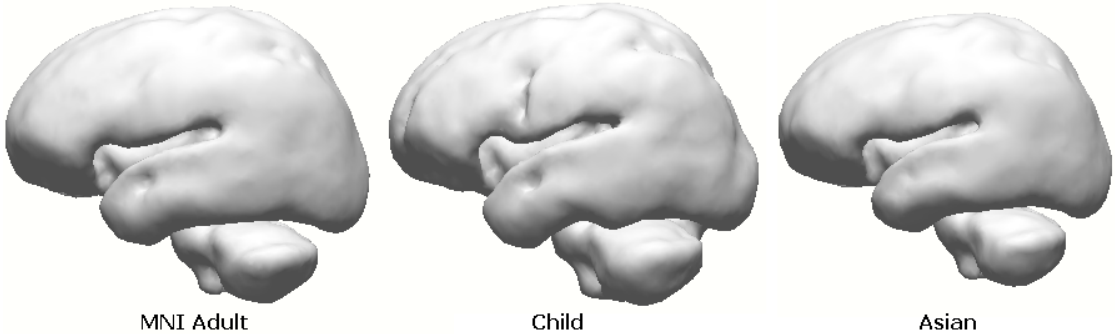
The fourth window on the right has tabs allowing you to select the *Segmentation Preview*, *Segmentation Result*, a *Histogram* of the gray values, the *Maximum Intensity Projection (MIP),* the *Grid View,* or the 

display.

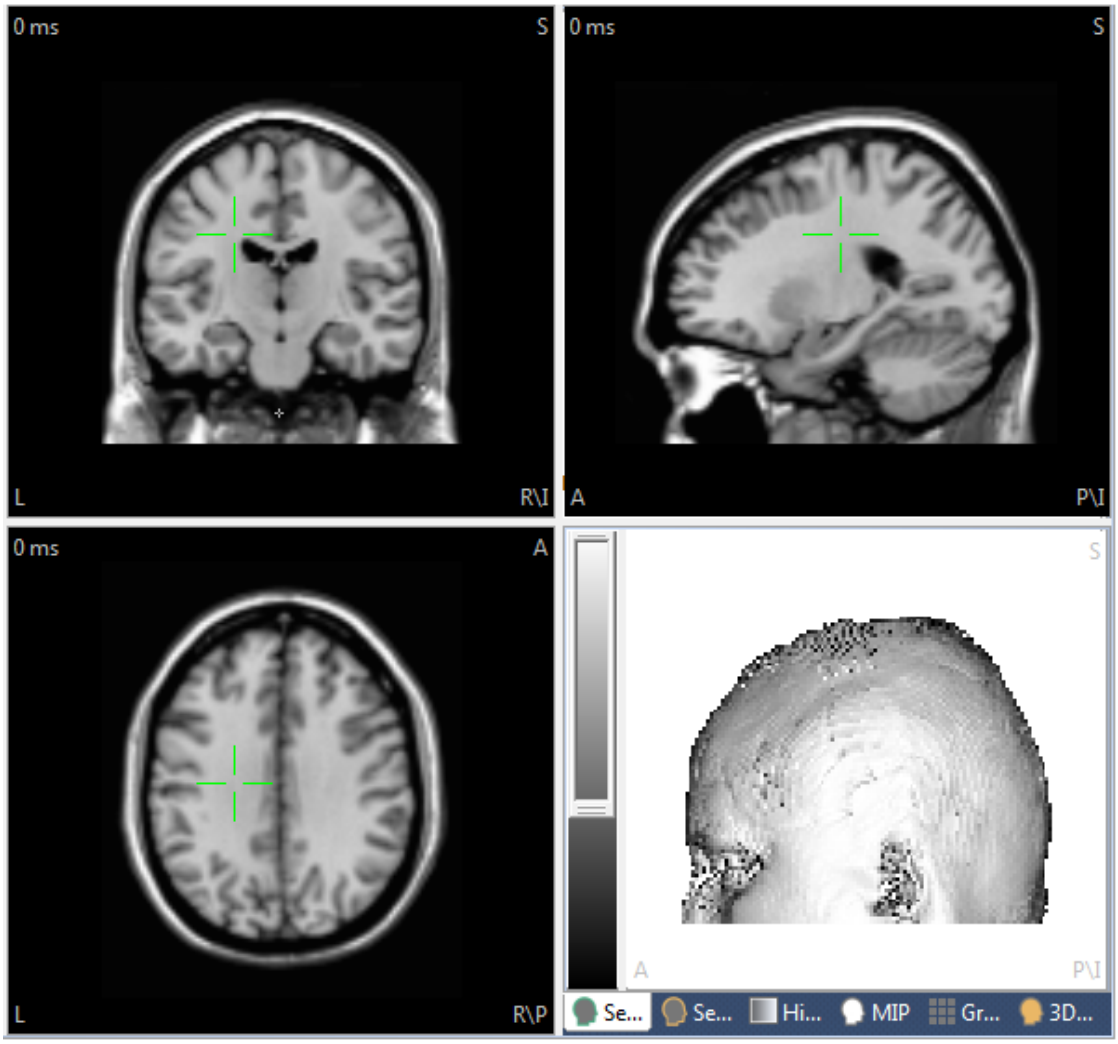


3. Click in any of the iso-image windows to display the orthogonal slices that intersect at the cursor position, or drag the mouse in any of the iso-image windows, and notice how the orthogonal views are updated.

The segmented cortex for each data set is shown for comparison purposes.



4. The hi-res MRI from a single subject data (Colin) is shown below. This is a good file to use if you do not have data for a given subject/patient.



2.5.2 Automated Segmentation and BEM Model Creation

The segmentation of the brain, skull, and skin surfaces is the most important image processing task in the context of functional source localization. Here, 3D region growing methods that are limited by gray value thresholds have proven to be very useful, and good initial estimates for the required thresholds can be calculated automatically for the typical MR images. One pass segmentations using the cortex threshold already lead to remarkable results for a large number of MR image data sets.

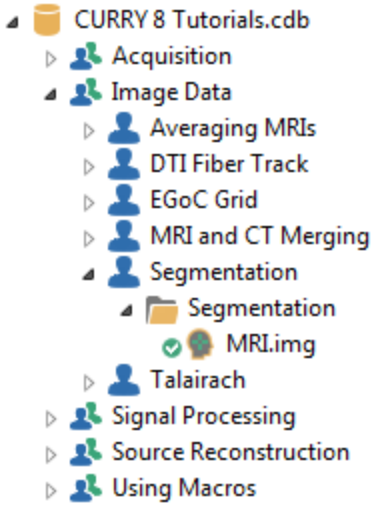
Segmentation is the process through which different surfaces are created from the MR data. Some of these surfaces are used to create a BEM (Boundary Element Method) Model. The BEM Model is a realistic head model. Unlike a three spherical shell head model to represent the head, the BEM Model has a more realistic shape for the skin, outer skull, and inner skull compartments. In many cases the realistic BEM Model will produce more accurate dipole localization. In the process of creating the BEM Model,

the cortex and skin surfaces are also segmented. These are used for displaying the results. The segmented cortical surface may also be used in Current Density Reconstructions, where the source can be constrained to the cortical surface.

CURRY has an automated routine that will often yield quite adequate BEM Models and segmented surfaces. In some cases, the segmentation of the cortex may be less than ideal, and it is possible to add some manual operations to improve the outcome. That is the subject of the next Tutorial (*Manually Assisted Automated Segmentation*). In some cases, it may be necessary to segment the cortex entirely by hand, and that is the subject of the third segmentation Tutorial (*Manual Segmentation*).

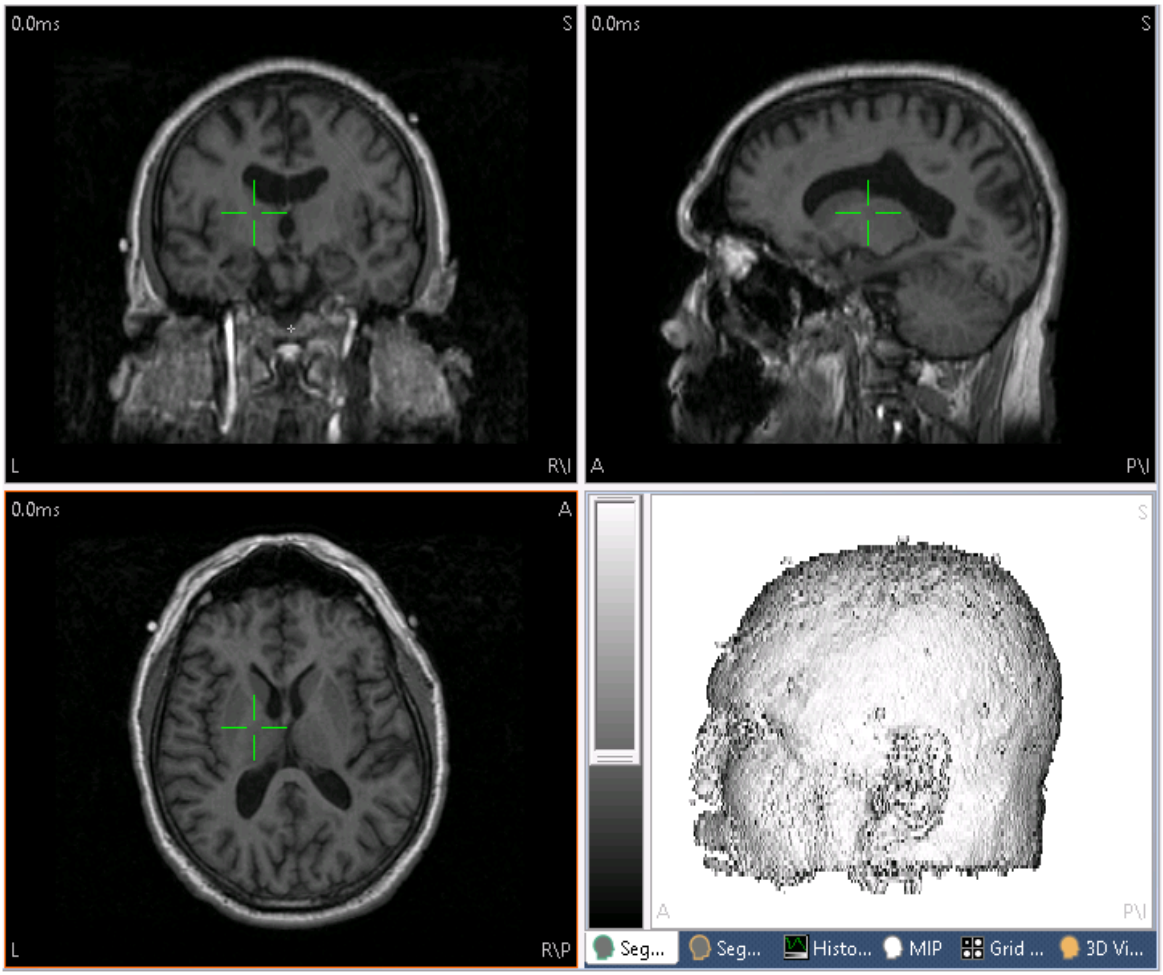
This tutorial describes the basic automated process for BEM Model creation and Skin and Cortex surface segmentation.

1. Locate the *Segmentation* Study in the *CURRY 8 Tutorials* Database.

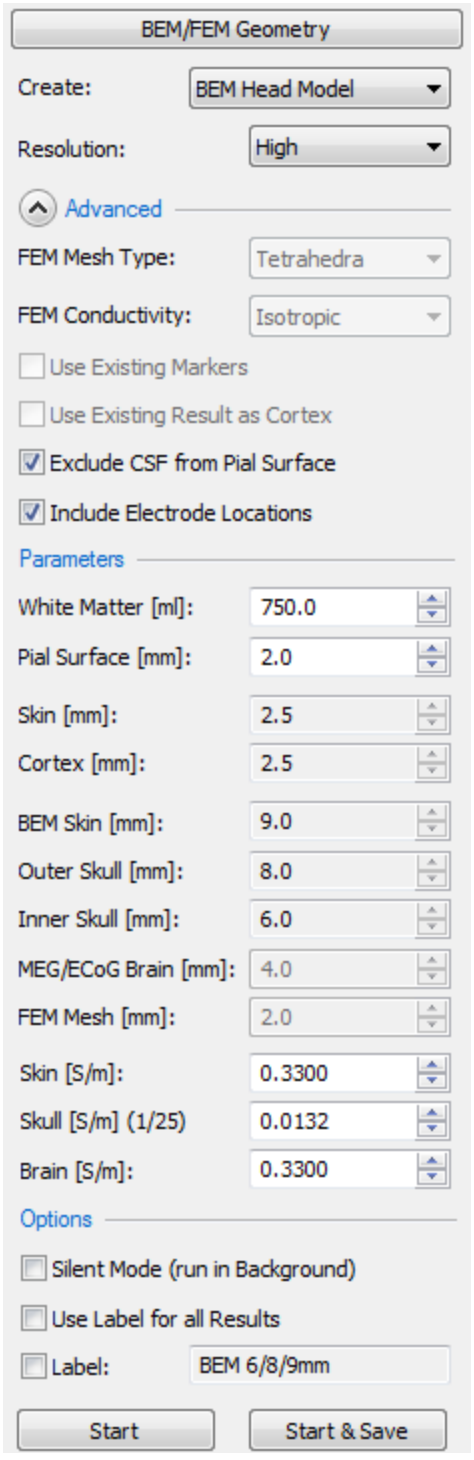


2. Open the Study and select the

display (if needed).

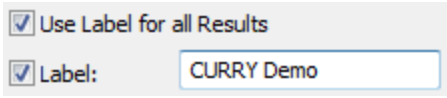


3. Click the **Setup BEM Geometry** icon on the Image Data toolbar inn the fourth rendered view, or just expand the BEM/FEM Geometry panel (add the Image Data 1 Image Data 1 panel, if needed).



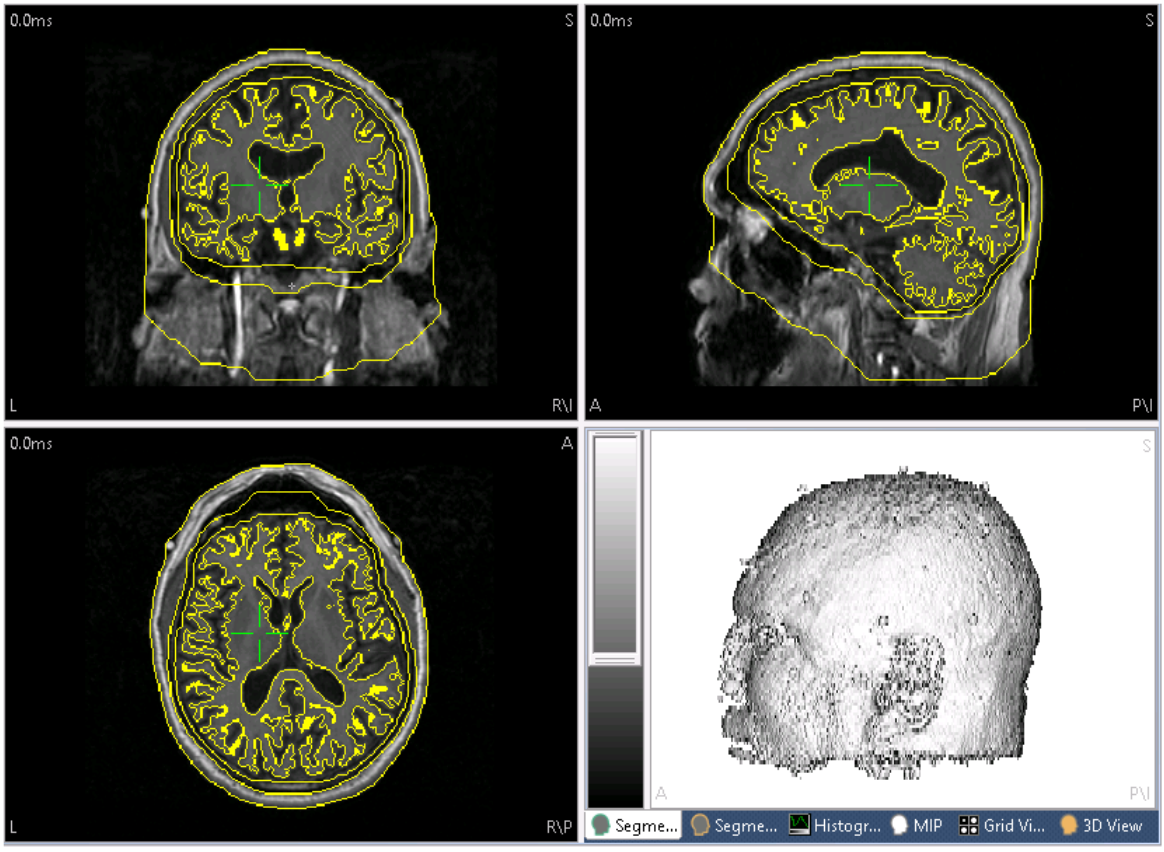
4. In this example, there are very few options we need to be concerned with. Under **Create**, select **BEM Head Model**. Select **High** for **Resolution**, if needed. The Skin and Cortex surfaces will be segmented in the process. Use the default parameters for everything else.

5. You can enter a label for the results, if desired. This is a good idea in that it helps keep track of which model is which if you are creating more than one. Enter **CURRY Demo**. Enable also the option above it to **Use Label for all Results**.

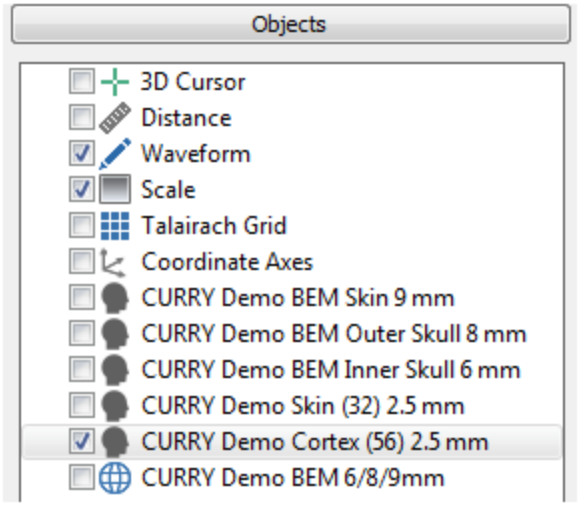


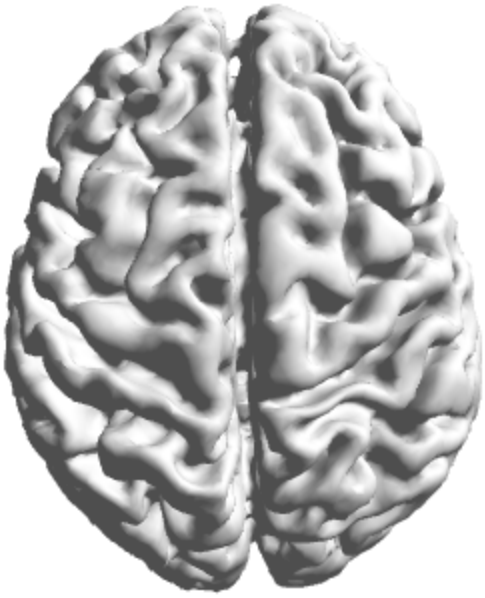
6. The Start button will initiate the process (don't click it). The results are saved only for use as long as the Study remains open. Use Start & Save if you wish to save the results to the hard drive, and have them available for later use.

7. Enter the parameters as shown above and click Start & Save. You will see a series of operations being performed, with yellow lines depicted the boundaries of the surfaces, and red (Stop Markers) and green (Pass Markers) defining regions that are included or excluded from segmentation. The final result will appear like the following.



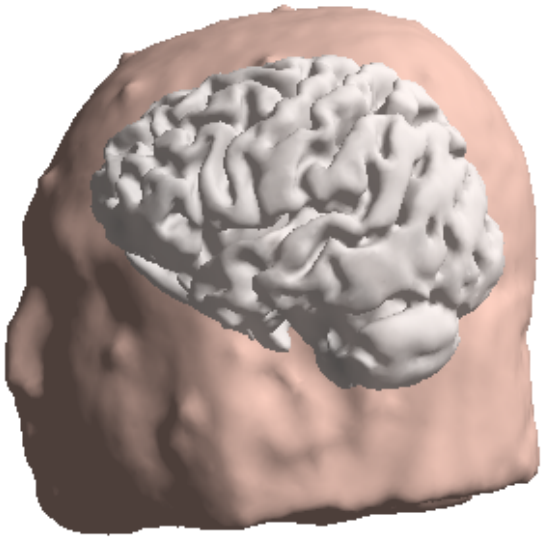
8. Now go to the 3D View display and look in the Objects panel. You will see the BEM Model and segmented Skin and Cortex that have been created.

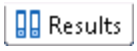




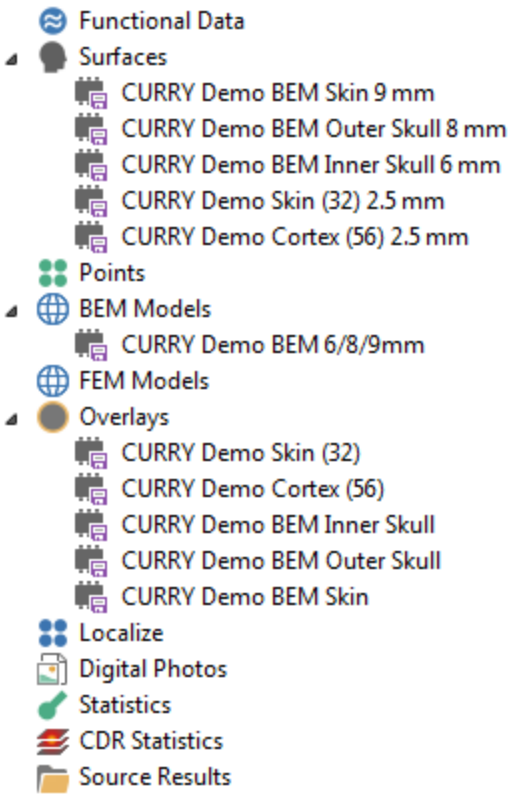
9. Viewing the results in

will be discussed in a later Tutorial, but feel free to enable the components of the BEM Model and segmented surfaces. By changing the **Transparency** for some components (in the **Properties** fields below the list), you may create multi-layered displays, as shown below.



10. Also look at the **Results** parameters 

. There you will see the Surfaces, BEM Models, and Overlays, etc. that were created. If you *right click* on them, you will see options for Loading, Unloading, Saving, Erasing, etc. The use of these will be discussed in later Tutorials and in the *CURRY 8 User Guide*. The symbols indicate that the files have been loaded and saved.



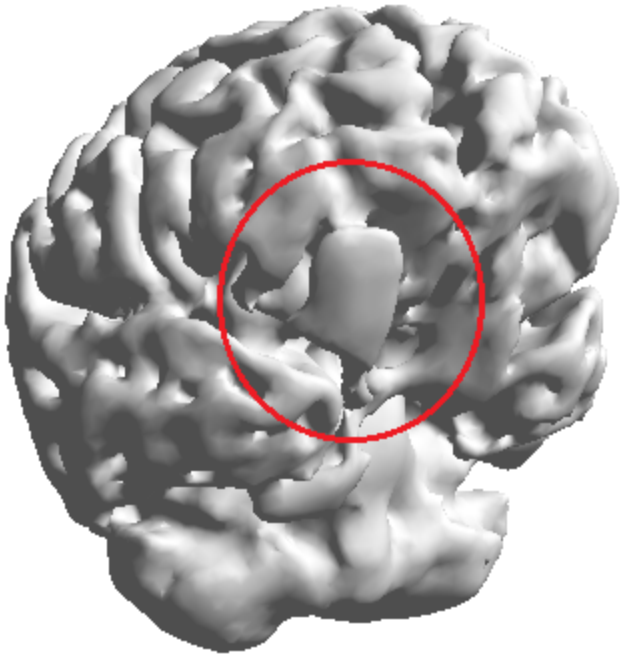
11. Continue on immediately with the next tutorial without closing the study, if desired.

2.5.3 Manually Assisted Automated Segmentation

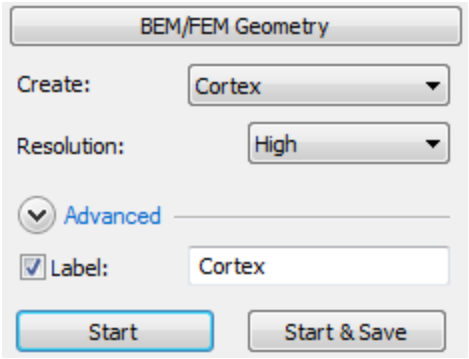
This Tutorial begins with the segmented cortex that was created in the previous Tutorial. You will need to complete those steps in order to follow along in this example.

1. Return to the

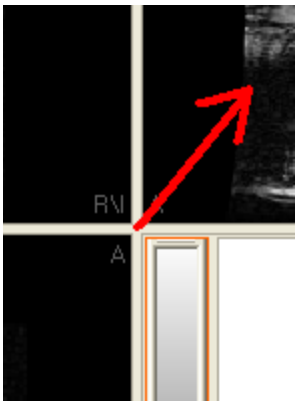
display and the CURRY Demo Cortex. Note, that some of the structures around the eyes have been segmented also (difficult to see in a static figure). This is not an uncommon occurrence, and it typically indicates that the segmentation bled into the boney structures around the eyes via one or both optic nerves.



2. Return to the Image Data display. First, we need just the cortex to work with. Set the parameters as shown to segment just the cortex. Click **Start**.

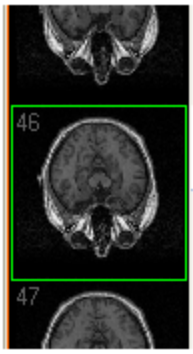


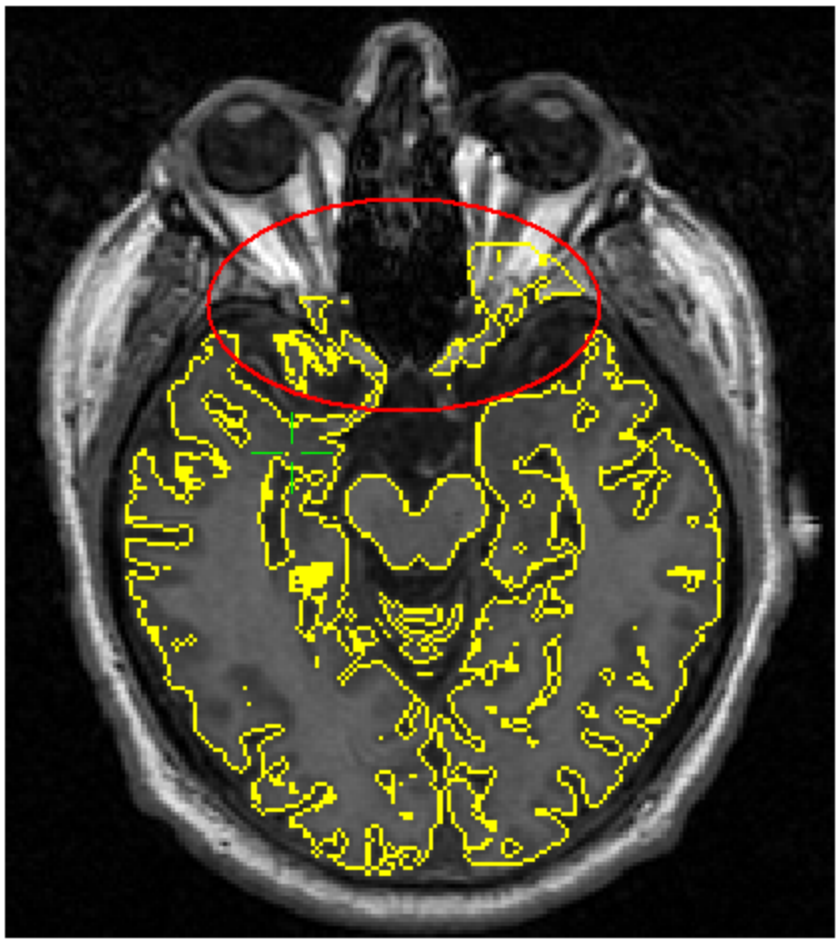
Slice **46** is shown below (selected from the film strip). The circled area shows the unwanted structures (the image size was expanded by dragging the intersection of the four views to the upper right area).



Also, if you position the mouse in the upper right corner, the full-size button will appear , providing another way to enlarge the display.

3. We can exclude the structures using **Stop Markers**. Incidentally, if you click on a structure in the **3D View**, you will see that slice in the **Image Data** display.

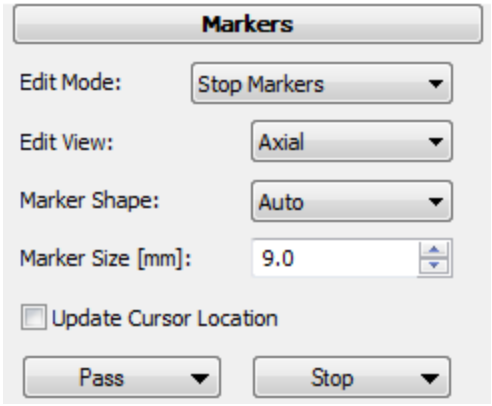




Right click in the axial view and select **Edit Markers**. The

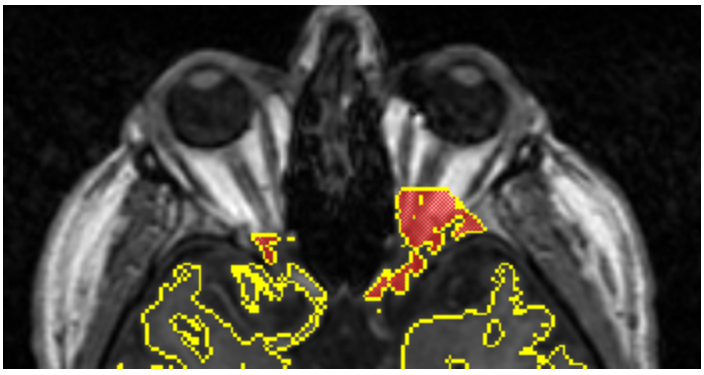
display is expanded and the **Edit View** is set to **Axial**. **Stop Markers** are selected

automatically. This will allow us to place stop markers in the axial view only, and to click in the other views without adding markers (which could happen by accident). Notice the cursor becomes a white cross when positioned in the axial view, and remains the white arrow when positioned in any other view. This serves as a reminder that Markers are On, and which view(s) is the active one(s).

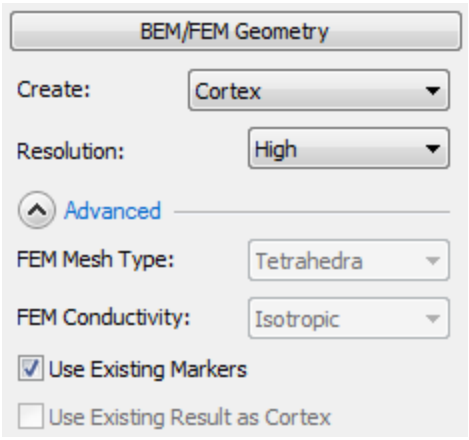


4. Now we will position the Stop Markers to block segmentation of the eye structures. Just click (or click and drag) where you want the Stop Markers to be placed. We also excluded the nerve on the left side as well. Step up and down through the slices (using the *mouse wheel*) to be sure you get all unwanted structures. If you can find and exclude the point that connects the brain to the eye structures, you need only to exclude that connection. If you make a mistake, and the entire exterior area turns red, for example, use **Undo** from the context menu, or click *Alt+Backspace*.

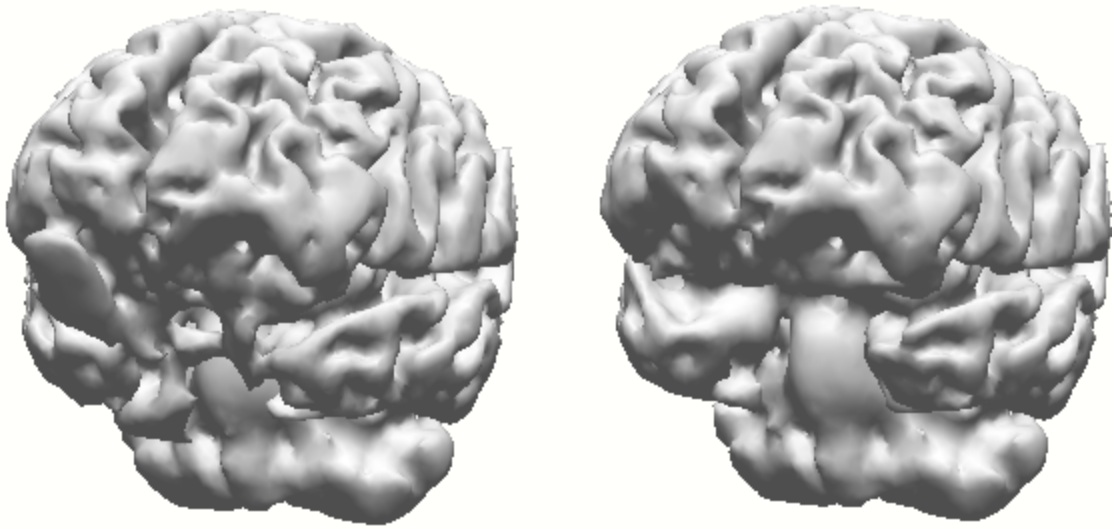
When finished, *right click* again and deselect **Edit Markers** (to avoid spurious marker placement). Reposition the dividers when finished.



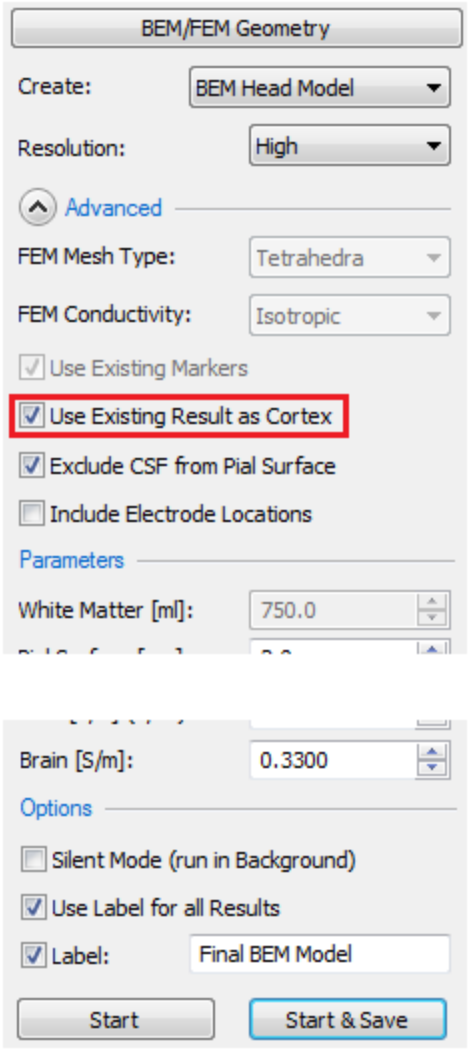
5. In the BEM/FEM Geometry panel, again select **Cortex** (if needed). Enable **Use Existing Markers**, since we want the Stop Markers we placed to be respected.



Enter "final cortex" for the **Label**, and click Start & Save. The resulting cortex with the eye structures removed is shown on the right.



6. Lastly, we can include the final cortex in a new BEM Head Model, if desired.



This is not strictly necessary, as the BEM Model itself will have only minor changes. The final segmented cortex will already be available in Source Locations, for use with Current Density Reconstructions. But if you want to simplify things, you can recreate the BEM Model and then delete the unwanted surfaces, models, and overlays from the Results list.

Close the Study without saving any of the results.

In the next segmentation Tutorial, we will segment the cortex manually.

2.5.4 Manual Segmentation

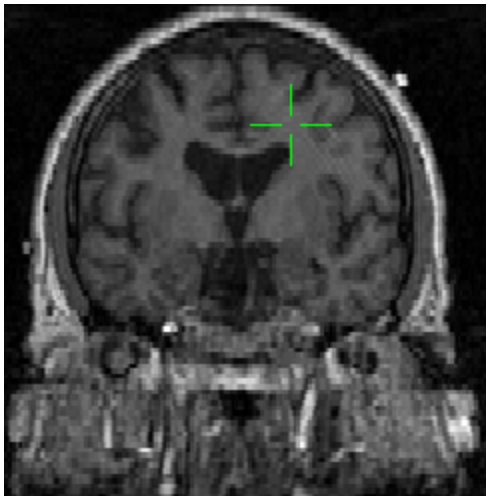
The quality of the source space (the cortical surface, optionally without the brain stem and cerebellum) and the BEM-model can be improved especially in the case of a noisy MR dataset by manual segmentation. This MR data file illustrates several of the difficulties you may encounter with some files.

These steps are for demonstration; the results will be discarded.

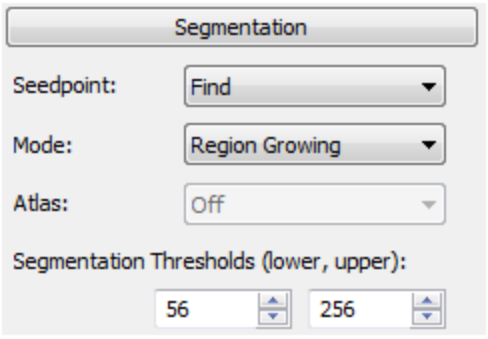
1. Using the same *Segmentation* Study as in the previous two Tutorials, open the Study and select the Image Data view, if needed. For the fourth view (lower right), switch to Segmentation Result (it will be blank).

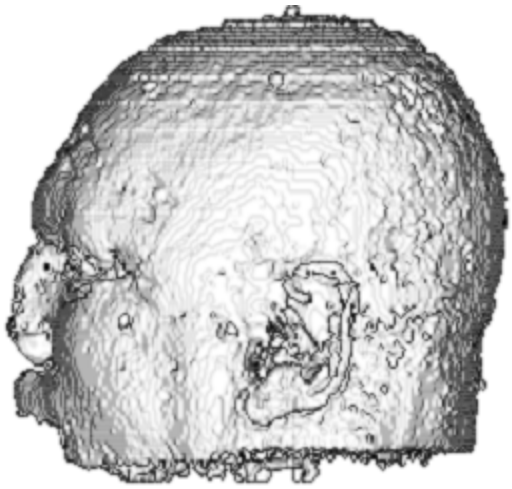
From the Main Menu Bar, select **Image Data** → **Segmentation Thresholds** (this is a shortcut to **Step 5** of the **Image Data Parameters** windows). Note that the **Cortex Threshold** is **56**. This is fine for the automated BEM Model algorithm, but we will encounter a problem when we attempt to segment the cortex manually using this threshold. Leave it at 56 for now, and click **Cancel** to exit the **Image Data Parameters** windows.

2. Position the cursor in the white matter of the coronal MR image (verifying the white matter position in the axial and sagittal views).



In the Segmentation section (under **Image Data**), select **Find** for the **Seedpoint**, **Region Growing** for the segmentation **Mode**, and a **Lower Threshold** of **56**. Click **Start**. The skin surface has been segmented instead of the cortex. This is the problem mentioned above - we need to use a different threshold.



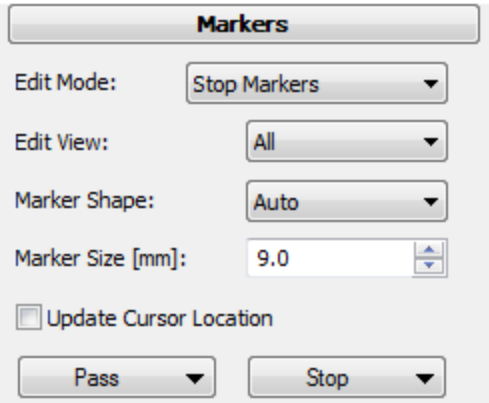


3. Increase the **Lower Threshold** to **70**, and click the **Start** button again. Now we see that the cortex has been segmented, but the brain stem and cerebellum have been included also. Both can be removed using **Stop Markers**.

Stop Markers are displayed as a red overlay and prevent segmentation at the voxel level. Analogously, Pass Markers (green overlay) enable segmentation. Where there are markers, image intensity is not taken into account. Markers can be drawn manually, or Segmentation results or their exterior can be transformed into markers.

4. In the

panel, select **Stop Markers**, **All** views, with **Auto** for the **Marker Shape**, and **9** for the **Marker Size**.

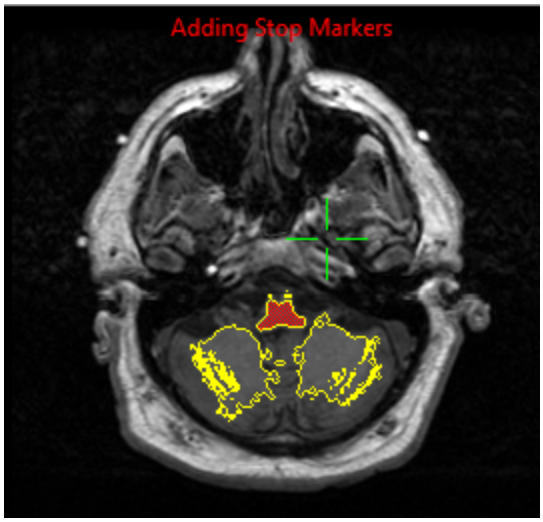


In the vertical thumbnails on the left of the images, select slice **32** (where the isolated brain stem structure appears).

In the Axial view, press the Plus key (*Shift*++) in order to magnify the MR image (use Minus to revert), or drag the dividers, or use the enlarge button, as in the previous Tutorial. All of these methods will give you a larger view.

In the axial view, click in the brainstem to place Stop Markers (red areas appear where markers are placed), then turn the Stop Markers **Off**

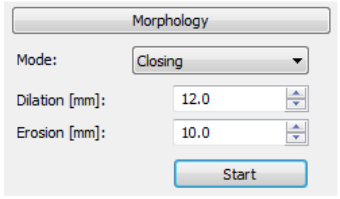
. (This is to avoid adding stop markers when you click in the image to select the white matter in the next step).

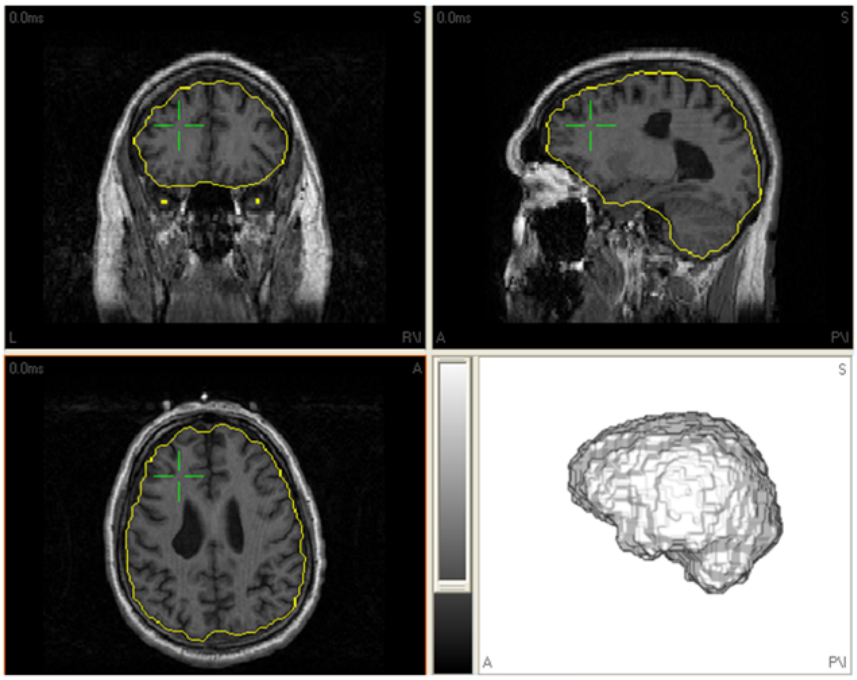


After placing the Stop Markers, select the white matter in the coronal image again. Repeat the segmentation by clicking the **Start** button (under Segmentation). The brain stem is then removed.

5. In order to lower the segmentation threshold further, which would result in better resolution of the gyri and sulci, as we saw in the previous Tutorial, the outside of the smoothed envelope of this segmentation result can be used as a constraint by converting it to Stop Markers.

In the Morphology section, set the **Mode** to **Closing**, with a **Dilation** radius of **12.0mm** and an **Erosion** radius of **10.0mm**. Press **Start** to generate a slightly dilated, smoothed version of the cortical surface.

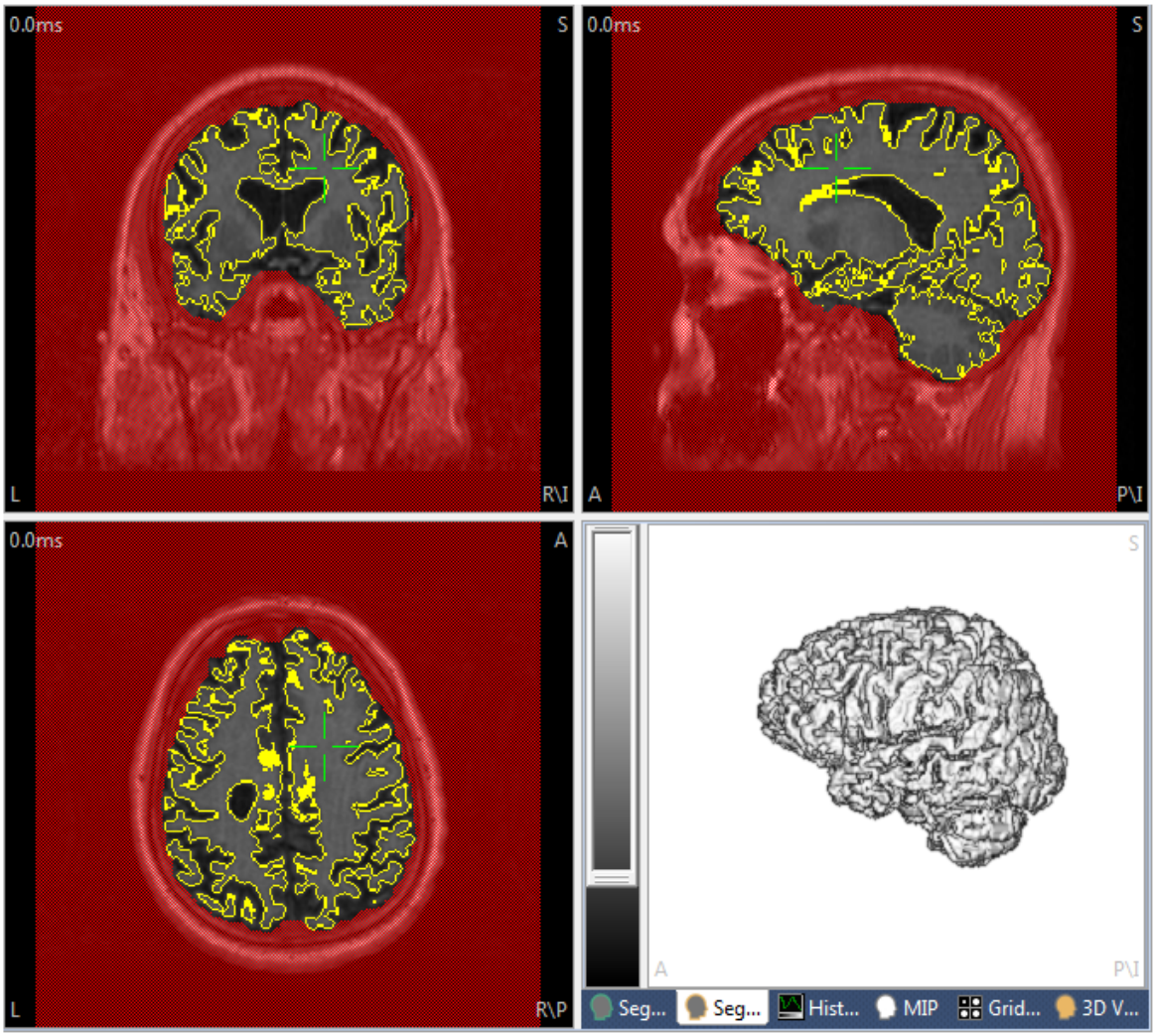




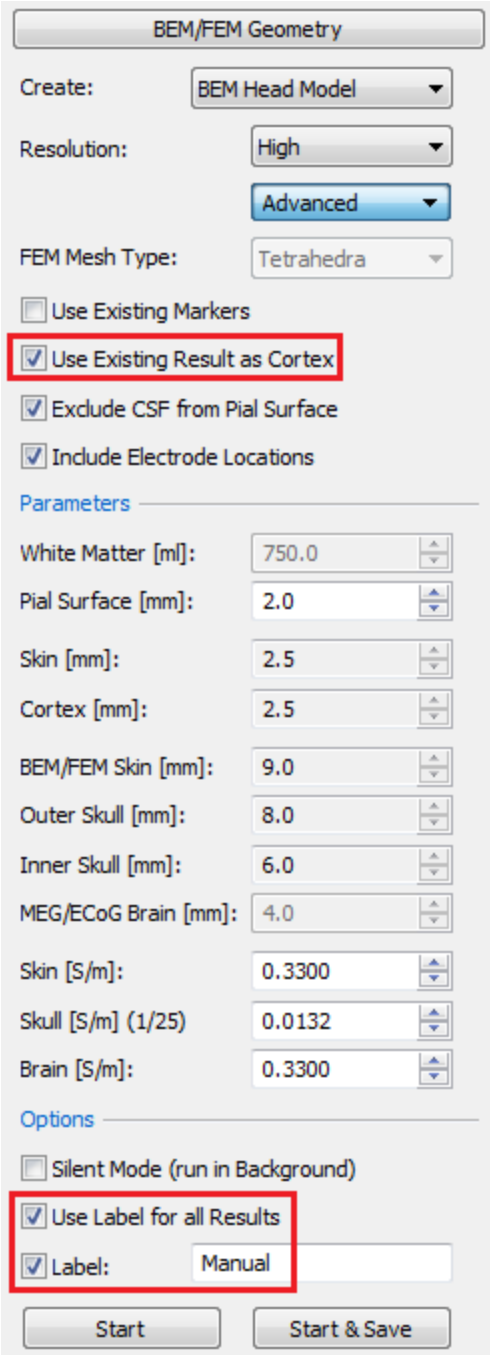
Morphological operations change the shape of the segmentation result. Markers do not interfere with morphological operations. The basic Morphological operations are **dilation** (inflation) and **erosion** (deflation). **Opening** is erosion followed by dilation. **Closing** is dilation followed by erosion. **Smoothing** is closing followed by opening.

6. Now use the exterior of this result as Stop Markers by selecting **Image Data** → **Segmentation Result** → **Add Exterior to Stop Markers**, or click the icon on the **Image Data** Toolbar.

7. In the Segmentation section, select a **Lower Threshold** of **60**. Place the cursor (seed point) into the white matter of the coronal view and press **Start**. The cortex now has a fuller definition, with better formed gyri and sulci.



8. The manually segmented cortex can be used for a new BEM model. In the BEM/FEM Geometry section, check **Use Existing Result as Cortex**, enable the **Label** field (call it *Manual*), and select a **High** Resolution. Enable **Use Label for all Results** to prepend "Manual" to all Surfaces and Overlays that are created. Press Start. The BEM Model will be created using the manually segmented cortex, and may be selected as the head model.



Because the BEM model keeps a certain minimum distance from the cortical source space, the new cortical model demands a new, enclosing BEM geometry.

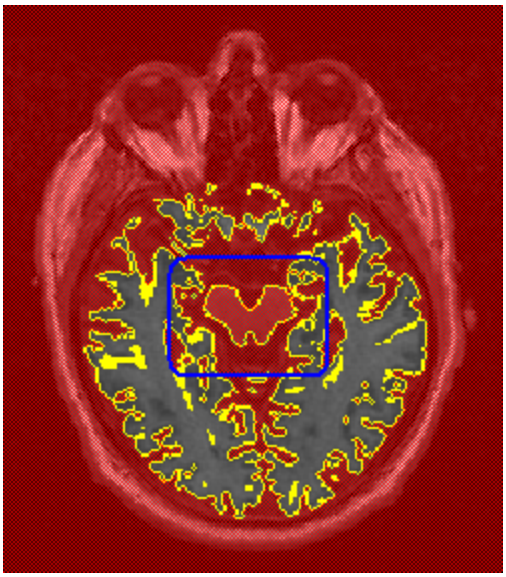
Next, we will remove the cerebellum manually by placing additional Stop Markers in an appropriate axial slice. Whether to remove the cerebellum or not is a matter of some debate. If you are performing CDR, the results may bleed into the cerebellum, and that might or might not make theoretical sense, depending on the activity that is being analyzed. For aesthetic reasons alone, people often elect to remove the cerebellum. What you should *not* do is create a BEM Model with the cerebellum removed. Doing so

will artificially alter the shape of the brain compartment, creating a compartment that does not conform to reality.

9. To re-import the segmentation result (overlay) for the cortex that was saved during the previous BEM setup, go to the Results list, *right click* on the Manual Cortex (manual) overlay, and select **Import Overlay**.

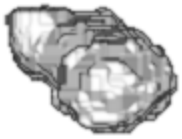
10. Use the exterior of the cortex as Stop Markers by selecting **Image Data** → **Segmentation Result** → **Add Exterior to Stop Markers**, or click the icon on the **Image Data** Toolbar.

11. Place additional Stop Markers in axial slice 46 to cut the cerebellum, as described above. Note that here we are placing the markers in a more superior slice than before.

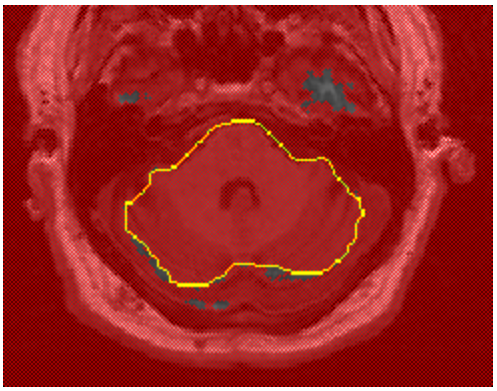


12. Set the Stop Markers to Off Edit Mode: Off. In the Segmentation panel, select **Find** for the **Seedpoint** and **Region Growing**. To segment the cerebellum, select a Lower Threshold of **68**, place the seed point into the *cerebellum* in any view (or use two views to be certain), and press **Start**. The segmented cerebellum will be seen.

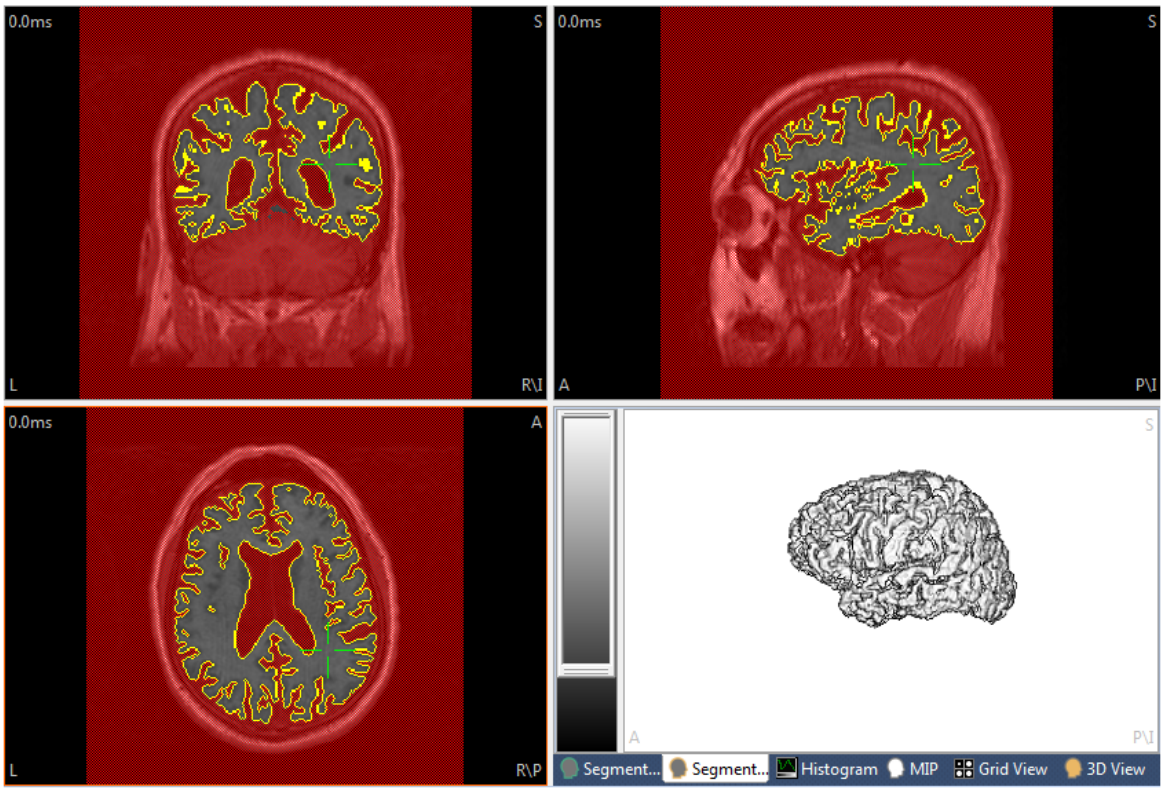
13. In the Morphology panel, set the **Mode** to **Closing**, with a **Dilation** radius of **12.0mm** and an **Erosion** radius of **10.0mm**. Press **Start**.



14. Select **Image Data** → **Segmentation Result** → **Add to Stop Markers** (*not* Add Exterior to Stop Markers, or use). The cerebellar areas are filled in with Stop Markers, and thus will be excluded from segmentation.



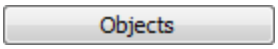
15. Select a **Lower Threshold** of **60**, place the seed point (cursor) in the *white matter*. Press **Start**. The cortex is segmented without the cerebellum.

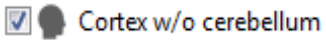


16. The next step is to create a triangle mesh of the cortex. In the

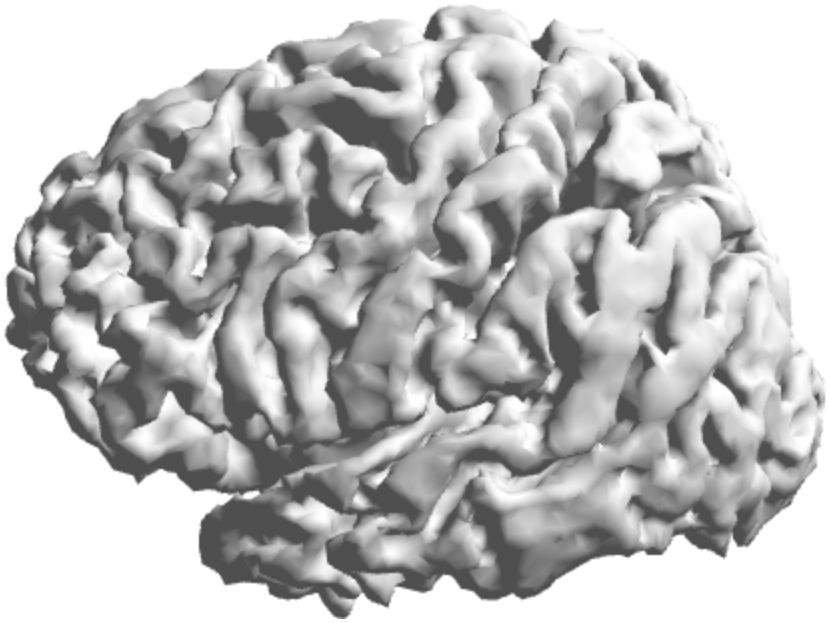
panel, select **Create Triangle Mesh** with a Resolution of **2.0mm**. In the label field, enter *Cortex w/o cerebellum*. Press **Start**.

17. Go to the



list, and see the new surface: 

, which can now be used for general purposes.

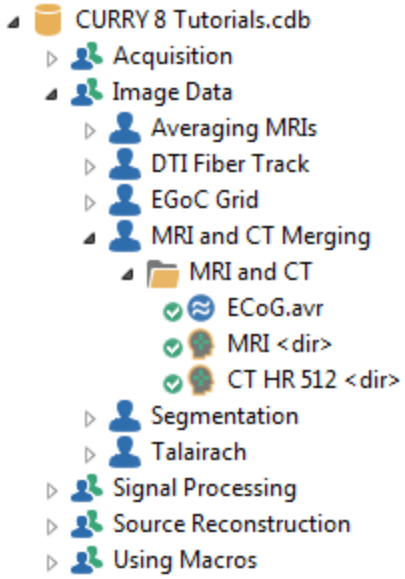


2.5.5 MRI and CT Grid Merging

One of the common uses of CURRY involves the combination of two image data sets, where, for example, the electrode positions for a cortical grid, as seen in the CT, need to be combined with the MR data that are used for creating the head model and source reconstruction.

The *ECoG.avr* file is the functional data recorded from an 8x8 cortical grid. There is as yet no file that contains the electrode positions for the grid - this is something we will create. The MRI and CT data were saved as individual slices, and the folders containing them were inserted into the Database. The MR and CT data have already been loaded into the Database, and the parameter files have been created.

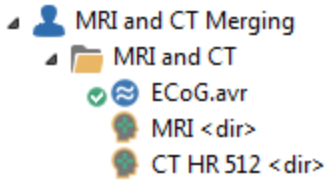
Locate the *MRI and CT* Study in the *CURRY 8 Tutorials* Database, a shown below.



Coregistering image data sets
When you load the image data for the first time, you will need to go through the **Image Data Parameters** windows. Once imported, parameter files are written and read in the future so you will not need to go through the **Image Data Parameters** windows again. In this Study, you can see by the green check marks that the image files have been imported previously. To simulate what you will experience when you import your own data files, we will first rename the existing parameter files, saving them in case you need to revert back to them.

To do this, *right click* on MRI <dir> and select **Open File Location**. This takes you to the folder containing the image data files. Go up one level to the *MRI + CT Co-registration* folder to see the parameter file: MRI.imd . *Right click* on it and **Rename** it to something like: Save MRI.imd . See also the CT HR 512.imd parameter file. Rename it as well. Again, this just saves the original parameter files should you need to revert back to them.

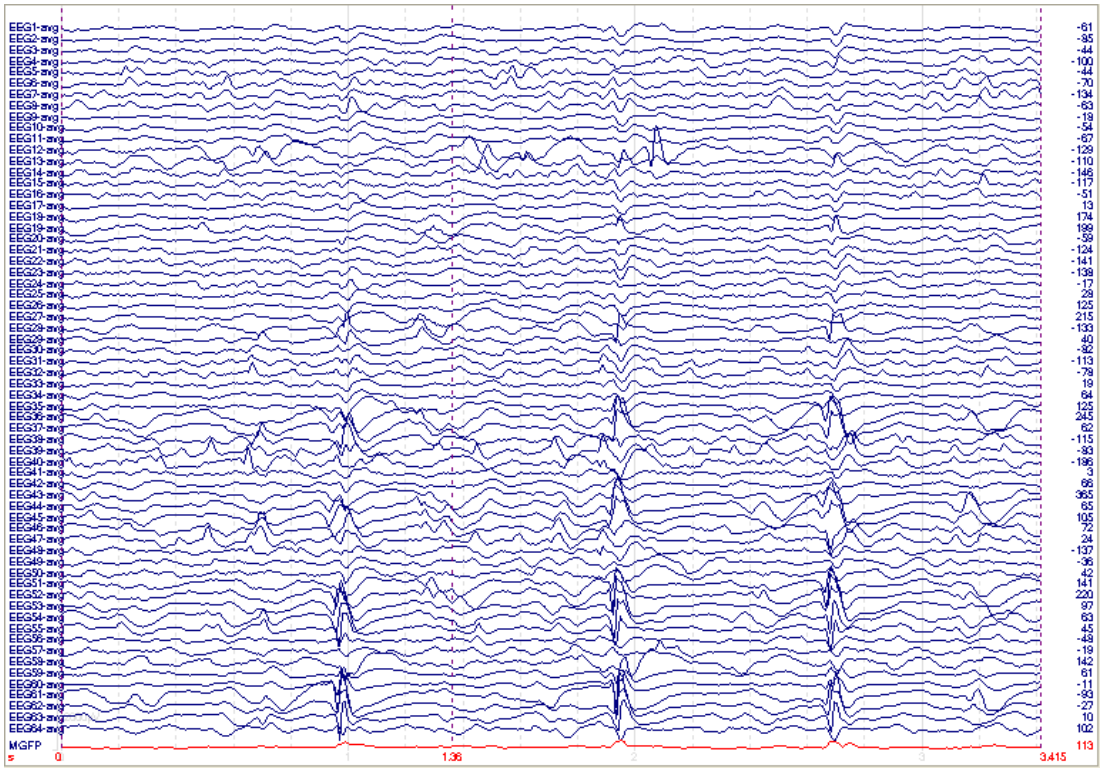
CURRY is at this point still displaying the green arrows. Close and reopen Curry. The green arrows are gone for the MRI and CT data, and this is now the state you will have when you load image data files for the first time.



Note that the MRI data are entered above the CT data - this is necessary for a couple of reasons. The MRI data are imported first, and the landmarks are measured. Then the CT data are imported, and the landmarks are approximated. Volume-based coregistration is used (via the **Autodetect** button described in Step 4 below), and the CT data set is in that way fitted to the MRI data set - and therefore the MRI data

need to be loaded first. Also, when verifying that the coregistration has been accomplished accurately (see the **Merging the two image data sets** section below, Step 1), you can only import the Image Data 2 results (CT bone segmentation) to Image Data 1 (MRI data) - you cannot do this step in the opposite direction. So again, the MRI data should be inserted into the Study above the CT data.

1. Open the Study. 64 channels of grid data are displayed.



Notice that there are additional display tabs.

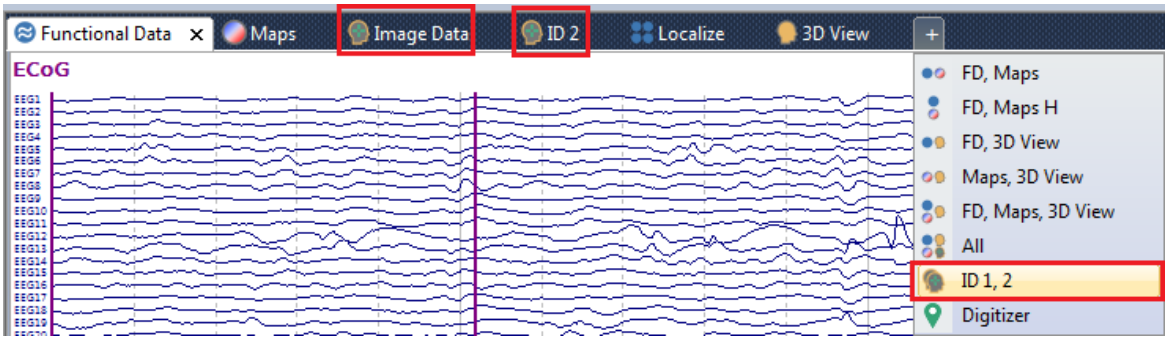
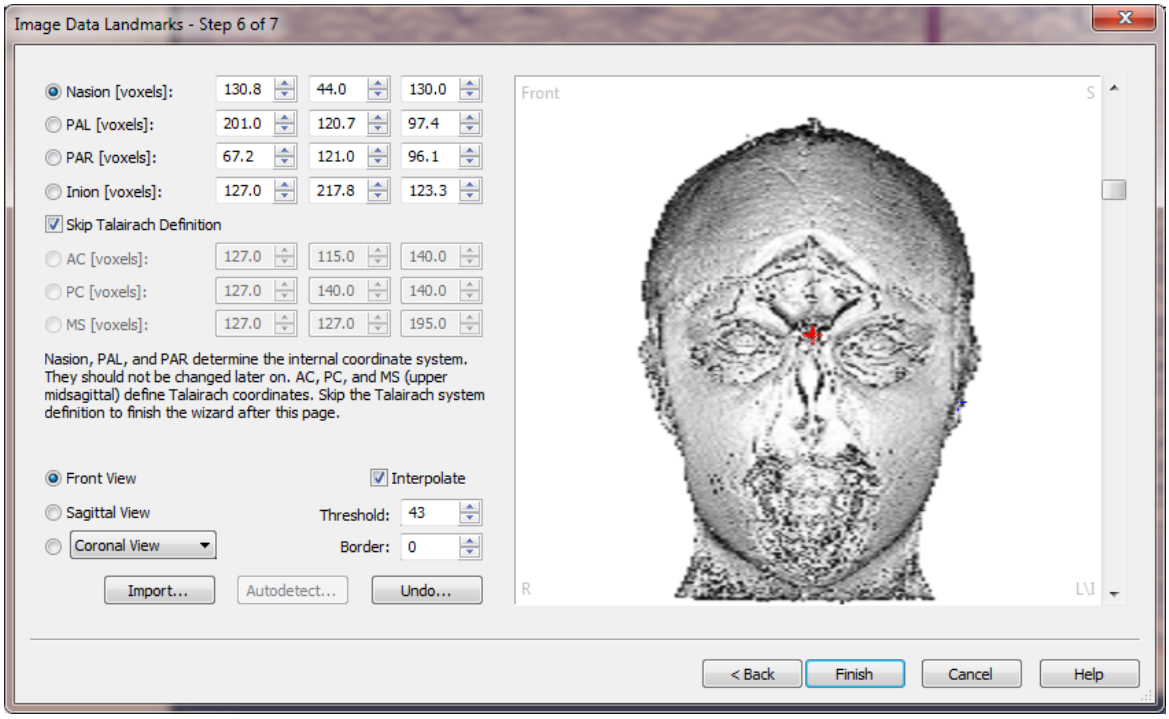


Image Data, or **ID 1**, contains the MRI data (it appears first in the Database). The MRI data need to come first because some options between data sets are uni-directional. **ID 2** contains the CT data, and **ID 1, 2** contains both. Some operations will be specific to the MRI data and others to the CT data. You can either switch back and forth from **Image Data** to **ID 2** to focus on the desired data set, or you can use **ID 1,**

2 and change the focus by clicking in the desired data set. We will switch back and forth to avoid confusion.

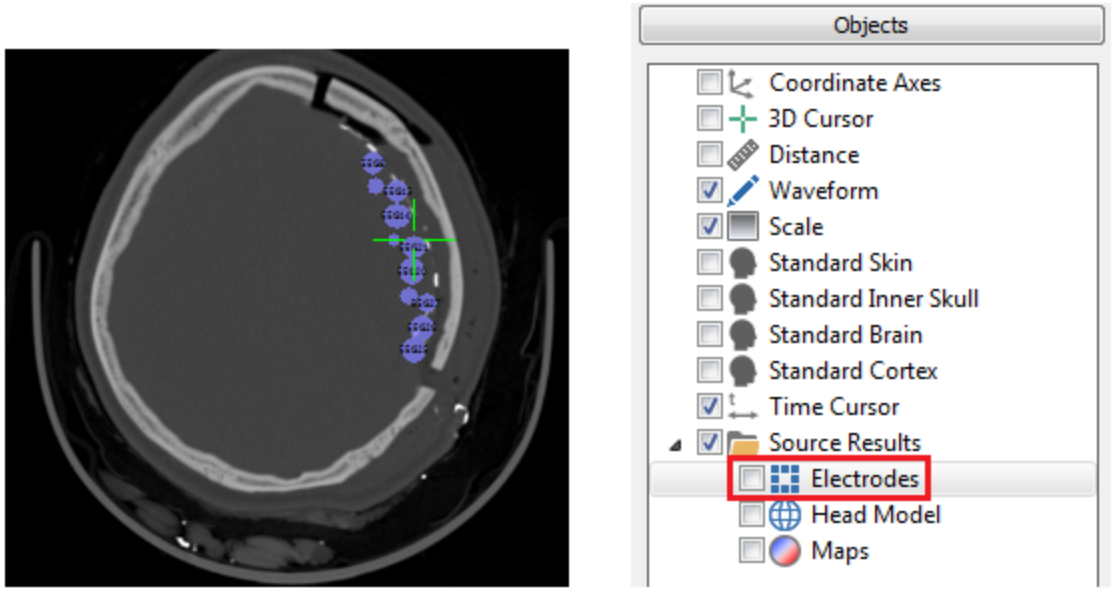
2. Click the Image Data tab. The **Image Data Parameters** windows appear. We could go through all of the steps, or we can see how well Autodetection works with this file. Click the Autodetect and Load Image Data option at the bottom of Step 1, and click **Finish**. The file is then displayed and it appears correct (this may not always be correct with other data files; some parameters may need to be entered manually).

3. We do need, however, to measure the Landmarks. Go to **Image Data** → **Landmarks**. This takes you back to Step 6 in the **Image Data Parameters** windows. Set the Nasion, PAL, and PAR landmarks. Note that there is some "wrap-around" in this file. Approximate the Nasion as best as you can (see Step 6 in the **Image Data Parameters** tutorial for more details). It is not necessary to define the Inion. Skip the Talairach settings. Then click **Finish**.



4. Click ID 2, and again the **Image Data Parameters** windows will appear. Click the **Autodetect and Load Image Data** option, and **Finish**.

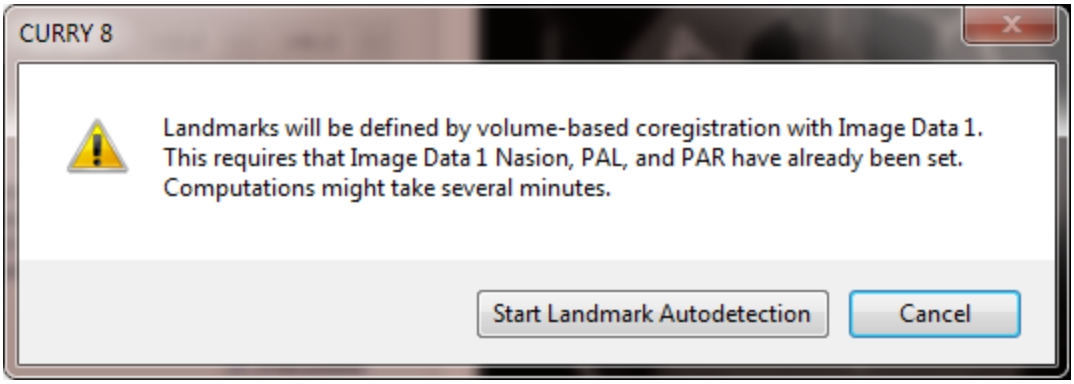
If you see electrodes from a previous tutorial where they had been located, select the 3D View, and then turn off the **Electrodes** in the **Objects** list. Then return to the ID 2 display.



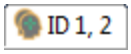
5. Both files have been loaded at this point, but they have not been coregistered. With the CT data still displayed, go to **Image Data → Landmarks**. This takes you back to Step 6 in the **Image Data Parameters** windows. Here we need only to approximate the landmark positions. Grossly measure the Nasion, PAL and PAR locations - excessive accuracy is not required here. We will use the landmarks from **Image Data 1** and perform a volume-based coregistration. **Skip Talairach Definition** should be enabled (default).

Click **Autodetect** and see the following message. In this case - as in most cases - simply click **Start Landmark Autodetection**. Note again that it is necessary to load

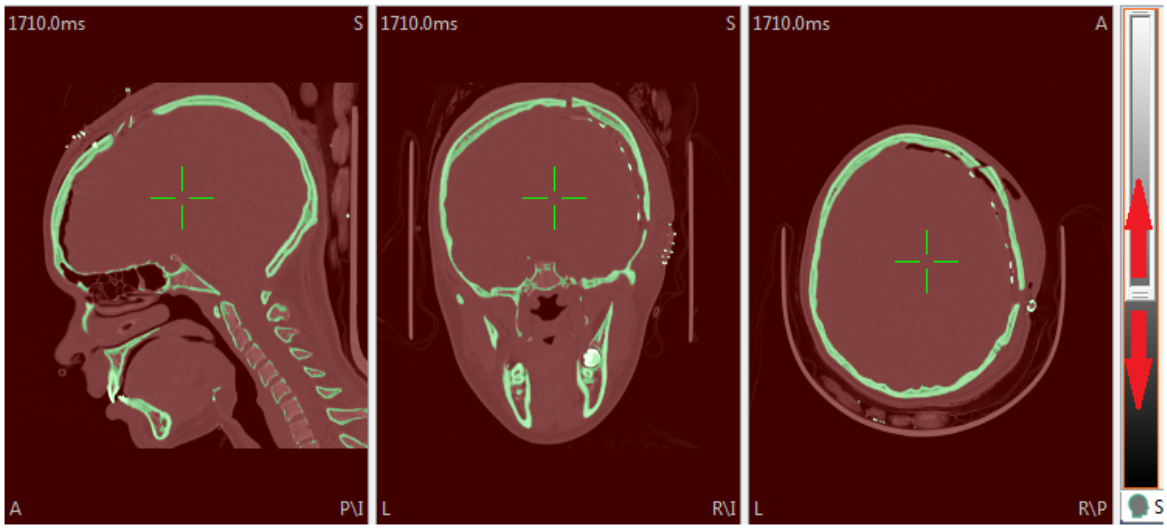
the MRI data first and measure the landmarks before using volume based coregistration with the CT (or other) data sets.



This will take a short while to run. When it is finished, click **Next** and **Finish**. Now the two image data sets are coregistered. If you have a third image data set, repeat the same steps you did for the second image data set.

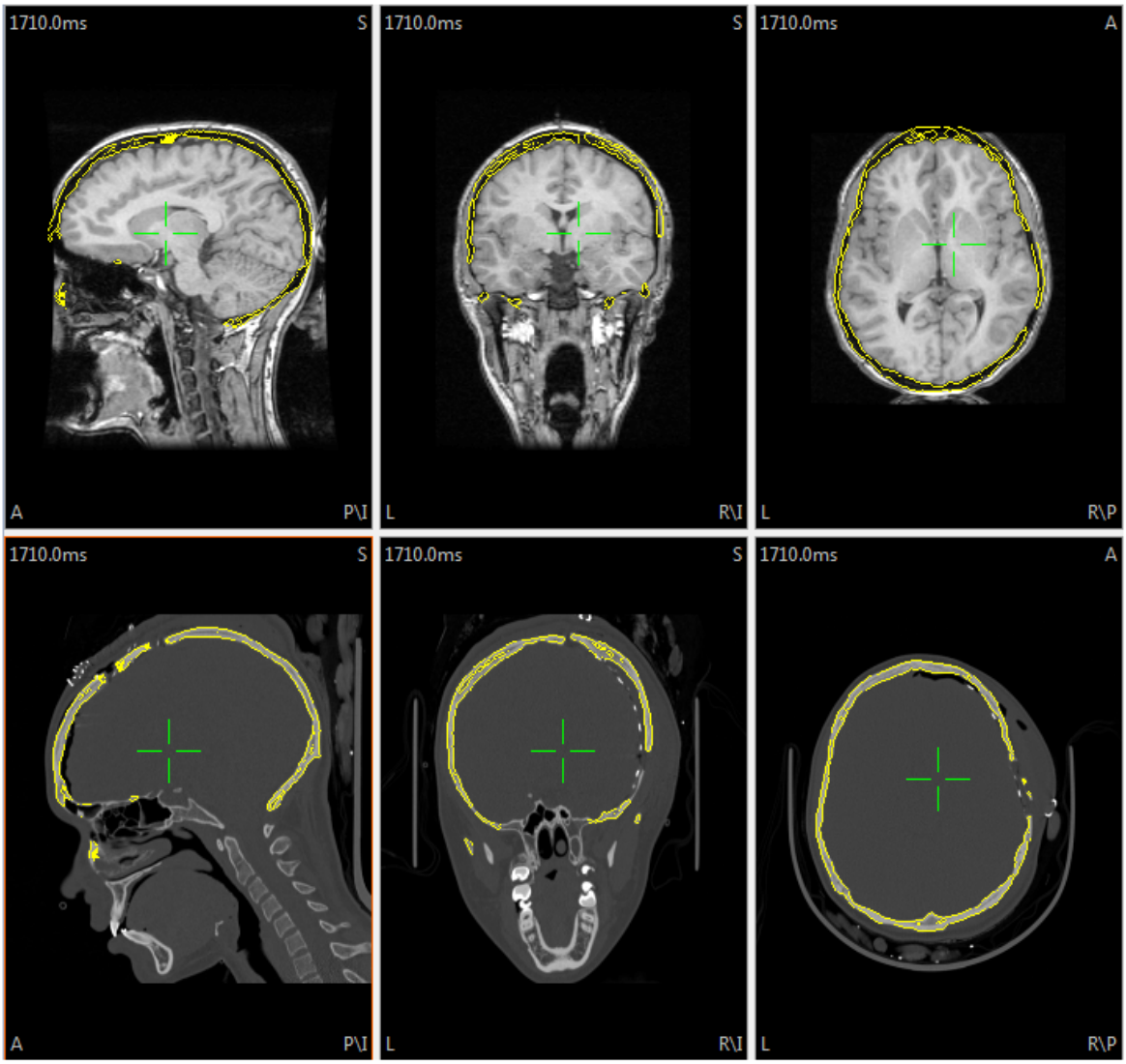
Merging the two image data sets
This is a continuation of the steps above.
1. First, we will perform a quick verification to ensure that the data sets have been coregistered properly. Select 

. Drag the slider to the right of the CT data to see green pass markers for the bone structures (click in the middle of the brain, if needed).



Expand the **Segmentation** panel and click

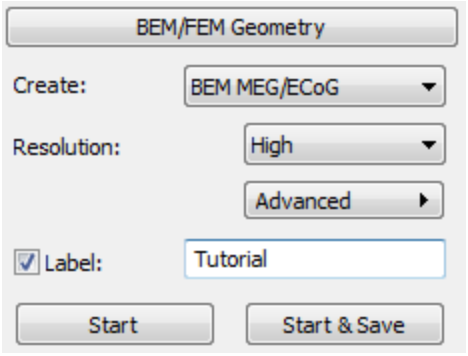
. (Use a lower Segmentation Threshold of about 103). Then go to **Image Data** → **Segmentation Result** and select **Export to Image Data 1** (make sure that one of the CT windows has the focus, i.e., outlined in red). If coregistration has been successful, the boney structures from the CT will be seen correctly in the MRI images.



If you find that your results are askew, or too large or small, this means there has been an error in importing one or the other data set (return to the **Image Data Parameters** windows and check file parameters).

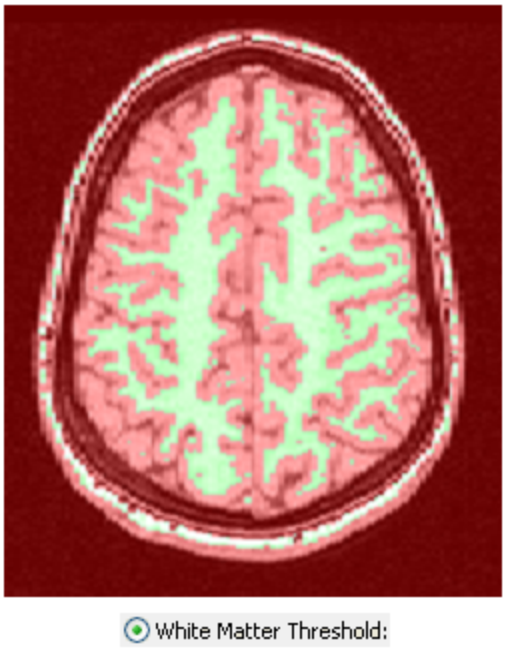
Click the **Clear Segmentation Result** icon for both data sets.

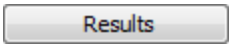
2. Select Image Data (the MRI data). Create a BEM model as shown. Since we have ECoG data, and we want to perform dipole modeling, we will select **BEM MEG/ECoG** for **Create**. Enter *Tutorial* for the **Label**. Click the Start button, as we will not save the results. This will take a few moments to run.



When using your own data files, you may sometimes encounter a message saying that you need to review the segmentation thresholds, and the process will be terminated. In other cases, the head model will be created, but the cortex, for example, may be under-segmented, and appear atrophied. In both instances, go to **Image Data** → **Segmentation Thresholds**.

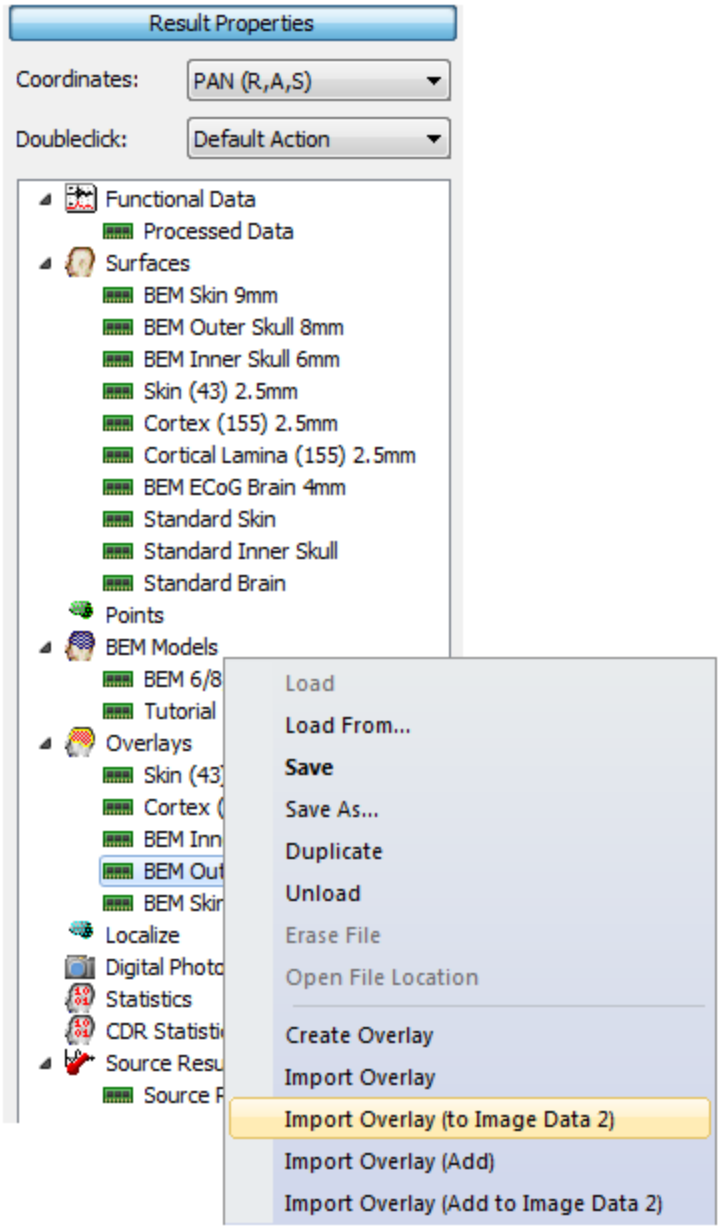
The Cortex Threshold is generally the most important one. It is what later determines the shape of the cortex created by BEM Geometry (automatic segmentation). If this value is too high, the cortex will look atrophic (eroded). In such a case, the cortex threshold will appear more like a white matter-gray 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.



3. In the 

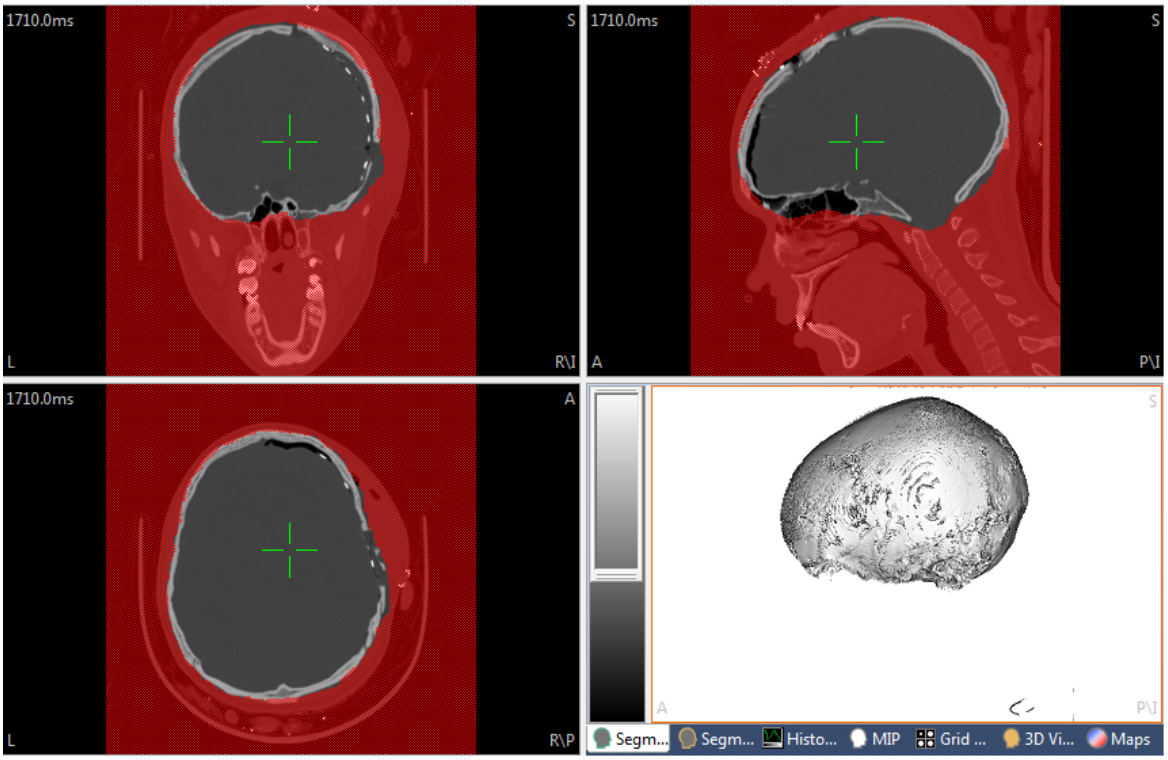
panel, *right click* on the **Overlay** for the **BEM Outer Skull** and select **Import Overlay (to Image Data 2)**. The outer skull is selected because

we want to see only the electrodes later on, and the Inner Skull might be too close to the actual electrodes.

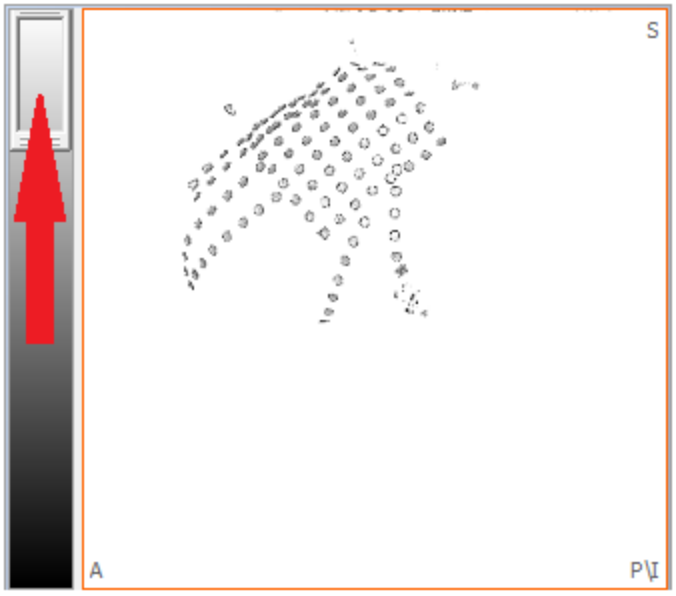


4. Select the ID 2 display. Click the **Add Exterior to Stop Markers** icon (on the Toolbar). Here we wish to remove the cables and other structures. Setting everything outside of the Outer Skull to Stop Markers will exclude the entire region.

Click the **Clear Segmentation Result** icon .



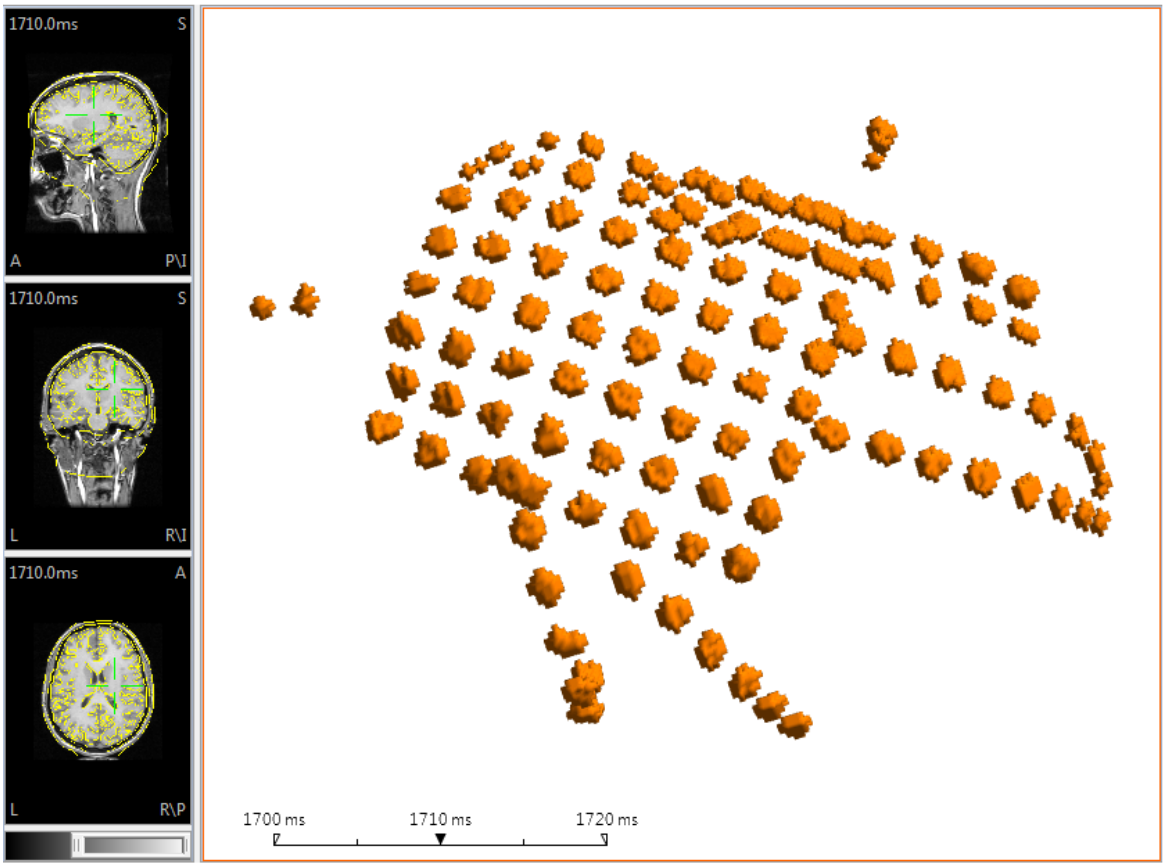
5. In the CT **Segmentation Preview** pane, *right click* and select **Omit Stop Markers** (if needed). Using the sliding scale to the left of the Segmentation Preview, change the threshold so that the electrodes become visible (drag it upward).



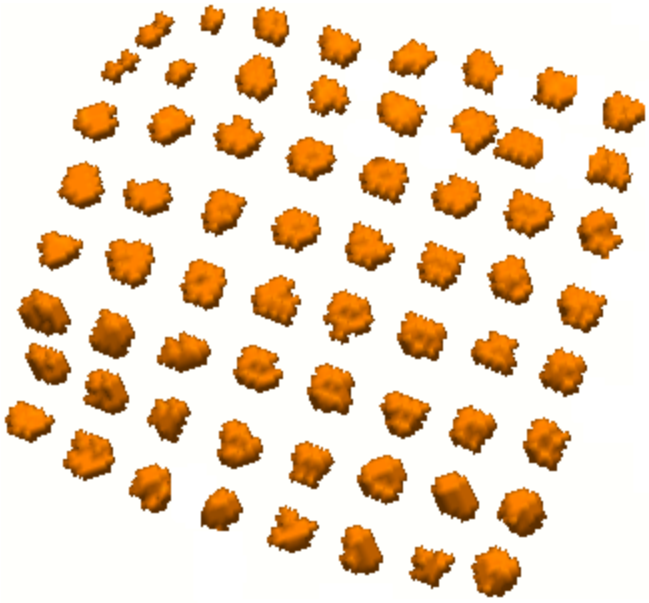
6. In the Segmentation panel, select **Dilated Thresholding** and click **Start**. You may not see anything happen. This is an optional step, not always needed, that can be used to enlarge the electrodes to make it easier to select them later.

7. In the CT **Segmentation Results**, *right click* and select **Create Voxel Mesh**. You will not see anything happen, but a new Surface has been created (seen in **Results** and in the **3D View**).

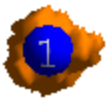
8. Select the Localize display, and select the 3D View display (at the bottom of the display). In this case, we selected **Right View** from the context menu, and used *Ctrl+drag* to reposition the display, *Shift+drag* to move the entire display, and the *mouse wheel* to enlarge it. If you do not see the grid electrodes, make sure the **Voxel Mesh** has been enabled in the **3D View** Objects list.



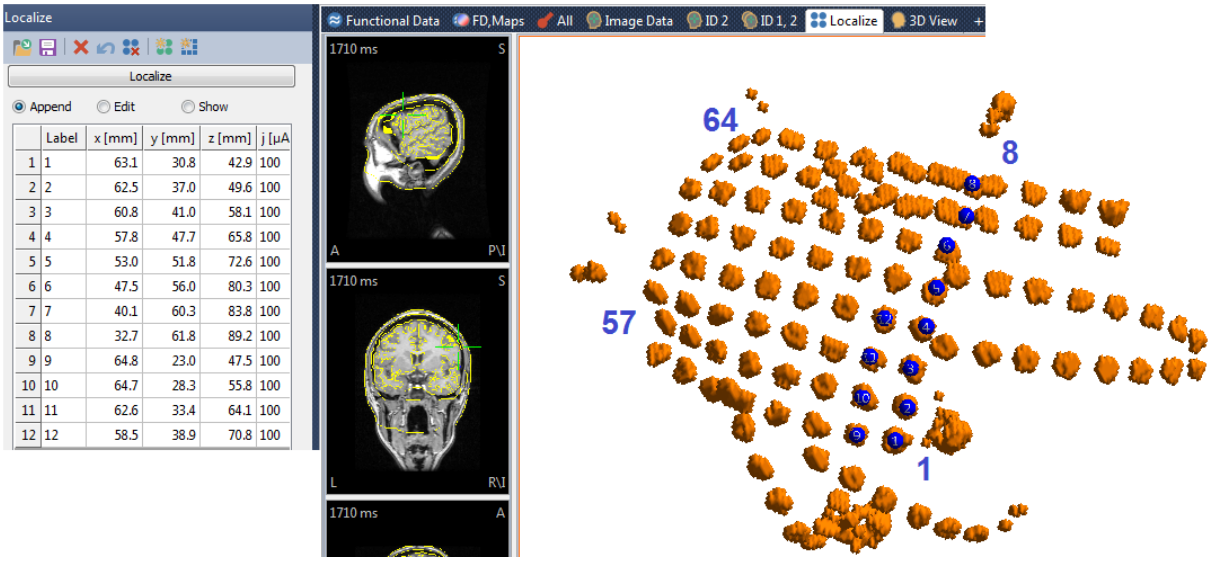
9. Now it is a matter of clicking the electrodes in the same order as they appear in the Functional Data. The Functional Data in this file were recorded from the 8x8 grid. Notice there are additional grids and strips. We can ignore these, and select only the electrodes in the 8x8 grid. Care must be taken to not select the other electrodes, which in some cases are very close. If we could magically remove the extraneous electrodes, the grid would appear much simpler, which may be the more likely case you will encounter.



Instead, we will just select the electrodes carefully. You need to know how the electrodes in the data file correspond to the digitized ones. The actual electrode labels are EEG1 through EEG64. EEG1 is the lower right corner, and EEG 64 is the upper left corner, moving from lower to upper. The electrodes must be clicked in the same order as they appear in the data file. The first 12 are shown below; note that they are numbered as you click them.

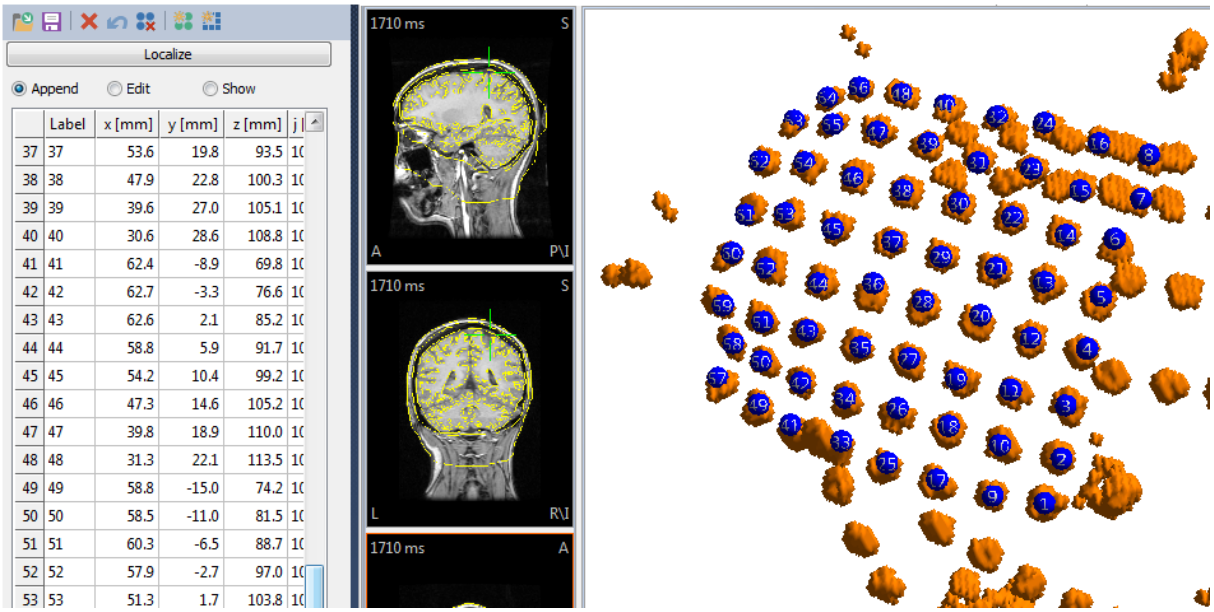


With each click, there is a new entry in the Localize list. If you make a mistake, *right click* in the Localize display and select **Delete Entry**, or **Delete All Entries** (or click the button above the localize list) to start over.

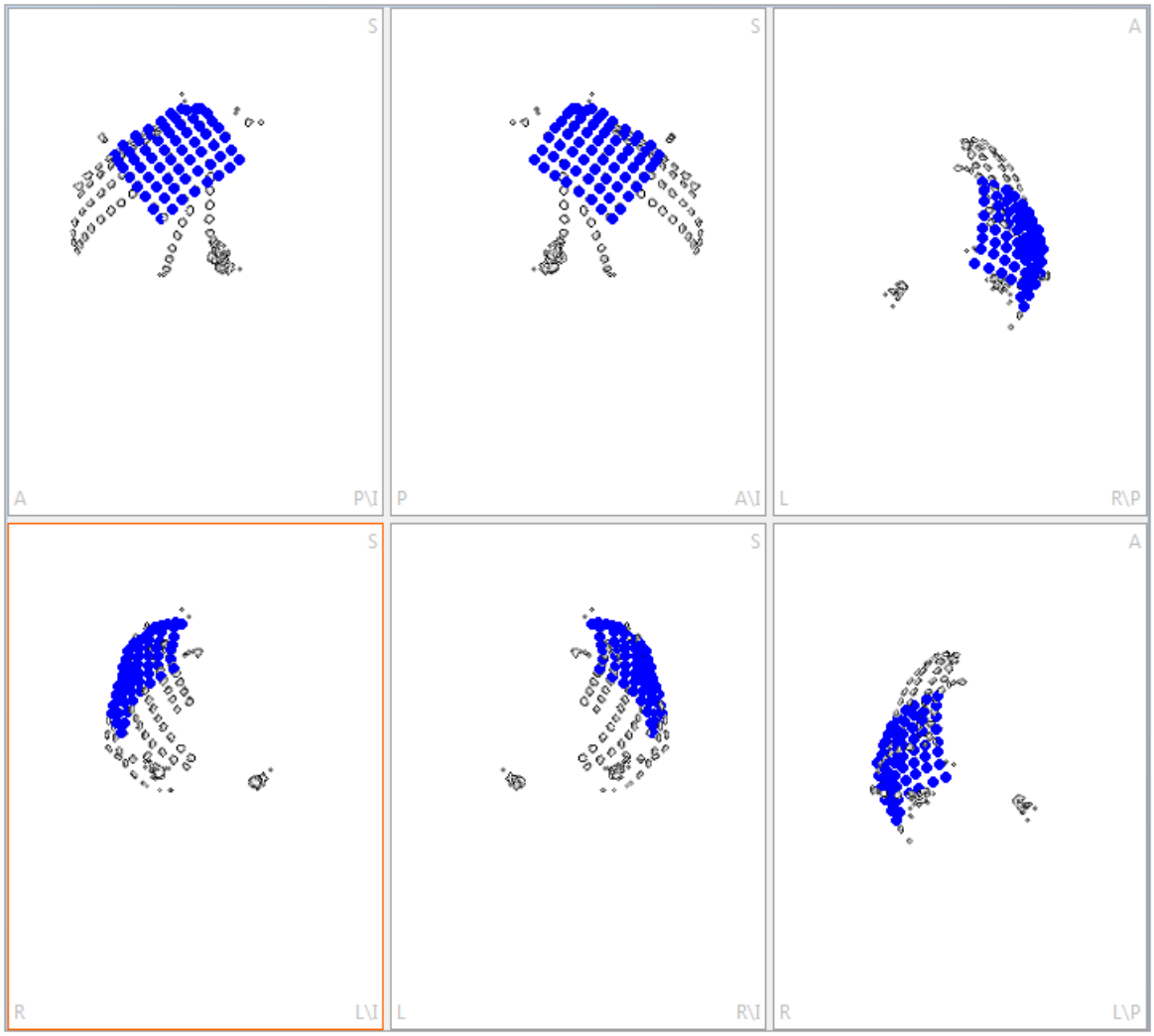


The complete grid appears as follows. It is not necessary to rename the electrodes to match those in the data file; the order is what matters.

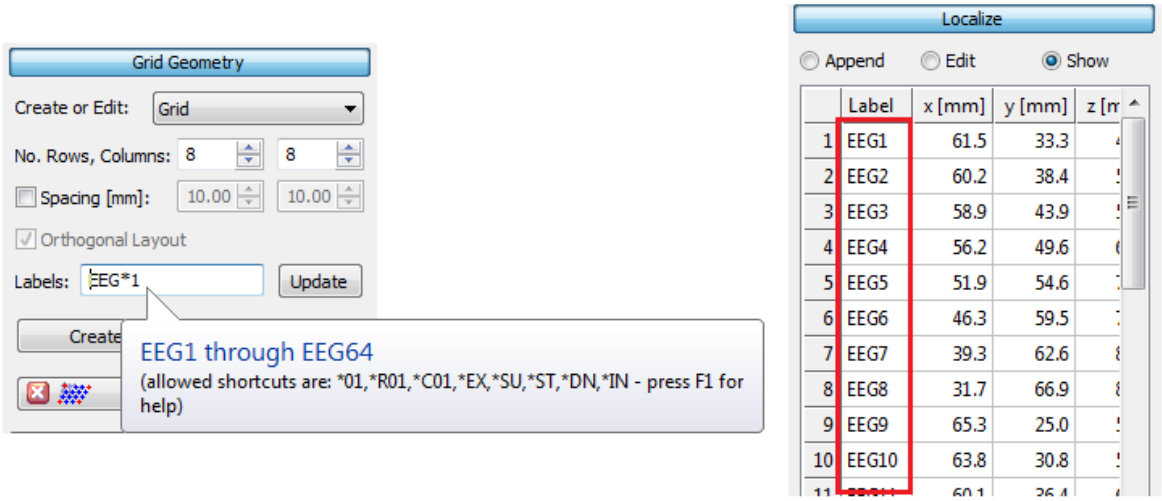
(Sometimes an electrode cannot be seen. In that case, click the next electrode instead and select **Move Halfway Towards Previous** from the context menu. The value of the estimated position will be entered into the list).



10. Still in **Localize**, switch to **Segmentation Result 2**, *right click* and select **Project All to Nearby Maxima**. This centers the dots within the electrode "blobs".

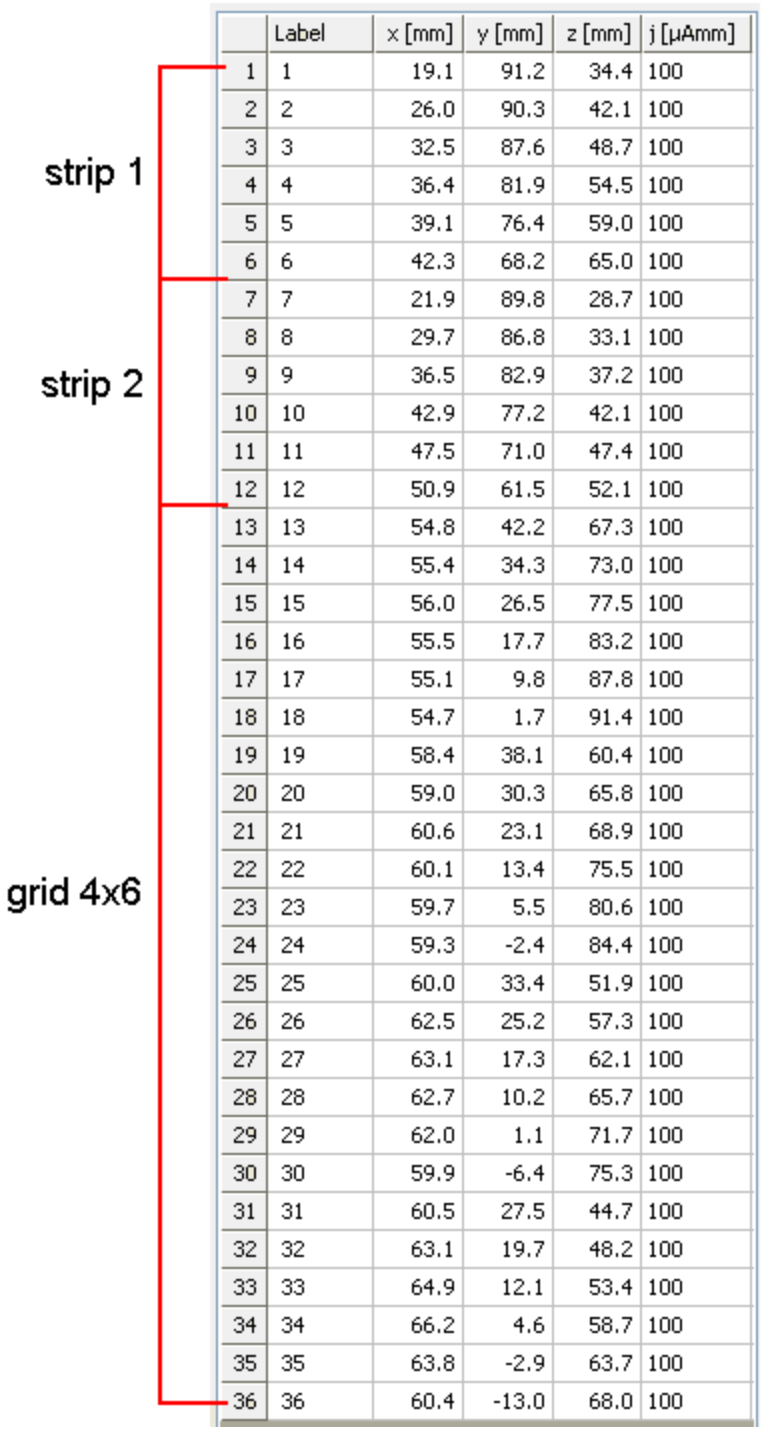


11. You may relabel the positions, if desired. This is not necessary, but it can be convenient to make the labels match, or nearly match, those used in the Functional Data file. In this case, we can make them exactly the same. The Functional Data labels go from "EEG1" through "EEG64". Expand the Grid Geometry panel (under **Localize**). Select **Grid** and set the Number of **Rows** and **Columns** to **8**. For the Labels, just enter "EEG*1". The Tooltip confirms that the new labels will also be "EEG1" through "EEG64". Then click the Update button to apply the changes, which are seen in the Localize list, and on the electrodes themselves.



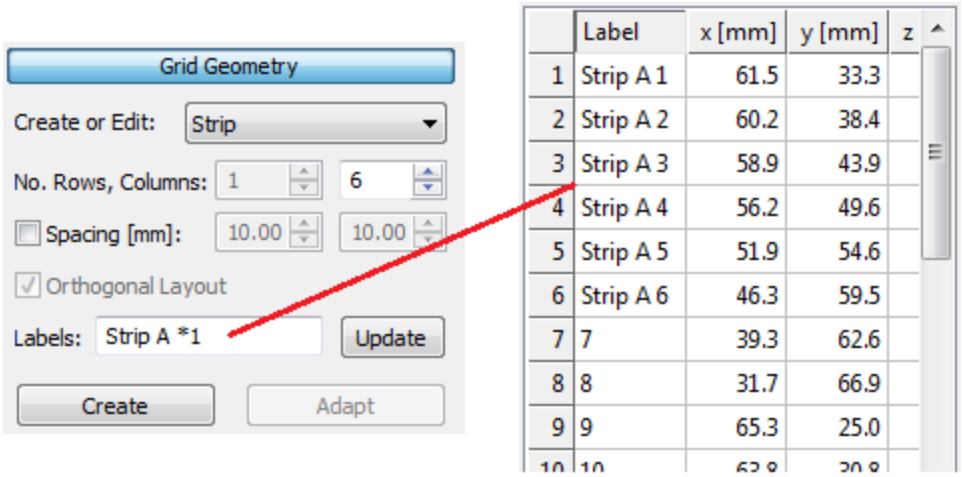
You may also relabel the electrodes manually by clicking a label in the **Label** column and entering the desired text.

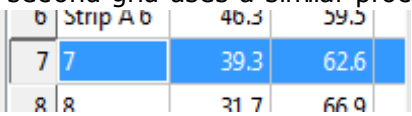
++++++



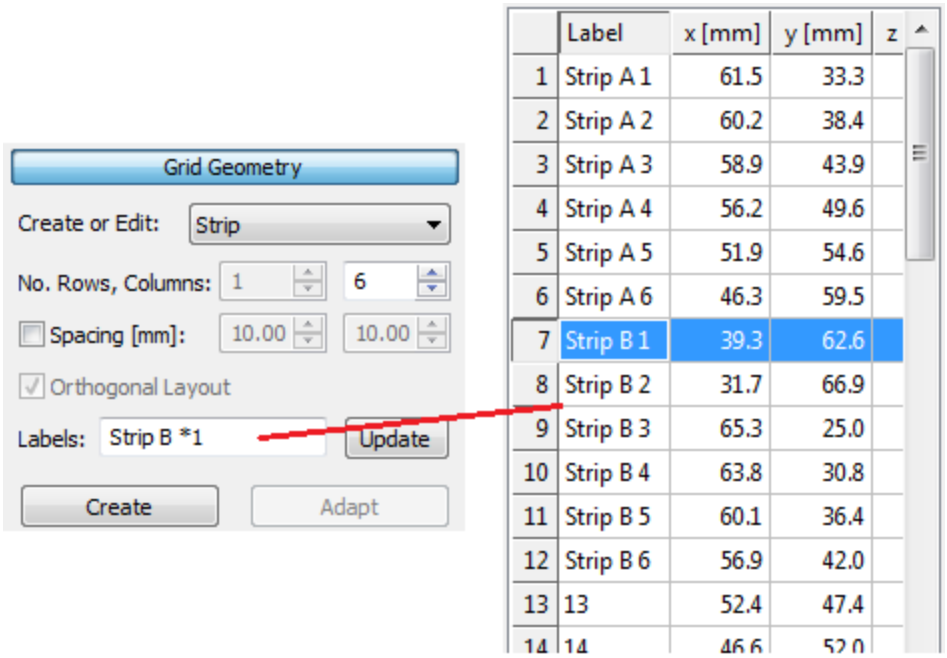
	Label	x [mm]	y [mm]	z [mm]	j [µAmm]
1	1	19.1	91.2	34.4	100
2	2	26.0	90.3	42.1	100
3	3	32.5	87.6	48.7	100
4	4	36.4	81.9	54.5	100
5	5	39.1	76.4	59.0	100
6	6	42.3	68.2	65.0	100
7	7	21.9	89.8	28.7	100
8	8	29.7	86.8	33.1	100
9	9	36.5	82.9	37.2	100
10	10	42.9	77.2	42.1	100
11	11	47.5	71.0	47.4	100
12	12	50.9	61.5	52.1	100
13	13	54.8	42.2	67.3	100
14	14	55.4	34.3	73.0	100
15	15	56.0	26.5	77.5	100
16	16	55.5	17.7	83.2	100
17	17	55.1	9.8	87.8	100
18	18	54.7	1.7	91.4	100
19	19	58.4	38.1	60.4	100
20	20	59.0	30.3	65.8	100
21	21	60.6	23.1	68.9	100
22	22	60.1	13.4	75.5	100
23	23	59.7	5.5	80.6	100
24	24	59.3	-2.4	84.4	100
25	25	60.0	33.4	51.9	100
26	26	62.5	25.2	57.3	100
27	27	63.1	17.3	62.1	100
28	28	62.7	10.2	65.7	100
29	29	62.0	1.1	71.7	100
30	30	59.9	-6.4	75.3	100
31	31	60.5	27.5	44.7	100
32	32	63.1	19.7	48.2	100
33	33	64.9	12.1	53.4	100
34	34	66.2	4.6	58.7	100
35	35	63.8	-2.9	63.7	100
36	36	60.4	-13.0	68.0	100

Expand the **Grid Geometry** panel and select **Strip**. Set the number of **Columns** to **6**. For **Labels**, we entered **Strip A *1**, and clicked **Update**. The resulting new labels are seen in the list.

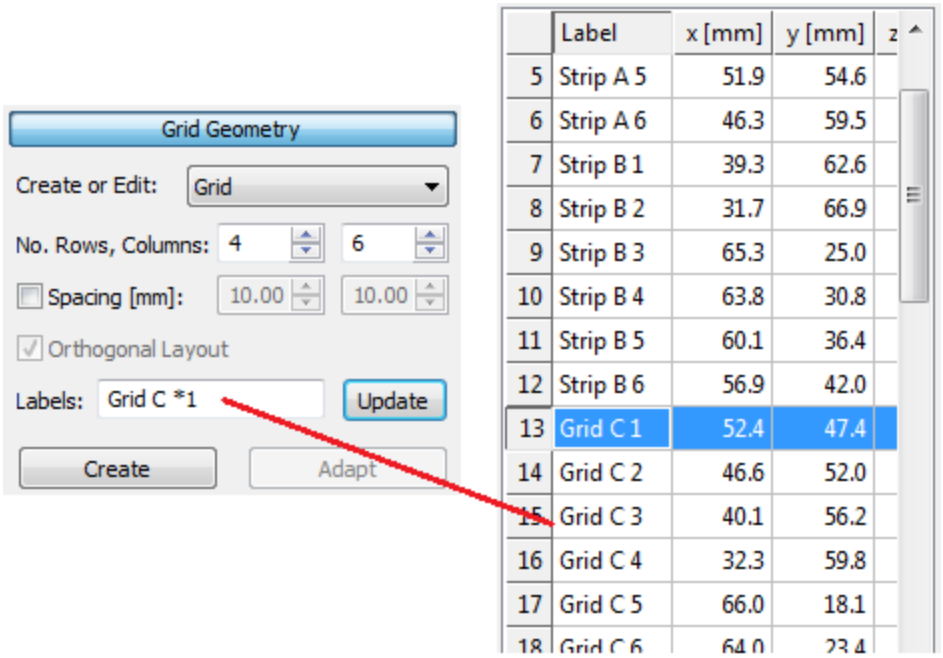


Relabeling the second grid uses a similar process. First, highlight the first line of the second strip: 

. Then just change **Strip A *1** to **Strip B *1** and click **Update** (and click **Yes** to the message).



Lastly, highlight line 13, set **Create or Edit** to **Grid**, and enter **4** for the number of **Rows**. Change the **Label** to **Grid C *1** and click **Update**.



When the electrodes are later displayed (as in the steps below), they will have these labels. Again, the most important thing to remember is that the list of Localize points must be in the same order as the channels in the functional data file; the labels may be different, but the order must be the same.

The individual grids and strips can be treated independently, as shown in the **Using Multiple Grids and Strips** section below.
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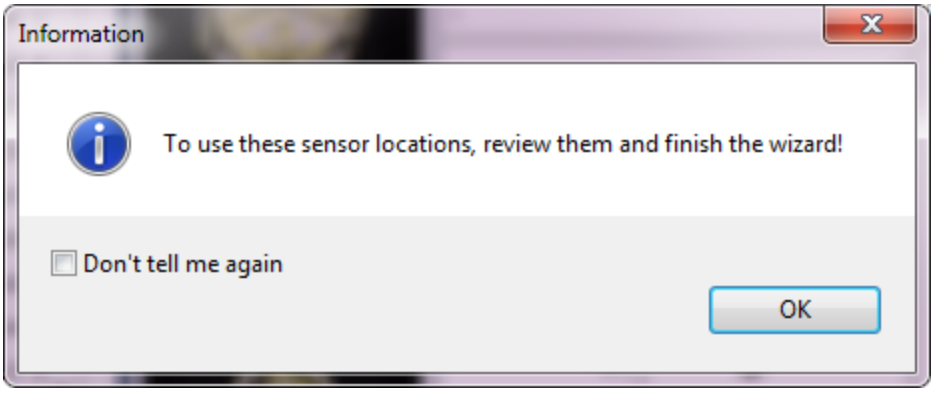
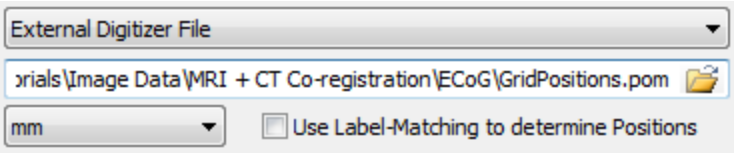
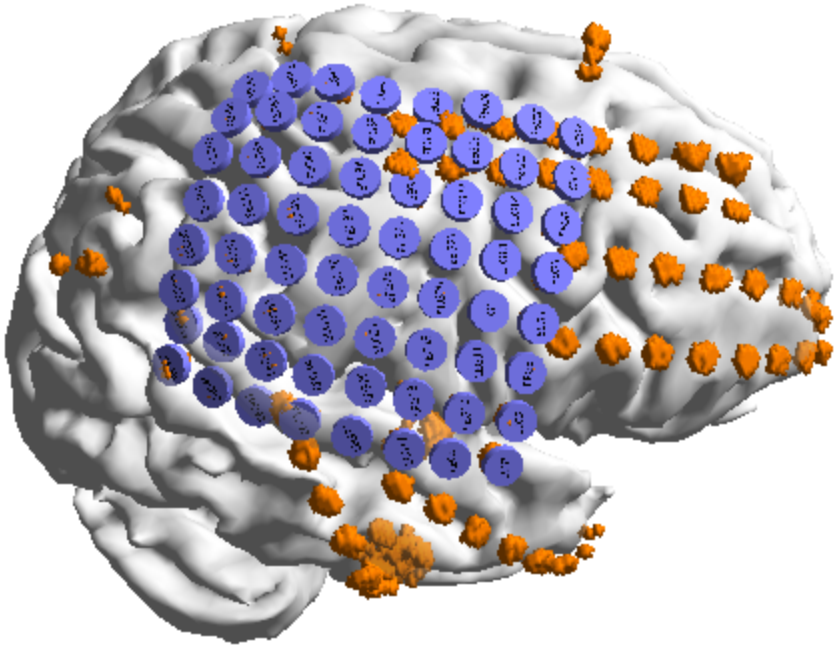
12. In the Localize panel, at the top of the panel, click the **Save and Use as Digitizer File** button. A Save As window will appear allowing you to select a folder and file name *(GridPositions.pom)* for the .pom file - the file containing the positions we have just created. A message appears, saying that if we want to use these new positions, we have to go to the Functional Data Import Wizard, review them, and save the results.



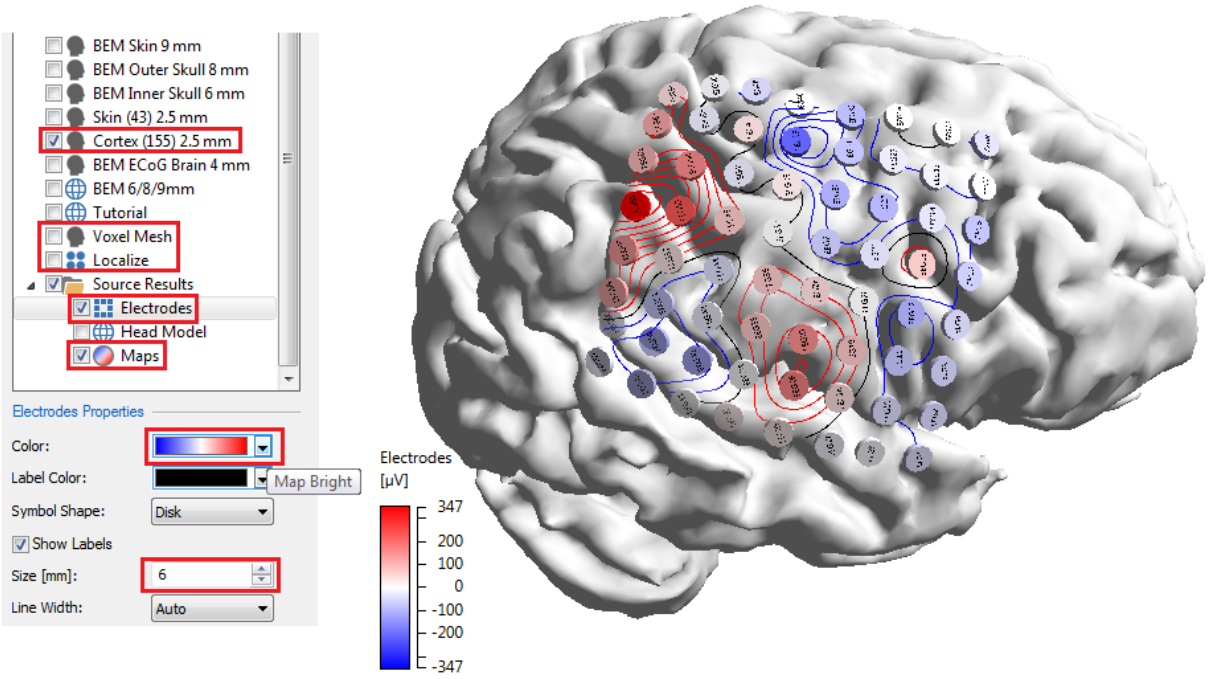
13. The second page of the Wizard appears, with the .pom file selected automatically.



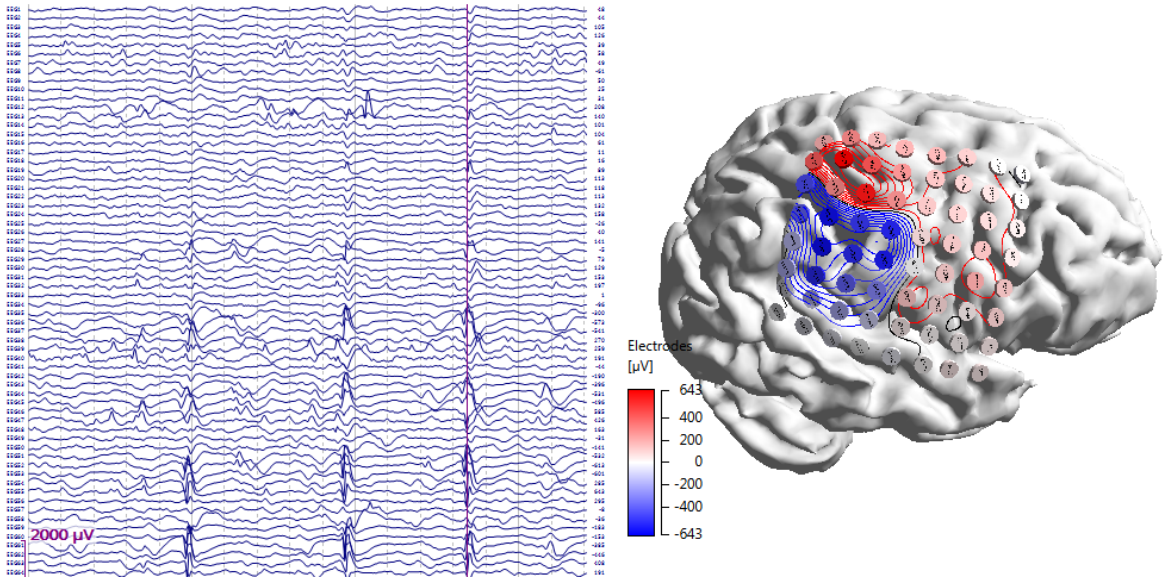
The grid electrodes are displayed. Then click **Finish**. Incidentally, you may also change the labels from within the Wizard. You will need to click the **Back** button to make the change(s), then **Next** and **Finish**. **Electrodes, Voxel Mesh**, and the **Cortex** were enabled. Set its **Transparency** to **100%**.



14. Now disable the display of the **Voxel Mesh**. In the **Properties** for **Electrodes**, select blue-white-red (**Map Bright**) for the **Color**. Each electrode will then become brighter (blue or red) as the voltage increases or decreases for the displayed time point (you must use a color scale with white as the middle color to use this option, or else the display will be confusing). Set the **Size** to **6mm**. Lastly, enable **Maps** to see the contours.

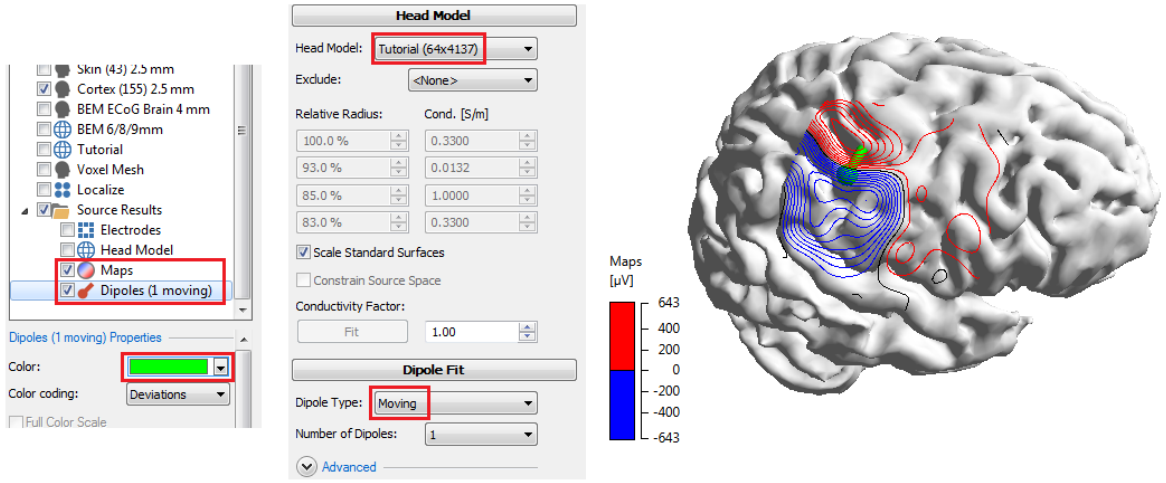


15. When you go to FD, 3D View, and select a Timerange (spike at 2685 ms), you will see the functional data displayed on the grid.



16. If you wish to perform source reconstruction*, select the **Tutorial ECoG Head Model** we created earlier, and select a **Dipole Type** (or CDR). The **Moving** dipole is seen in red below. The **Electrodes** were turned off and the **Line Width** for **Maps** was set to **1** to make it easier to see the dipole.

*Source reconstruction with depth electrodes, grids, strips, etc., is questionable and should generally be avoided, or used with caution.

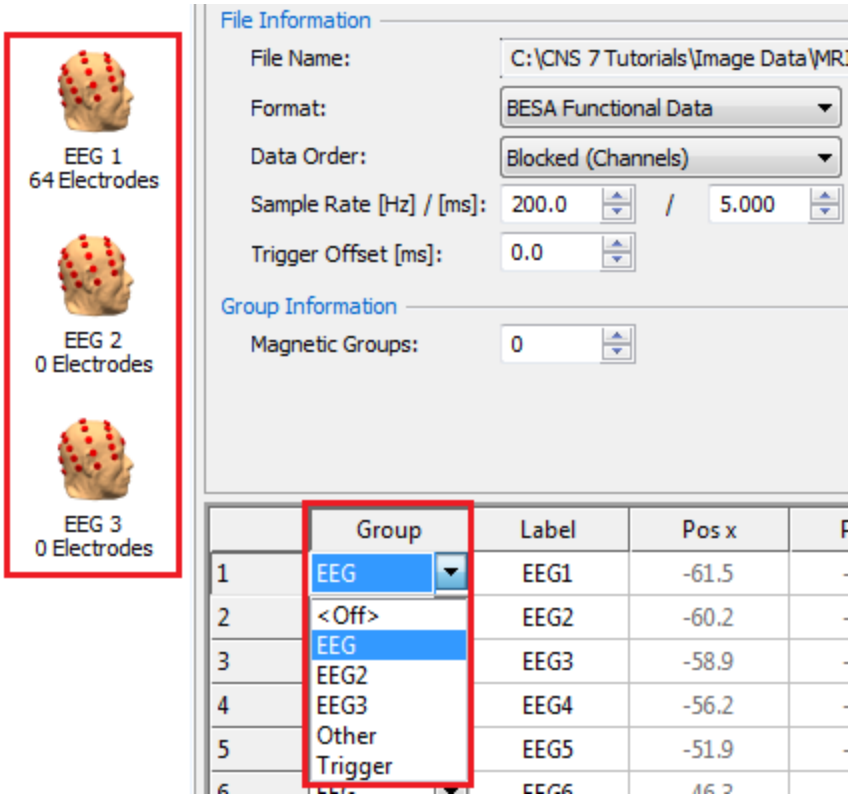


Close the Study without saving the results.

Using Multiple Grids and Strips

It is common to have more than one grid or strip, and you will likely wish to treat these independently. Pretend for the sake of demonstration that the 8x8 grid we have been using is really a 4x8 and two 2x8 grids. Go to the Data Parameters wizard .

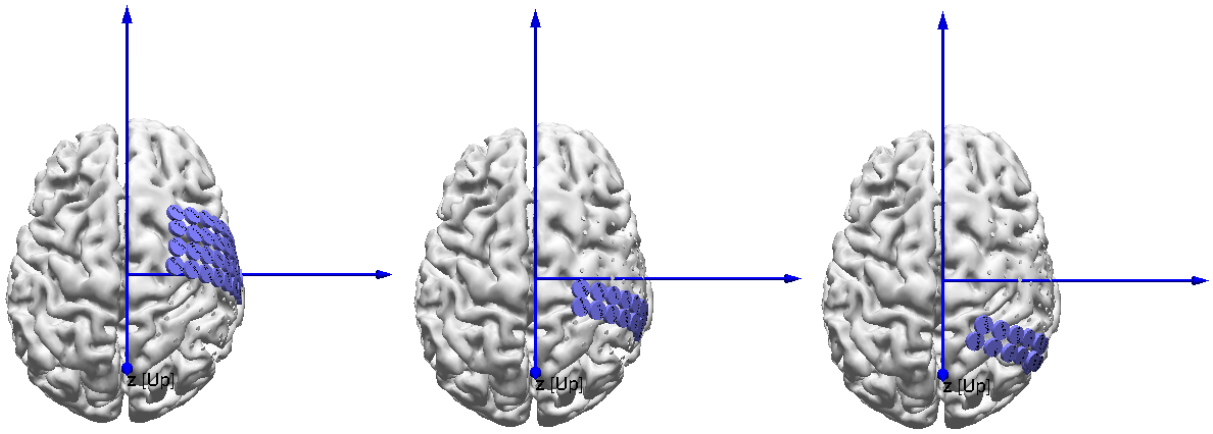
Increase the Electric Groups to 3 Electric Groups: 3 . You will then see the three electrode group symbols on the left, and the Group drop down list will have the addition EG2 and EEG3 options. You may have up to 10 Groups.



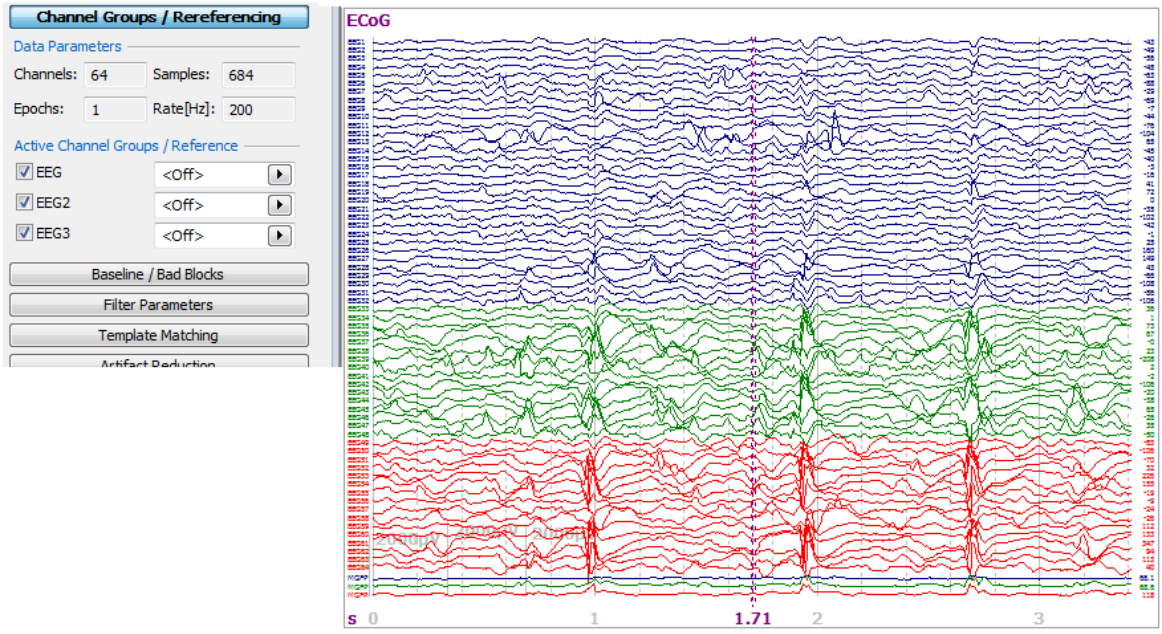
Now it is just a matter of selecting the correct Group for each channel. In this case, the first 32 channels will remain in the first EEG group. The second 16 will be assigned to the EEG2 group, and the final 16 will be assigned to the EEG3 group.

	Group	Label	Pos x	Pos y	Pos z
31	EEG	EEG31	38.5	40.5	102.0
32	EEG	EEG32	30.2	43.7	104.3
33	EEG2	EEG33	62.5	2.0	66.9
34	EEG2	EEG34	61.9	7.5	74.5
35	EEG2	EEG35	60.0	13.1	82.3
36	EEG2	EEG36	56.4	18.5	89.4
37	EEG2	EEG37	51.1	23.5	95.9
38	EEG2	EEG38	44.9	28.2	101.6
39	EEG2	EEG39	37.8	32.0	106.3
40	EEG2	EEG40	28.8	35.2	109.5
41	EEG2	EEG41	59.3	-5.5	71.6
42	EEG2	EEG42	58.7	-0.1	79.6
43	EEG2	EEG43	58.7	5.2	87.5
44	EEG2	EEG44	55.5	10.4	94.6
45	EEG2	EEG45	50.2	15.5	101.3
46	EEG2	EEG46	44.0	20.2	107.2
47	EEG2	EEG47	36.9	24.5	112.1
48	EEG2	EEG48	28.9	27.8	116.0
49	EEG3	EEG49	54.5	-12.7	76.6
50	EEG3	EEG50	53.9	-6.9	84.4
51	EEG3	EEG51	56.7	-2.9	92.8
52	EEG3	EEG52	54.1	2.5	100.0
53	EEG3	EEG53	48.4	7.2	106.0

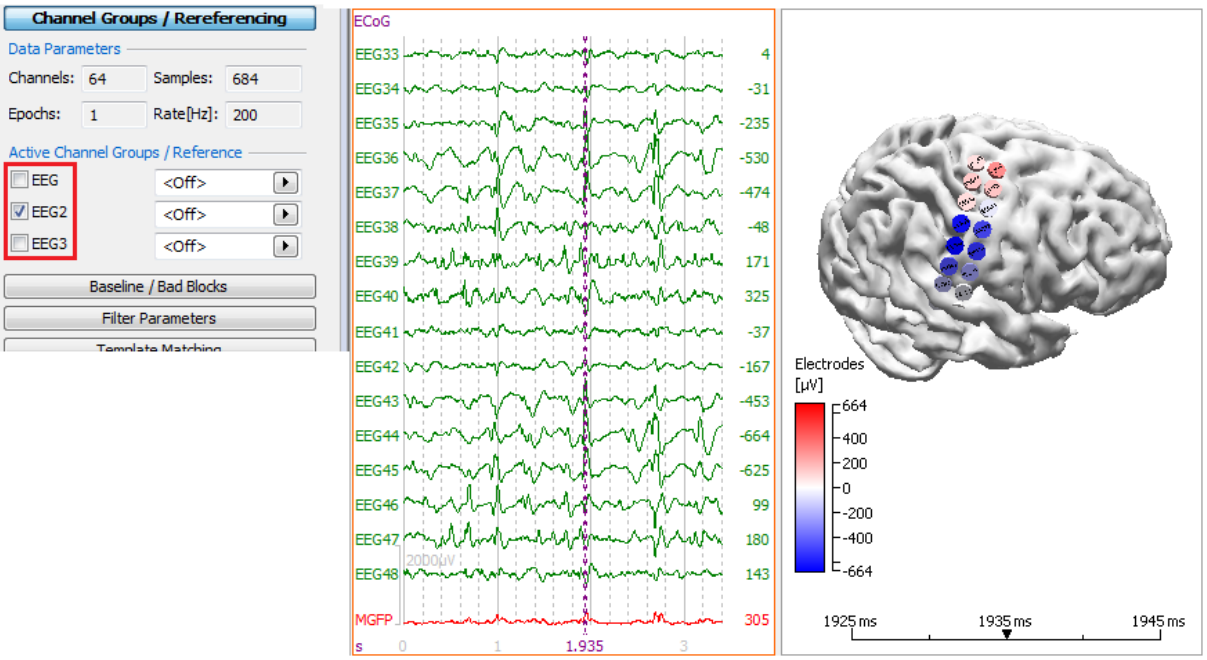
When you click **Next**, you swill see the first group only. Click **Next** again to see the second group, and **Next** again to see the final group.



Then click **Finish**. In the **Channel Groups / Rereferencing** panel, you will see the three Groups, and in the Functional Data display you will see that the groups have different colors (you can select the color in the Colors panel, as was done below).



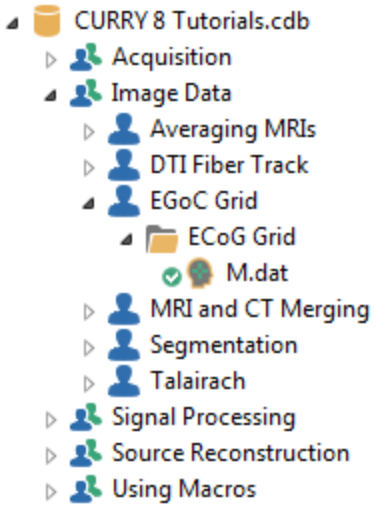
By selecting just the desired group, you will be selecting only the desired grid or strip. In the **3D View**, you will see only those electrodes.



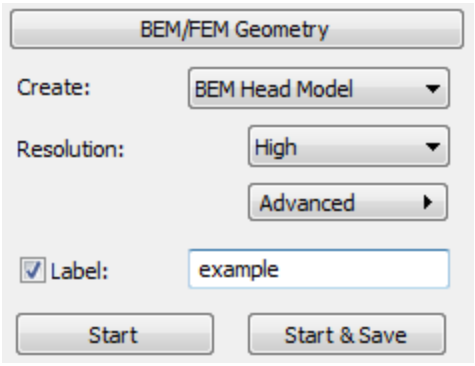
2.5.6 Grid Placement Planning

Typically, these steps are followed if you wish to plan placement of cortical grids or strips. If you already have data recorded from a grid, and you wish to display that grid on the segmented cortex, please see the **MRI and CT Grid Merging** tutorial.

Locate the *ECoG Grid* Study in the *CURRY 8 Tutorials* Database, as shown below. Open the study and select the Image Data display (if needed).

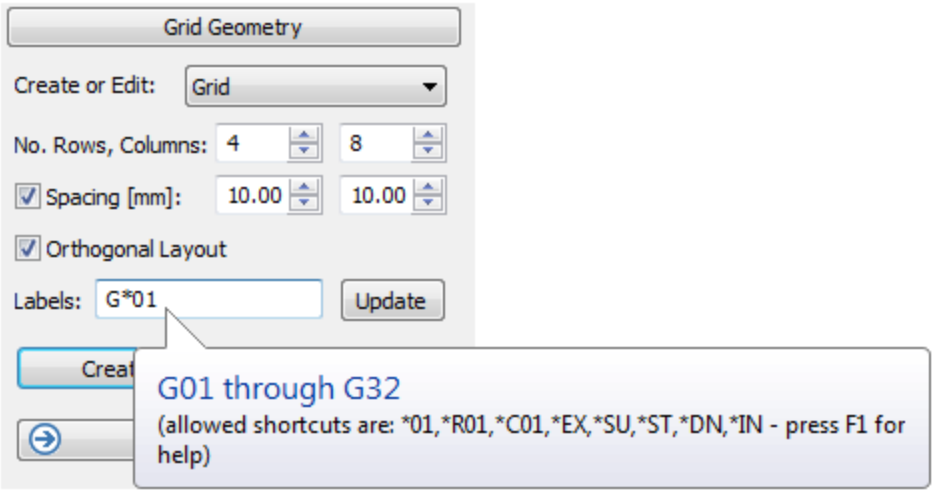


1. To create a cortical grid, you need a smooth surface on which to position the electrodes. CURRY will facilitate the process. Start by creating a **BEM Head Model**, using the default settings in the BEM/FEM Geometry panel, with a label of your choice ("example"). Click **Start & Save**.

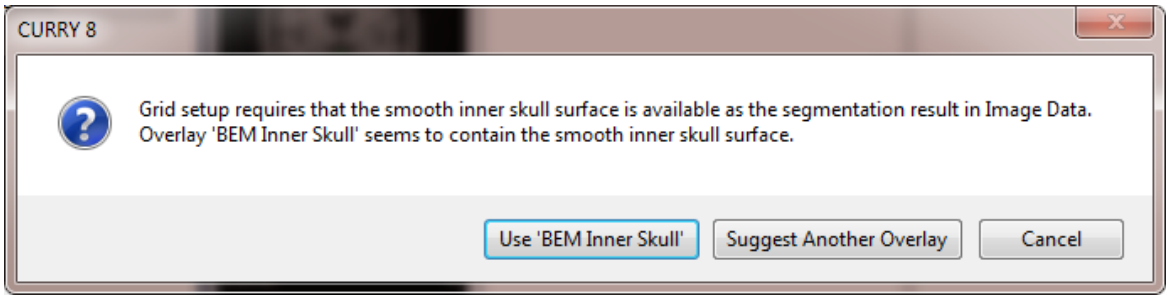


2. To use an upcoming shortcut, it is necessary to close and reopen the Study at this point. When the Study is reopened, select the Localize display and select the Segmentation Result tab at the bottom. The display will be empty.

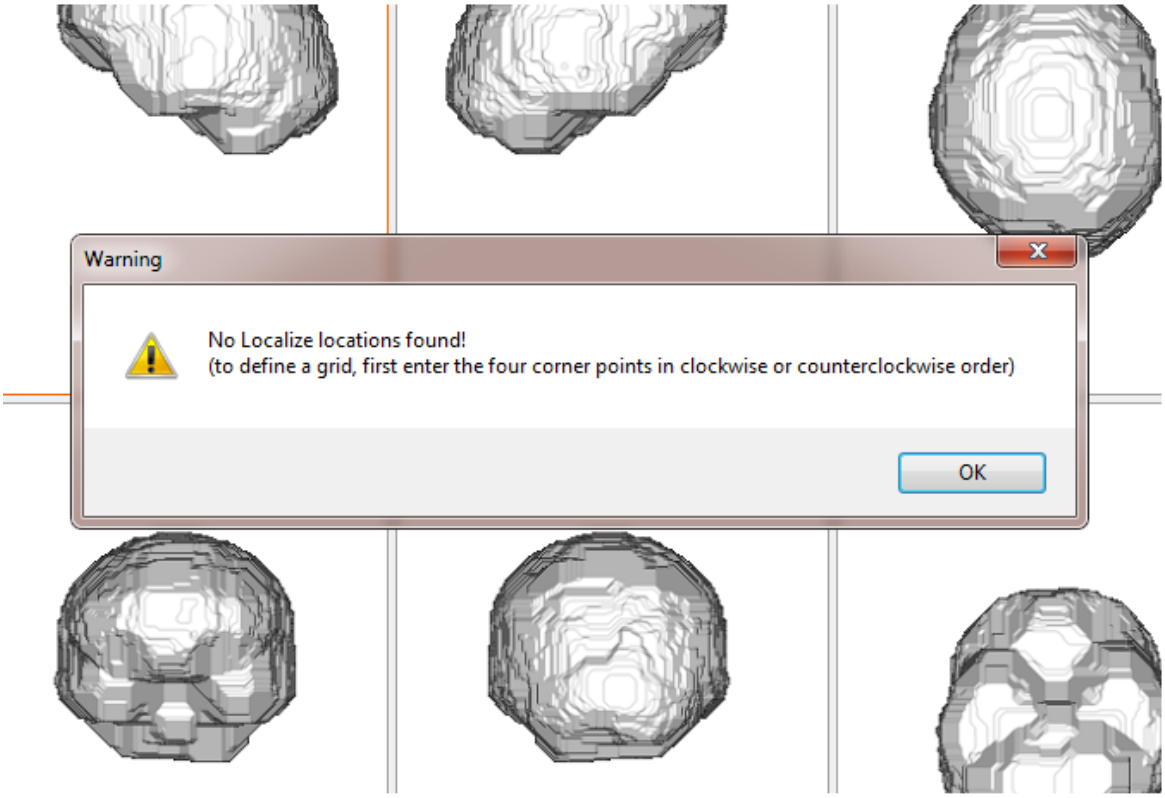
3. Expand the Grid Geometry panel. We will create a 4x8 orthogonal grid, with 10mm spacing among the electrodes. The G*01 label means that labels from G01 to G32 will be created automatically. Click the Create button.



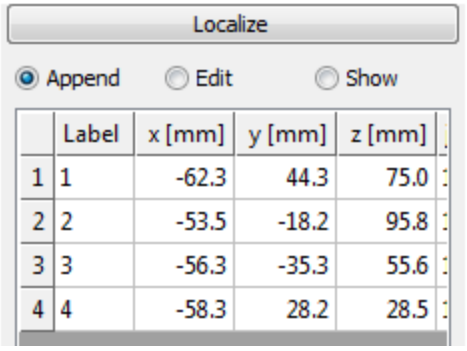
4. You will now see the following shortcut message. Here CURRY is saying you need a smooth surface to create the grid(s), and that the BEM Inner Skull is the recommended surface. (You can also select the same surface manually from the Results list, and select **Import Overlay** from the context menu). (You can also segment just the cortex and perform a Closing operation to slightly enlarge and smooth the surface). Click Use 'BEM Inner Skull'.

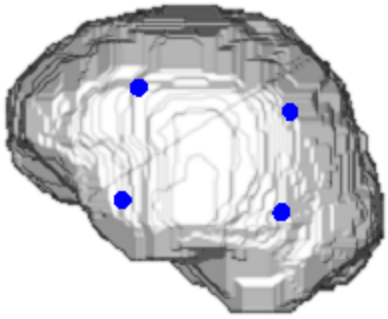


Now you see the segmented inner skull surface with another message instructing you to define a grid. Click **OK**.



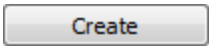
5. Now we need to position the four corners of the grid. Select one of the views and click-to-enter the approximate positions of the four corners of the grid in either a clockwise or counterclockwise direction (or three sequential positions if you are creating a strip). If desired, position the cursor in the upper right corner area to see the Enlarge button . The entries appear on the Localize list.





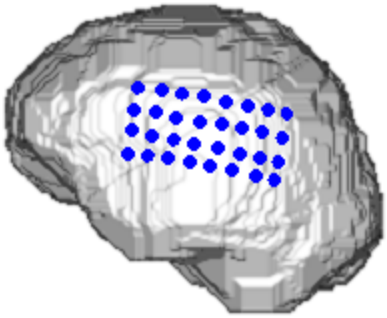
If you make a mistake in placing the positions, *right click* in the

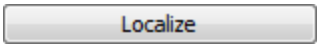
display and note the relevant options.

Click the 

button again under

. **Spacing** is used if you know how far apart the electrodes are in the grid. If selected, the program will take the first corner point you enter, and base the positions of the other electrodes on that, using the distance apart you enter. If you do not select Spacing, the electrodes will be placed within the four corners you designate. If you select **Orthogonal Layout**, the electrodes will be spaced at 90 degree angles from each other.



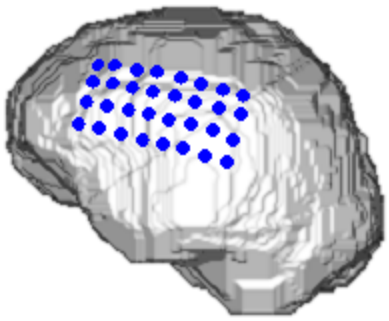
6. In the 

display, you will see that the grid entries now appear. The labels are Grid01 through Grid32. Notice the **Symbol Shape** option at the bottom, where you can select different shapes for the electrodes.

	Label	x [mm]	y [mm]	z [mm]	j [µAmm]	nx	ny	nz	Color	Group
1	G01	-62.2	44.0	75.2	100	-0.795	0.560	0.232	<Default>	<Undefined>
2	G02	-64.7	34.8	78.9	0	-0.936	0.205	0.287	<Default>	<Undefined>
3	G03	-64.4	26.1	81.2	0	-0.930	0.133	0.342	<Default>	<Undefined>
4	G04	-64.9	16.9	84.8	0	-0.947	0.160	0.280	<Default>	<Undefined>
5	G05	-64.5	7.4	87.6	0	-0.976	-0.074	0.204	<Default>	<Undefined>
6	G06	-64.1	-2.2	90.4	0	-0.899	-0.198	0.390	<Default>	<Undefined>
7	G07	-60.7	-10.8	92.7	0	-0.876	-0.385	0.289	<Default>	<Undefined>
8	G08	-54.5	-18.3	94.5	100	-0.697	-0.490	0.523	<Default>	<Undefined>
9	G09	-64.2	41.2	65.6	0	-0.955	0.260	-0.142	<Default>	<Undefined>
10	G10	-66.7	31.9	69.3	0	-0.954	0.263	0.146	<Default>	<Undefined>
11	G11	-68.3	23.2	71.7	0	-0.931	0.297	0.214	<Default>	<Undefined>
12	G12	-67.9	13.6	74.5	0	-0.997	0.044	0.058	<Default>	<Undefined>
13	G13	-68.4	4.4	78.1	0	-0.970	-0.093	0.223	<Default>	<Undefined>
14	G14	-65.1	-4.1	80.4	0	-0.986	-0.103	0.132	<Default>	<Undefined>
15	G15	-62.8	-12.7	82.7	0	-0.841	-0.352	0.411	<Default>	<Undefined>
16	G16	-57.5	-21.2	84.9	0	-0.873	-0.435	0.220	<Default>	<Undefined>
17	G17	-63.2	38.0	57.4	0	-0.896	0.397	-0.199	<Default>	<Undefined>
18	G18	-66.7	29.2	59.8	0	-0.983	0.145	-0.110	<Default>	<Undefined>
19	G19	-67.3	19.6	62.5	0	-0.951	0.309	-0.031	<Default>	<Undefined>

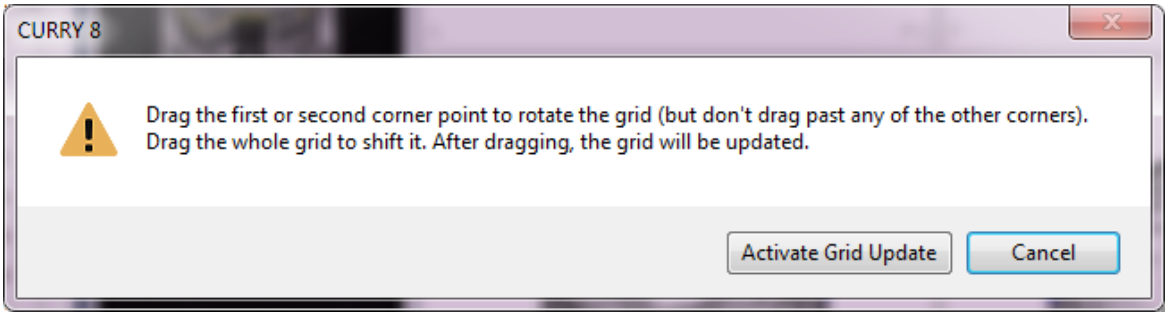
Symbol Shape: Sphere

7. If you wish to move the location of the grid, *grab and drag* a corner to a new location (be sure **Append** is selected). Then click the Adapt button in Grid Geometry. If **Spacing** were not being used, the grid would be stretched to include the new location. Since Spacing is being used, the grid is moved to the new location.

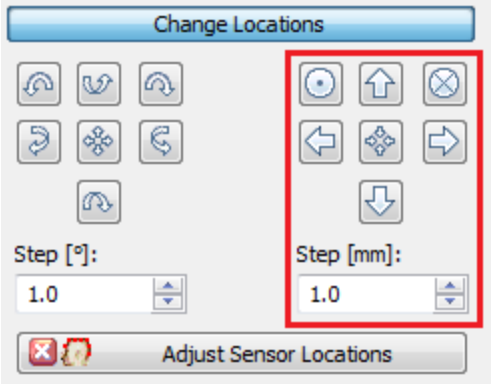


8. If you select the Update Grid mode, you will see the following message. This bypasses the need to click the Adapt button when moving the grid, and lets you move the entire grid. Position the mouse over the grid so that the cursor changes to a finger pointer. Then *click-and-drag* the grid to a new location.

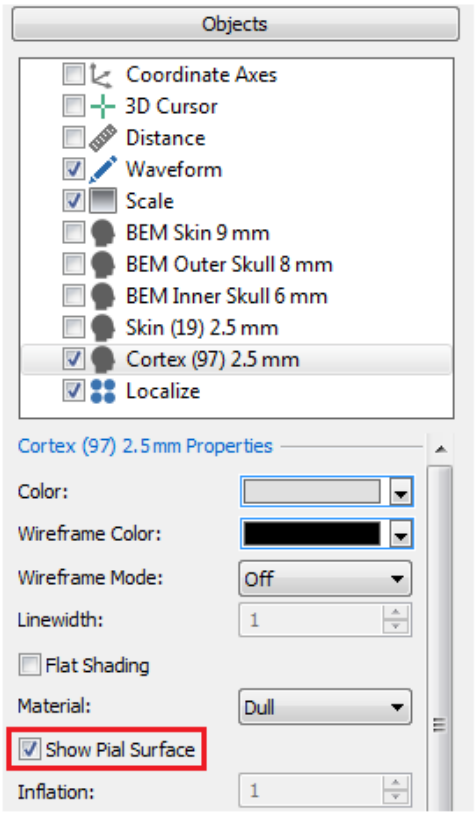
Position the mouse over the first or second corner, and the cursor changes to a plus with arrows. *Click-and-drag* to rotate the grid.

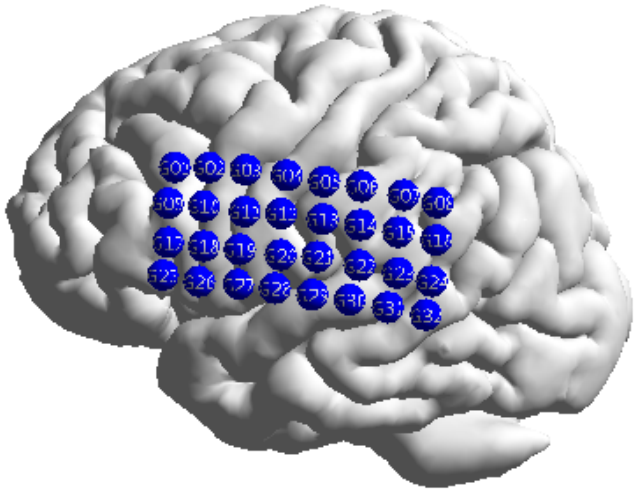


You may also use the Move options under **Change Locations**. After moving the grid, you may see that the electrodes are no longer on the surface (either exterior or interior to it). Click the Adapt button in **Grid Geometry** to place them on the surface.

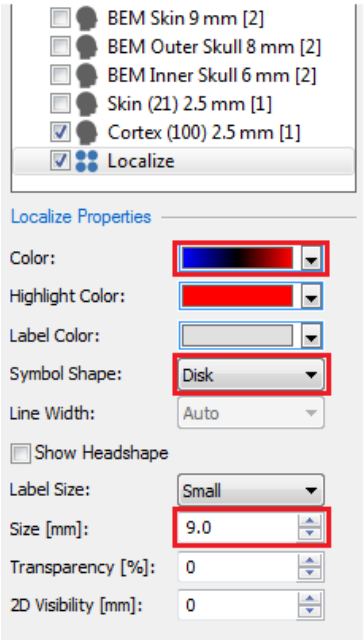


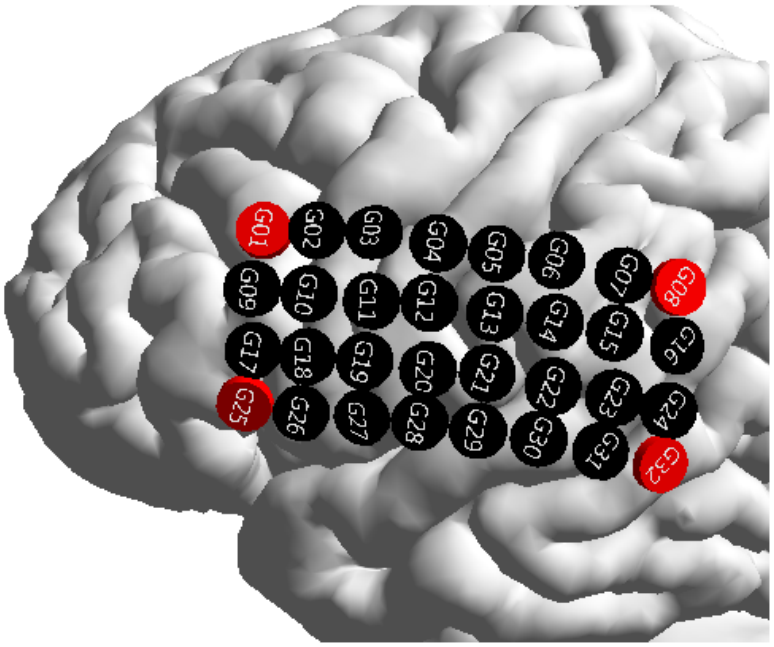
9. You can view the grid on the cortex in the 3D View (use *Ctrl+left mouse* to rotate the display to different views; use *Shift+left mouse* to drag the entire display). You may need to increase the **Transparency** for the cortex. In this example,



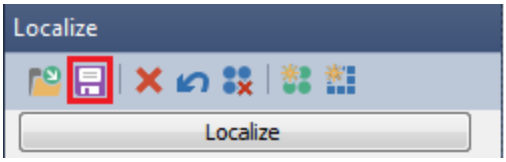


You can change the "Xs" to be more realistic. Go to the **Localize Properties** list. **Shape** was changed to **Disk**, and **Size** was set to **9mm**. A **Color** scale was selected. In the Localize matrix above, note the column for strength (j[μAmm]). All values are 0 except for the corners which are 100. By selecting a color scale, you can highlight the corners. This is helpful when there are multiple grids and strips.

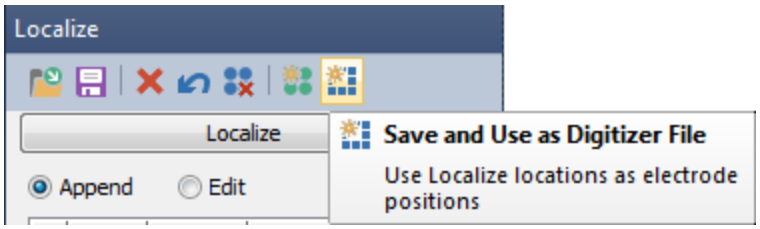




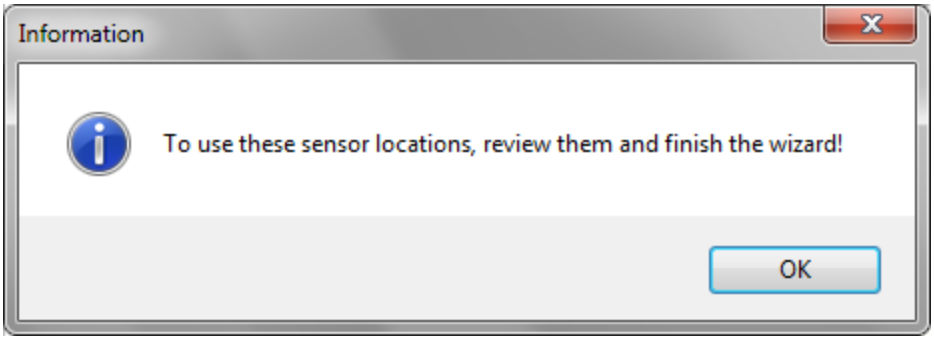
10. When you have the grid in the desired location, and you wish to save it, click the **Save** button at the top of the panel. The results will be saved as a .pom file.



If you have data using these grid positions, you can click the **Save and Use as Digitizer File** button (save as .pom file).



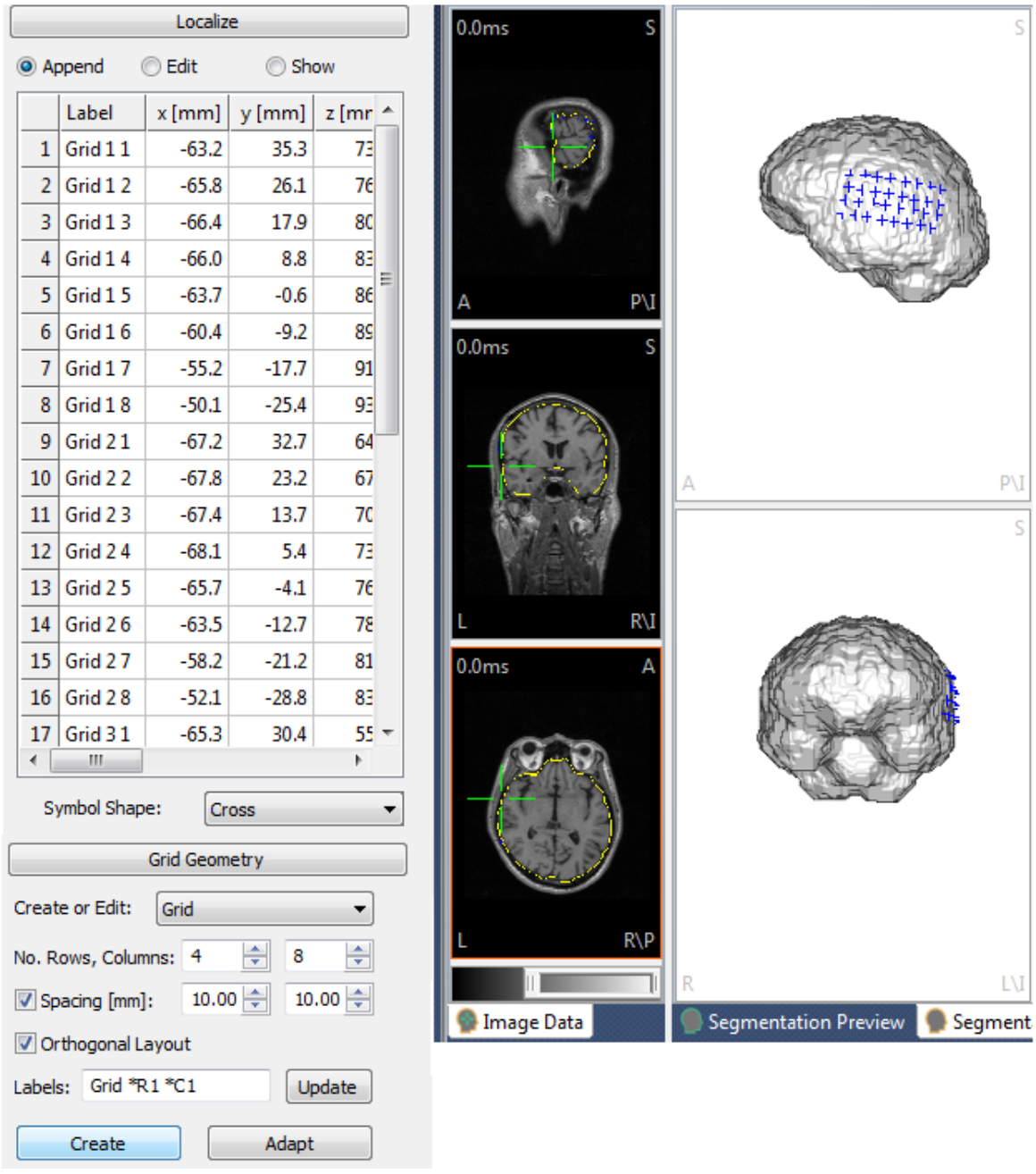
You will see a message saying that to use these positions, you need to review them and then click **Finish** in the Functional Data Import Wizard. There are no functional data in this Study, so click the red X to close the message.



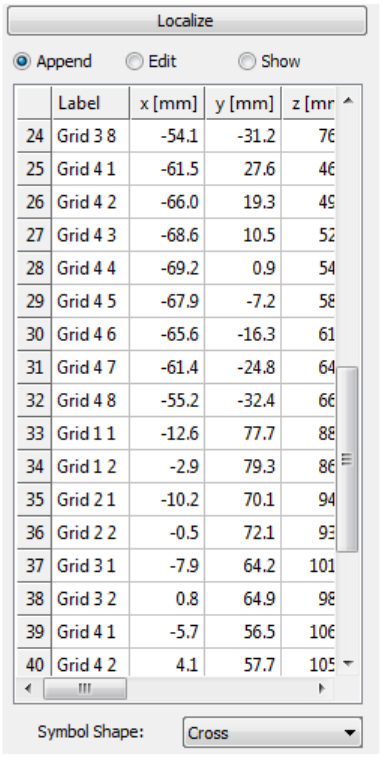
Creating Multiple Grids and Strips

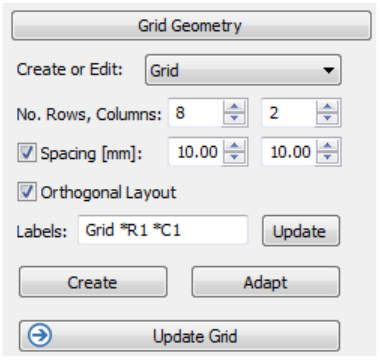
Creating multiple Grids and Strips is accomplished in basically the same way. Let's say you will be using a 4x8 grid, an 8x2 grid, and a 1x8 strip.

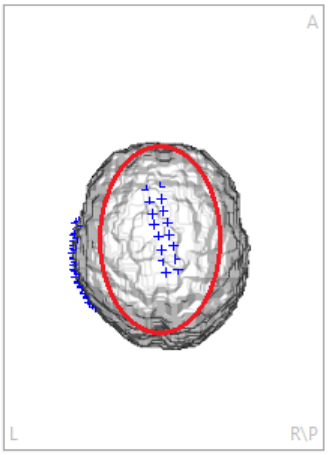
1. Start by entering the 4 corners (clockwise or counter-clockwise), as above. Select **Grid** for **Create or Edit**. Enter **4** rows and **8** columns. Click **Create** to see the grid and the entries in the Localize list.



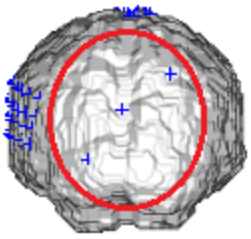
2. Enter the 4 corners for the second grid. In this case, we want 8 rows and 2 columns. The entries for the second grid appear in the Localize list below the first ones. (Always make sure **Append** has been selected when creating new grids or strips). If you make a mistake and want to delete a grid (or strip), highlight the lines in the Localize list (you can use the conventional *Ctrl+Shift+click*), and then click the *Del* key on the keyboard. You can also use **Undo** (*Ctrl+Z*) to remove the last entry (or entries).



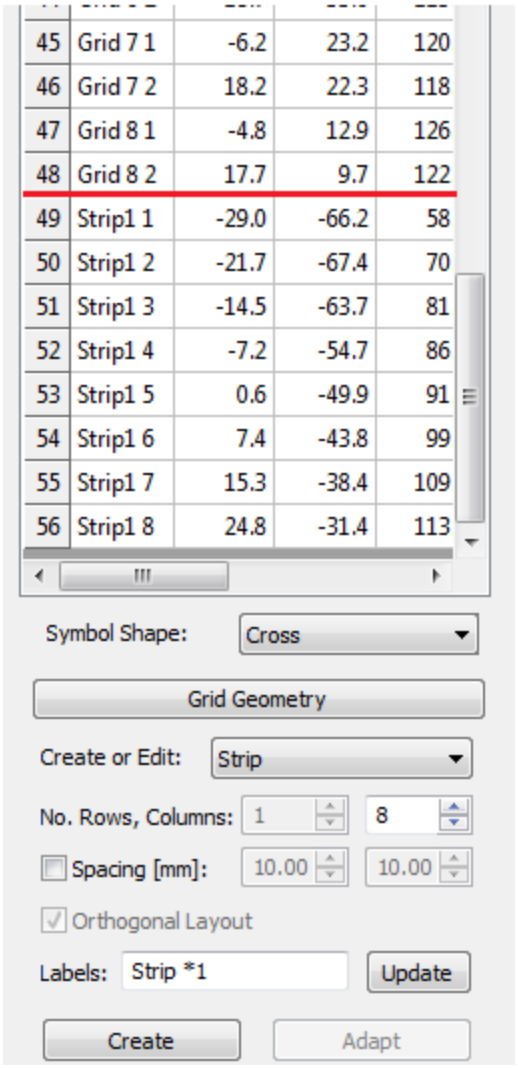


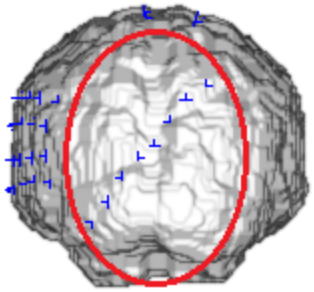


3. To create a strip, you must select the first, intermediate, and last positions, in that order.



Select **Strip** for **Create or Edit**. Enter the number of electrodes (**8**) for **Columns**. Click **Create**. The remaining electrodes will be filled in, and displayed in the Localize list.





4. From here, you may reposition or resize the grids and strip, as described above.

5. Save the positions as described above.

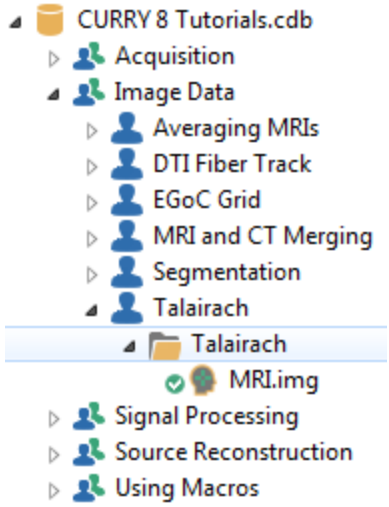
2.5.7 Talairach Coordinate System

The Talairach system identifies brain structures in the MR data either in terms of their anatomy or function. Different brain areas are indicated by different colors. You may display all structures or selected ones, and you may click on a point in the MR data to see what structure you have selected.

To use the Talairach system accurately, you need to define the anterior commissure (AC), posterior commissure (PC) and the Midsagittal (MS) points accurately, as well as define the brain limits in Step 7 of the **Image Data Parameters** windows when the file was loaded. If you did not define the landmarks and boundaries when the image data were first loaded, or if the file was loaded in a previous version of CURRY, you

can complete these steps by clicking **Image Data** → **Talairach Parameters**. This will take you to **Step 6** of the **Image Data Parameters** windows, where you can define the landmarks and boundaries.

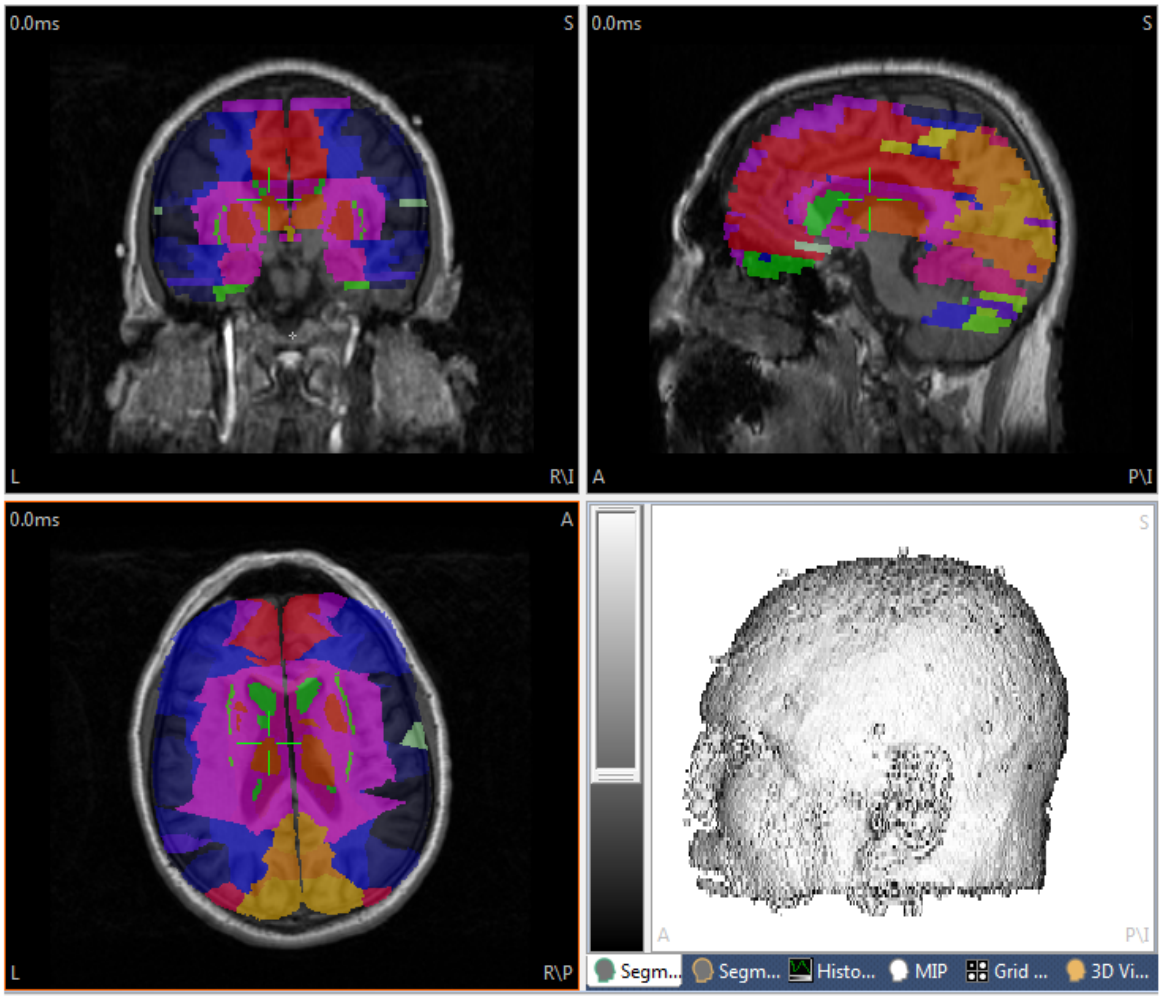
1. Locate the *Talairach* Study in the *CURRY 8 Tutorials* Database. Open the Study to the Image Data display.



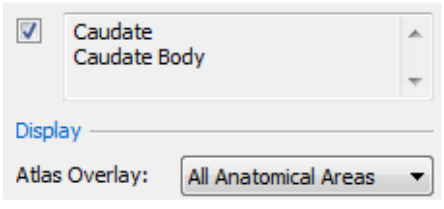
2. Expand the Options panel.

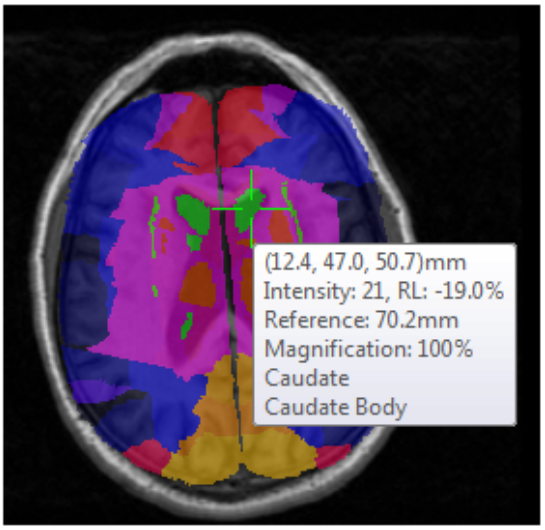
3. Initially, there is **No Overlay** selected for the **Atlas** Atlas Overlay: <Off>. Click the drop-down list to see all of the options. They are **All Anatomical Areas**, **All Functional Areas** (including Brodmann areas), and then lists for each of the anatomical and functional areas.

4. Select **All Anatomical Areas** and see the overlay on the Image Data display. The colors can be set in the **Atlas Maps** option under Colors.

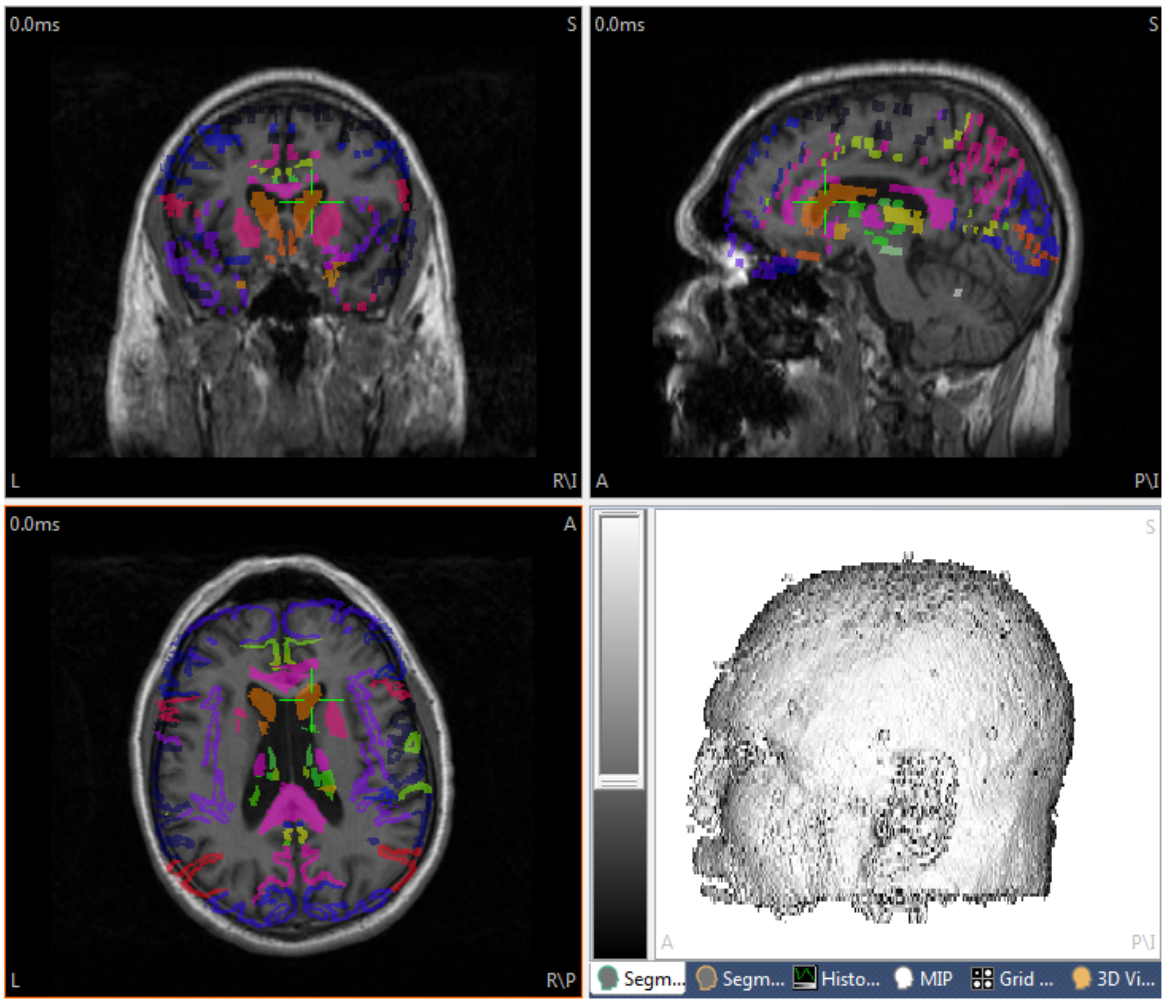


5. Click the 3D Cursor in a new location, and read the anatomical structure in the field in the Options panel. In this way, you can identify any structure in the MR images. A Tooltip displays additional information.

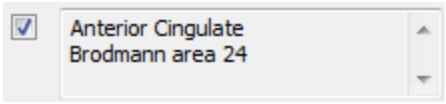




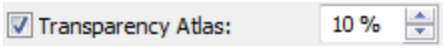
6. Now select **All Functional Areas**.

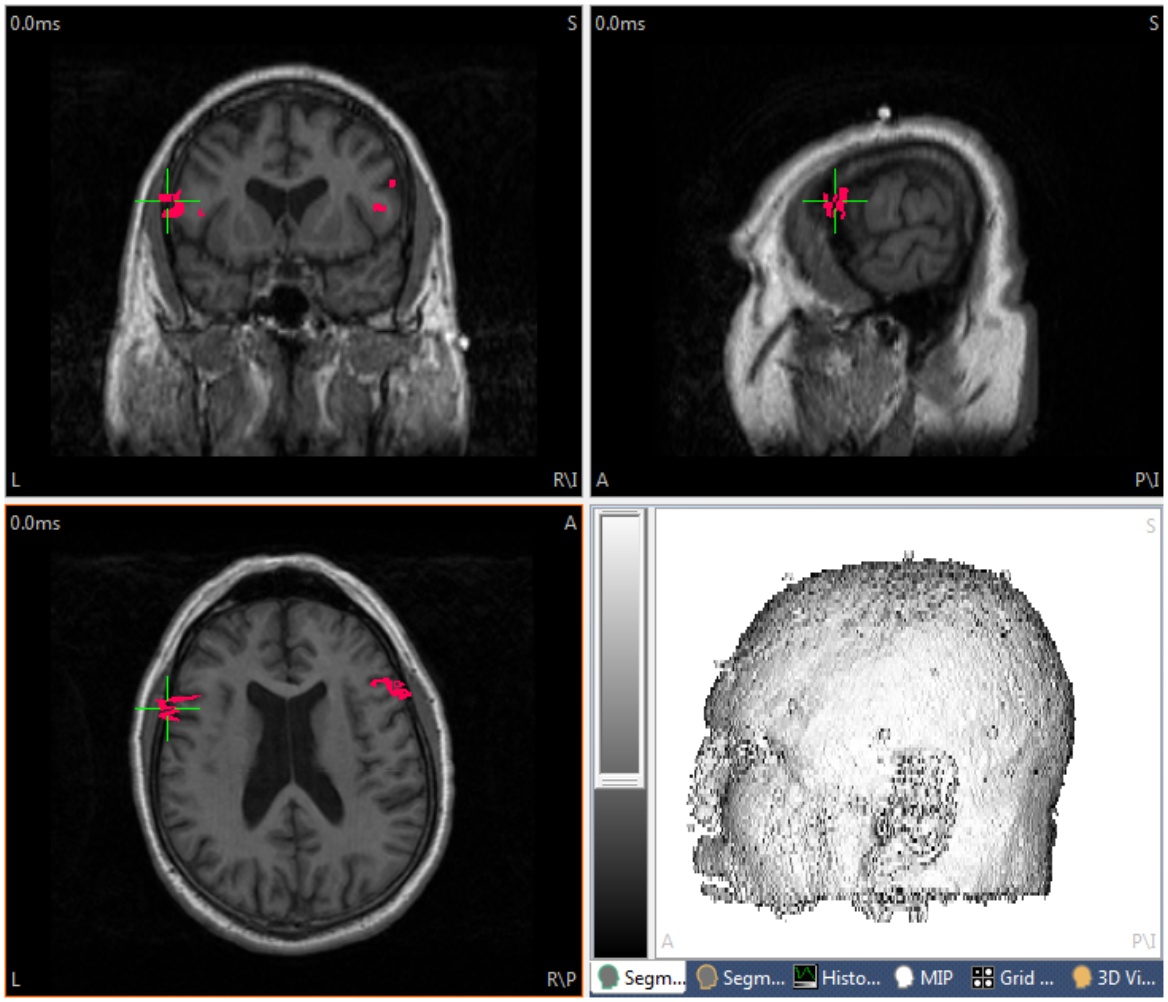


You will see the various functional regions. Click on one and see the structure and Brodmann area (where applicable) in the display.

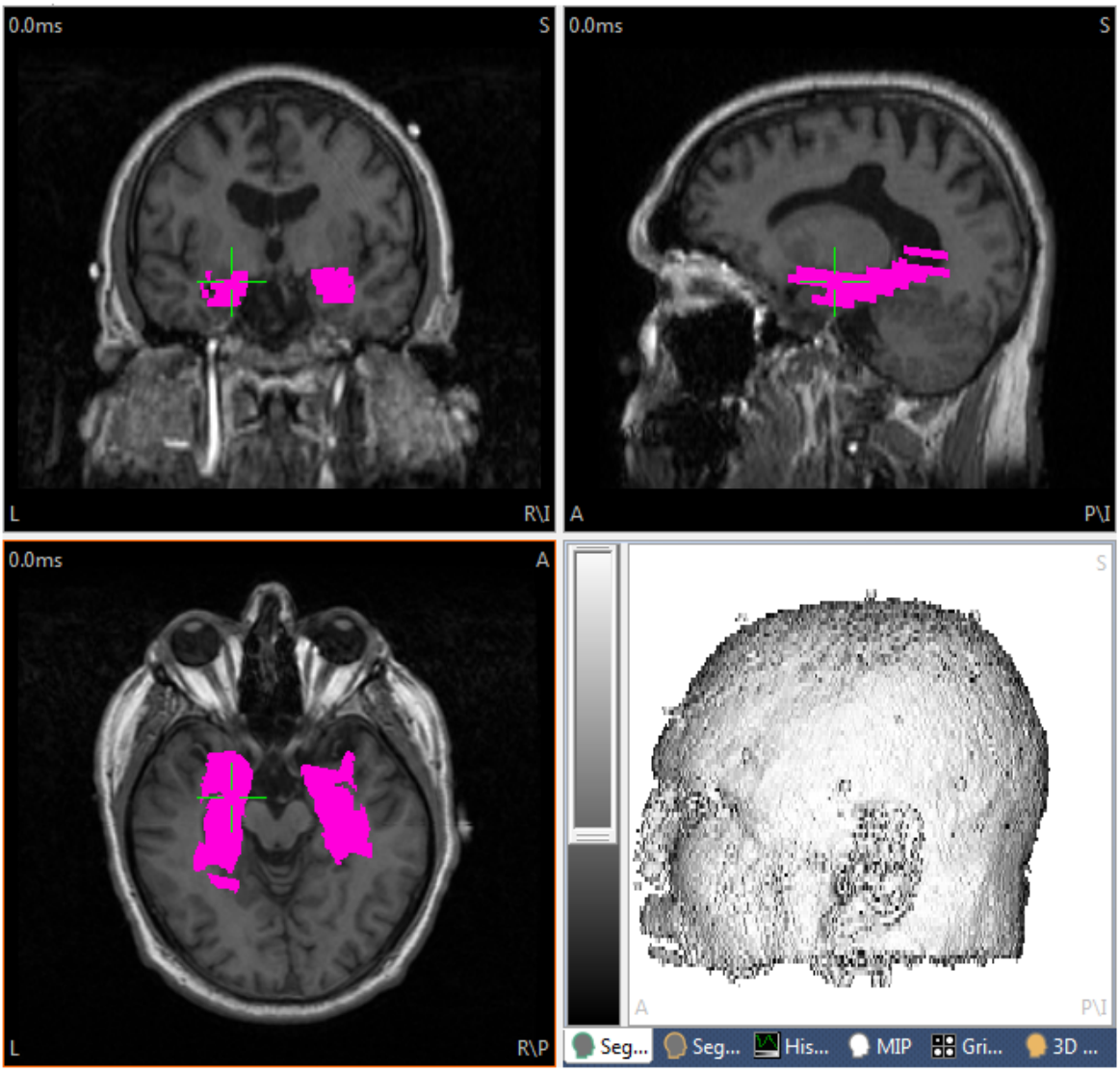


7. Now go to the drop-down list and select an area of interest, such as **Brodmann Area 44** (Precentral Gyrus). That functional area is shown in the Image Data display. Position the 3D Cursor on the area in all views to see it most clearly. Decrease the **Transparency** for the Atlas to make the colored areas stand out more brightly



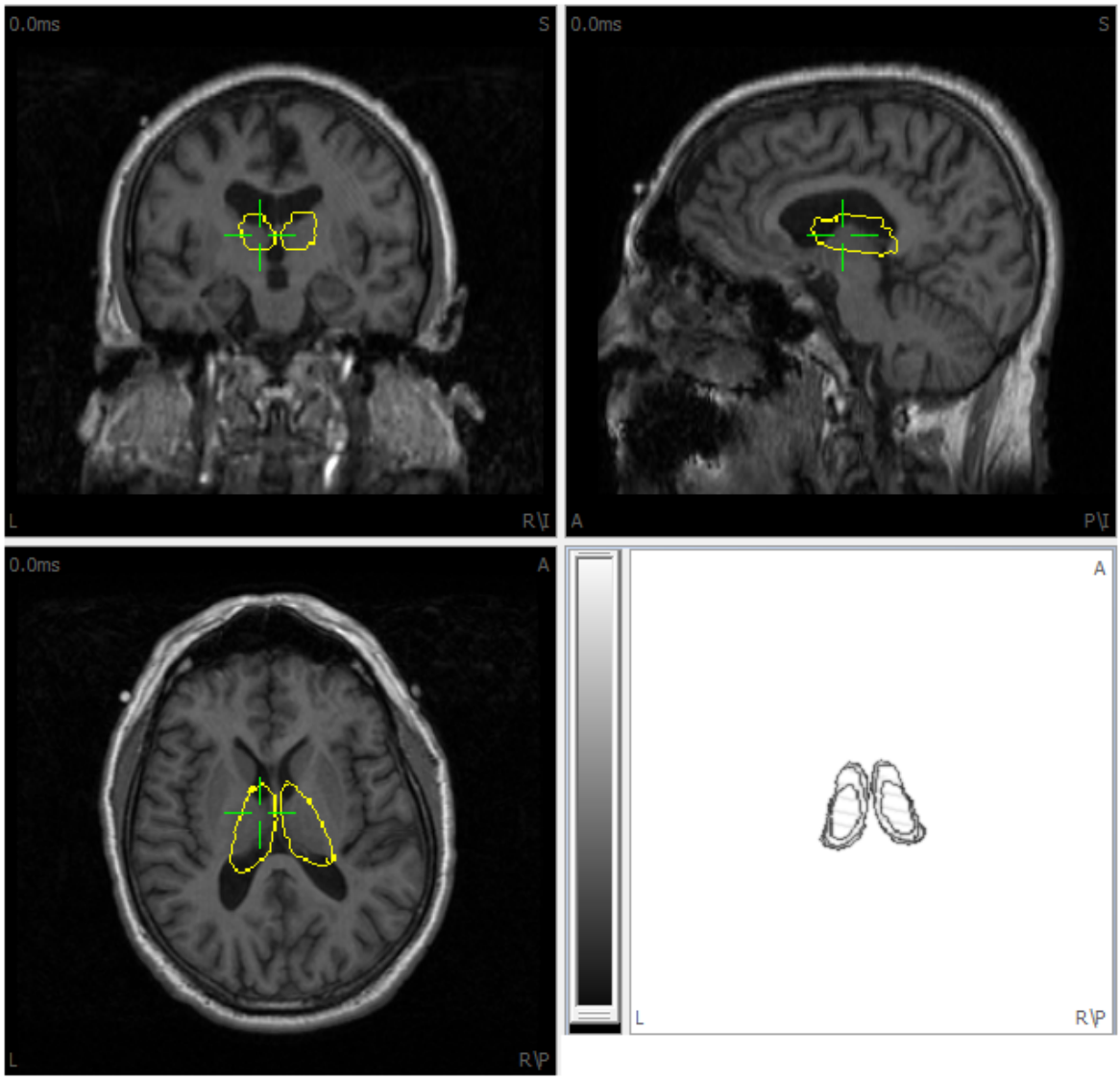


Select the **Parahippocampal Gyrus**. That area will be shown.



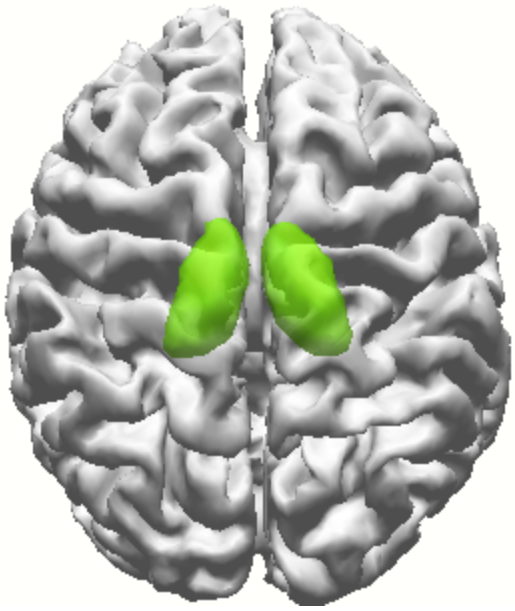
8. The more commonly used options are described next. If you have dipole results and wish to display them also, enable Show Results (or click the icon on the **Image Data** Toolbar). Interpolate will blend the pixels in the MR images to form a less pixelated view. The data in this file were loaded such that the right side of the brain appears on the right of the display. If you wish to reverse the view, enable Radiological Orientation (R,L).

9. You can also use the Talairach system to segment a specified structure. Expand the Segmentation panel, and select **Thresholding**. The **Atlas** field will then become active. Select a structure (**Thalamus**) and press the **Start** button. The segmented structure will appear in the Segmentation Result display. (Note: the **Lower Threshold** is used here, and if the value is too large, you may lose all or parts of the structure in the segmentation). Use a **Lower Threshold** of **10** in this example.



10. In the Morphology panel, perform an **Opening** (using **Dilation** and **Erosion** values of **4.0**). The result will be a smoother surface (enlarged).

11. Then create a triangle mesh (or **Image Data → Create Triangle Mesh**) to create a *Surface x* that can be displayed in the 3D View. For example, the thalami may be displayed within the segmented cortex (increase the cortex Transparency). Select a color for the new Surface (and perform a Rotation to see the deeper structures).

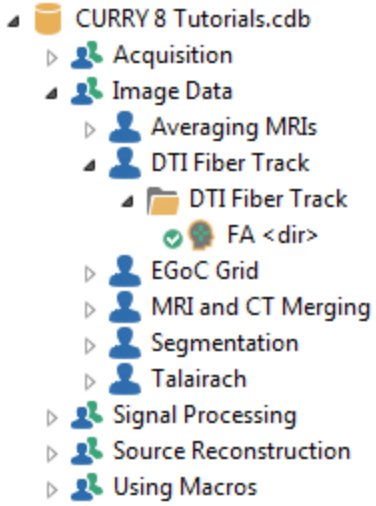


2.5.8 DTI Fiber Track Imaging

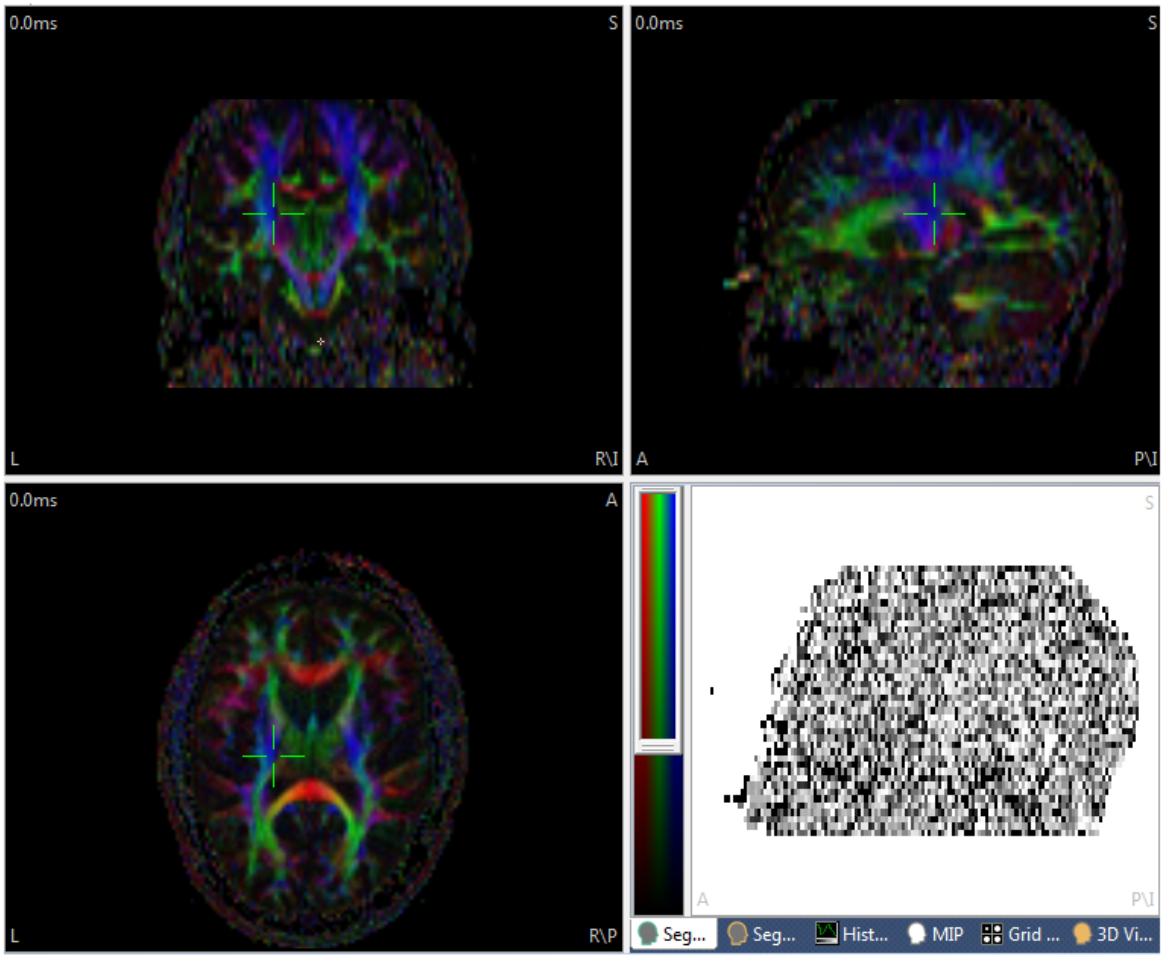
DTI FA image data allows you to view image data in color, where the different colors indicate the primary orientations of the fiber tracks. The results can be segmented in order to display the fiber orientations in very fine detail.

This type of imaging is used to show connectivity, such as the dominating fiber tracks involved where there is a seizure disorder, or to show how currents are conducted within the brain.

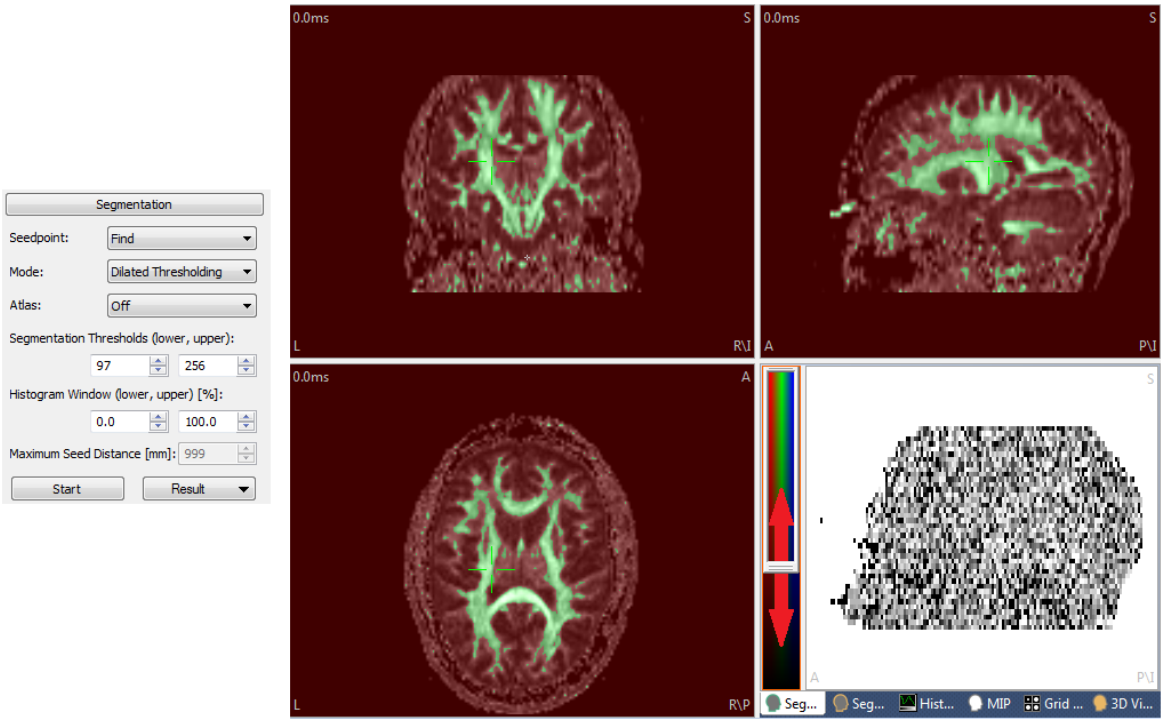
This tutorial uses the files shown below (contained within a single folder). The file has been imported previously and the parameter files have already been created (to bypass the **Image Data Parameters** windows).



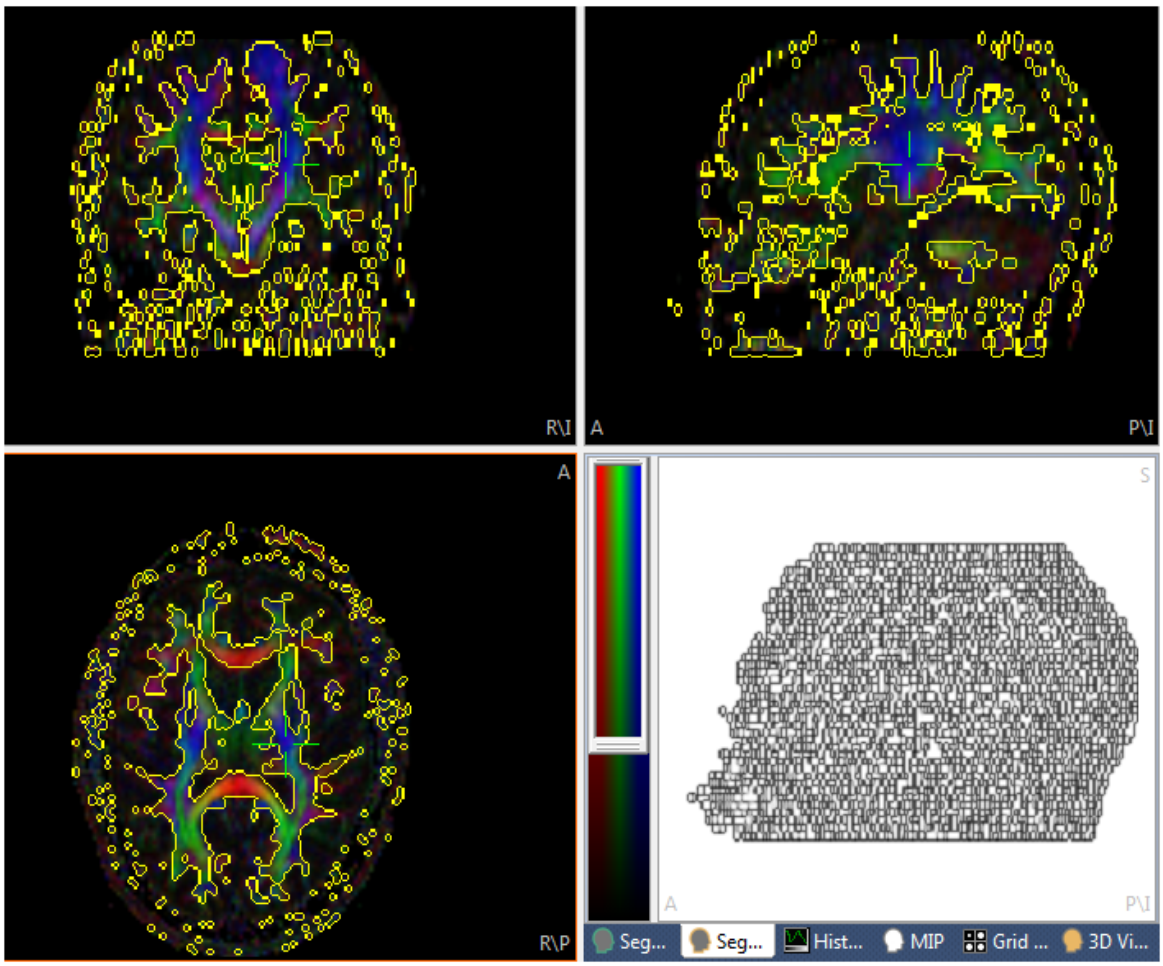
1. Open the Study to the Image Data display. The colors represent the directions of the major fiber tracts. Red tracts are left/right, blue tracts are dorsal/ventral, and green tracts are anterior/posterior. Reposition the cursor as usual to see other views.



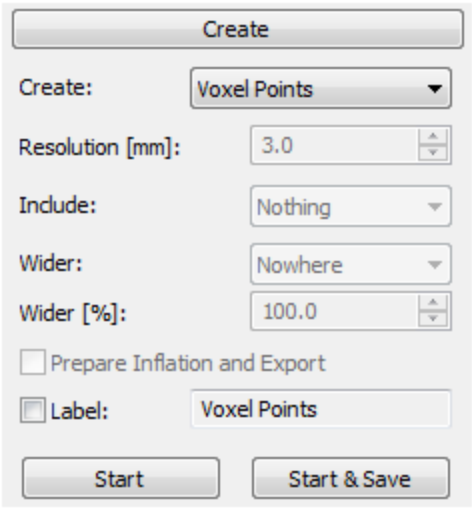
2. Expand the Segmentation panel and select **Dilated Thresholding**. To determine the **Lower Threshold** level, you can either use the *mouse wheel* to change the Lower Threshold values, or else drag the scale bar up or down. Your are looking for the setting that gives the brightest intensity for the tracts, without bleeding into other areas. A Threshold of **97** will work well. Click **Start**.

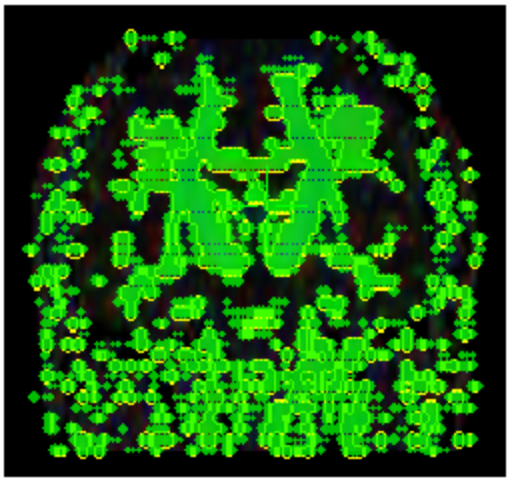


Click **Start**. The results are seen in the Segmentation Result display.

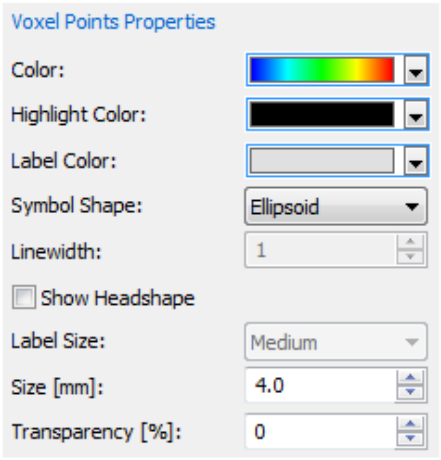


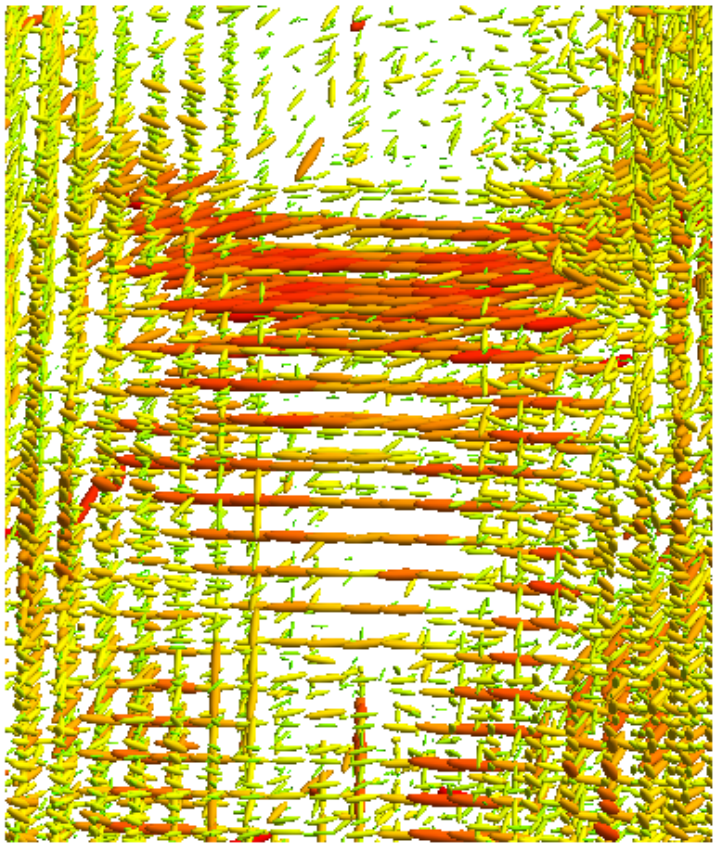
3. Expand the Create panel and select **Voxel Points**. Click **Start**. The Points have been created and are listed in the Objects panel for **3D View**.





4. Select the 3D View display. Zoom in (greatly) to see the fiber orientations. As usual, you may select different **Shapes**, **Color** and **Size** schemes for the points.



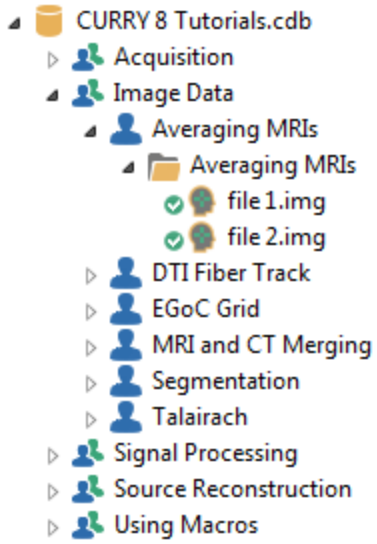


You may superimpose DTI data on the MR data (from the same subject). Load the MR data first in the Database. Make sure the MR data has the focus, then select **Image Data** → **Show Thresholded** → **Image Data 2** to display the DTI data on the MR data. The same result may be obtained by selecting the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

2.5.9 Averaging MRI Data Files

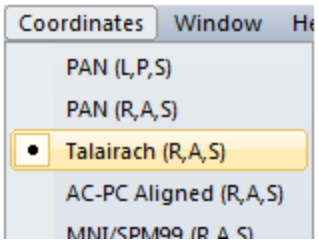
MRI data files may be averaged to create your own averaged data sets. Normalization using Talairach space allows the differently sized brains to be averaged together with minimal distortion.

We will use a simple example where there are just two image data sets that we want to average together. Locate and open the Study shown.

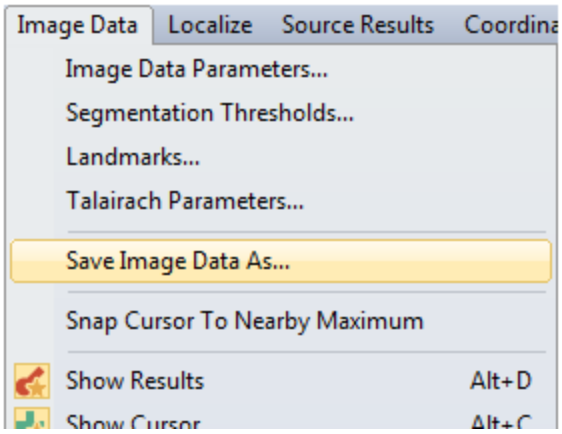


1. These files have been imported previously, so you will not need to go through the **Image Data Parameters** windows. When you import your own files, *you must not Skip the Talairach Definition steps*. Carefully mark the position of the anterior (AC) and posterior commissures (PC), as well as the upper, midsagittal position (MS). It is helpful to use the coronal view to be certain you have the correct positions of the AC and PC. In Step 7 of the **Image Data Parameters** windows, carefully measure the boundaries that define Talairach space. The space is subdivided into 12 sub-spaces: Anterior to AC, AC to PC, PC to Posterior, above and below the horizontal AC-PC plane, left and right of the vertical AC-PC plane. The data are averaged within each subspace to preserve more detail.

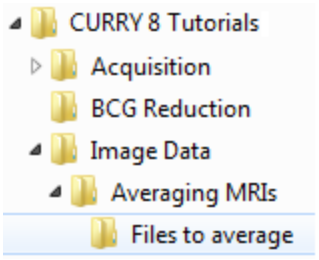
2. Set the **Coordinates** to **Talairach (R,A,S)**.



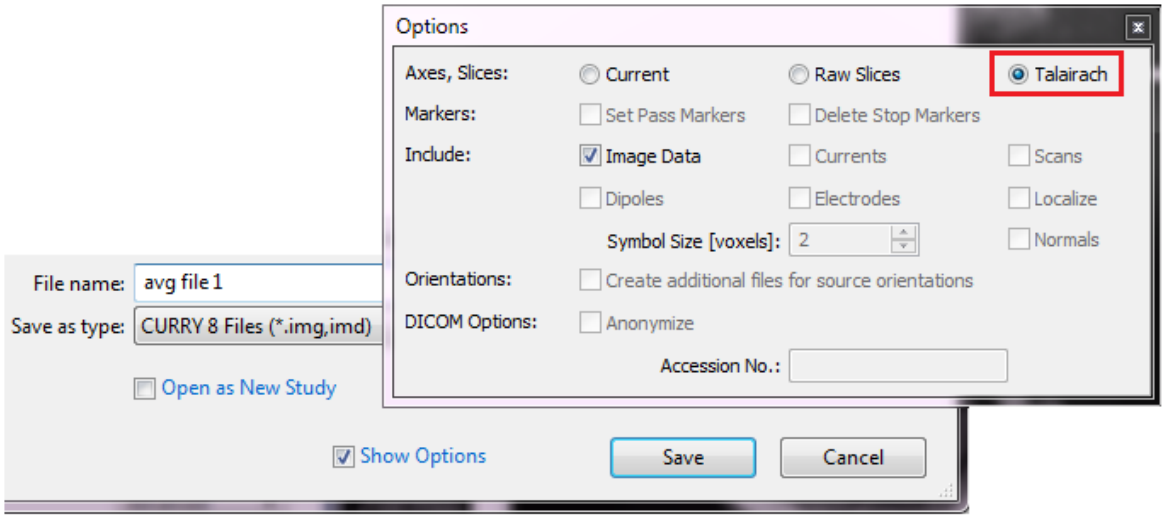
3. For both (all) image data sets, select **Image Data** from the Main Menu Bar and then **Save Image Data As**.



Select a folder for the image data you will be saving. All of the files you will be averaging should be in the same folder, with no additional image data files. You may create the folder from the Save As dialog.

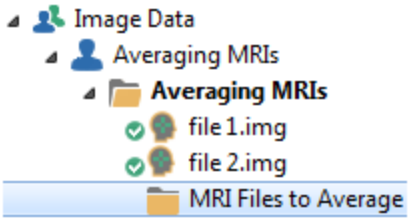


Enter a file name (*avg file 1*), and save the files in **(*.img,imd)** format. Enable the **Talairach** option.

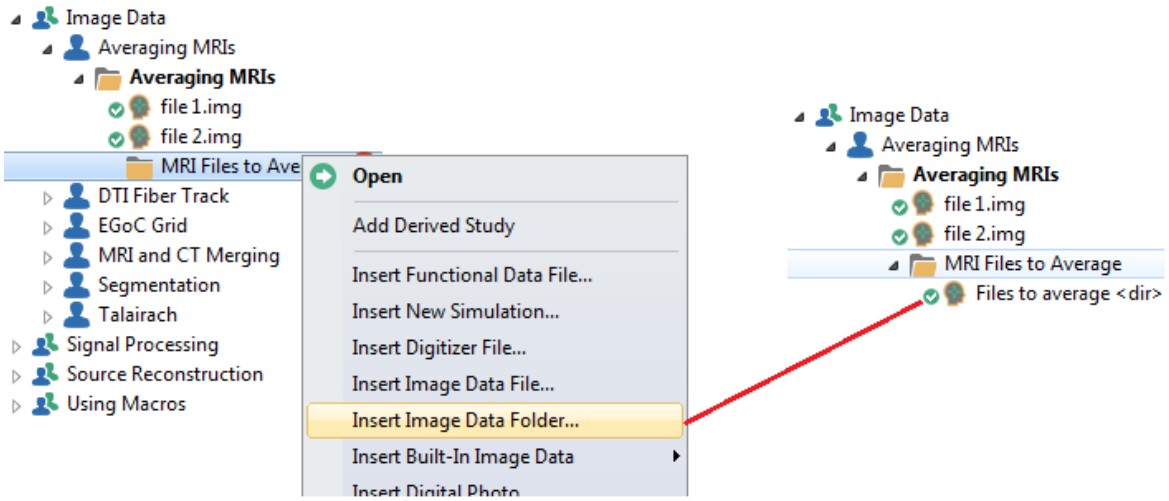


4. Repeat the process for the second image data set (using *avg file 2* for the file name). Then close the Study.

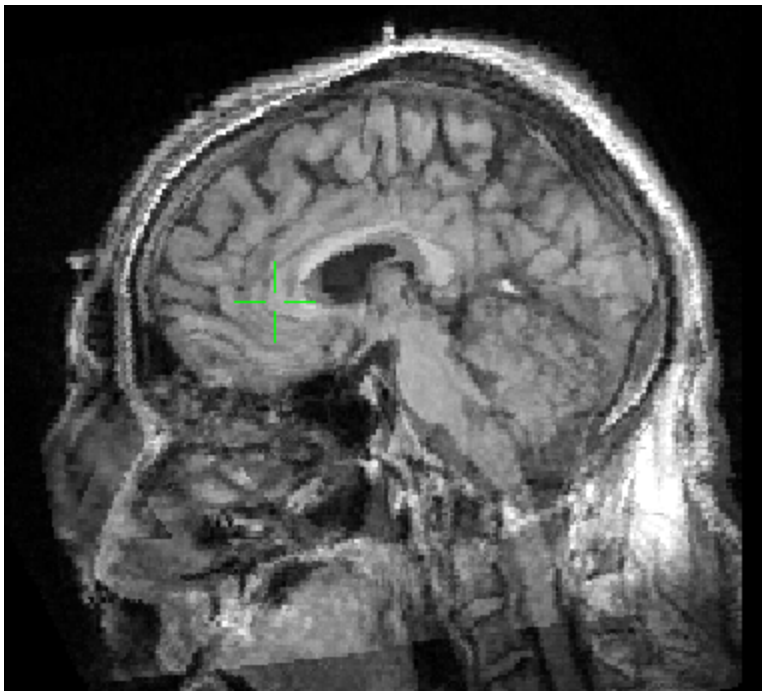
5. Create a new Study in the Database. In this case, we created a Derived Study called *MRI Files to Average*, below the *Averaging MRIs* study.



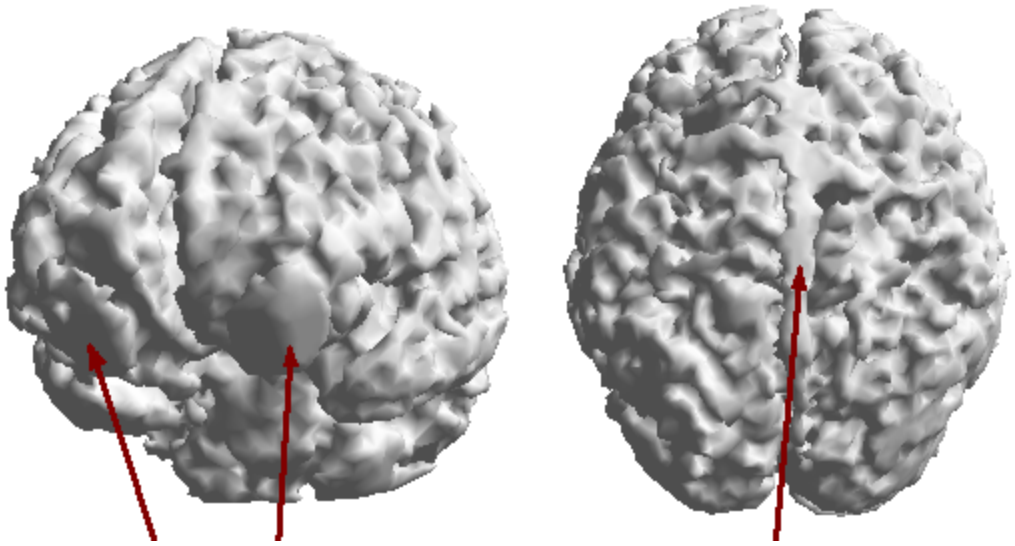
Use the **Insert Image Data Folder** option to select the folder containing the .img files you have created. Select the folder containing the files you saved.



6. When you open the Study, the average of the image data files will appear in Image Data. These two files do not have the same orientation, so the fit is not that good.



7. If you go on to create a BEM Model from the averaged MRI data, you may need to perform some manual segmentation to obtain an acceptable cortex. In the figure below, 4 MRI data sets were averaged and the automatic BEM Model was created. You can see that parts of the structures around the eyes, as well as parts of the skull were included.



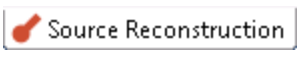
These may be removed using Stop Markers, as described in the **Manually Assisted Automated Segmentation** section above. If that is not successful, it may be necessary to perform **Manual Segmentation**.

2.6 Source Reconstruction

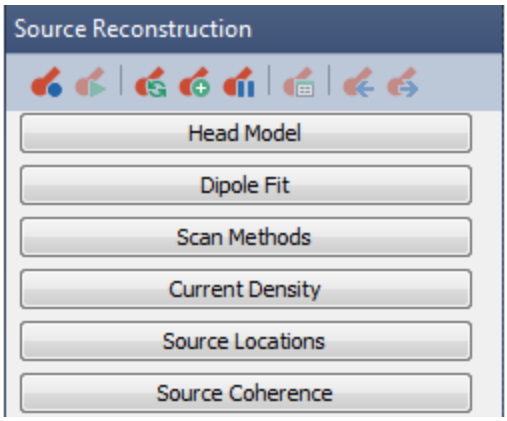
The tutorials in this section are all concerned with finding the source(s), or generator site(s), for the activity recorded at the scalp. These include several different single dipole models, several Scan methods (which scan a surface for multiple single dipoles), and Current Density Reconstruction (a layer of dipole sources constrained to a surface). Source reconstruction with FFT (spectral power) data is demonstrated. Different methods for creating simulated dipoles are described. Combining fMRI data with other anatomical and functional data sets is illustrated. The final tutorial describes the idea of multi-modal source reconstruction, where electric and magnetic data sets are combined.

2.6.1 Dipole Models

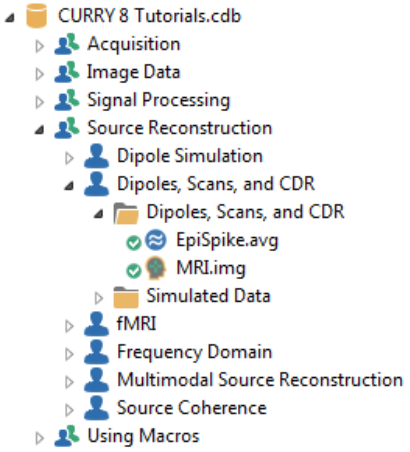
In this Tutorial we will demonstrate how to perform source reconstruction using some of the basic dipole models.

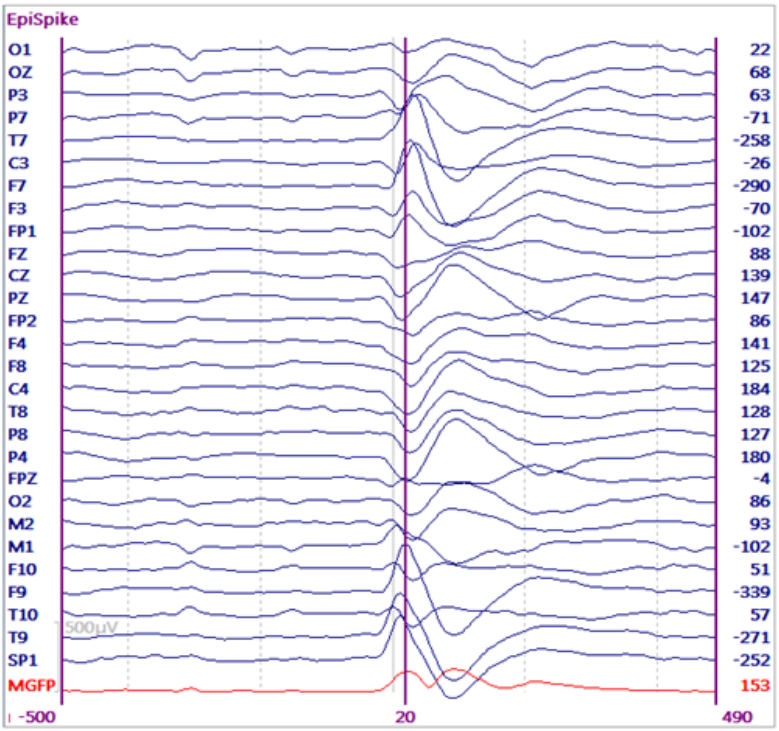
The **Source Reconstruction** tab 

displays the relevant options.



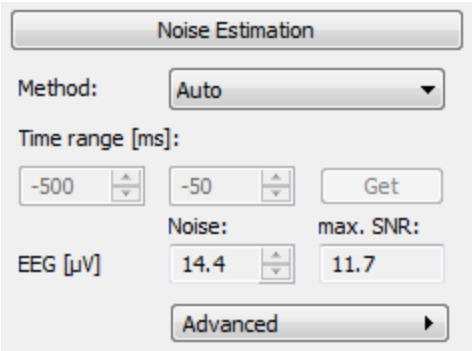
Locate the *Dipoles, Scans, and CDR* Study in the *CURRY 8 Tutorials* Database, as shown. Open the Study.



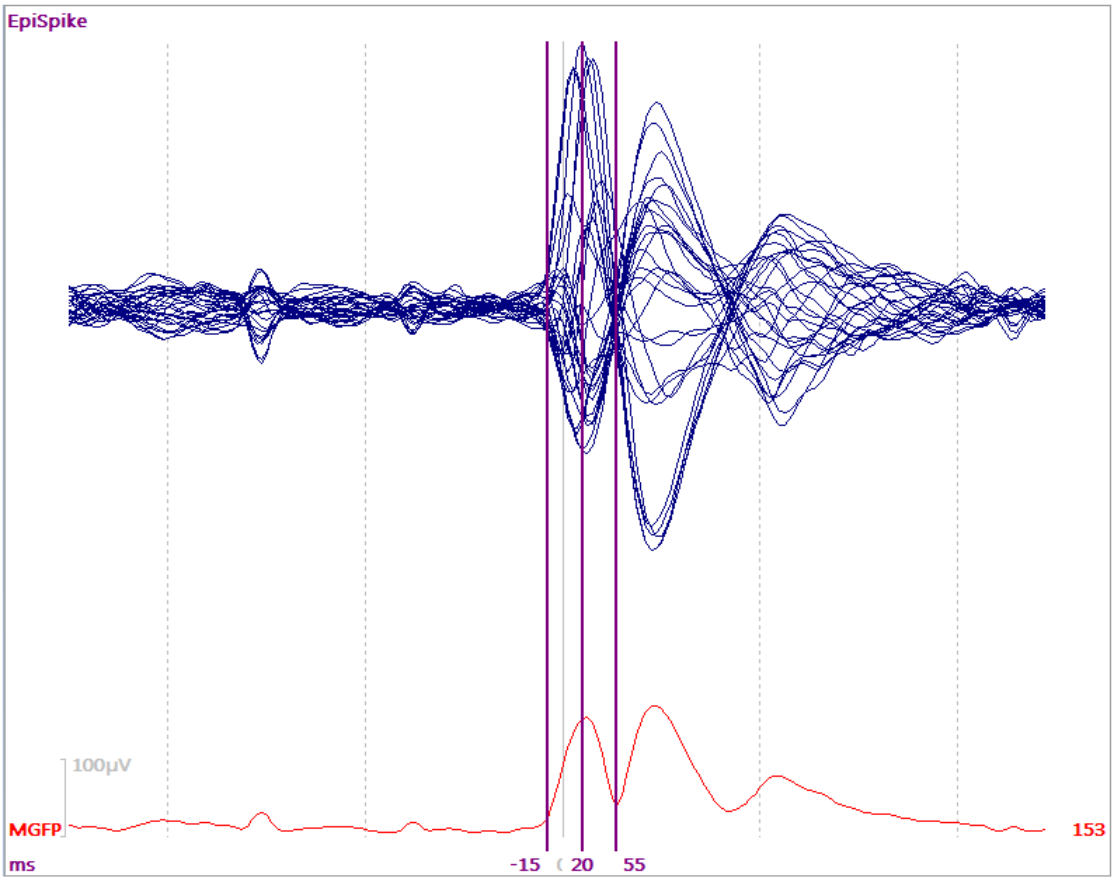


1. CURRY automatically performs **Noise Estimation** using the Timerange starting at the beginning of the epoch interval, in this case, -500 ms, to -50 ms before the 0 ms time point. Typically, epileptic spikes are detected at the peak of the spike, so the noise estimate ends 50 ms prior to that. You can override that by selecting **User Defined Interval**, and set the time points as desired. Noise estimation must be performed prior to source reconstruction, as parts of the analyses use a noise estimate in the computations. The noise estimate is being computed and recomputed all of the time. **Percentile 50** is the default option for continuous data grater than 10 seconds (unless you have selected **Curry 7** for the **Scope**, in which case **Percentile 20** is used), which is not always the best option, depending on the data you are working with. In this case, we have an interval in the file that has

no signal (where signal refers to the spike and slow wave). In these cases it is often preferable to select the "non-signal" interval for noise estimation, thus the -500 to -50 ms range.



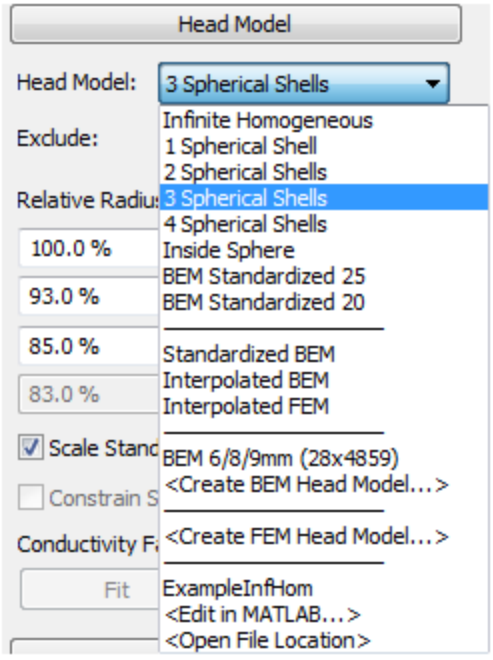
2. Select a Timerange in the Functional Data from **-15** to **55**ms (**Butterfly Plot** selected). Why this interval? It depends on the question you are asking. If you wish to determine the origin of the spike, then select that interval. With evoked responses, there could be several intervals of interest. If you are computing moving dipoles, a dipole solution will be computed for each data point in the Timerange. If you are using the fixed dipole models, the dipoles will be computed using all data points combined.



With other data sets, you may wish to perform **PCA/ICA Analyses** to analyze components separately, or to filter out any unwanted components. In this file, there are three genuine ICA components, and are all related to the progression of the epileptic spike across time and location (additionally, ICA is a statistical method and there are relatively few samples in this Timerange). See the **ICA Source Reconstruction** tutorial for an example using the ICA results.

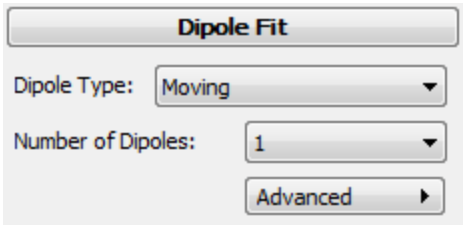
3. Select the All display. Generally, the next step is to create a BEM Model from the MRI data. In this example, we have already computed this. Those procedures are described in the **Image Data Processing** tutorials above. Briefly, in BEM/FEM Geometry, set **Create** to **BEM Model**, use the default **Label**, and press **Start**. We will use a couple of head models.

If you do not have the MR data, you have other options. Expand the Head Model panel under **Source Reconstruction**, and look at the drop-down list for the **Head Model**. Please refer to the *User Guide* for a description of the various models. In this case there is one new model (BEM 6/8/9mm) that we will use shortly. We will compare the differences among some of these models in the steps below.

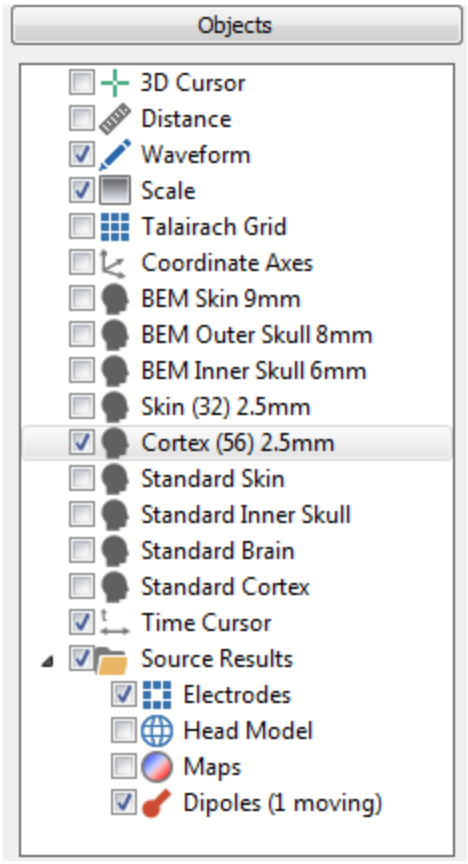


For now, select the **3 Spherical Shells** model.

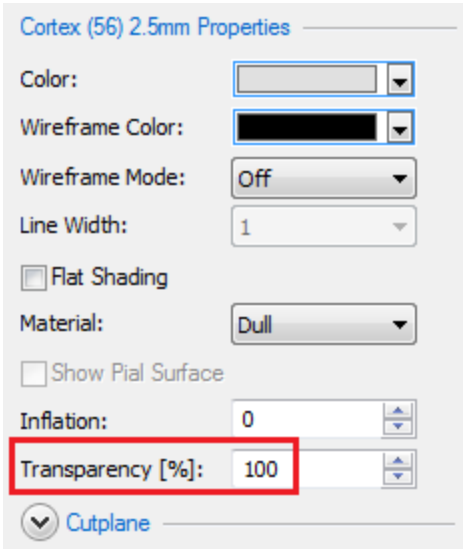
4. Expand the Dipole Fit panel and look at the drop-down list for **Dipole Type**. As mentioned above, the Moving dipole option will compute a solution for each latency point independently in the Timerange. This is generally a good option to use with spikes, where you wish to determine the probable origin. The remaining options will create a dipole solution for all points combined within the Timerange. Select **Moving**.



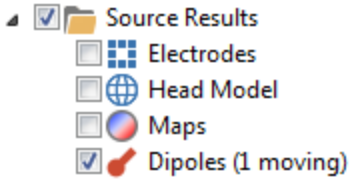
5. The moving dipole results are seen in the 3D View. Select a **Left View** (using or the context menu), and select Cortex (56) 2.5mm from the Objects list under **3D View** 3D View.



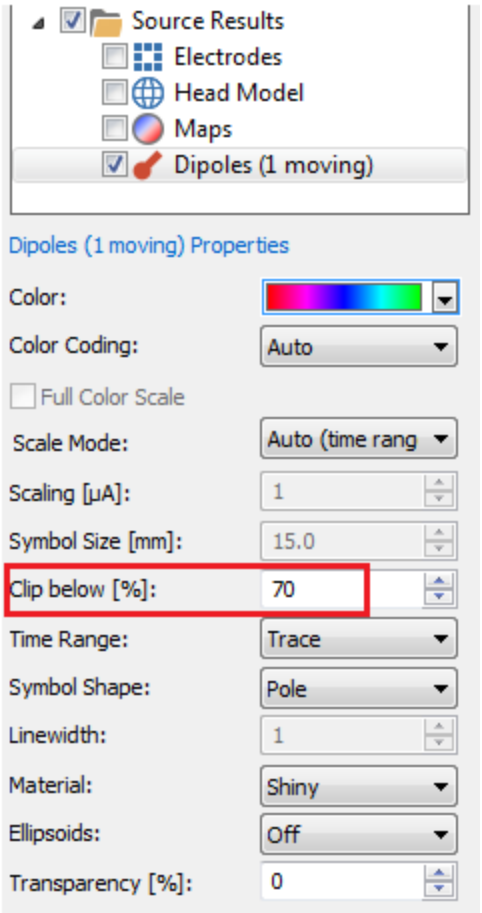
In the Properties list for the Cortex, set **Transparency** to **100%**.



In the **Objects** list, disable the display of the **Electrodes** (to simplify the display).

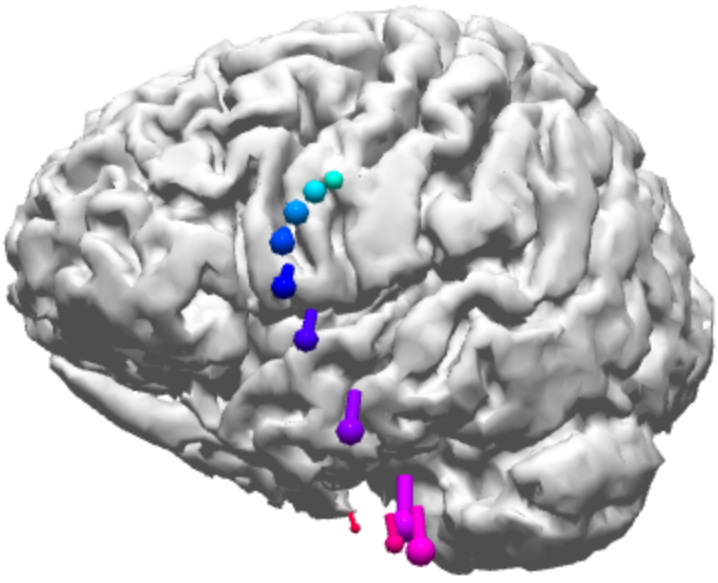


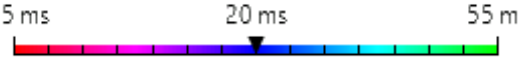
Click on **Dipoles (1 moving)** in the **Objects** list to highlight it. In the Properties section, set **Clip below** to **70%**. This removes the dipole solutions from the display that have "poorer" goodness of fits (not strength). Disable the display of the **Confidence Ellipsoids** .



You should now see the moving dipole results on the cortex, using the 3 Spherical Shell model. Use the *mouse wheel* to enlarge or reduce the display. Grab and drag it to change the perspective. Use *Shift+left mouse* to move the entire display.

Click the **Rotate** icon on the Toolbar to rotate the display through 360°.

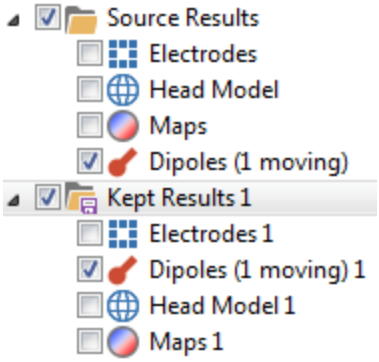


Disable the **Timerange Display Mode** icon on the 3D View Toolbar. A single dipole is seen. Grab and drag the pointed in the time scale to see the dipole move across time 

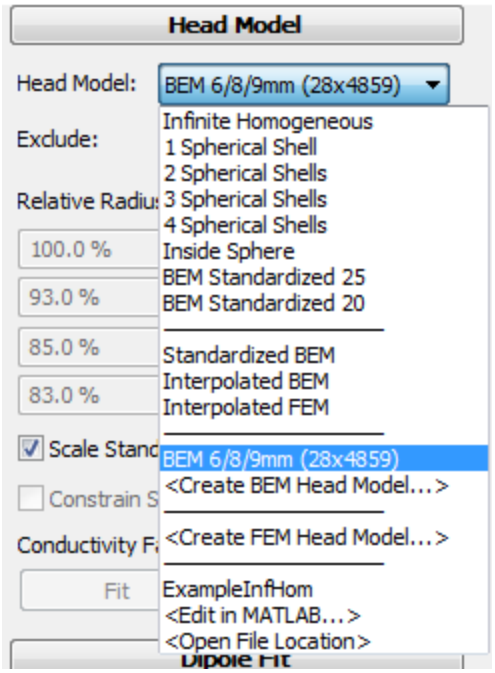
. Click the **Show Movie** icon on the Main Toolbar (upper left area) to play a movie of the moving dipole.

Enable the **Timerange Display Mode** option again.

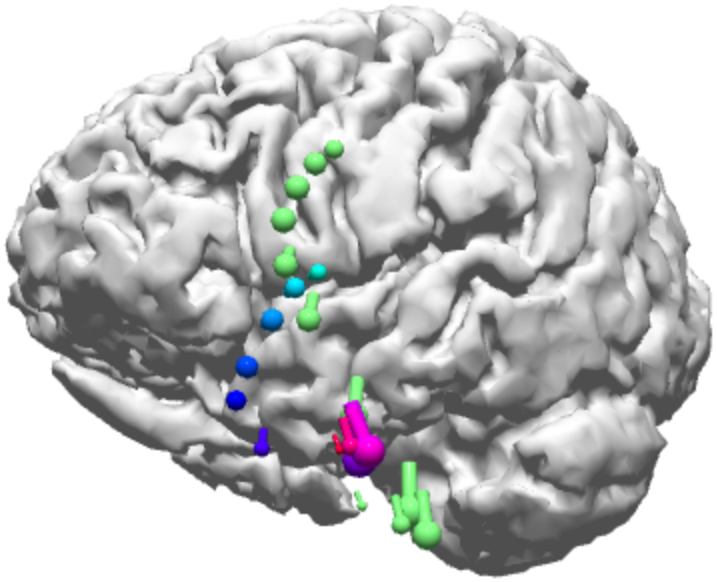
To "keep" these results, click the **Keep Results** icon on the Source Reconstruction Toolbar, or go to **Source Results** (Main Menu bar) → **Keep Results**. The Kept Results are now seen in the **Objects** list (and in a single color).



6. Now we will repeat the same analysis using the patient's Head Model. Select **BEM 6/8/9mm** for the **Head Model**.

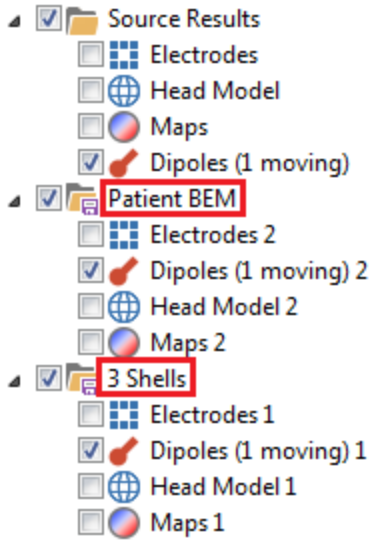


The results are seen in the 3D View, superimposed on the previous ones. You can see that the realistic head model results in dipoles (multicolor) that trace the tip of the left temporal lobe.

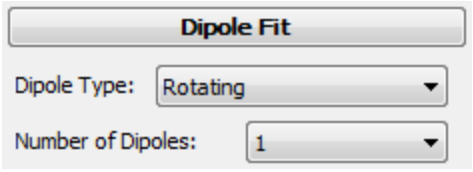


Keep these results by clicking the icon on the Toolbar.

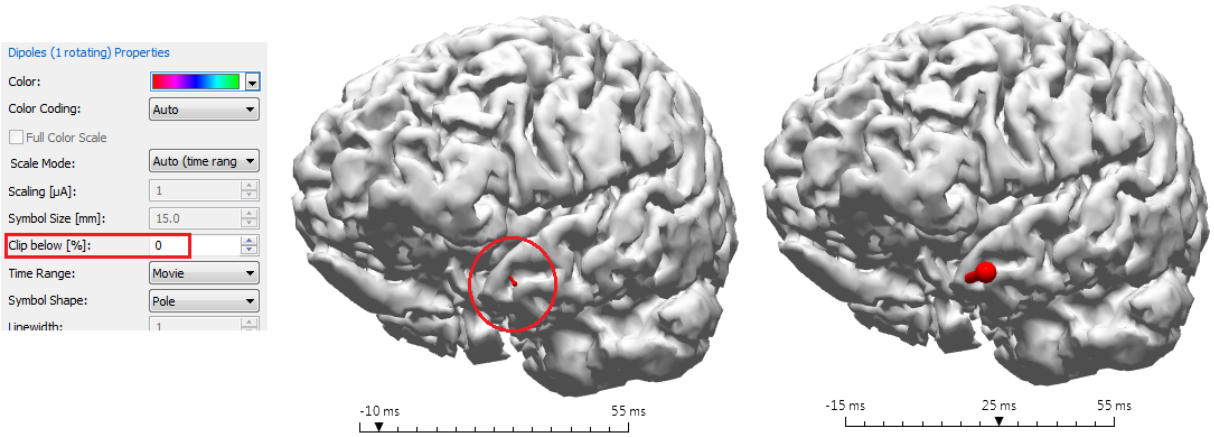
7. You can rename the Kept Results to avoid confusion. Click on Kept Results 1 to highlight it, and then press the *F2* function key. You will then be able to rename the Kept Results (*3 Shells*). Rename Kept Results 2 to *Patient BEM*. Note that you can display any or all of the Kept Results for comparison.



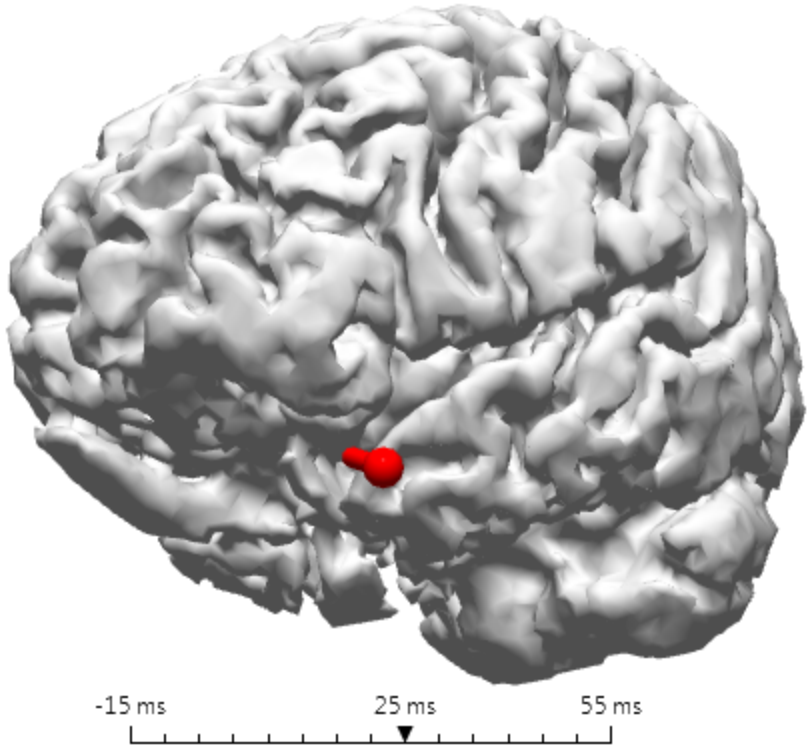
8. Now deselect the display of all of the Kept Results. This leaves only the latest results (using the patient's BEM Model). Go back to Dipole Fit and select **Rotating** for the **Dipole Type**.



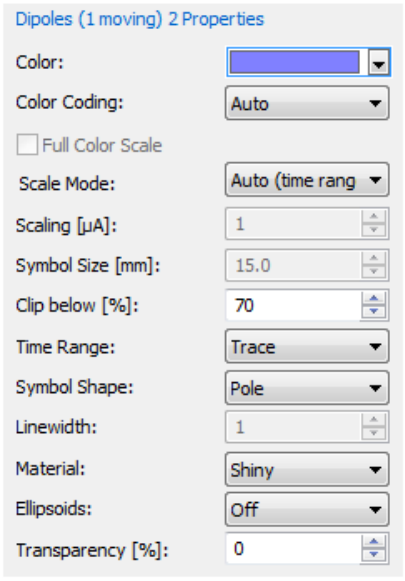
Now there is a single dipole with a fixed position. Deselect the Timerange Display Mode icon again. Decrease **Clip below** to **0%** in the **Dipoles (1 rotating) Properties** (so that all solutions will be seen). Drag the pointer in the time scale to see the dipole rotate across time. The position is fixed, but the orientation is free to change.

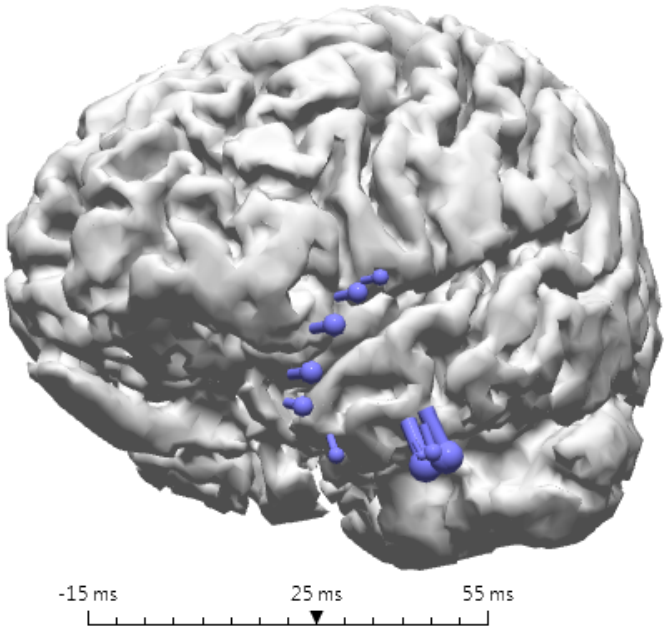


Go back to Dipole Fit and select **Fixed Coherent**. Now when you move through the Timerange, you will see that the position and orientation are both fixed, and only the dipole strength (and confidence ellipsoids) changes across time.

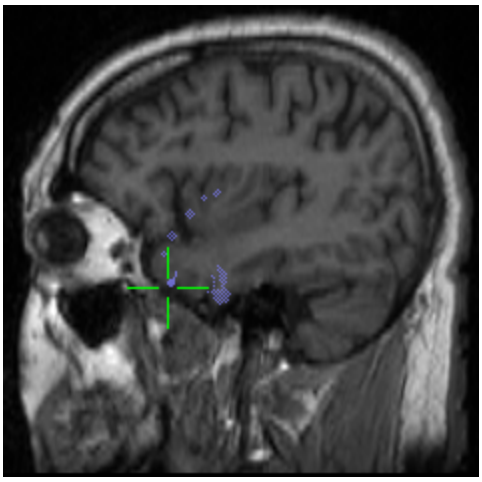


9. Display only the results with the patient's BEM Model (Kept Results 2). Click on the cortex surface and note that the Cortex properties are displayed below the Objects list. Click on a dipole to see its properties. These are shortcuts to the properties of any object that is displayed.



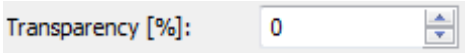


Go to the Image Data display and enable the Timerange Display Mode icon again. The dipole results are superimposed on the MR data.



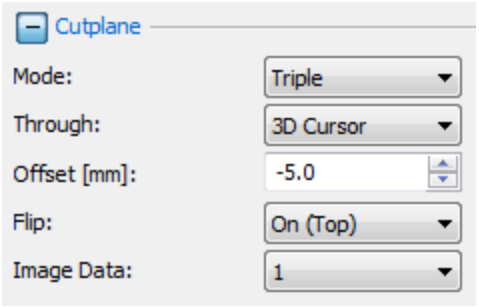
Go to the

display. Enable the display of the Skin

, with its Transparency set to 0% 

in the Skin properties. Only the Skin surface is displayed.

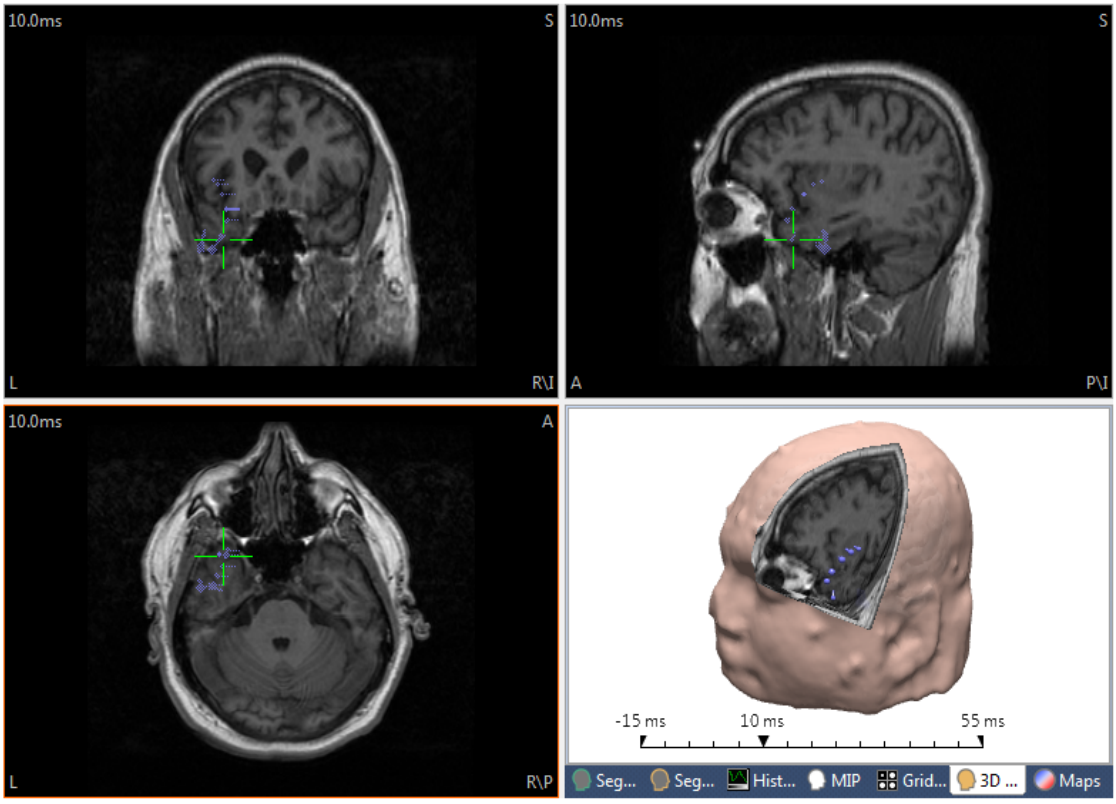
In the Skin properties, set **Mode** (in the **Cutplane** section) to **Triple**. For **Through**, select **3D Cursor**. Set **Offset** to **-5mm**. Set **Flip** to **On (Top)**.



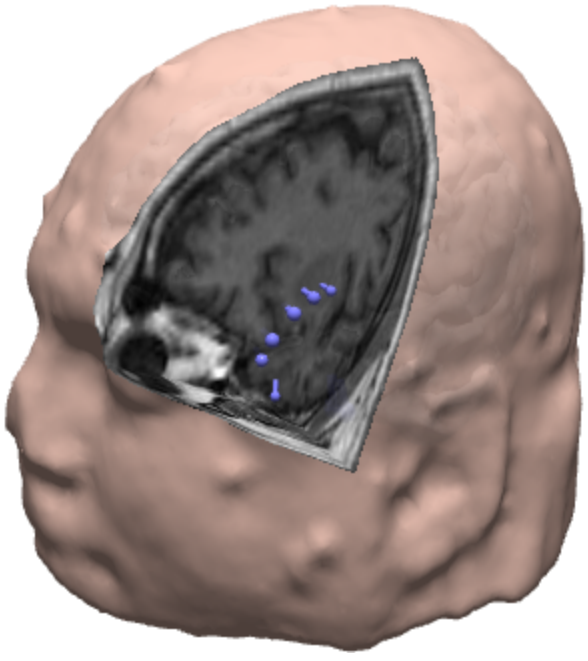
Return to the

display and select the **3D View** display

for the lower right display. Now drag the cursor (green crosshair) in any of the image displays to control the position of the cut planes. Rotate the head in the 3D View part of the display to make the cut section shift.



When you have a view you like, return to the 3D View display.



This concludes the tutorial for single equivalent dipoles. Not all of the functionality was presented, but you should have sufficient familiarity to explore the additional options.

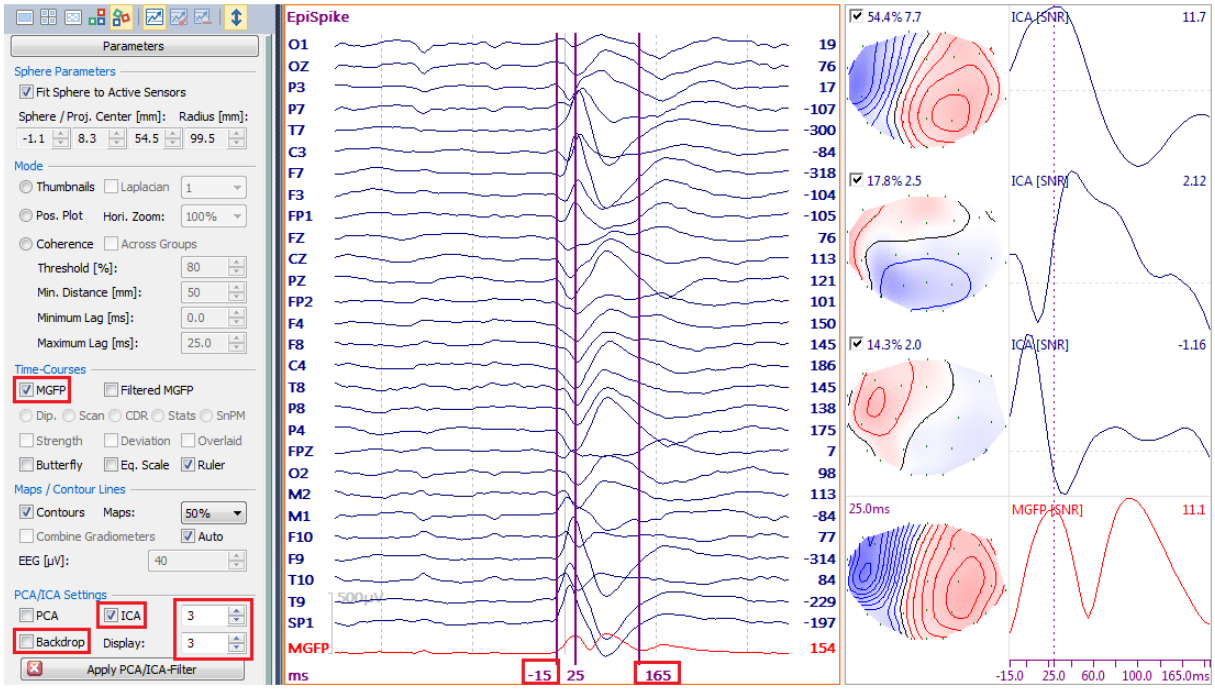
The same Study is used in the **Scan Methods** tutorial below. The Kept Results will not be needed. Click **Source Results** → **Remove All Results** to clear them. Close the Study, if desired.

2.6.1.1 ICA Source Reconstruction

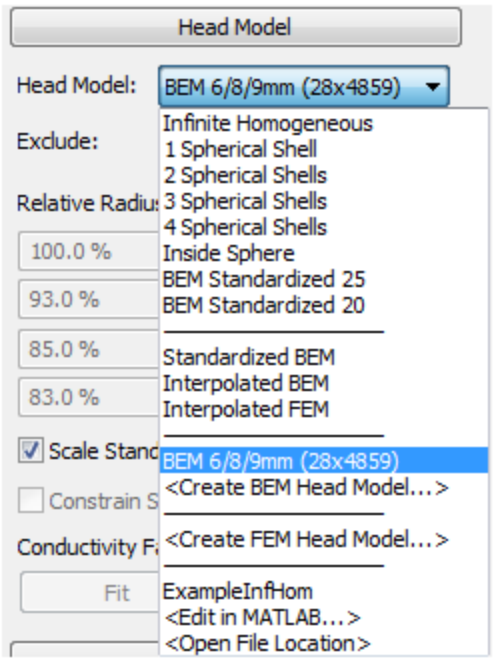
ICA Source Reconstruction allows you to compute a fixed dipole source for each ICA component. The results are more meaningful with more samples - it is better not to restrict the Timerange too much.

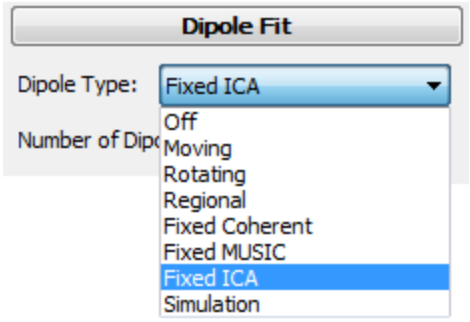
We will use the same file (*epispike.avg*) as in the previous tutorial. Noise Estimation has been performed automatically (-500 to -50 ms), and a Timerange from -15 to 165 ms has been selected (the spike and slow wave).

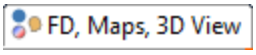
1. Select the FD, Maps display. ICA has been performed (using the Maps parameters), and three components have been detected. **MGFP** was enabled, and the **Backdrop** was disabled (just to reduce the visual complexity).



2. Select Source Reconstruction and in the Head Model panel, select the pre-computed patient's **BEM Model** (BEM 6/8/9). Select **Fixed ICA** as the **Dipole Type**.



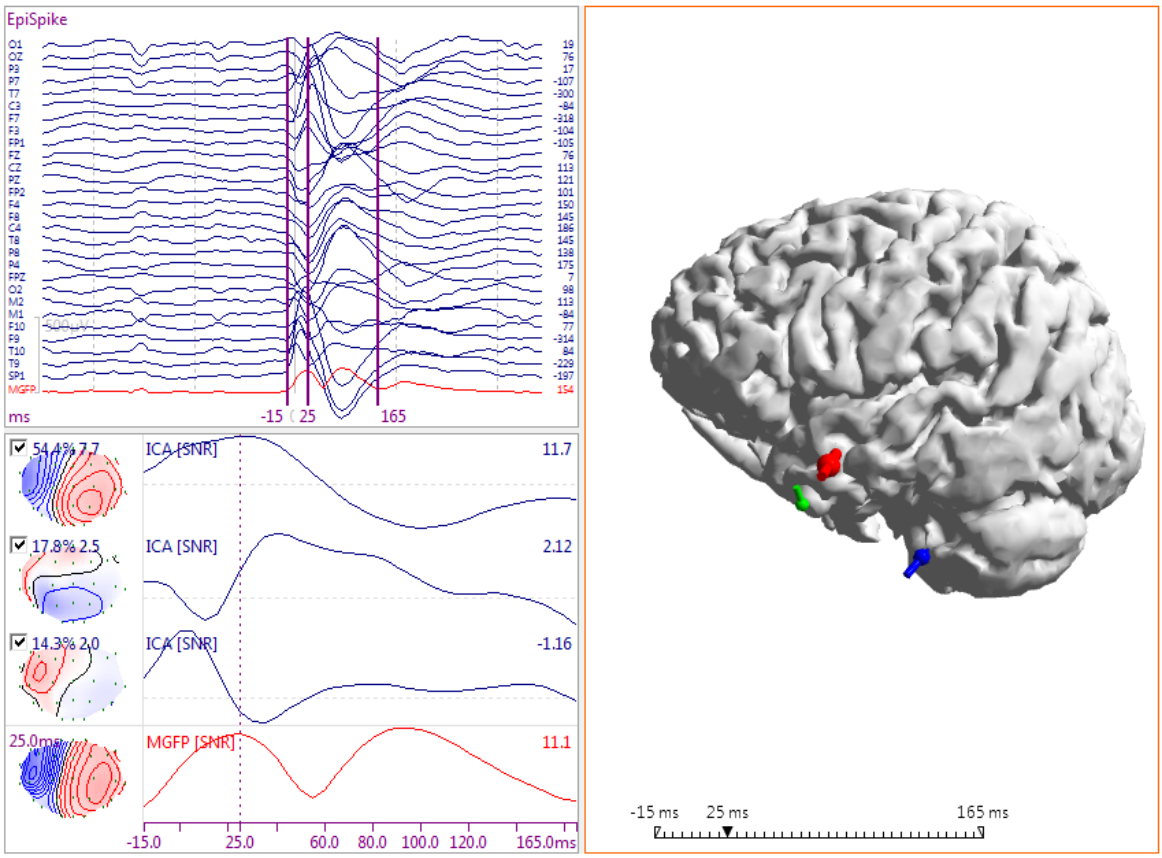


Select the 

view.

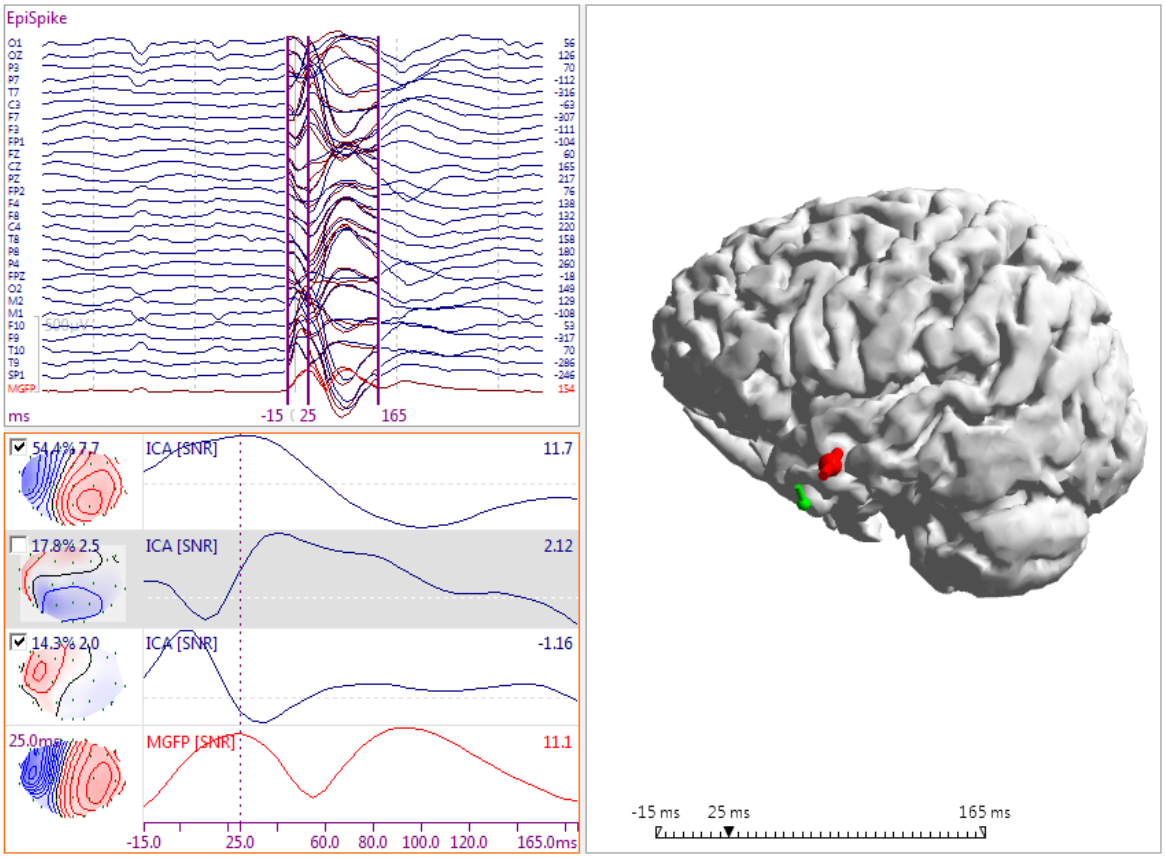
3. You will see three dipole solutions in the **3D View** display. The cortex was selected (left view and Transparency of 100%) and the electrodes were deselected for display. The Confidence Ellipsoids were turned off (in the **Dipoles** properties:

).



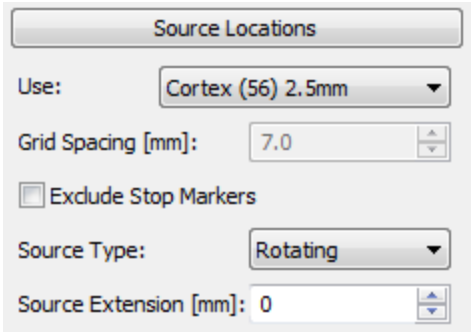
4. Deselect individual ICA components to see the effects on the dipoles and click the

button. In this way you can see the dipole solutions of the individual ICA components.

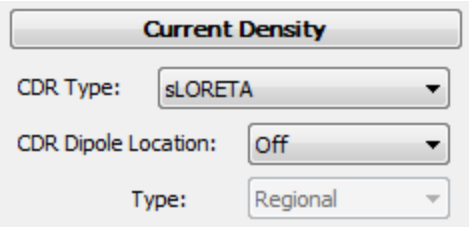


5. The same type of analysis may be performed with CDR as well.

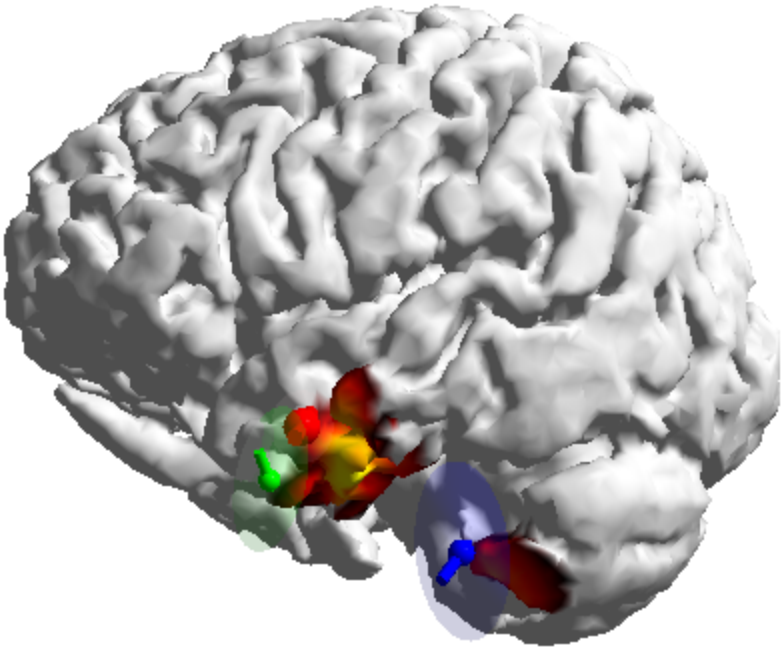
In the Source Reconstruction parameters, in the Source Locations panel, set **Use** to the patient's **Cortex** (constrains CDR solutions to the cortex).



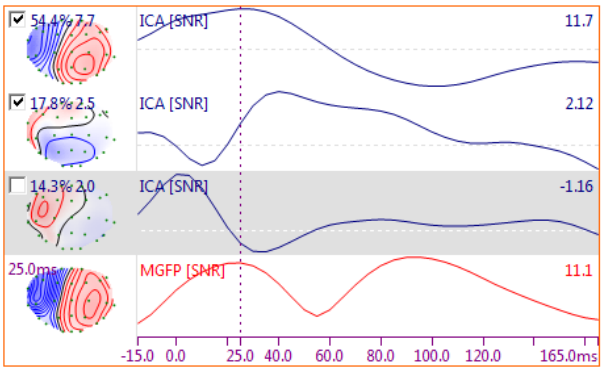
6. In the **Current Density** panel, set **CDR Type** to **sLORETA**.

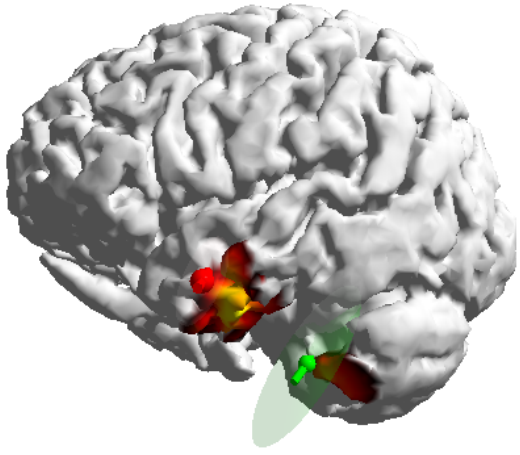


7. The Fixed ICA Dipoles and the sLORETA CDR results are seen in the **3D View**. Increase **Transparency** of the **CDR (sLORETA)** results to **100**% to see all of the Fixed ICA dipoles. Adjust **Clip below [%]** as desired (95% selected below).



8. Now when you deselect an ICA component, you will see the dipole be removed as well as the loss of its contribution to the CDR results.



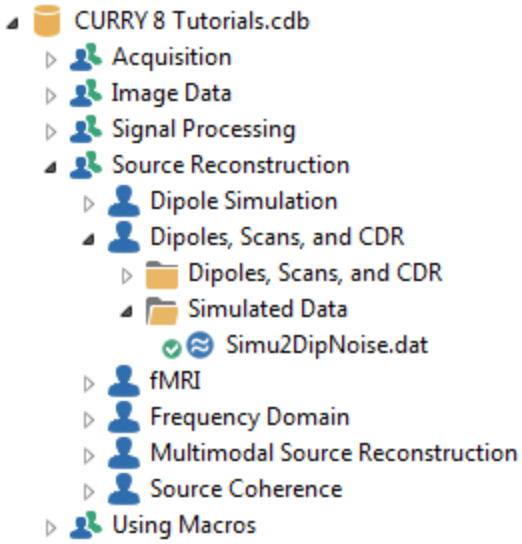


Close the study without saving the results.

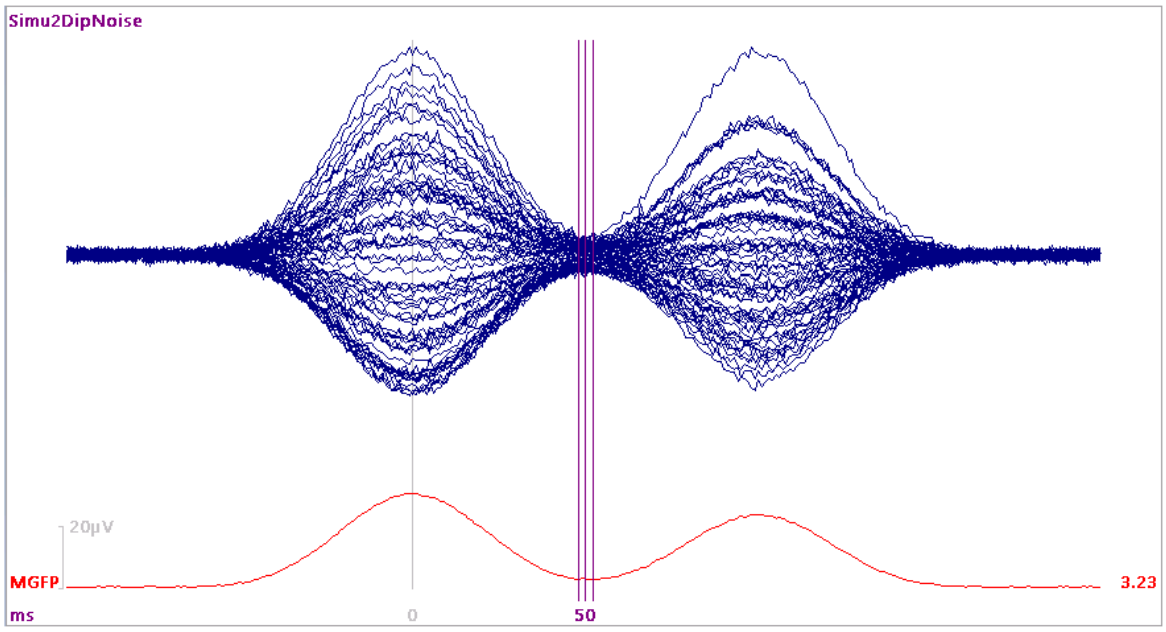
2.6.1.2 Simulated Data

In this example, we will combine PCA/ICA analysis with source construction, using a simulated data set. This will illustrate the relationship between ICA filtering and more than one dipole source.

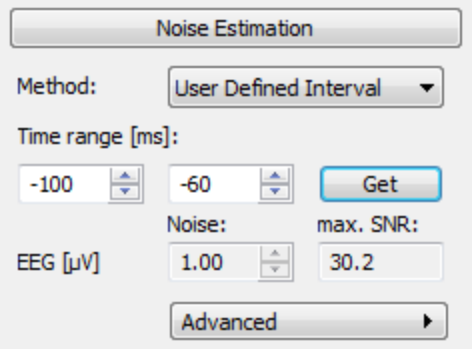
The data may be found in the Study shown below, in the *CURRY 8 Tutorials* Database. Open the Study.



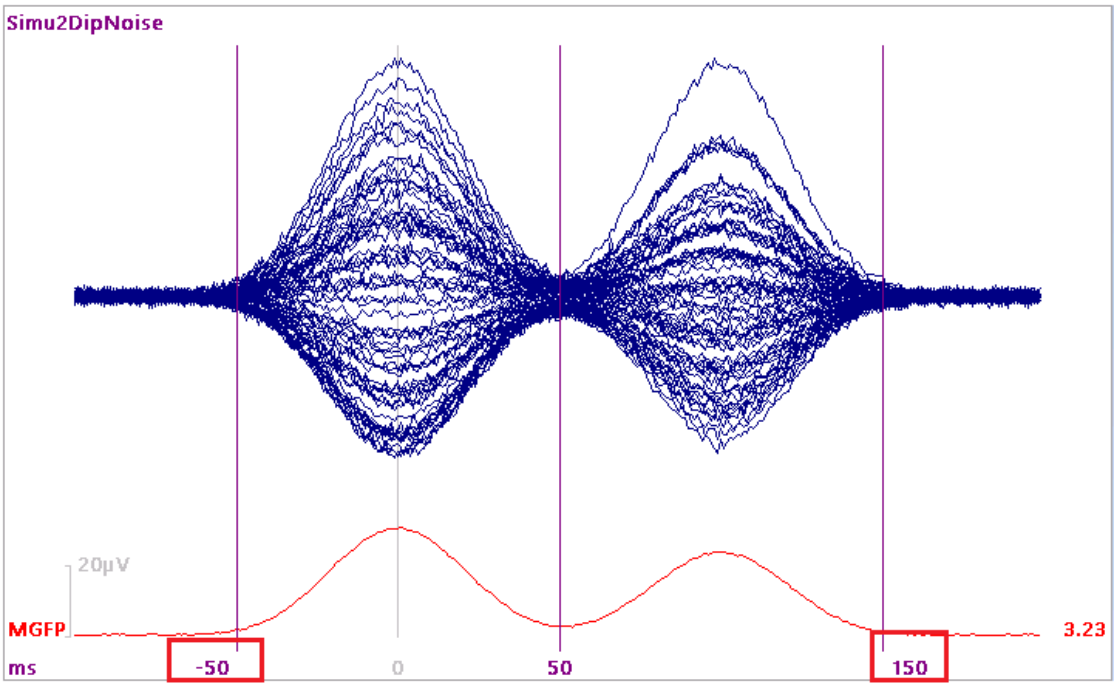
There are 2 peaks in the MGFP.



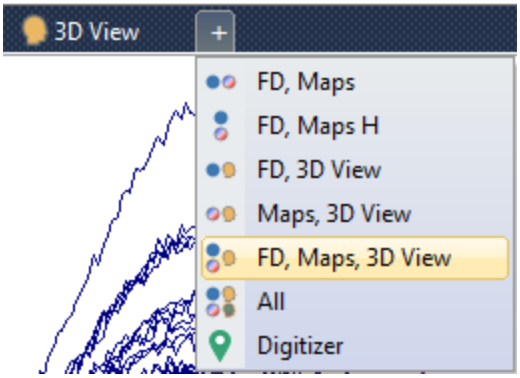
1. As usual, the first step is to compute a **Noise Estimation**. The **Auto** setting is not appropriate in this case, since the "signal" begins around -60 ms and Auto uses the 0 ms time point. Set the two outer cursors at **-100 ms** and **-60 ms**, and expand the Noise Estimation panel. Select **User Defined Interval** and click the Get button to transfer the cursor latencies.



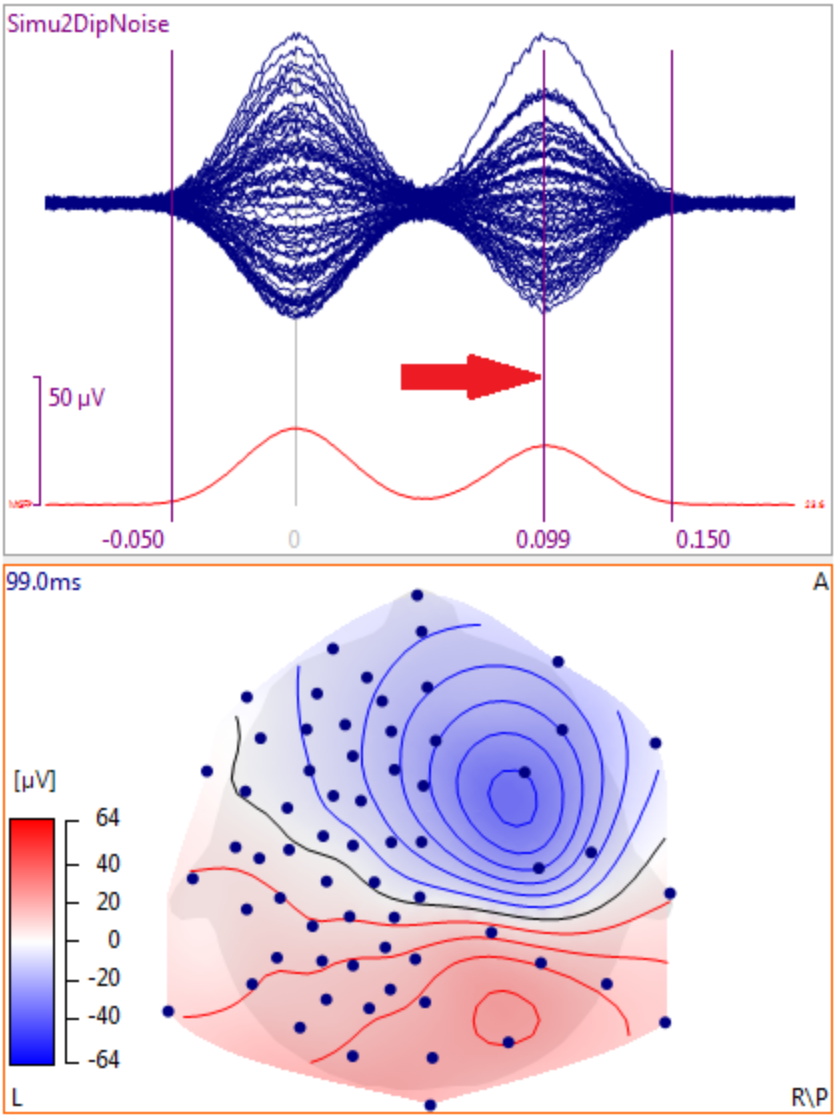
2. Set the outer cursors to **-50** and **150**ms.



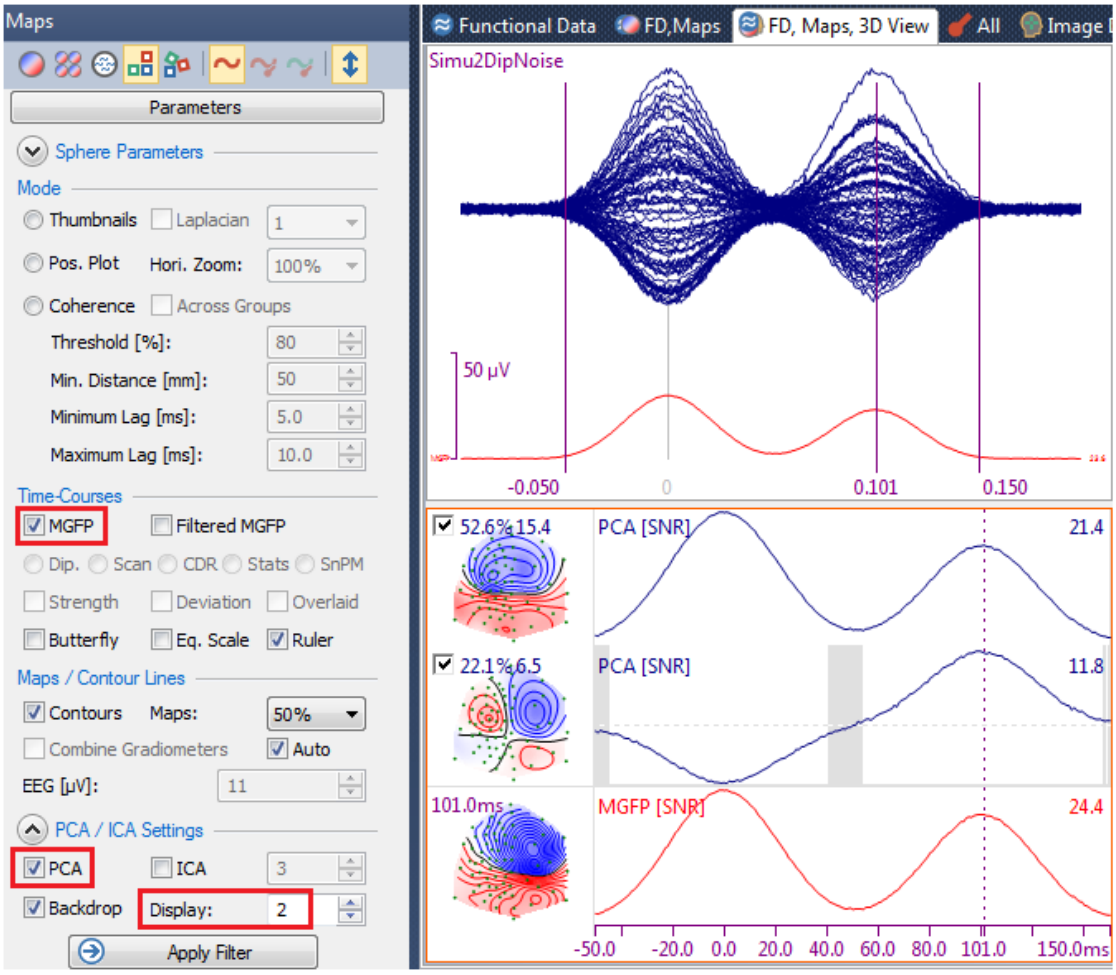
3. Select the FD, Maps, 3D View display.



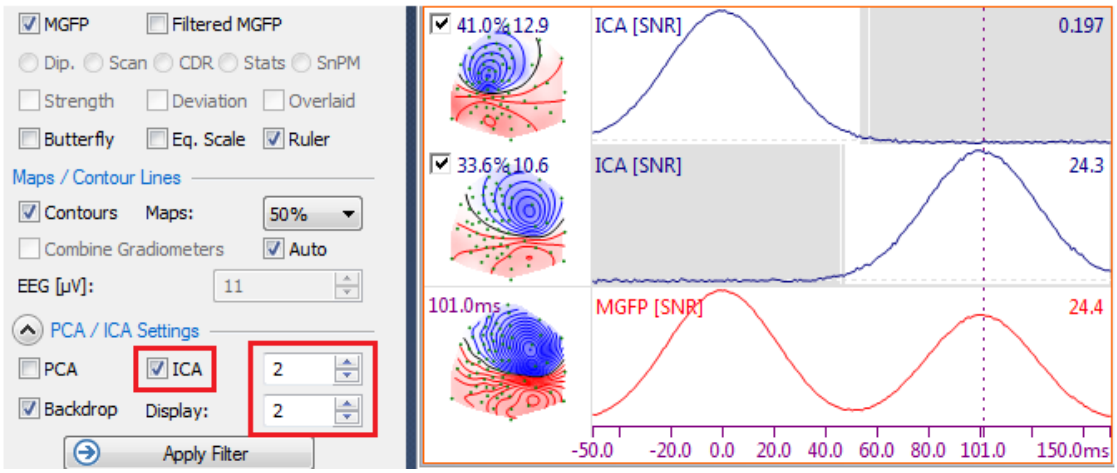
Drag the middle cursor in the Functional Data display to see the change in the contours in the Maps display.



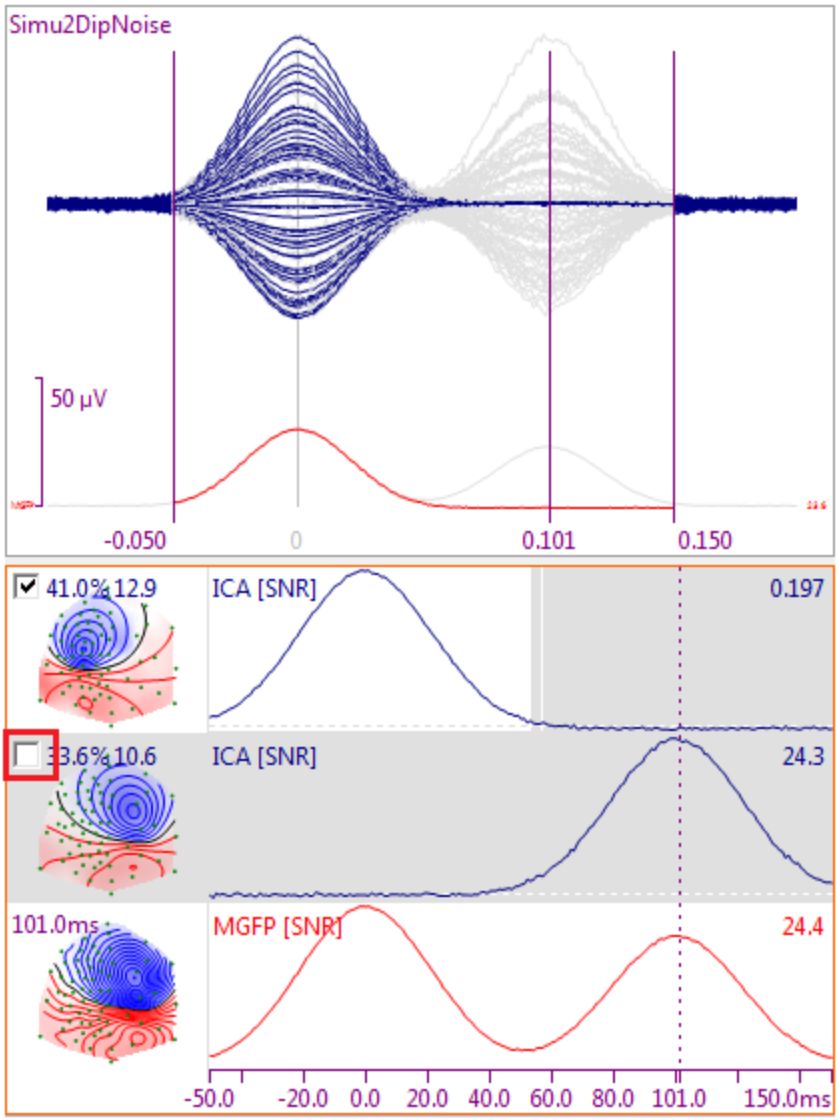
4. Select the Maps parameters. Enable MGFP and PCA, and set **Display** to **2** components (the others being noise only).



5. From the PCA we see that there are two valid components, so select ICA with 2 components computed and displayed. Now you can see the two independent components. The gray areas are where the SNRs are less than 1.0. The components can be removed selectively. Incidentally, the results also illustrate a difference between PCA and ICA. The original waveforms are decomposed into independent components with ICA.



6. Deselect the second component (click on the check mark to remove it; it will gray out), and then press the button. In the Functional Data display, you can see that the second component has been replaced by essentially flat lines. The grayed out lines show the previous waveforms. The second peak in the MGFP has been replaced by a nearly flat line (in the Functional Data display).

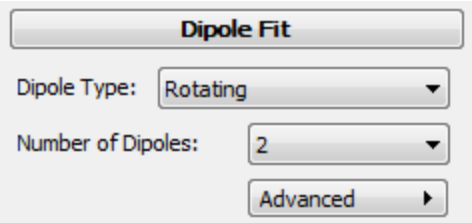


Reselect the second component and deselect the first component. The first component has been removed.

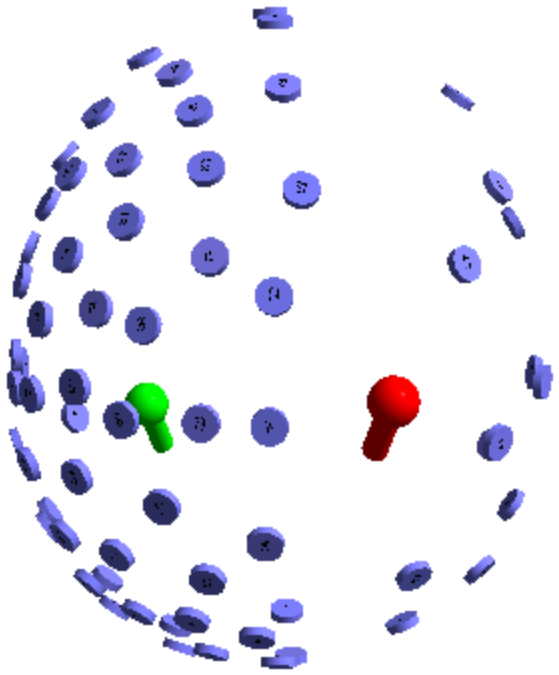
7. Click the Apply Filter button to remove the filtering, and reselect both components. Thus far, you have seen how to selectively remove independent components. What effect does this have on source reconstruction?

Select the Source Reconstruction parameters, and expand the Head Model panel. Select the **3 Spherical Shells** head model (if needed).

8. Expand the Dipole Fit panel, and select **Rotating** for the **Dipole Type**, and **2** for the **Number of Dipoles**.



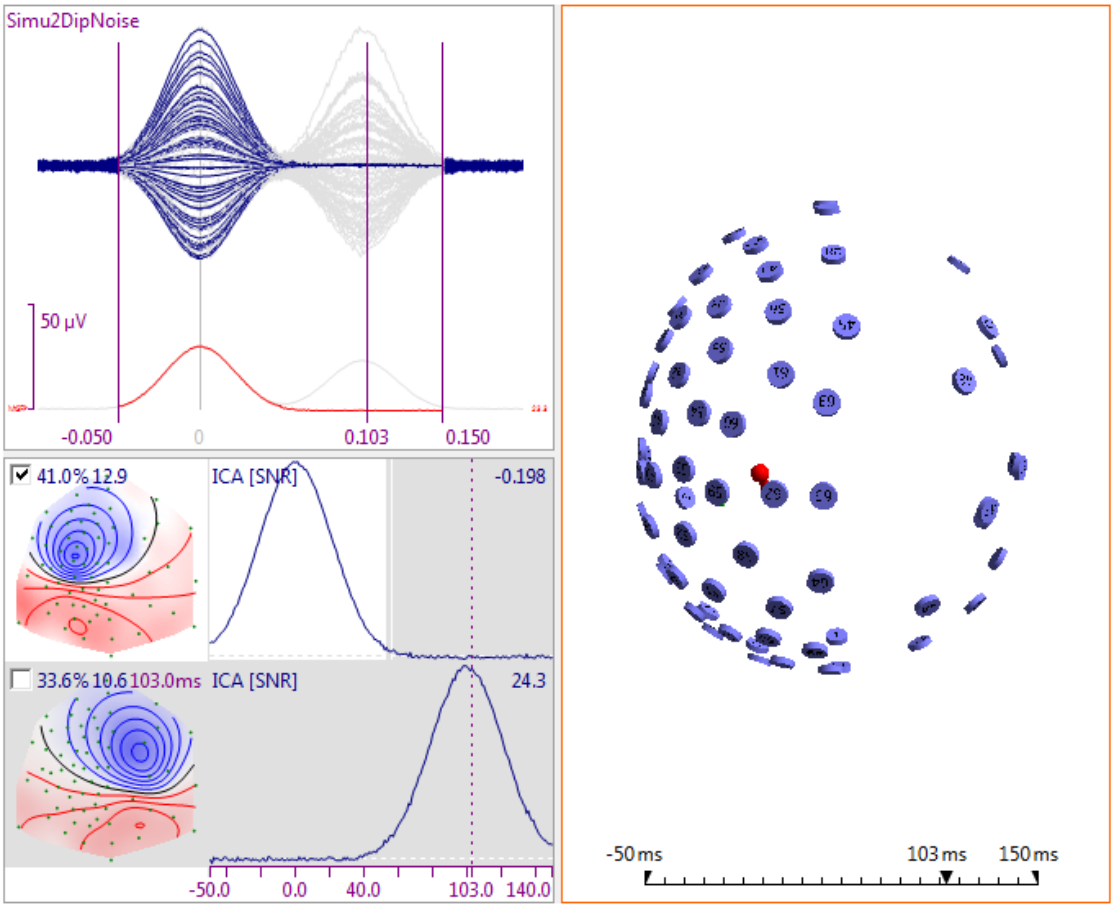
9. Select the 3D View display, and disable the **Confidence Ellipsoids** from the **3D View** toolbar. You will now see the two dipole solutions.



Deselect the **Timerange Display Mode** (**3D View** toolbar) and play a **Movie** (Main toolbar). You will see first the left side dipole develop and wane, followed by the same on the right side.

Select the **Timerange Display Mode**.

10. Deselect the second ICA component, click the Apply Filter button, and see the second dipole result disappear (or nearly so). Reselect it and deselect the first component to see the first dipole result disappear.

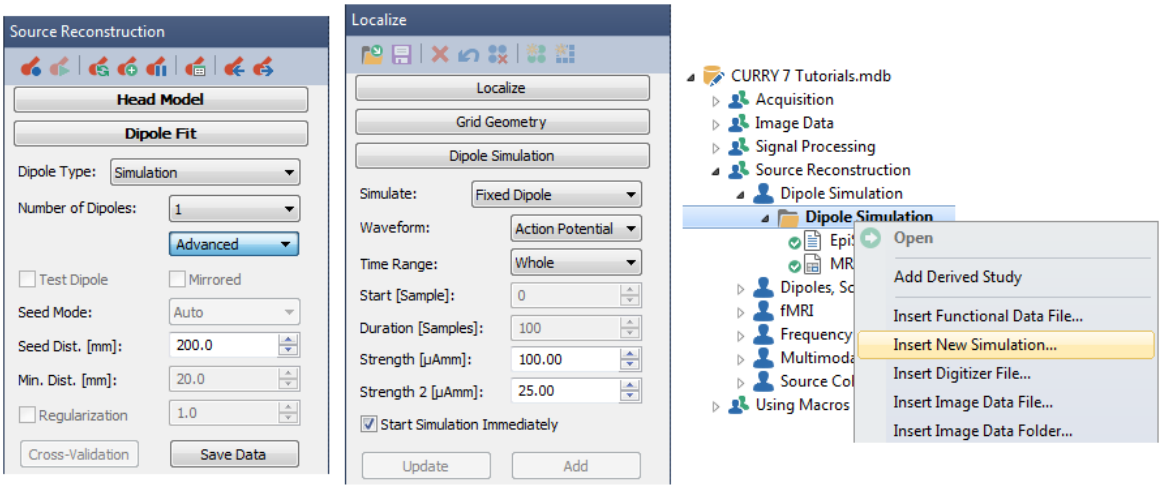


In this way you can see how multiple dipoles can be used to explain the data, and how to selectively filter single components. See also the **ICA Source Reconstruction** tutorial.

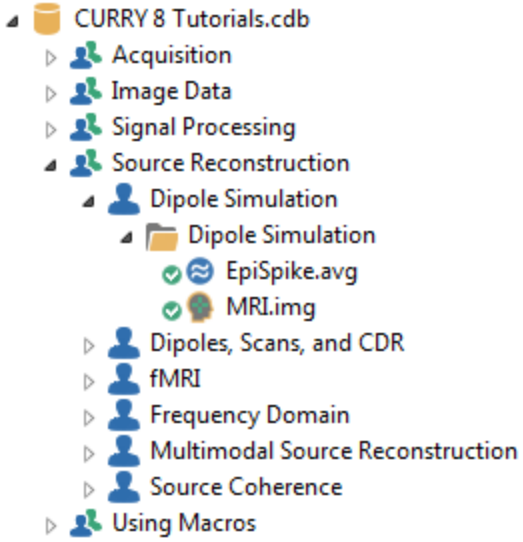
2.6.1.3 Dipole Simulation

Dipole simulation is used when you wish to see the scalp data that would be present with dipole sources in various locations. They are also used for testing your own algorithms and for teaching purposes.

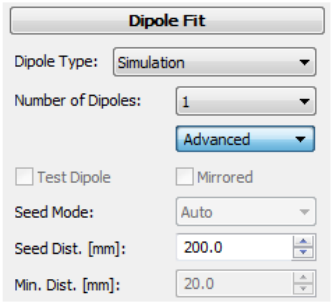
There are two different ways to create simulated dipoles. One way uses the **Simulation** option for Dipole Fit in the Source Reconstruction parameters. The other uses a more involved approach found in the Dipole Simulation parameters panel under Localize, and the **Insert New Simulation** option in the Database.

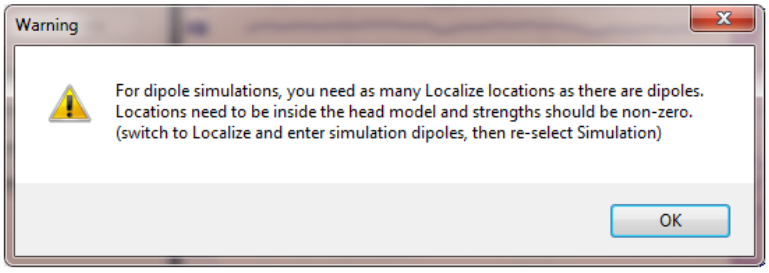


Locate and open the *Dipole Simulation* study shown below. Any file can be used; the waveform data are ignored. The file is selected only to provide the electrode position information. In this case, we have the MRI data also.

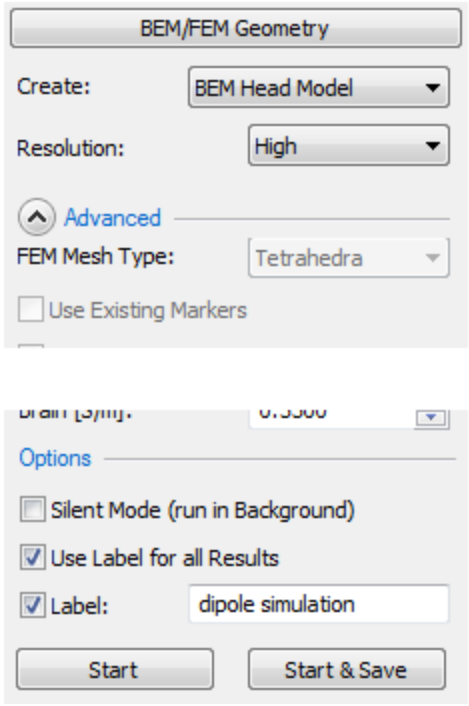


1. In this example, we are using an average file with the Timerange set for the entire interval (*Ctrl+double-click* will set the cursors automatically). Expand the Dipole Fit panel and select **Simulation** for the **Dipole Type** (acknowledge the message if it appears).

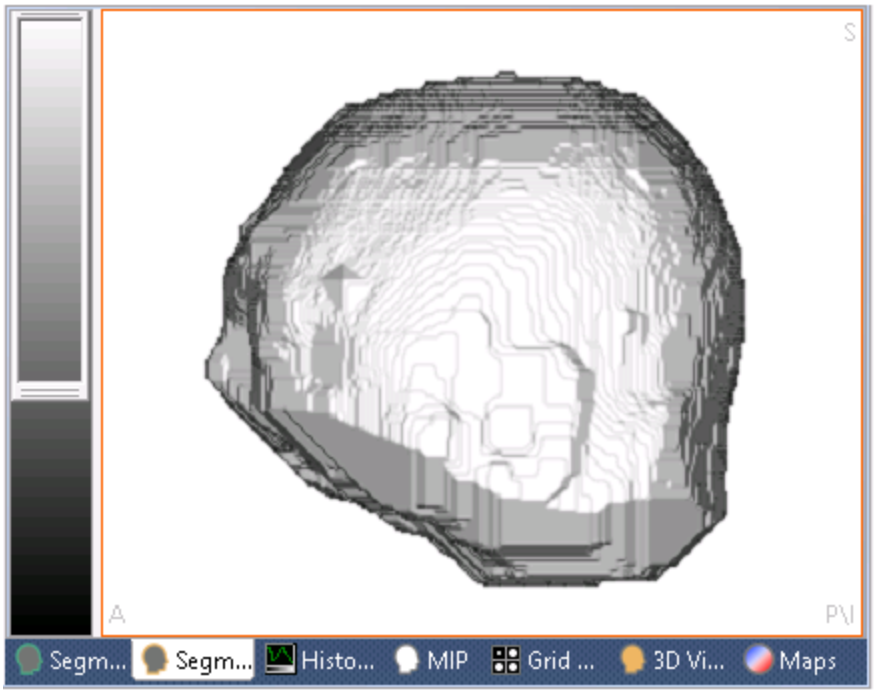




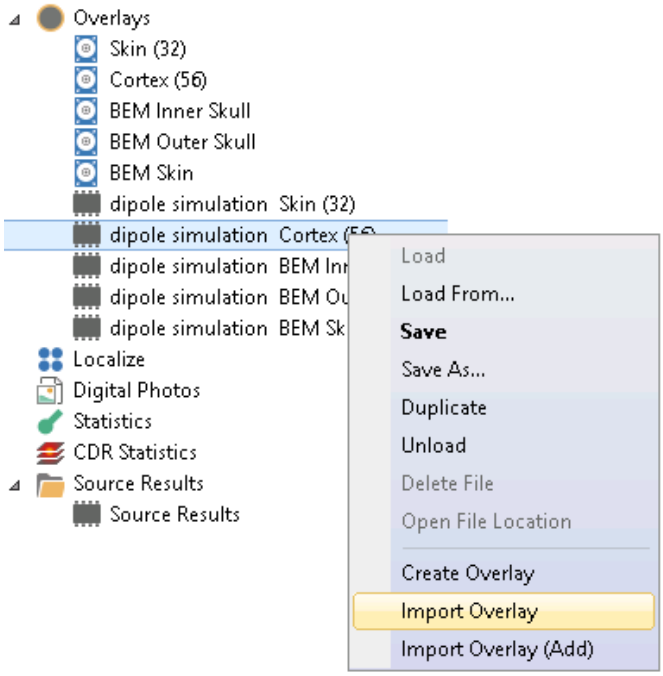
2. The next step is to create a **BEM Head Model** so we will have a surface to place the dipole positions on, if one has not already been created. If you do not have the MRI data, you can use the supplied averaged MR data set. In this case we have the MR data. The default parameters were used, with *dipole simulation* as the **Label**. Enable Use Label for all Results. Click **Start**.

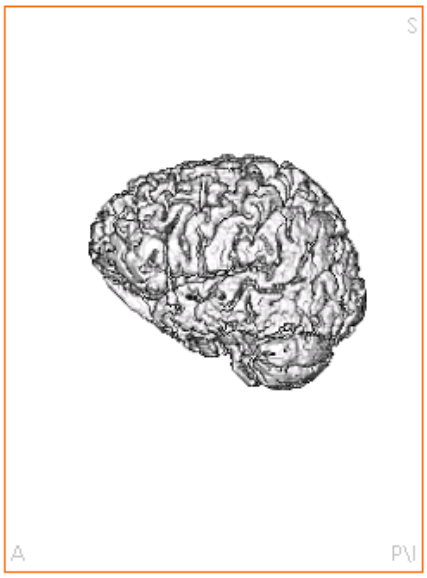


Select Segmentation Result in the **Image Data** display. The segmented Skin surface is displayed. We could use that, but more likely we would want to use the segmented cortex. To use the cortex, we will need to import its **Overlay** from Results.

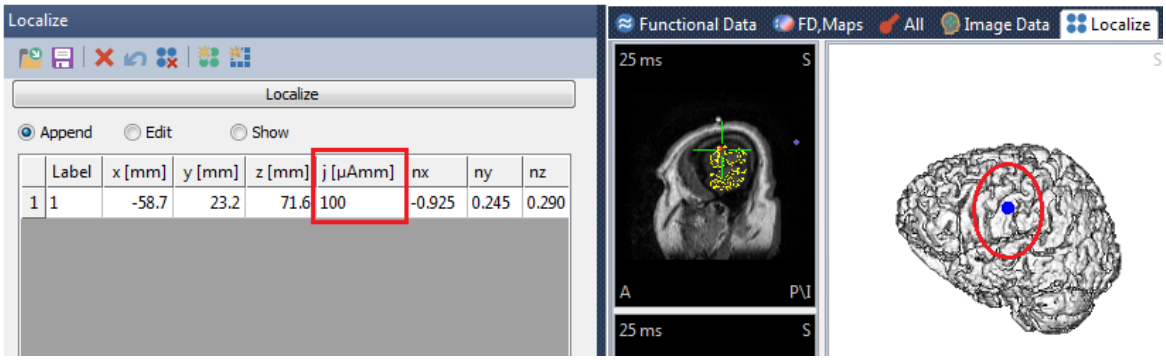


Go to the Localize display and select Segmentation Result. Then go to the Results panel (under **Results**), locate the cortex **Overlay** that was just created, *right click* on it, and select **Import Overlay**. Now we see the cortex in the Segmentation Result.

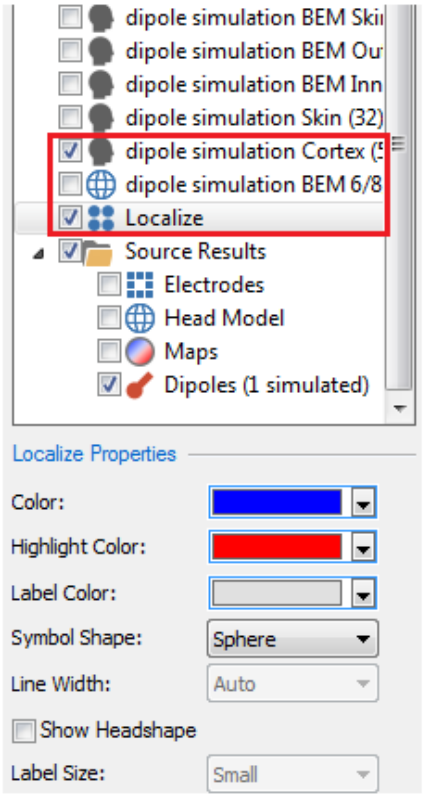


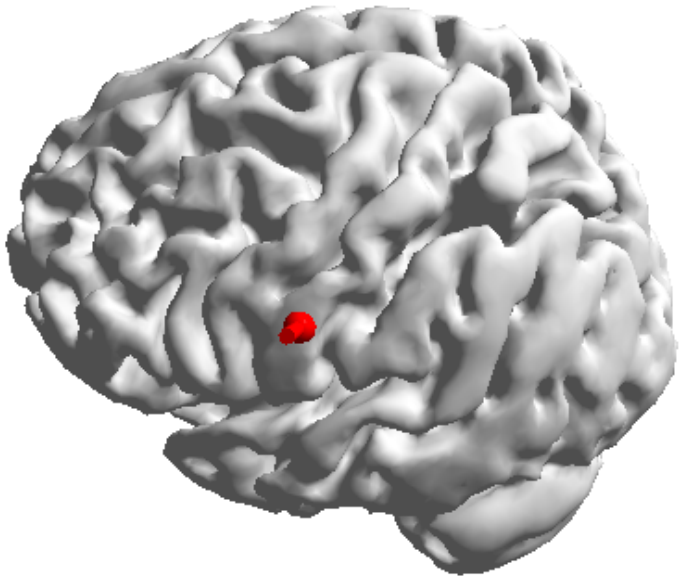


3. Still in the Localize display, click on a surface in the segmented cortex to create a dipole location, seen also in the Localize list. Note that the Strength (**j[µAmm]**) is set to **100** by default.

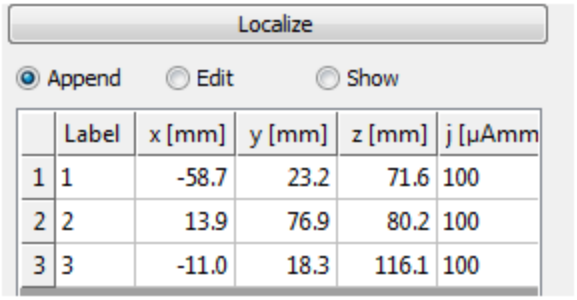


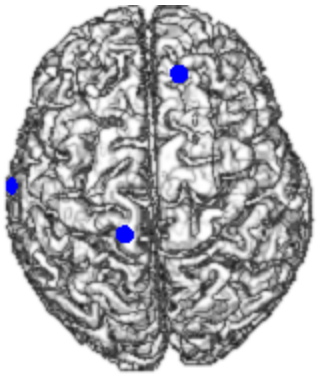
4. The simulated dipole is seen in the 3D View. In the 3D View Objects list, select the **Cortex**, and change the **Localize Properties** to show the dipole.



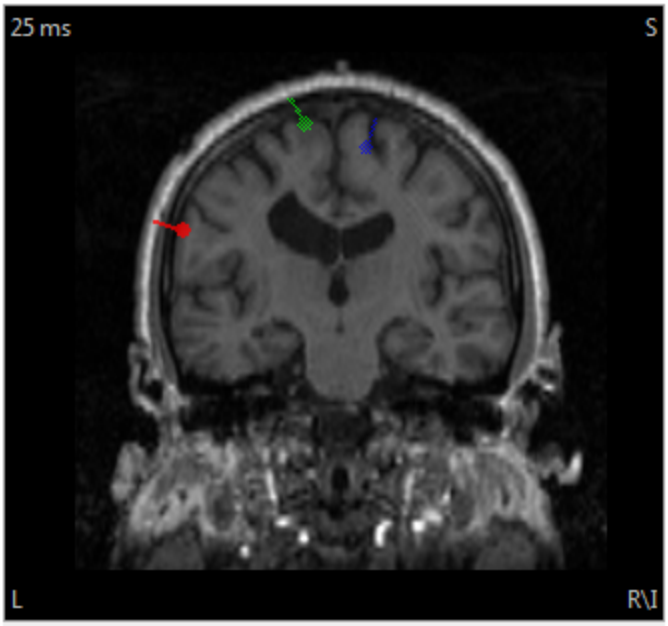


5. To add more simulated dipoles, click in the **Localize** display in a few more locations. If you want to change the dipole **Strengths**, you can do so from the Localize list.





6. The simulated dipoles are also seen in the **Image Data** display.

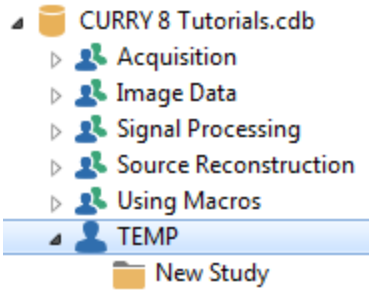


The above illustrates the procedure for creating simple simulated dipoles. Next we will look at the more complex options using the Dipole Simulation parameters under Localize.

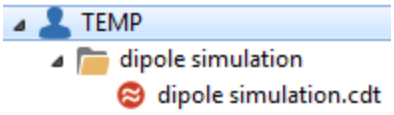
Close the Study without saving any of the results.

The second method has more flexibility, and begins by setting up the waveforms that you want to use (the previous method ignored the waveforms, and used the positions only).

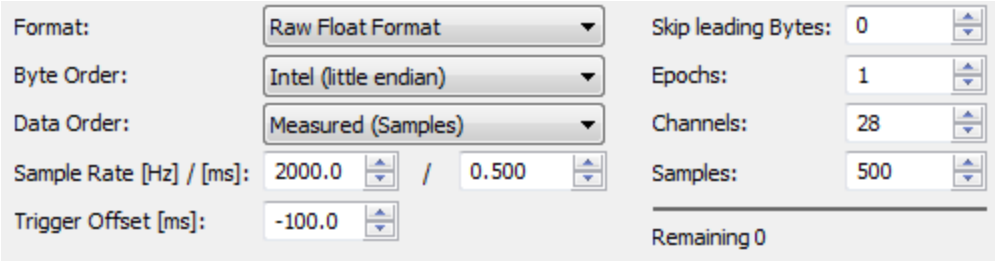
1. We will begin by creating a temporary Study in the Database. Highlight the Database name and click the **Add Subject** icon. Rename the Subject name to *TEMP*.



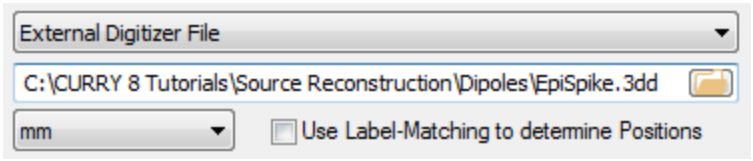
2. *Right-click* on the New Study and select **Insert New Simulation**. A Save As dialog appears, allowing you to select a target location and enter a file name (use, for example, *dipole simulation.cdt*, saved to the Desktop). The study is renamed in the process, and the simulated file is seen. Then open the Study.



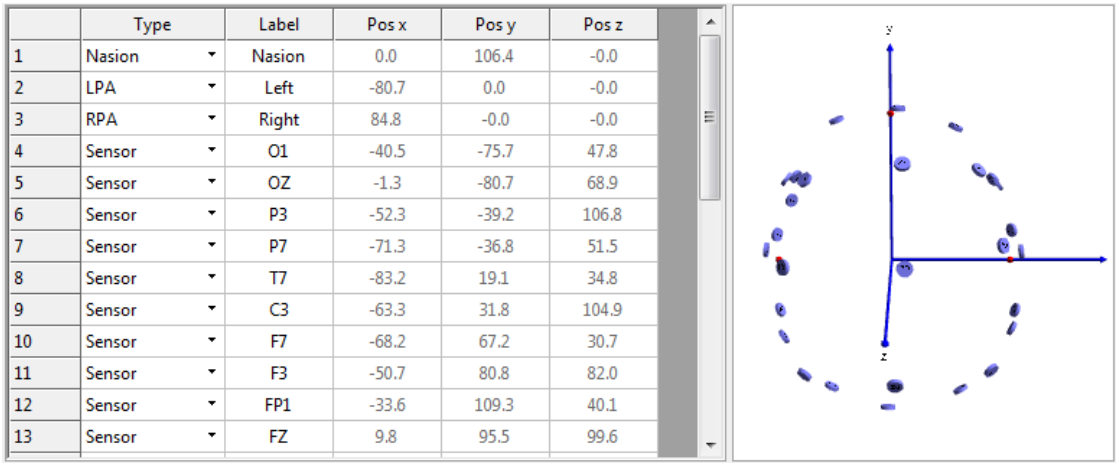
3. The Functional Data Import Wizard will appear. Here we decide how many channels to use, what the Sampling Rate will be, and so on. This is determined by the file that we will be referencing. We will use **2000**Hz for the **Sample Rate** and a **Trigger Offset** of **-100**ms. We know that the file has **28 Channels**, and that there are **500 Samples**. Then click **Next.**



4. On the second screen of the Wizard, select the sensor file - in this case, the *EpiSpike.3dd* file found in the *C:\CURRY 8 Tutorials\Source Reconstruction\Dipoles* folder.



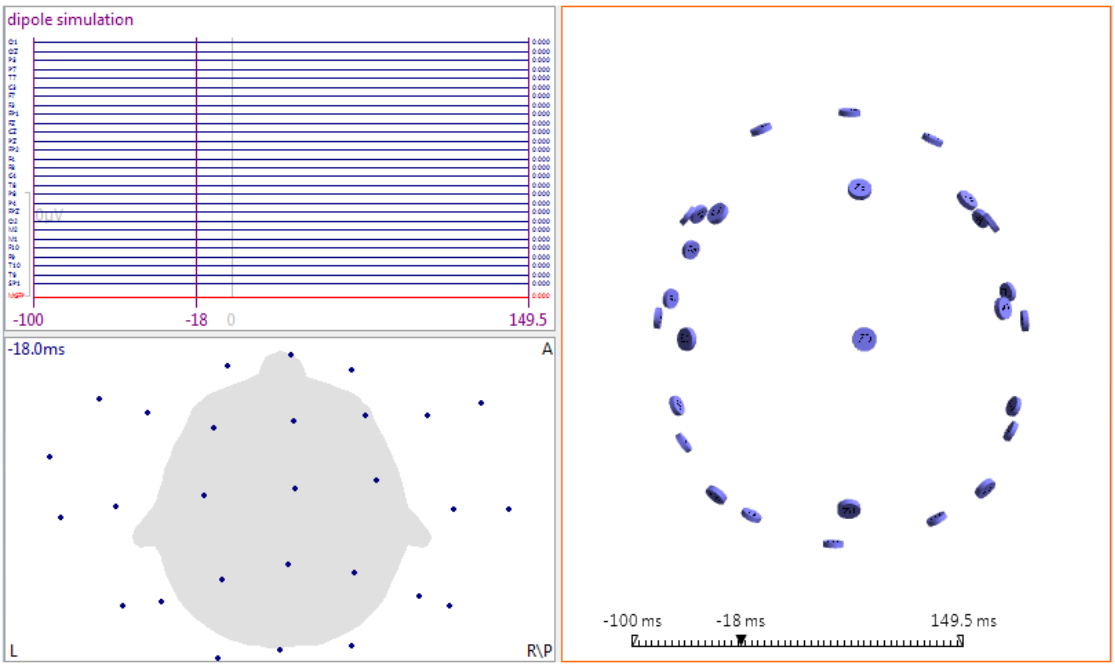
The positions are seen in the list and in the preview display. Click **Finish**.



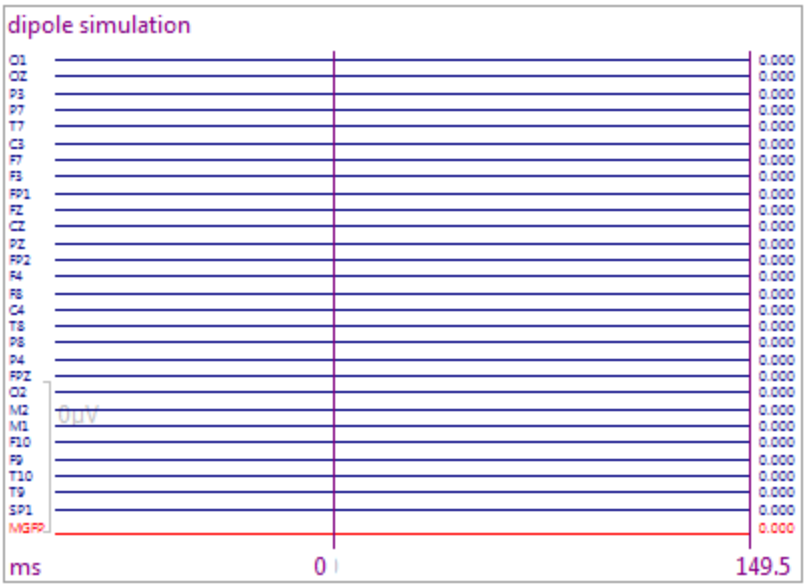
	Type	Label	Pos x	Pos y	Pos z
1	Nasion	Nasion	0.0	106.4	-0.0
2	LPA	Left	-80.7	0.0	-0.0
3	RPA	Right	84.8	-0.0	-0.0
4	Sensor	O1	-40.5	-75.7	47.8
5	Sensor	OZ	-1.3	-80.7	68.9
6	Sensor	P3	-52.3	-39.2	106.8
7	Sensor	P7	-71.3	-36.8	51.5
8	Sensor	T7	-83.2	19.1	34.8
9	Sensor	C3	-63.3	31.8	104.9
10	Sensor	F7	-68.2	67.2	30.7
11	Sensor	F3	-50.7	80.8	82.0
12	Sensor	FP1	-33.6	109.3	40.1
13	Sensor	FZ	9.8	95.5	99.6

5. Select the

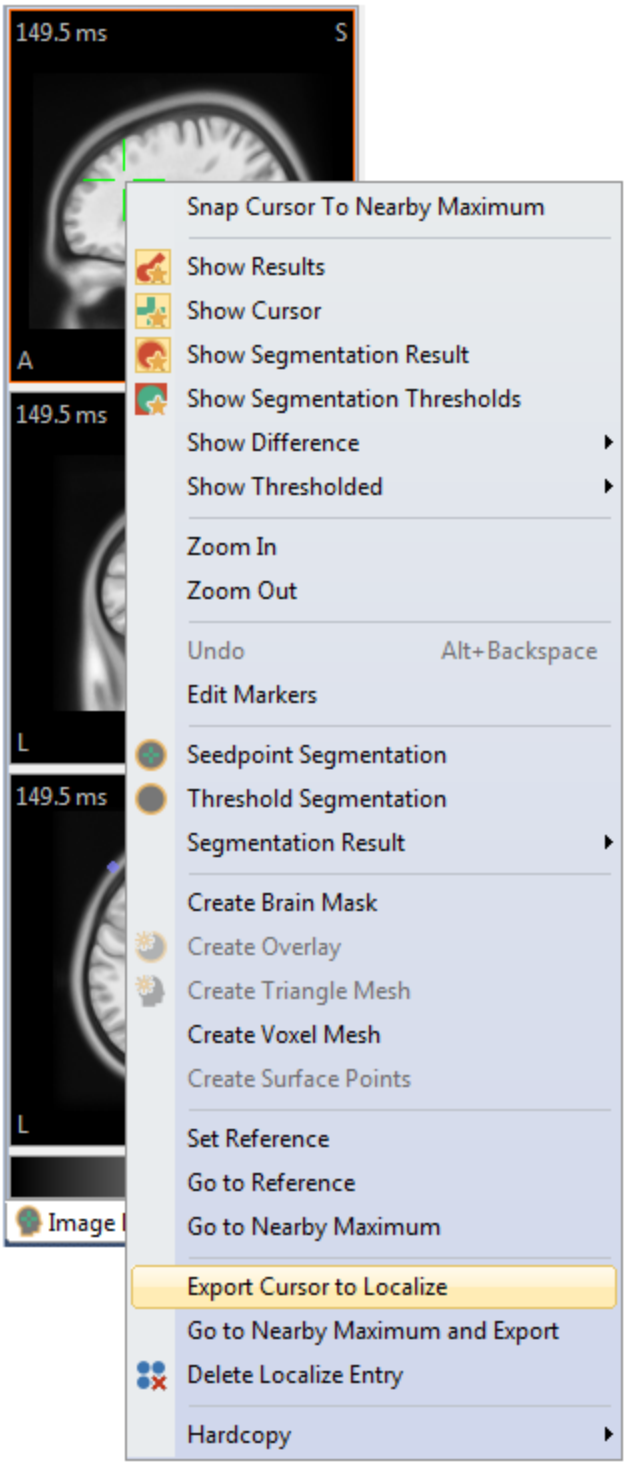
display. The waveforms are flat lines at this time, and are displayed from -100 to 149.5 ms.



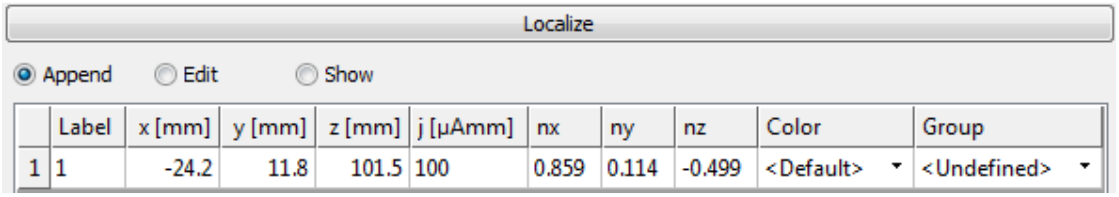
Select a Timerange from **0** to **149.5 ms**. The simulated waveforms we will create will be in this range.

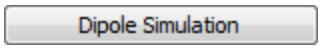


6. Select the Localize display. Click a desired dipole location in the MRI filmstrip, then *right click* and select **Export Cursor to Localize**.

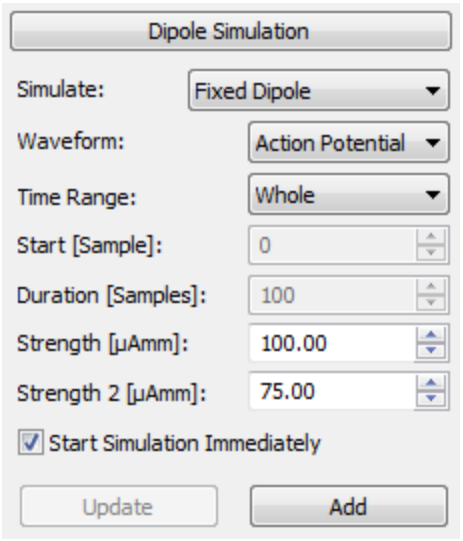


The position is added to the Localize list (with a Strength of 100).

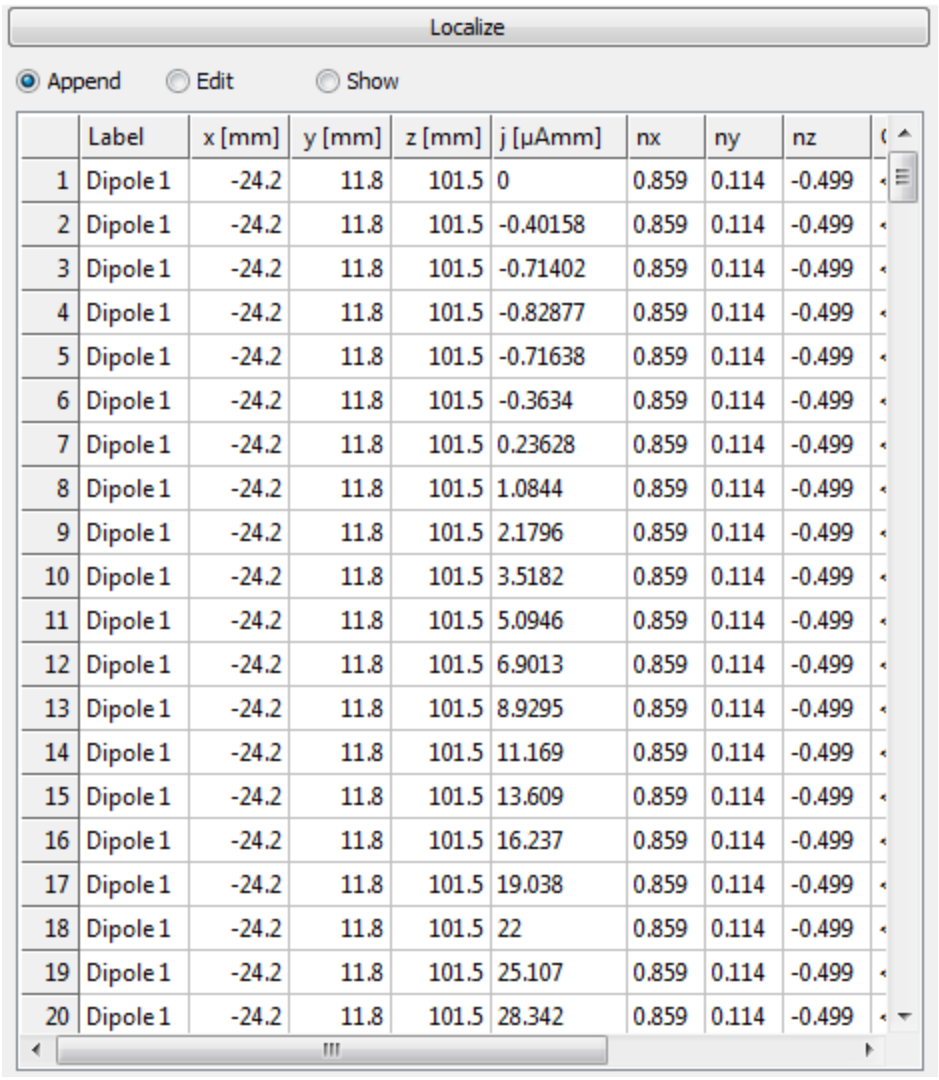


7. Expand the 

panel, and use the parameters shown below. Click **Add**.

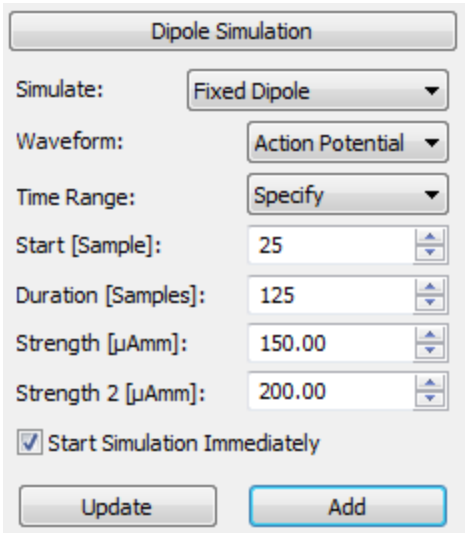


The dipole values are added to the Localize list, with one entry per sample point, across the selected Timerange. Since we selected **Fixed Dipole**, the positions and normals do not change. Selecting **Action Potential** creates Strengths that go positive to 100, then negative to 75, and then back to 0.



	Label	x [mm]	y [mm]	z [mm]	j [µAmm]	nx	ny	nz
1	Dipole 1	-24.2	11.8	101.5	0	0.859	0.114	-0.499
2	Dipole 1	-24.2	11.8	101.5	-0.40158	0.859	0.114	-0.499
3	Dipole 1	-24.2	11.8	101.5	-0.71402	0.859	0.114	-0.499
4	Dipole 1	-24.2	11.8	101.5	-0.82877	0.859	0.114	-0.499
5	Dipole 1	-24.2	11.8	101.5	-0.71638	0.859	0.114	-0.499
6	Dipole 1	-24.2	11.8	101.5	-0.3634	0.859	0.114	-0.499
7	Dipole 1	-24.2	11.8	101.5	0.23628	0.859	0.114	-0.499
8	Dipole 1	-24.2	11.8	101.5	1.0844	0.859	0.114	-0.499
9	Dipole 1	-24.2	11.8	101.5	2.1796	0.859	0.114	-0.499
10	Dipole 1	-24.2	11.8	101.5	3.5182	0.859	0.114	-0.499
11	Dipole 1	-24.2	11.8	101.5	5.0946	0.859	0.114	-0.499
12	Dipole 1	-24.2	11.8	101.5	6.9013	0.859	0.114	-0.499
13	Dipole 1	-24.2	11.8	101.5	8.9295	0.859	0.114	-0.499
14	Dipole 1	-24.2	11.8	101.5	11.169	0.859	0.114	-0.499
15	Dipole 1	-24.2	11.8	101.5	13.609	0.859	0.114	-0.499
16	Dipole 1	-24.2	11.8	101.5	16.237	0.859	0.114	-0.499
17	Dipole 1	-24.2	11.8	101.5	19.038	0.859	0.114	-0.499
18	Dipole 1	-24.2	11.8	101.5	22	0.859	0.114	-0.499
19	Dipole 1	-24.2	11.8	101.5	25.107	0.859	0.114	-0.499
20	Dipole 1	-24.2	11.8	101.5	28.342	0.859	0.114	-0.499

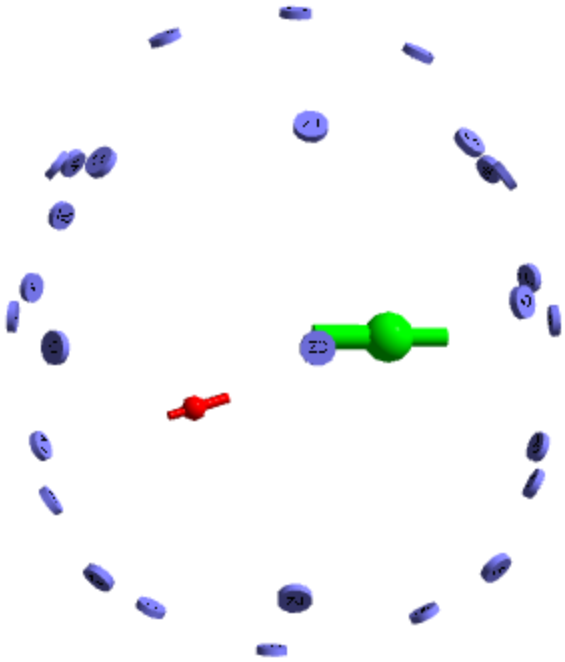
8. Select a second dipole location, and again select **Export Cursor to Localize** (added to the bottom of the list). This time, we will select **Specify** for the **Timerange**, enter **25** samples for **Start**, and **125** samples for the **Duration** of the waveforms that will be created. Increase the **Strength** to **150** and **Strength 2** to **200**. Then click **Add**.

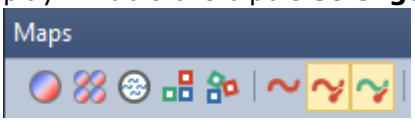


Dipole 2 has been added along with Dipole 1.

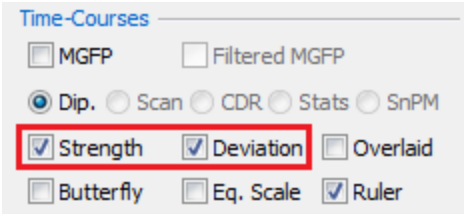
	Label	x [mm]	y [mm]	z [mm]	j [µAmm]
1	Dipole 1	-24.2	11.8	101.5	0
2	Dipole 2	33.0	33.0	99.0	0
3	Dipole 1	-24.2	11.8	101.5	-0.40158
4	Dipole 2	33.0	33.0	99.0	0
5	Dipole 1	-24.2	11.8	101.5	-0.71402
6	Dipole 2	33.0	33.0	99.0	0
7	Dipole 1	-24.2	11.8	101.5	-0.82877
8	Dipole 2	33.0	33.0	99.0	0
9	Dipole 1	-24.2	11.8	101.5	-0.71638
10	Dipole 2	33.0	33.0	99.0	0
11	Dipole 1	-24.2	11.8	101.5	-0.3634
12	Dipole 2	33.0	33.0	99.0	0
13	Dipole 1	-24.2	11.8	101.5	0.23628
14	Dipole 2	33.0	33.0	99.0	0
15	Dipole 1	-24.2	11.8	101.5	1.0844
16	Dipole 2	33.0	33.0	99.0	0
17	Dipole 1	-24.2	11.8	101.5	2.1796

9. The dipoles are seen in **3D View**.

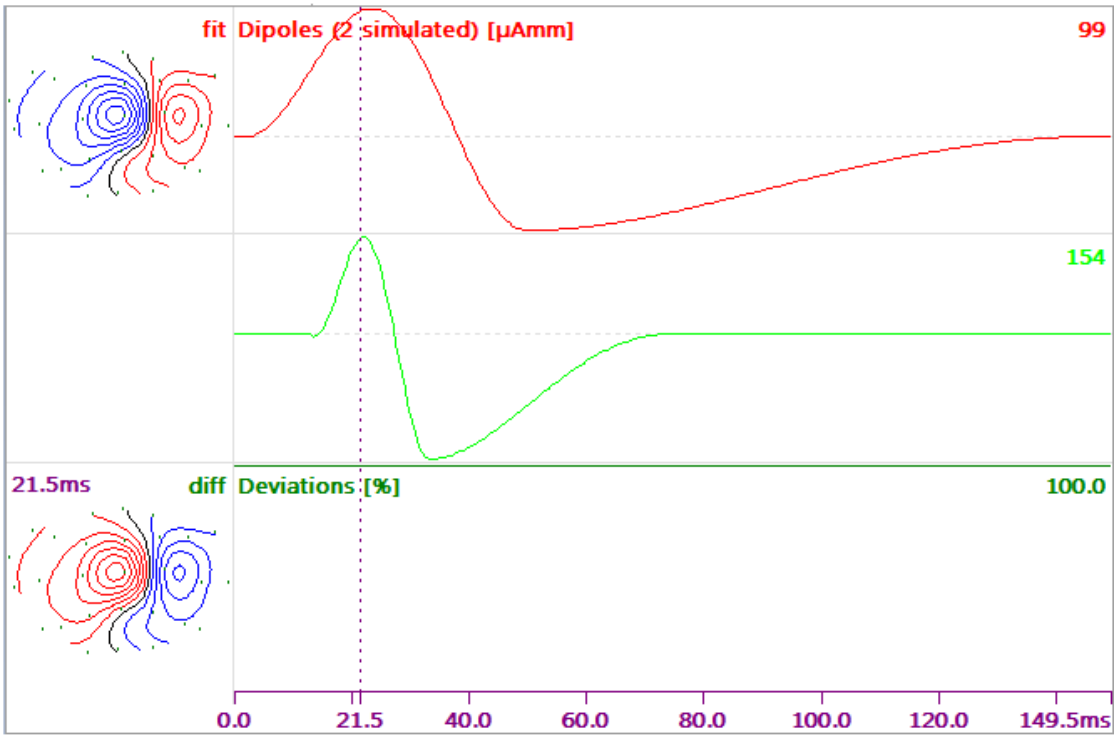


10. Go to the **Maps** display. Enable the dipole **Strength** and rresidual **Deviations** icons from the Toolbar 

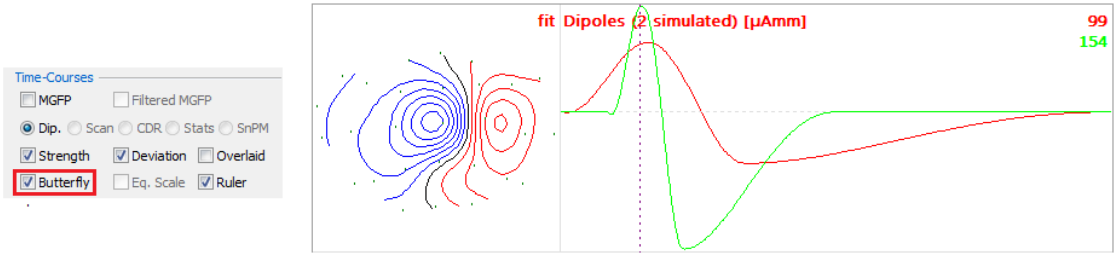
or from the **Parameters** dialog.



In the display itself, the top line is dipole 1 and the middle line is dipole 2. The Deviations are meaningless at this point because there are no data (flat lines). Drag the cursor back and forth to see the distributions.

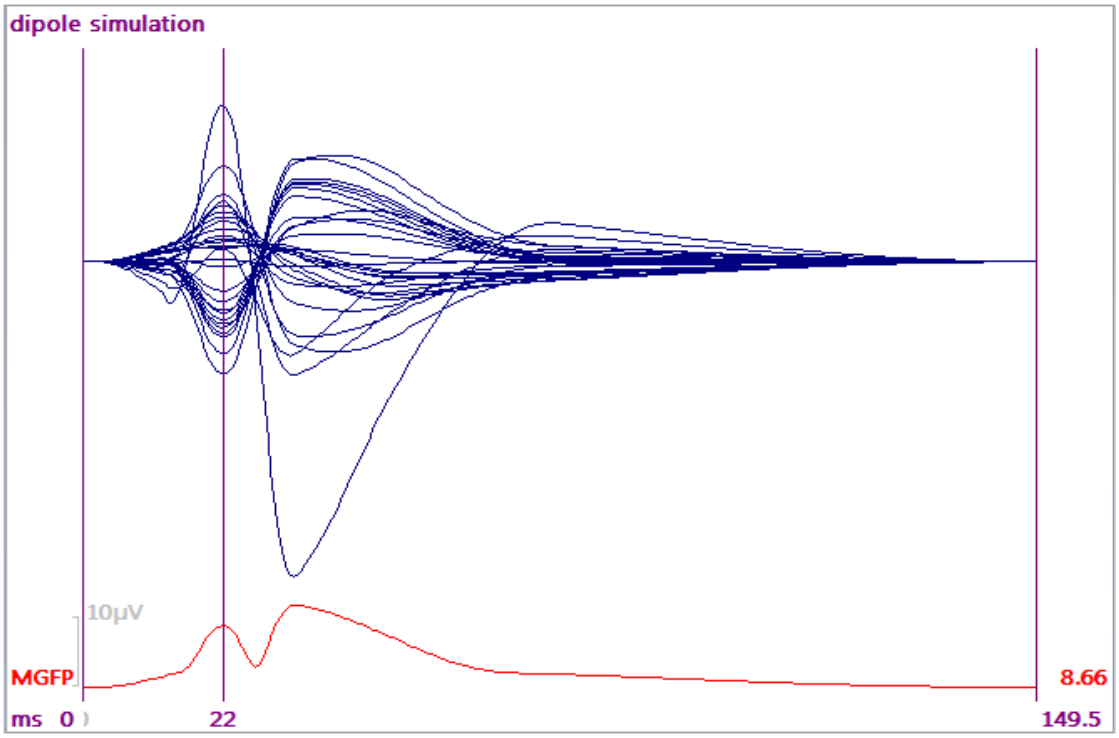


In the **Parameters** panel for **Maps**, in the **Time-Courses** section, select the **Butterfly** option. This overlays the two dipoles.

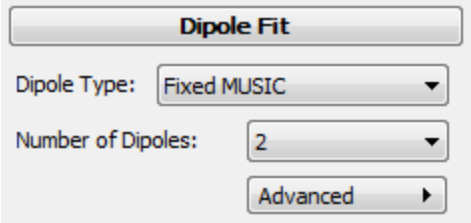


11. Expand the **Dipole Fit** panel under **Source Reconstruction**. Here there is the Save Data button (in the **Advanced** section). Before clicking it, realize that only the data within the Timerange will be saved. If we want to save the entire epoch, we would set the Timerange accordingly (*Ctrl+double-click*). Then click **Save Data**. Overwrite the existing file you created in Step 2, after clicking Insert New Simulation.

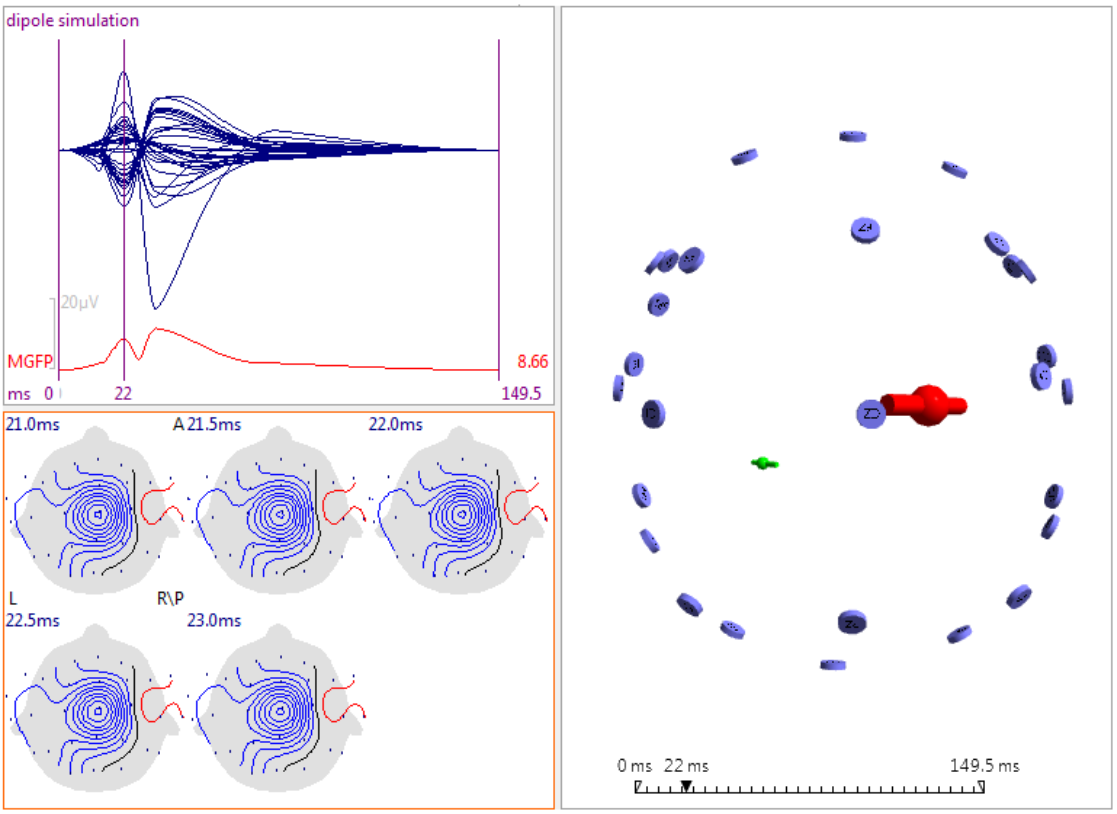
12. Open that Study (if needed). Now we see the waveforms that were created (**Butterfly Plot** selected). Select the entire epoch for the Timerange.



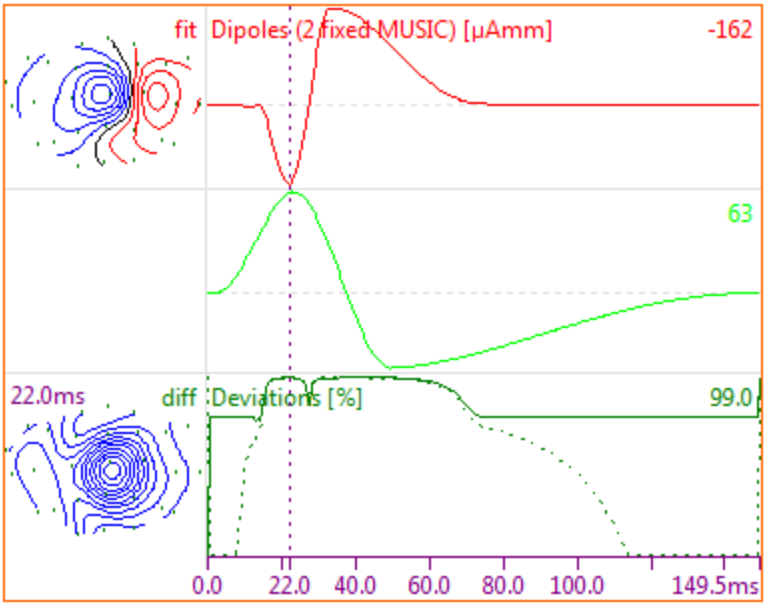
13. Select the FD, Maps, 3D View display. Now expand the **Dipole Fit** panel. Select **Fixed MUSIC** for the **Dipole Type**. Set the **Number of Dipoles** to **2**.



The two dipoles are seen.

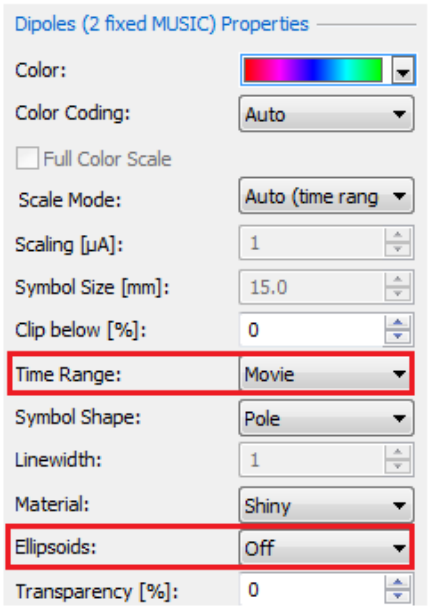


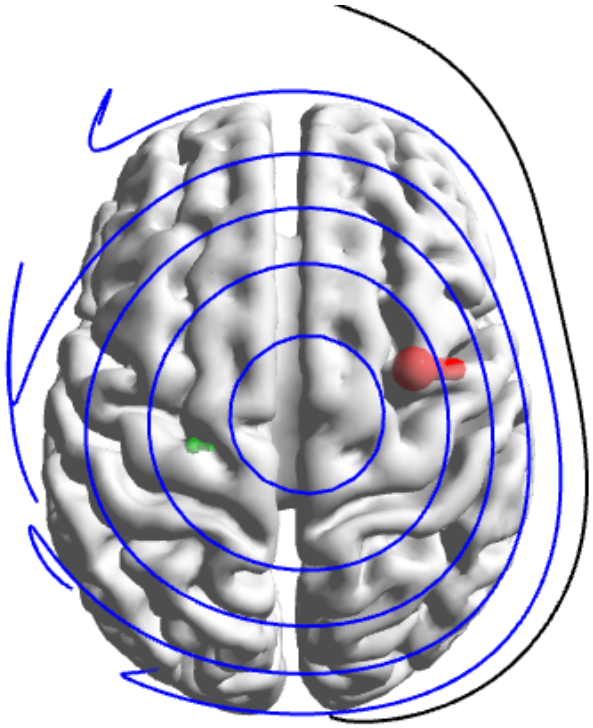
14. Enable again the **Dipole Strengths** and **Residual Deviations** icons from the Toolbar . The two dipoles are again seen and now the deviations make sense.



15. If you want to see the scalp contours in the 3D View, you can use the **Standard Cortex** in the **3D View**. Enable **Maps**. In the Dipoles Properties area,

set **Time Range** to **Movie** and **Ellipsoids** to **Off**. Play a Movie (Standard Toolbar) to show the progression of the scalp distribution across the epoch.

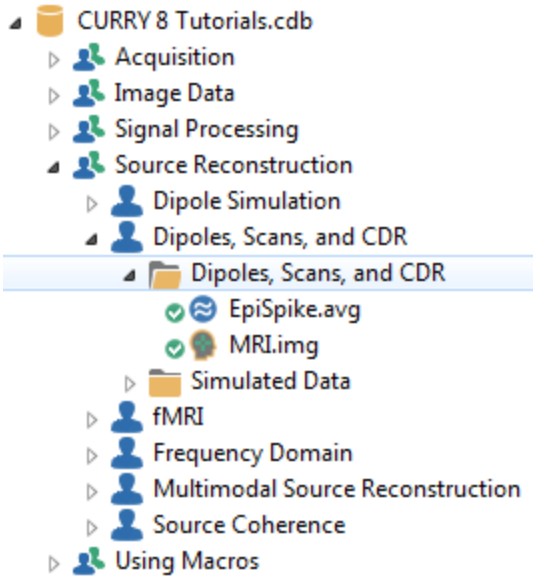




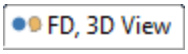
Close the studies without saving any of the results. Delete the TEMP subject you created in the Database (unless you want to save it).

2.6.2 Scan Methods

This Tutorial uses the same Study as in the **Dipole Models** tutorial. It is recommended that you go through that tutorial first for familiarization (although the results from that one are not used in this one).

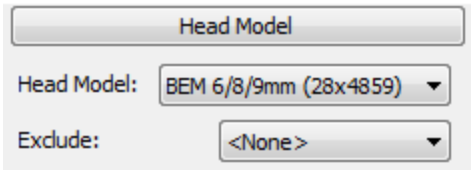


As a further verification of the dipole results, a complete *scan* of the MUSIC metric (Multi Signal Classification) for a large number of points on a regular 3D grid will now be performed. In contrast to the nonlinear optimization that is applied in the dipole fits, Scans are used to step through a predefined list of points. At each location, the MUSIC metric (or, for Scans, the unexplained variance) is evaluated. Scans can thus be used to verify the results of dipole fits and to measure the uncertainty regarding the fitted locations, since they visualize confidence regions and reveal additional local minima.

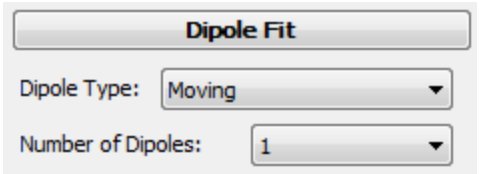
1. Open the Study and select the 

display. The **Auto** option for **Noise Estimation** has already estimated the noise level using the **-500** to **-50 ms** interval. Select a Timerange from **-15** to **55 ms**.

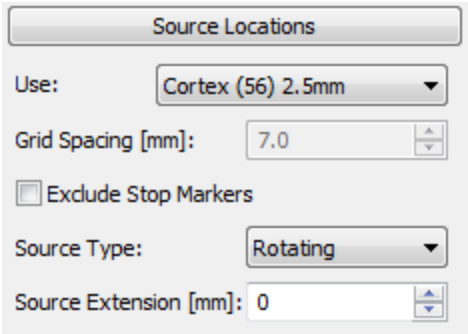
2. Select the patient's **Head Model**.



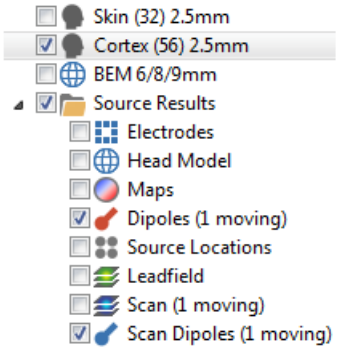
3. In the **Dipole Fit** panel, select **Moving**, for comparison's sake.

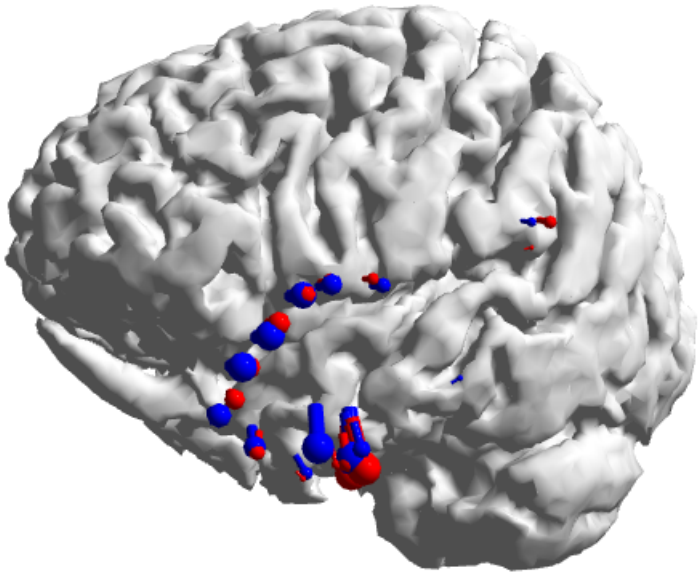


4. Go to Source Locations and select the **Cortex**. The scan results will be constrained to the cortical surface.



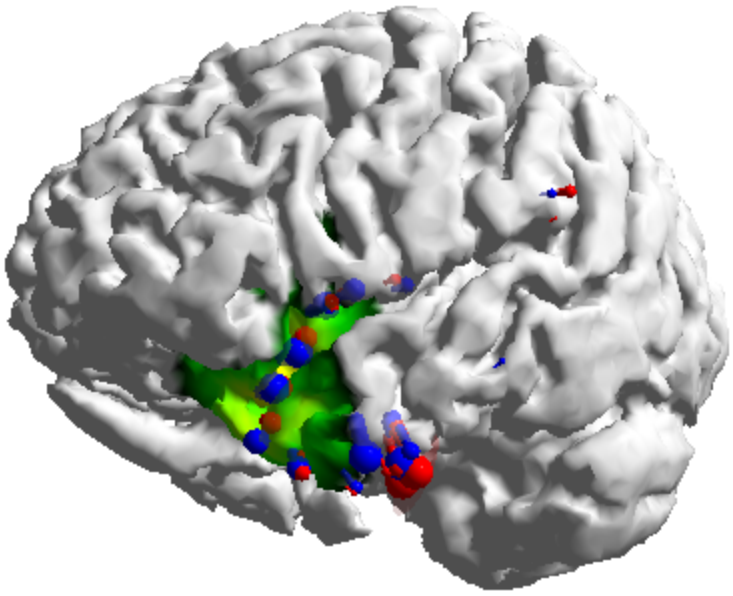
5. Expand the **Scan Methods** panel, set the **Scan Type** to Scan Type: Moving. The resulting objects are seen in the **Source Results** part of the list under **Objects** (*double-click* in a clear area in the 3D View display have the Options list displayed automatically). These include **Source Locations**, the **Leadfield**, **Scan**, and **Scan Dipoles** results. Disable all but the **Scan Dipoles** display (leave the **Dipoles** enabled). Disable the display of the **Electrodes**. Change the **Color** of the **Dipoles** to a solid color, such as **Red**. Change the **Color** of the **Scan Dipoles** to a solid color, such as **Blue**. Enable the Cortex and set its **Transparency** to **100%**. The results are very similar.





6. Enable the **Scan (1 moving)** results. Go to the **Scan (1 moving) properties**, change **Clip below** to **75%**, and make sure that Adapt Color Scale is enabled, if needed (to use all of the colors on the displayed range). Change the **Color** to a different range, such as **Black, green, yellow**. Set its **Transparency** to **50%**.

Deselect the Cortex (56) 2.5mm display - Scans include the cortical surface. Set **Timerange** to **Movie**.



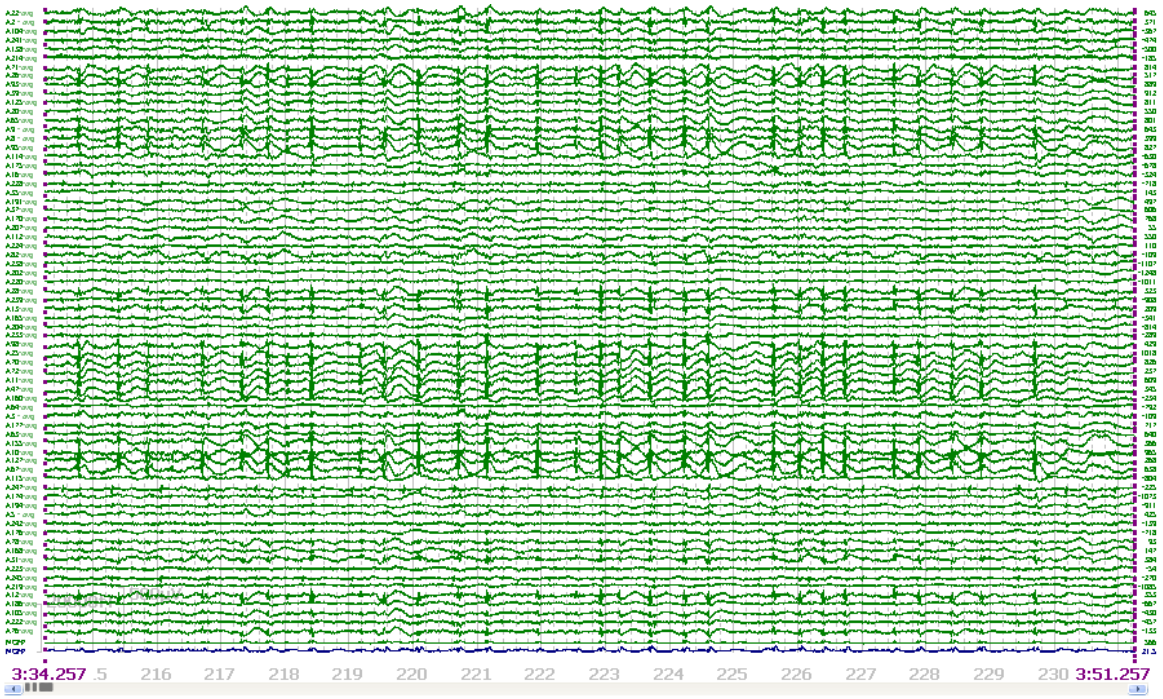
The Scan, Scan Dipoles, and Moving dipoles all track very closely. Close the Study; do not save the results.

Vector Beamformer

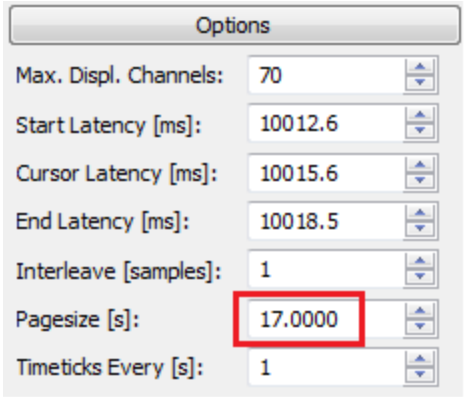
The Beamformer was developed for use with MEG data, and in CURRY it works best with MEG data, as opposed to MEG+EEG combined or EEG data alone. Unlike the other source reconstruction methods, where you typically define a relatively narrow Timerange about a feature of interest, Beamformer uses thousands of data points, which means many seconds of data.

The CURRY Tutorials Database does not include a suitable file for using Beamformer, so we will demonstrate with a different file. The steps will be similar to those you should try with your own data files.

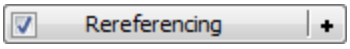
This file has many spikes throughout. The file contains MEG (shown) and EEG data channels.



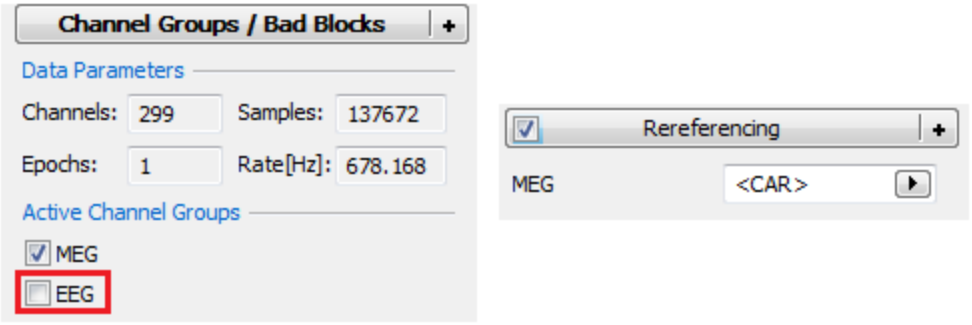
1. Set a Timerange to include the entire data display (use *Ctrl+double click* to spread the outer cursors all the way apart). In this case, 17 seconds are displayed.



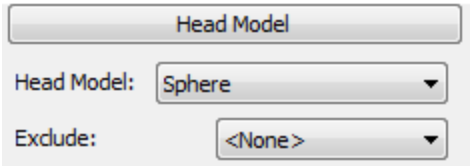
2. Disable the EEG channels in the

panel. Select the CAR for MEG, if needed, in the 

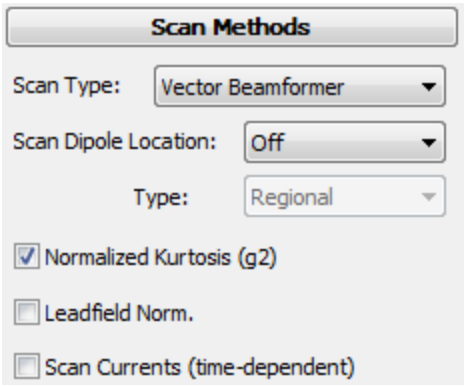
panel.



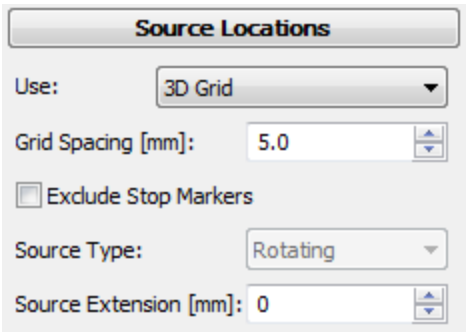
3. Select **Sphere** for the **Head Model.**



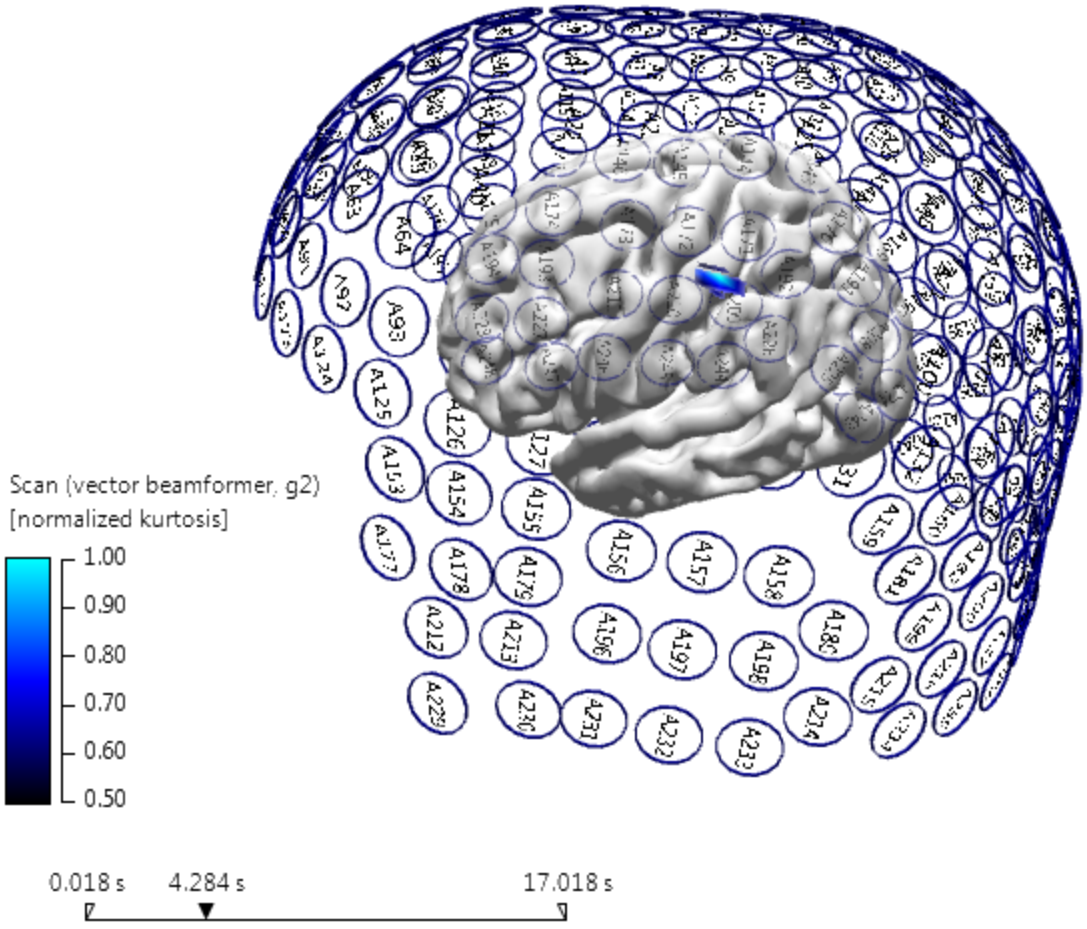
4. Select **Vector Beamformer** for the **Type** of **Scan Method**. Enable **Normalized Kurtosis (g2)**. This will accentuate the peaks and usually result in a tighter localization.



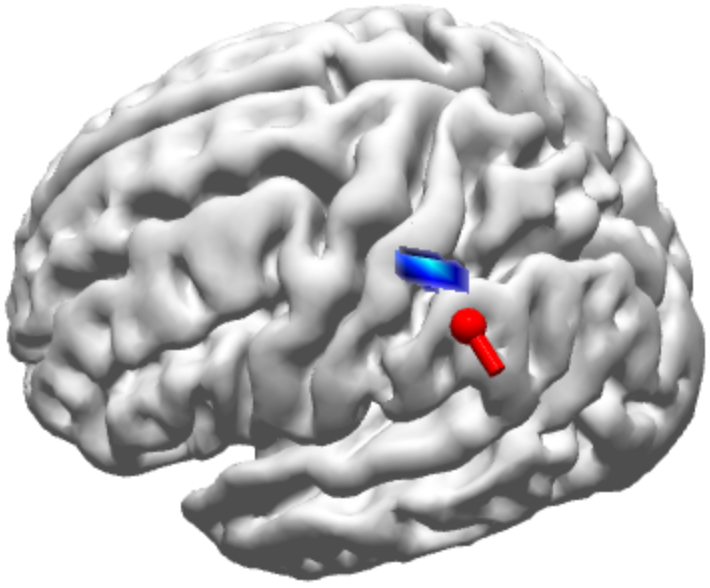
5. Under **Source Locations**, decrease **Grid Spacing [mm]** to **5.0**. This gives a finer resolution in the results.



6. The results are seen in the **3D View**. In this case, we did not have the patient's MR data; the Standard Cortex is displayed instead for reference.



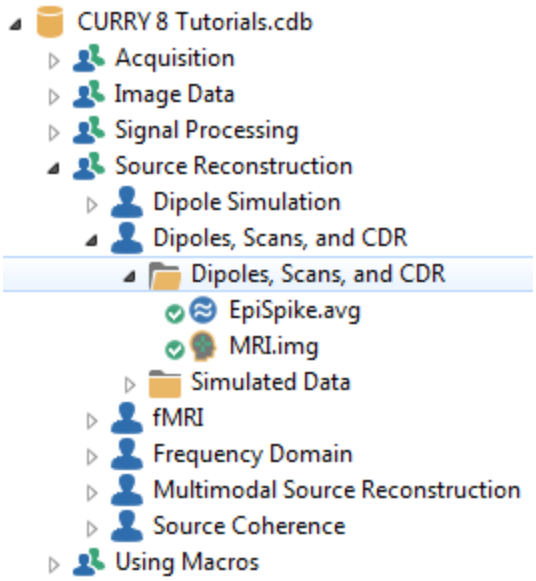
7. For comparison sake, we computed a Fixed Coherent dipole for a single spike, using a 3 sphere head model, with combined MEG and EEG data.



2.6.3 Current Density Reconstruction

In contrast to the assumption of a limited number of dipolar sources, current density methods allow many distributed sources to be concurrently active. Please refer to the *User Guide* for information about the various CDR types. The one we will be using is perhaps to most frequently used one - **sLORETA**. sLORETA is a modification of **MNLS (Minimum Norm Least Squares**), 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.

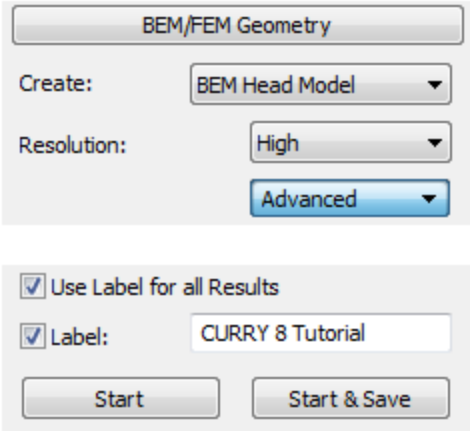
The next sequence represents a realistic application of CURRY's capabilities. This tutorial uses the same Study as the previous two - shown below. If you have that Study open already, close it without saving any results.



We have a functional data file - *EpiSpike.avg* - and we have already added its electrode and Functional Landmarks from the *EpiSpike.3dd* file (or have created its parameter file). We have the MR data file - *MRI.img*. We have co-registered the Functional and Anatomical Landmarks. We will now create a realistic BEM model, and then perform realistic source localizations using the cortical surface.

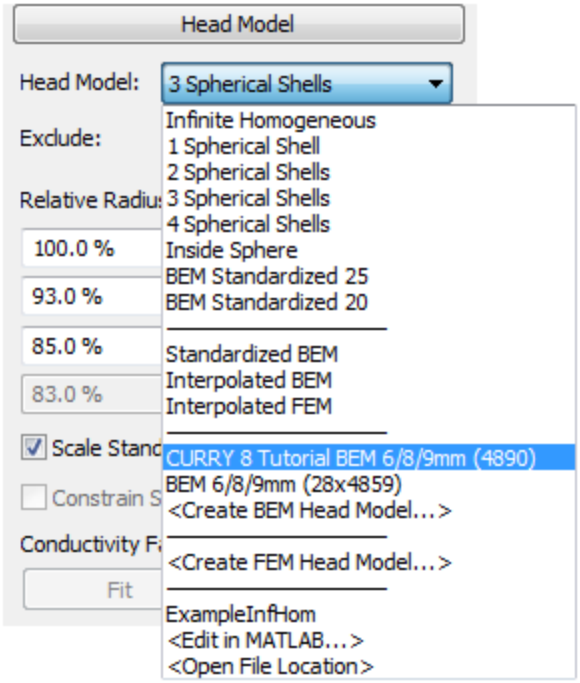
This is a good place to explain how CURRY saves and uses the various surfaces, BEM models, and other files that are created.

1. Open the Study and click the Image Data display. Expand the BEM/FEM Geometry panel. Use the settings shown in the figure, and then click Start. This will take a few moments - watch the various processes in the **Image Data** display and the **Status Bar**.

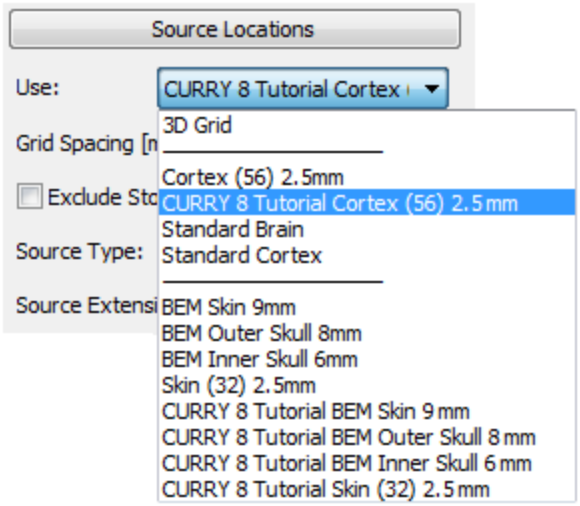


2. We will use the BEM model in two examples of Current Density Reconstruction (CDR). Since we restarted CURRY, we will need to redefine the Timerange for source reconstruction (unless you saved the parameters as **Study Parameters**). For the Timerange, use **-15** to **55 ms**, as we have done before.

3. Go to Source Reconstruction and expand the Head Model panel. In the **Model** drop-down list, notice that now there is the BEM model we created. Select it.

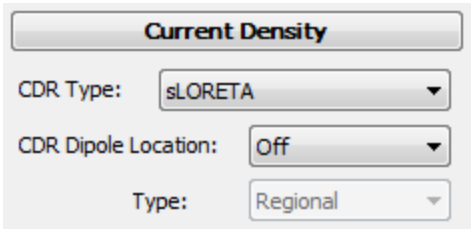


4. Expand the Source Locations panel, and see that the new surfaces are now included in the **Use** list. When performing a Current Density Reconstruction, you can constrain the results to a selected surface. Select **CURRY 8 Tutorial Cortex (56) 2.5mm** for this example.

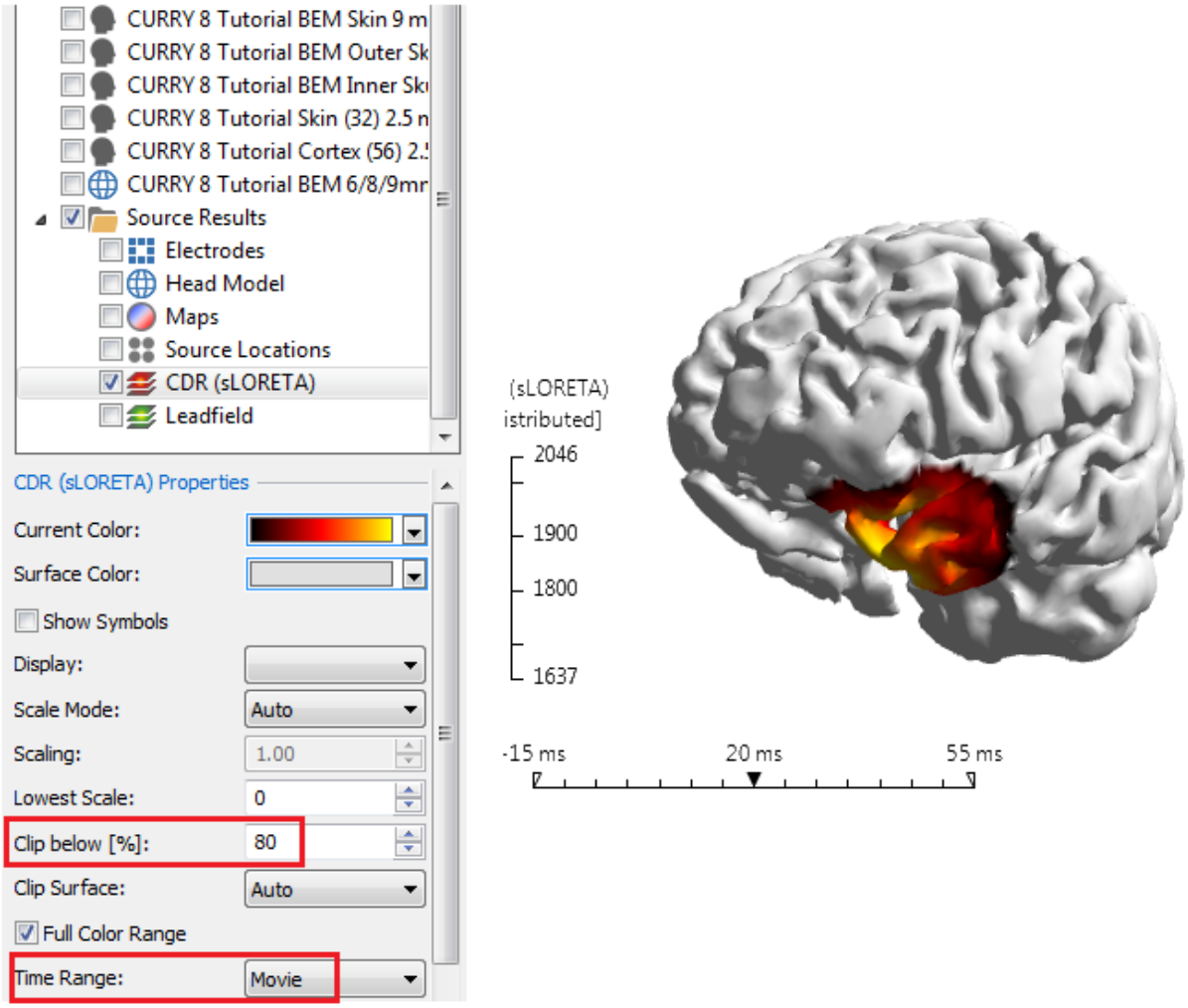


Set **Source Type** to **Rotating** and **Extension** to **0**mm (if needed).

5. Expand the Current Density panel, and select **sLORETA**. Leave the other parameters in their default settings. This will start the current density reconstruction on a list of approximately 25,000 cortex points, which will take a little while to complete (including - once - the leadfield setup time).



6. *Double-click* in the 3D View part of the display (if needed) to see the **Objects** panel. In the **Results** section there are the **Source Locations**, the **Leadfield**, and **CDR** results. The CDR results for the 20 ms time point are shown below, using the **CDR properties** indicated. The left view is shown (the Electrodes were turned off).

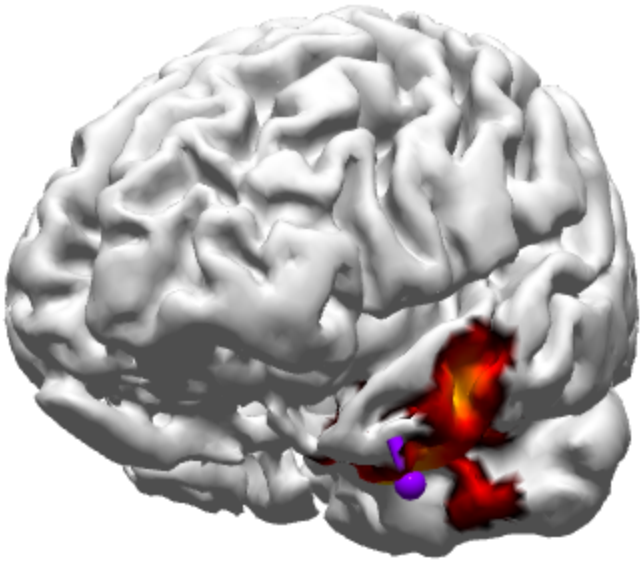


If you enable the **Source Locations**, you will see that the points used were from the surface we selected - the **Cortex 2.5 mm** surface.

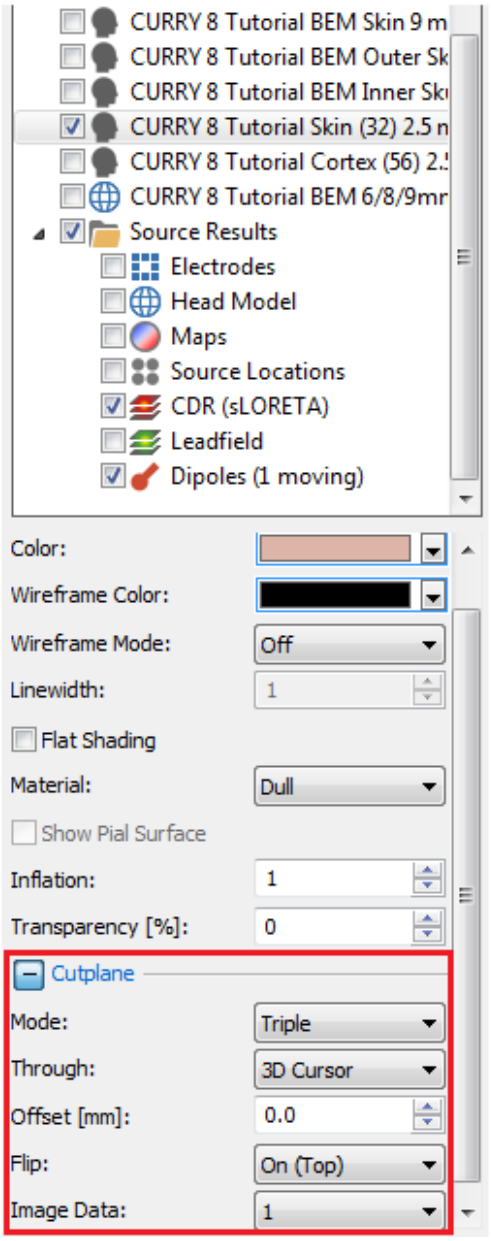
7. Return to the Source Reconstruction parameters, and select **1 Moving** dipole under Dipole Fit. Both sets of results are now seen in the **3D View**.

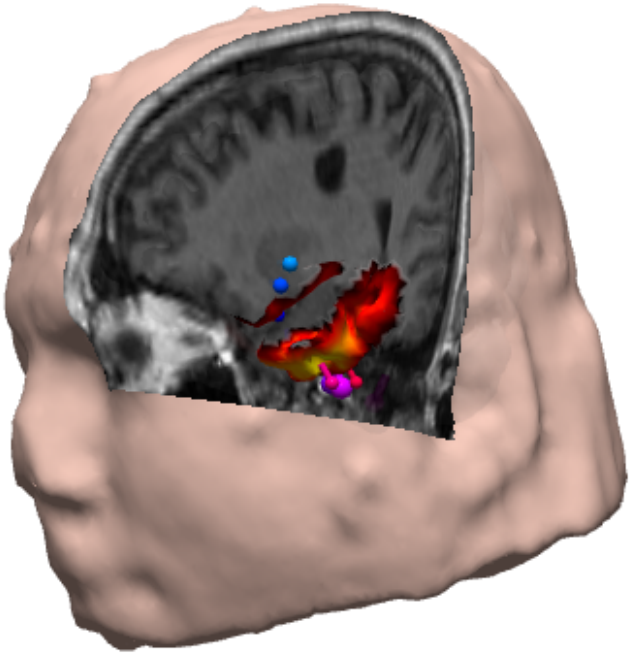
In the **Dipoles Properties**, set **Clip below** to **80%**, **Time Range** to **Movie**, and **Ellipsoids** to **Off**. In the **CDR (sLORETA) Properties**, set the **Transparency** to **100**%.

Now step one time point at a time and see the close agreement between sLORETA and the moving dipole results.



8. As was demonstrated in the *Dipole Models* tutorial, you can display the results in a cutaway view (see that section, if needed). The relevant parameter settings are shown. Set CDR **Transparency** to **0**%.





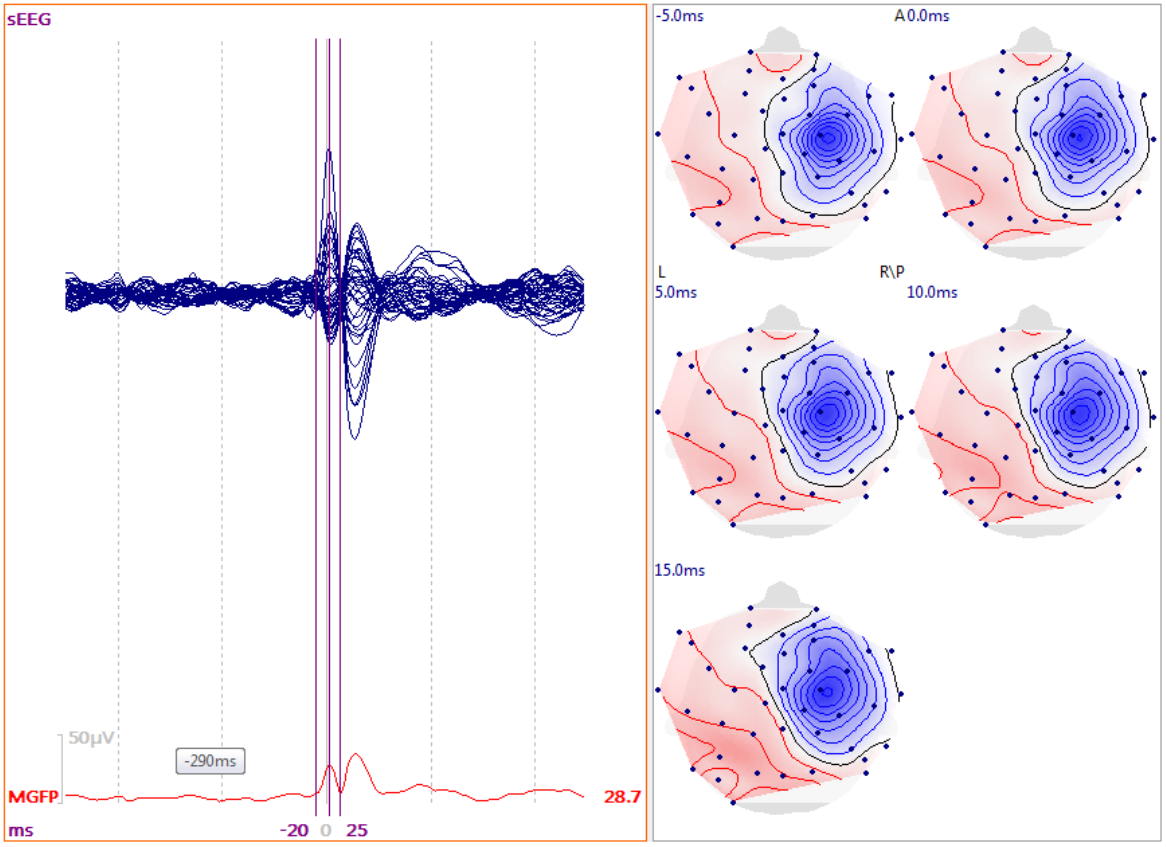
Close the Study without saving any results.

2.6.4 Some Tips for Using Source Reconstruction

When using any of the source reconstruction models, it is important to keep in mind that these are mathematical models that will compute the theoretical source, based on the constraints imposed by each model. All involve solving the inverse problem - finding the best source in the brain for the activity seen on the scalp (or grid) - and there are an infinite number of solutions to this problem. Each model has its own set of constraints that allow the problem to be solved. The solution is a theoretical one, which may or may not be interpreted literally. To fully understand the various source

reconstruction results, you need to have at least a general appreciation for the differences among the models. These are addressed briefly in the **Source Reconstruction in Detail** section in the *CURRY 8 User Guide*. More complete information may be obtained from various other resources.

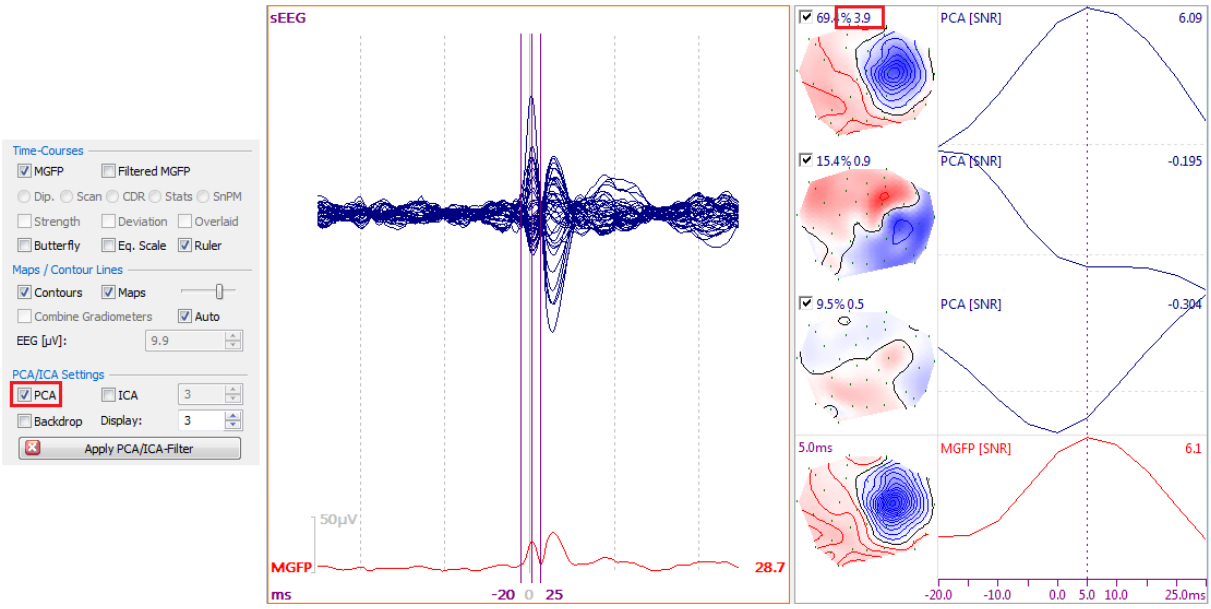
Consider the following example. This is a single epileptic spike, taken from a longer continuous scalp recording (not included with the tutorial data files). We wish to determine the dipole source for the spike.



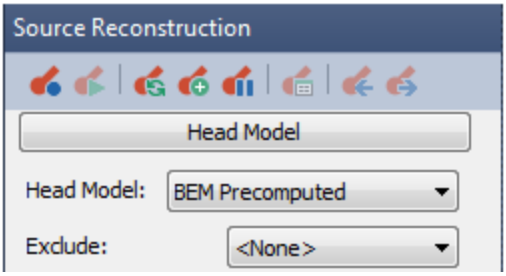
1. Select a Timerange for analysis. The Timerange (set by the two outer cursors) is determined largely on the basis of the question you are asking. Are you interested in finding multiple dipoles corresponding to all parts of the spike and slow wave? Are you trying to determine the earliest part of the spike? Are you interested in the whole Timerange? In each case, you would set the Timerange accordingly. In this case, we wish to determine the earliest source of the spike, and so we set the Timerange from -20 to 25 ms about the peak of the spike. Typically, Timeranges are selected based on the peak(s) of MGFP, as these are the ranges where dipoles are most likely to occur.

Noise Estimation was set automatically from -500 to -50 ms, so we do not need to do anything more with it.

2. The next question is, how many sources could there be for the spike? Is there a single source, or could there be more? A PCA for the selected Timerange shows one main component (SNR = 3.9). It appears that a single dipole solution will likely explain the data sufficiently (the second component is marginal and could be contributory).

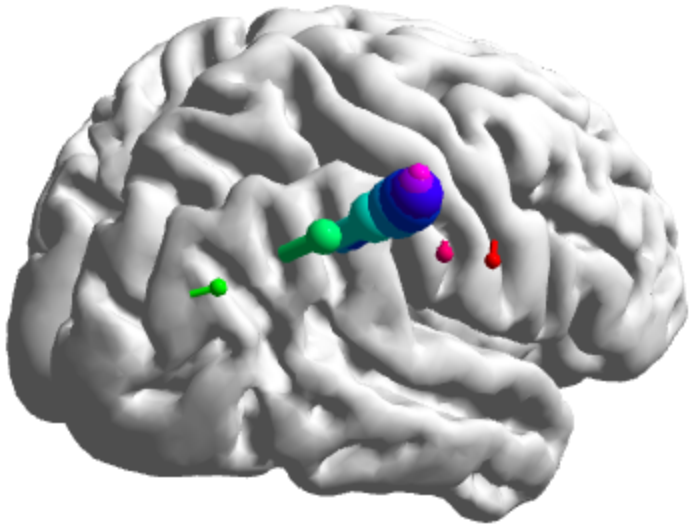


3. Select a Head Model. Generally speaking, the most accurate Head Model will be the one created (from BEM/FEM Geometry) using the subject's own MRI data. If that is not available, you can use one of the pre-computed models. If you are making a first pass analysis and you want to get a faster solution, you can use the 3 Spherical Shells model. Depending on the location of the source (is it from a spherical head area), the 3 Spherical Shell model may or may not be similar to the pre-computed models. In this case where we do not have the subject's MRI data, we are using the **BEM Precomputed** model.

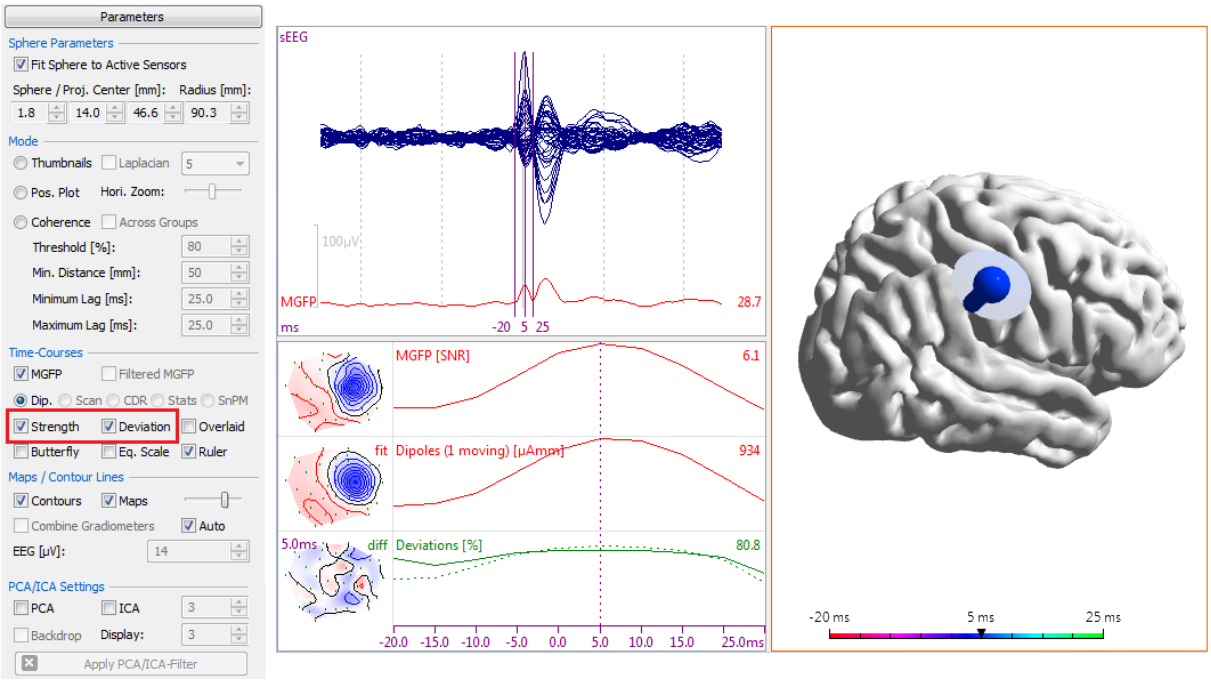


4. We do not have the measured electrode positions for this subject; Label-Matching was used to estimate the positions. There may be some loss of accuracy in that case.

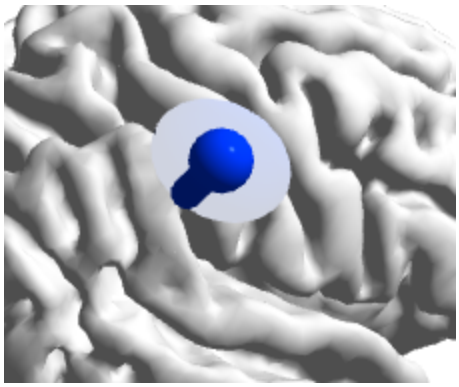
5. Next, we decide which dipole model to use. There is certainly nothing wrong with trying different models. In fact, if the different models all produce similar results, that is an argument for the validity and stability of the source. With an epileptic spike, where there is often a propagation of the activity over time, we would use a moving dipole. The colors show the progression of the dipoles over the Timerange.



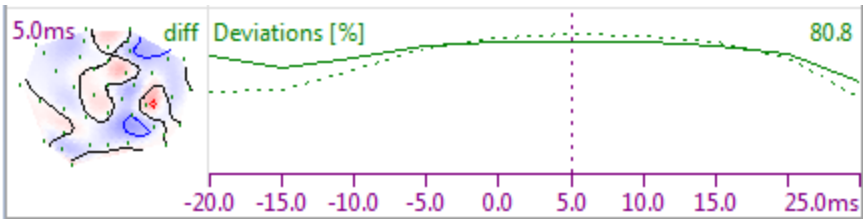
6. In the **Parameters** panel for **Maps**, **PCA** was deselected and **Strength** and **Deviation** were selected (as well as **MGFP**). The Timerange mode was set to **Movie** to see the dipoles one at a time. The display of the **Confidence Ellipsoids** was enabled.



There are several things to look at when evaluating the validity of a dipole solution. First, look at the confidence ellipsoid. At this time point, the ellipsoid is pretty good. There is about a 68% chance that the dipole will be located within the ellipsoid, with the greatest probability of it being in the center of the ellipsoid. If the ellipsoid were very large, such that it encompasses areas outside of the brain/head, then the solution becomes questionable or dubious. If the location appears reasonable, but the ellipsoid is large, it may be that there is too much noise in the recording.

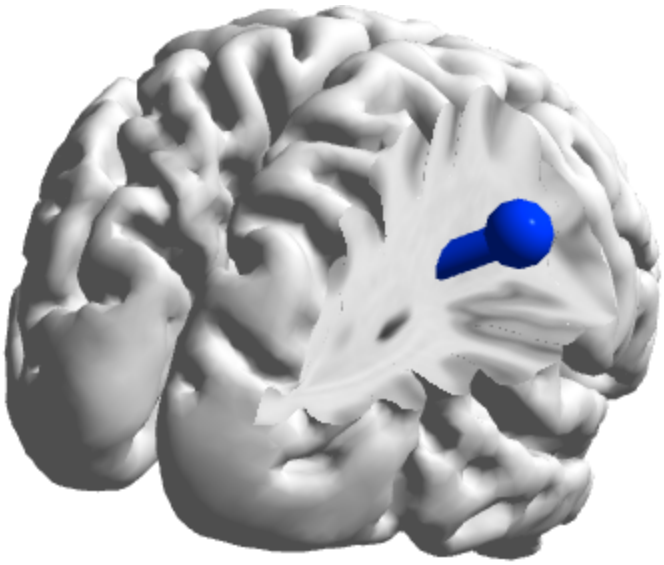


Next, look at the Deviations in the Maps display. Deviations are a measure for the fit quality (how well the source model explains the measured data). The solid line is the achieved goodness of fit, and the dotted line is the expected goodness of fit. The closer these two measures are, the better, and the larger they are, the better. (In this case, there is an overfit, where the algorithm is attempting to fit noise as well). The horizontal dotted line is the **Clip below** value for Dipoles. At the indicated time point (vertical line), the achieved goodness of fit is very close to the expected.

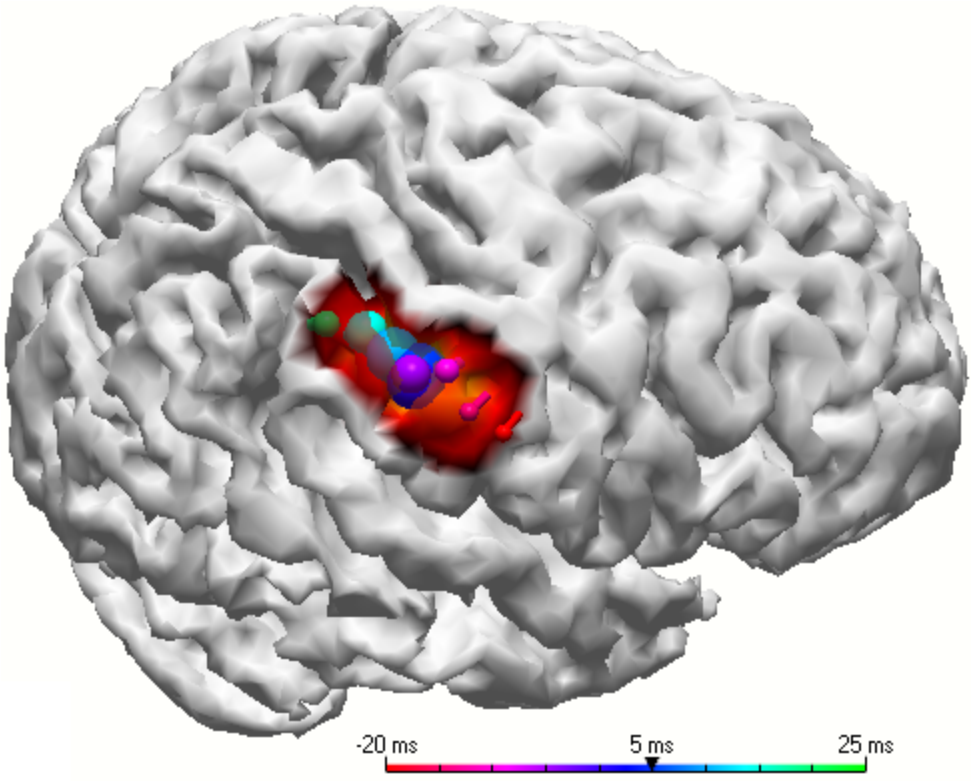


The numerical results for the residual deviations are found in the Output window. In this case, the moving dipole model does a fairly good job of explaining the measured data, at least at the peak of the spike.

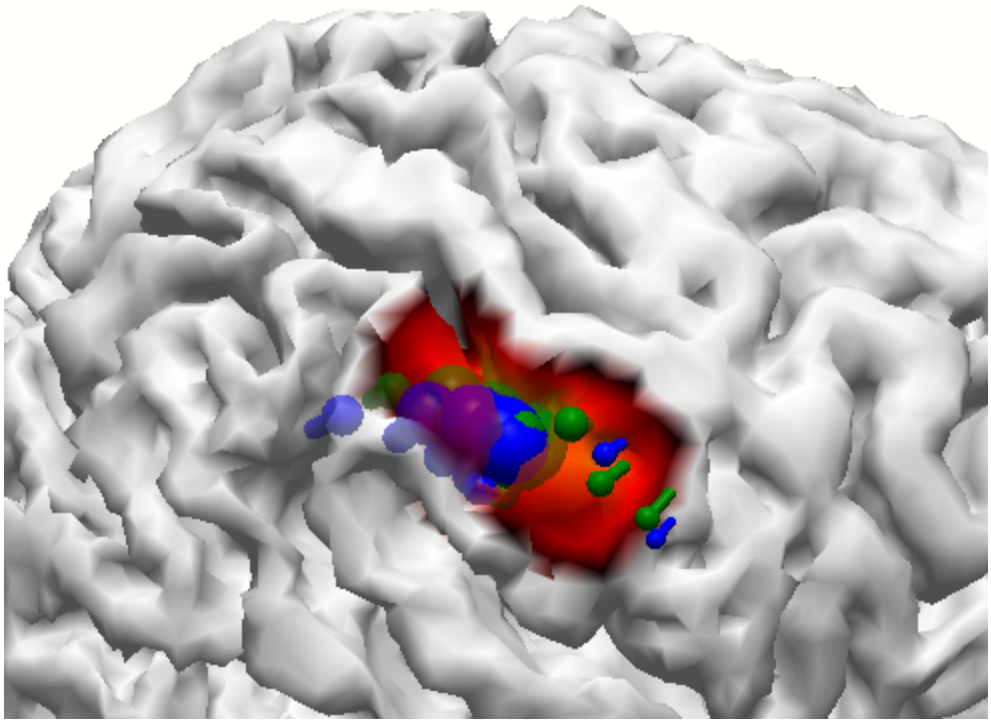
7. Now we look at the actual location of the dipole. If we use a triple Cutplane, we can see that the dipole sources are actually located a little deeper, almost in the white matter - a doubtful source for epileptic spikes. In selecting one of the Dipole Fit models, we were telling the program to find a single location (for each time point with moving dipoles) in 3D space that best explains the scalp data. CURRY did that. However, we know that the spike is most likely originating from the layers in the cortex, and not from deeper sources in the white matter. The *negative direction* of the dipoles (the ball end) may be more informative than the *location*. Think in this case of a flashlight shining on the interior surface of the cortex. It points to where the cortical sources may well be. Epileptic spikes typically originate from several square centimeters of brain area, and not single points.



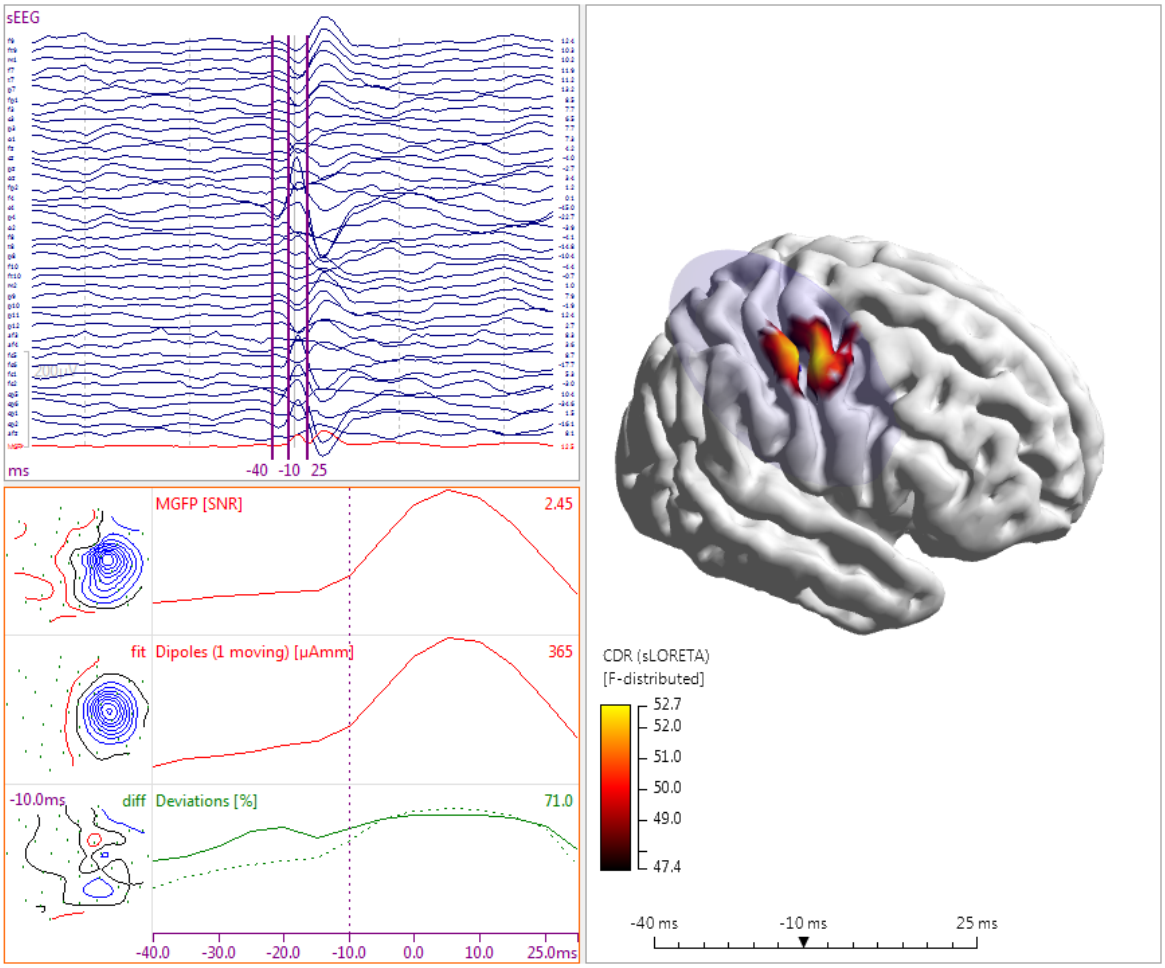
9. So in addition to a single equivalent dipole, we decide to use one of the distributed source models. We must first decide whether we want to constrict the solutions to the cortex, or to the 3D Grid, which means that the current density solutions can be at multiple points within the volume. We decide to constrict the solutions to the cortex, as we have reason to assume that is where the actual generator sites are. We selected the sLORETA model, as it is a good compromise between processing time and accuracy (similar results were found with Minimum Norm and SWARM), with a Moving CDR Dipole (where the colors show the progression across time).



In comparing the CDR moving dipoles (green) with the Dipole Fit moving dipoles (blue), we find that the results are very similar.



10. As to the question of the earliest source of the spike, we find in this example that the confidence ellipsoids become unacceptably large, the goodness of fit decreases, and the Deviations become smaller as we move toward the beginning of the spike. Thus, we cannot say with certainty where the spikes originate in this example, although the location does not really change as you move more toward the peak, where the results do appear genuine.

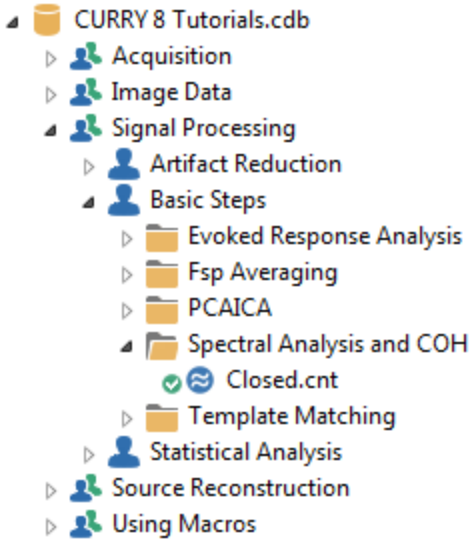


2.6.5 Frequency Domain Source Analysis

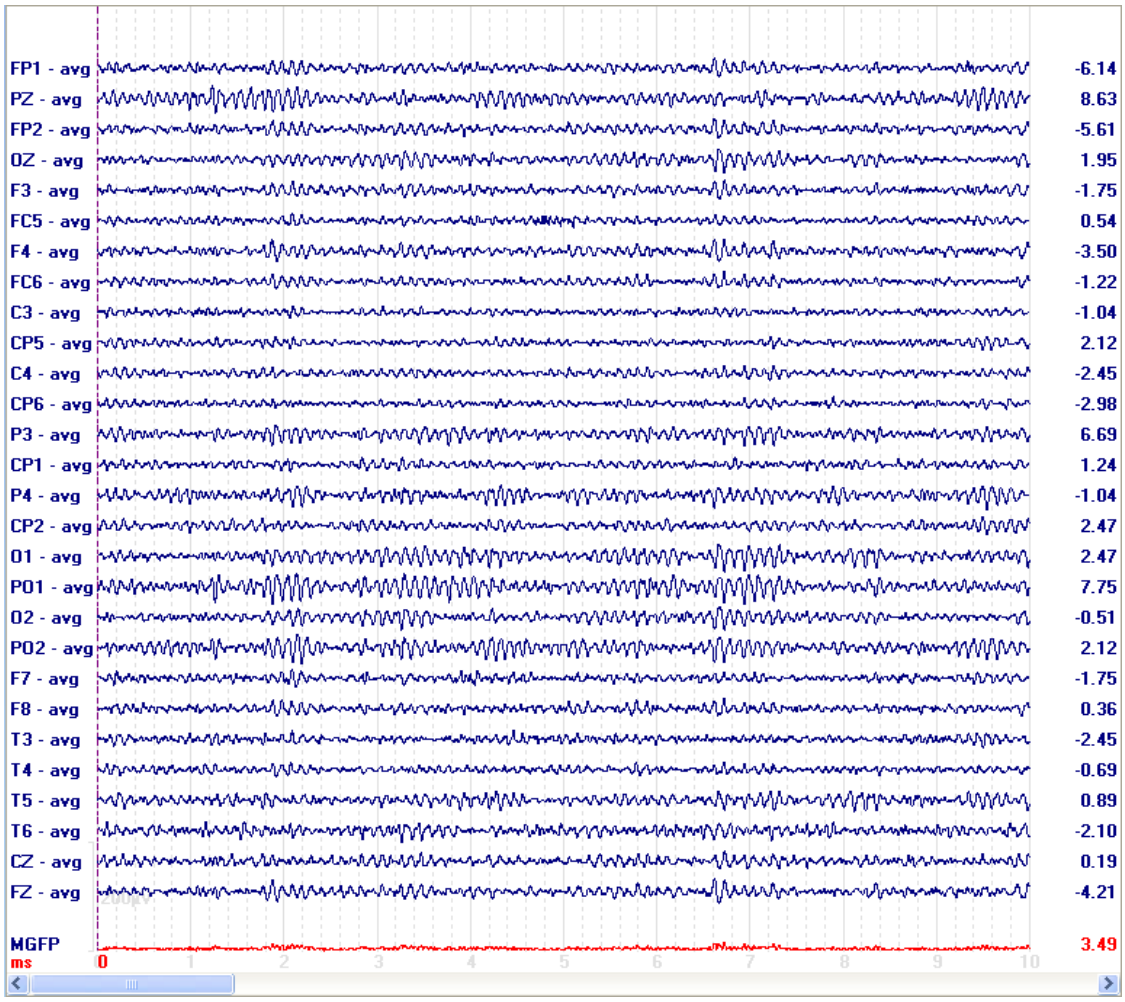
Source Reconstruction with frequency domain data (FFT power spectra) is very similar to time domain data. Instead of setting the Timerange to delineate an interval of time, it defines a frequency range. The results are computed across the entire Timerange; temporal resolution is lost.

You need to have a general familiarity with source reconstruction in CURRY 8 to complete this tutorial (some details are assumed to be known).

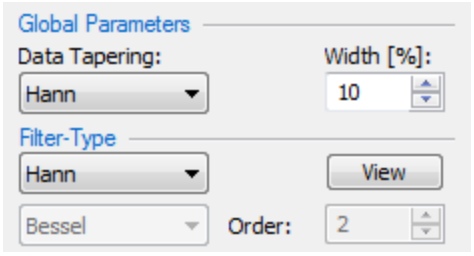
For this example, we are using a simple eyes closed EEG recording, found in the Study shown below.

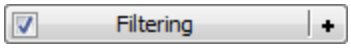


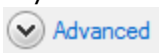
Open the Study and rescale as desired.



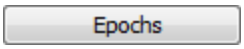
1. Since we will be performing an FFT, we need to Window the epochs that we will create. This happens automatically with the default settings shown.



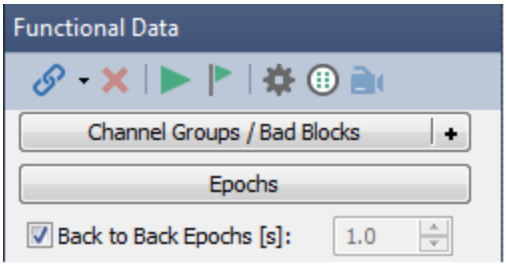
If you want to change them, expand the 

panel and click the 

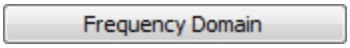
button. Select a type of windowing (**Data Tapering**) and **Width [%]**. Select a **Filter-Type**. If in doubt, use the defaults.

2. Expand the 

panel under **Functional Data**. In this case we will create epochs of 1 sec duration. Enter **1.0** in the **Back to Back Epochs** field, and then enable it. The continuous file has now been cut into 52 consecutive epochs of 1.0 sec duration. (Sweeps do not need to have the number of data points be a power of 2 - extra points are added automatically as needed).

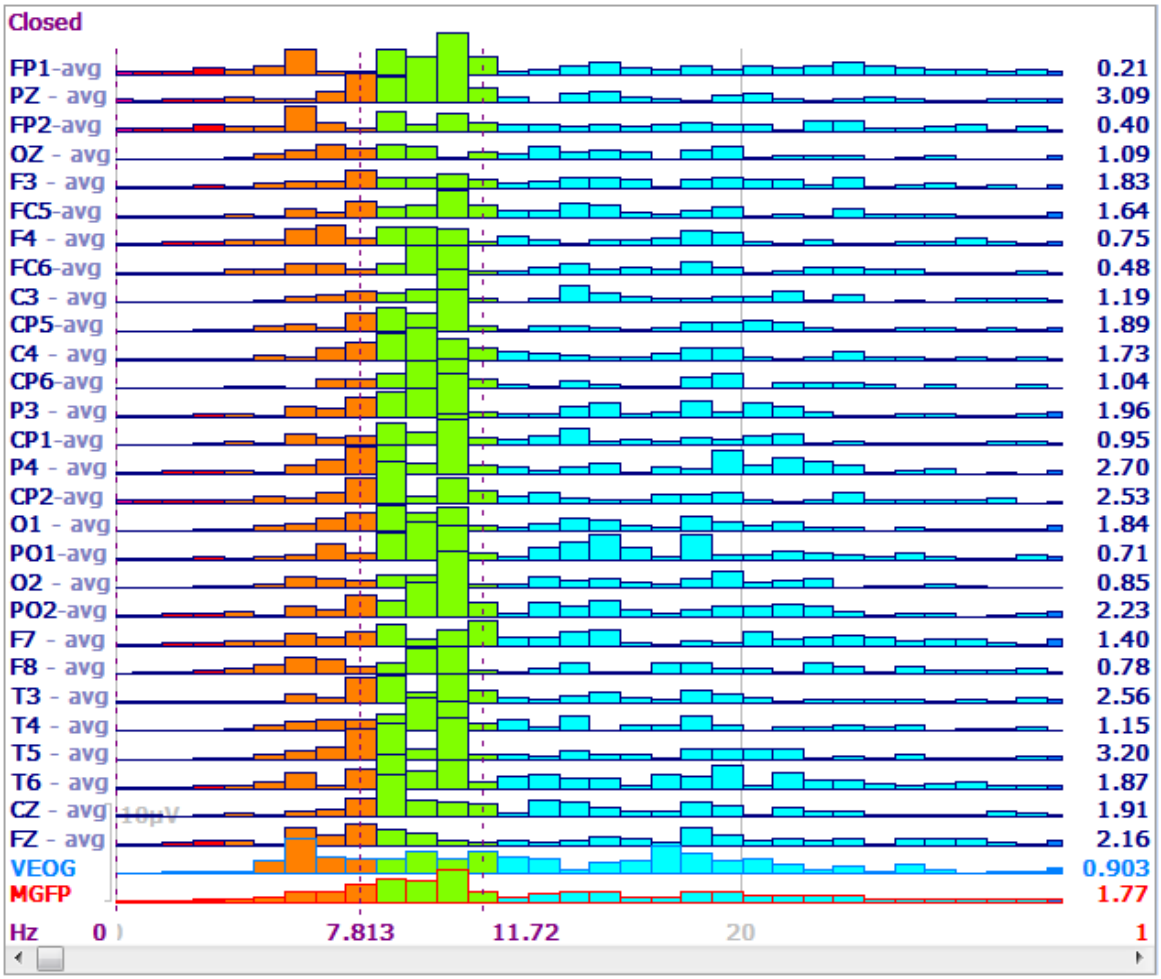


There is no appreciable artifact in this file, but if there were, we would then use either the voltage threshold or the SNR based method, or both, to reduce the artifact.

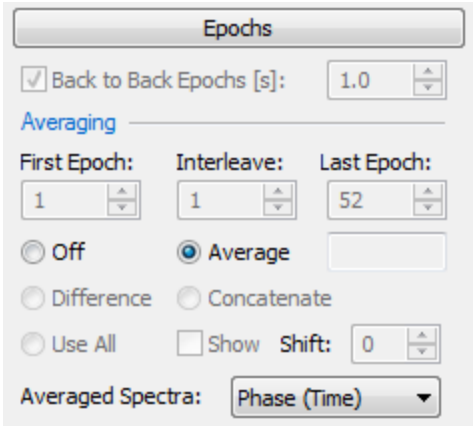
3. To compute the FFT for each epoch, expand the 

panel and enable **Spectra**.

Position the outer two cursors to define a general frequency range of interest (like 0-30 Hz). *Right click* in the data display and select **Zoom In**. Position the outer two cursors to define a precise frequency range of interest. Note that you are looking at the first epoch. You can step through the file, or drag the cursor below the file, to select a different epoch.



If you want to use the average of all epochs, go to the Epochs panel and select the **Average** option. For **Averaged Spectra**, select either **Phase (Time)**, **Amplitude (Freq)** or **Power (Freq)** to see the results in either microvolts or microvolts squared. Select **Phase (Time)**.



Reminder: The **Phase (Time)** option averages the waveform data first, then computes the FFT on the averaged waveform data (out of phase activity will tend to cancel

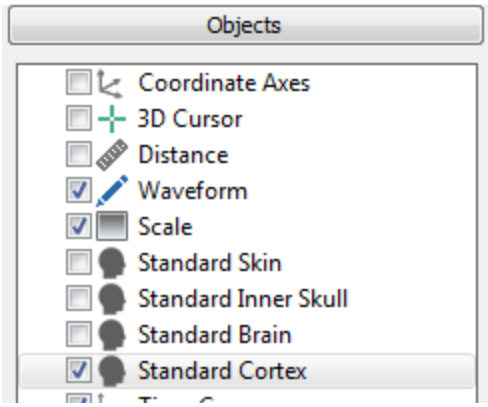
out). If you select the **Amplitude (Freq)** option, an FFT is computed for each epoch, scaled to μV, and then the FFT'd epochs are averaged. If you select the **Power (Freq)** option, an FFT is computed for each epoch, scaled to μV^2, and then the FFT'd epochs are averaged. The results will be displayed in μV or μV^2, depending on whether you selected Power or Power, in the **Frequency Domain** panel.

4. From here, the source reconstruction process is basically the same as with time domain data.

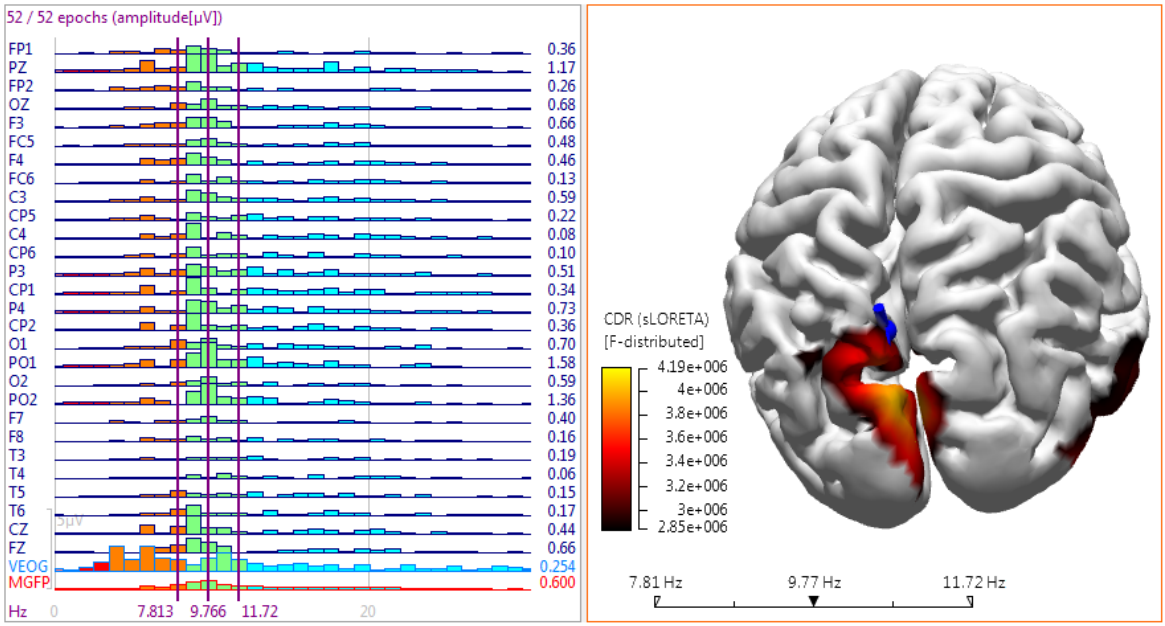
Expand **Noise Estimation** and select **Auto** (which is the default). This will apply the **Percentile 50** method (since there are no "signal free" sections in the epochs).

Select the type(s) of source reconstruction method to use. A **Rotating** dipole is the method of choice for frequency domain source reconstruction (it forces the real and imaginary values into a single location). sLORETA and Scan Methods can also be used with frequency domain data. Real and imaginary results are seen in the 3D View and Image Data displays.

Select the **Standard Cortex** in the **Objects** list for **3D View**.



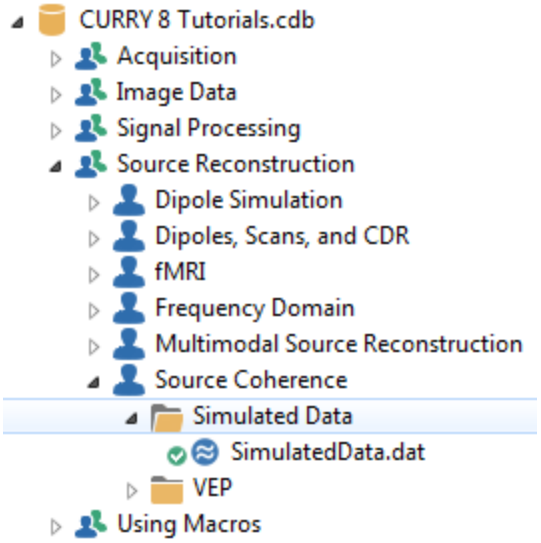
In this example, we used the interval from about 9-12Hz, and computed a **Rotating** dipole fit as well as **sLORETA** constrained to the cortical surface. Both show the expected posterior localization for alpha.



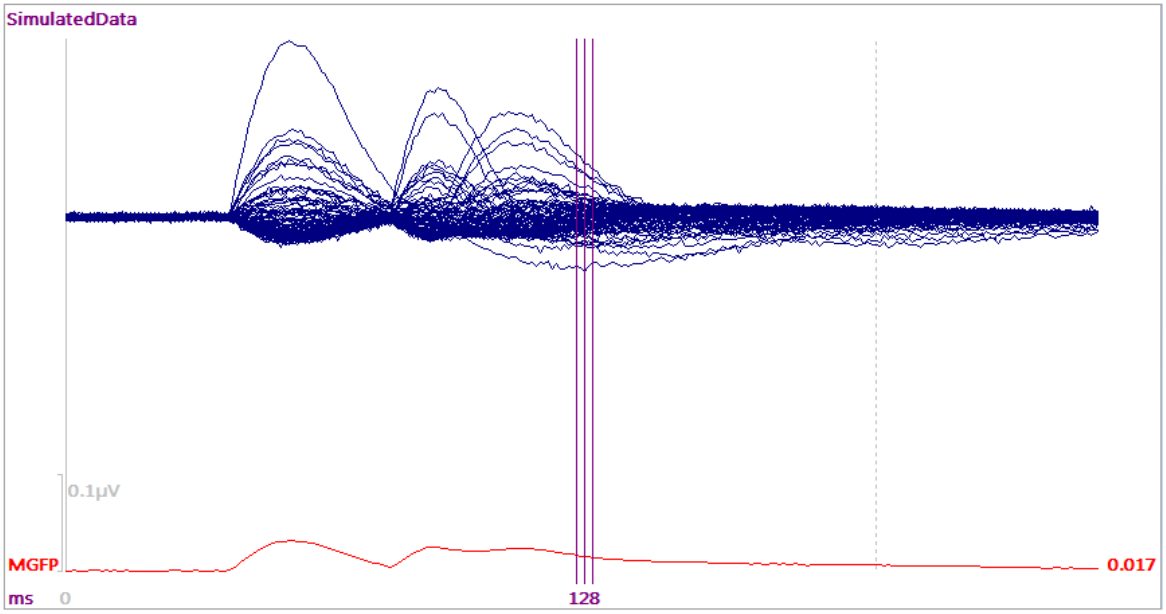
2.6.6 Source Coherence

Coherence, or sensor coherence as it is sometimes referred to in CURRY, is a correlational measure between pairs of sensors, based on the EEG or MEG 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 *CDR*.

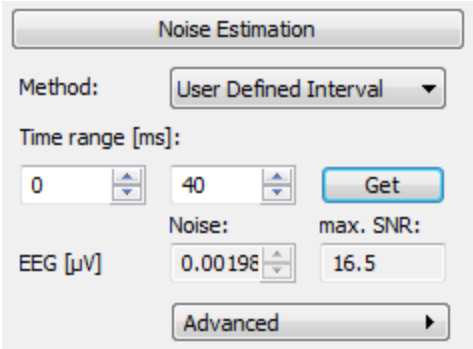
To illustrate how CURRY uses source coherence, which emphasizes the lag time among sites, we will start with a simulated data file. This file is found in the Study shown below.



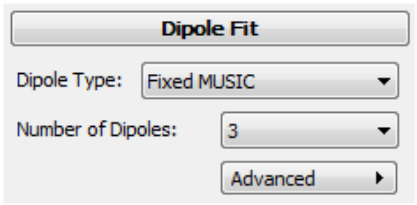
1. Open the Study and select the **Butterfly Plot**. There are 3 simulated dipoles.

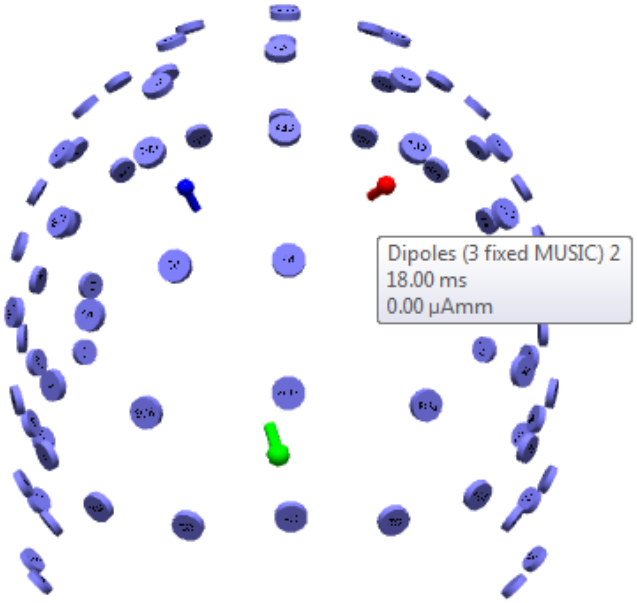


2. As usual, when doing source reconstruction with EP-like data, it is best to use the pre-stimulus interval for **Noise Estimation**, or, in this case, from **0** to **40**ms.



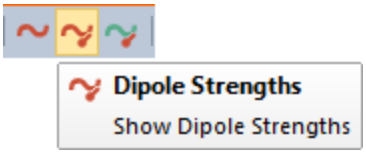
3. Select the full Timerange. Select the FD, 3D View display. Use the default **3 Spherical Shells** head model. In the **Source Reconstruction** panel, select **Fixed MUSIC** for **Dipole Type** under **Dipole Fit** (using the default head model). Enter **3** for the **Number of Dipoles**. The 3 dipoles are seen in the **3D View**. Position the mouse over the dipoles to see which one is which.



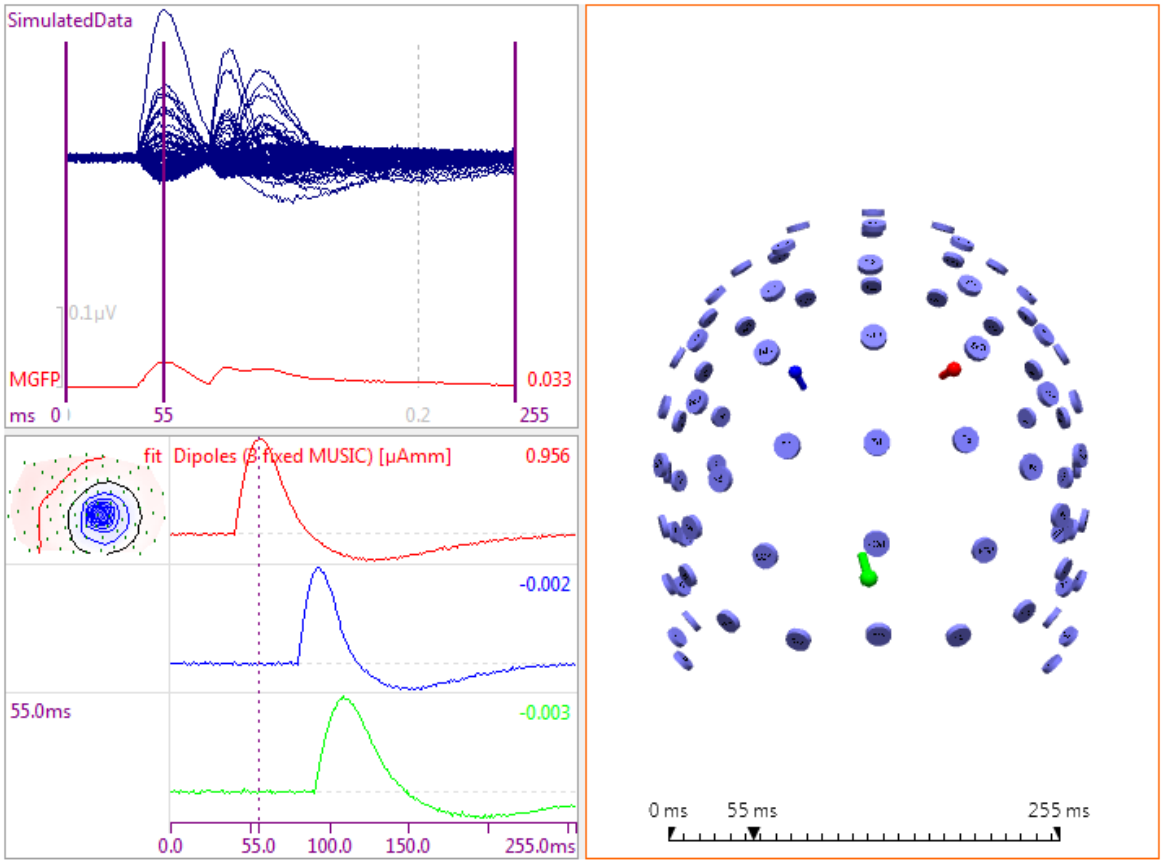


Deselect the **Ellipsoid Display Mode** and the **Time Range Display Mode** . Drag the time cursor back and forth to see how the waveforms relate to the individual dipoles.

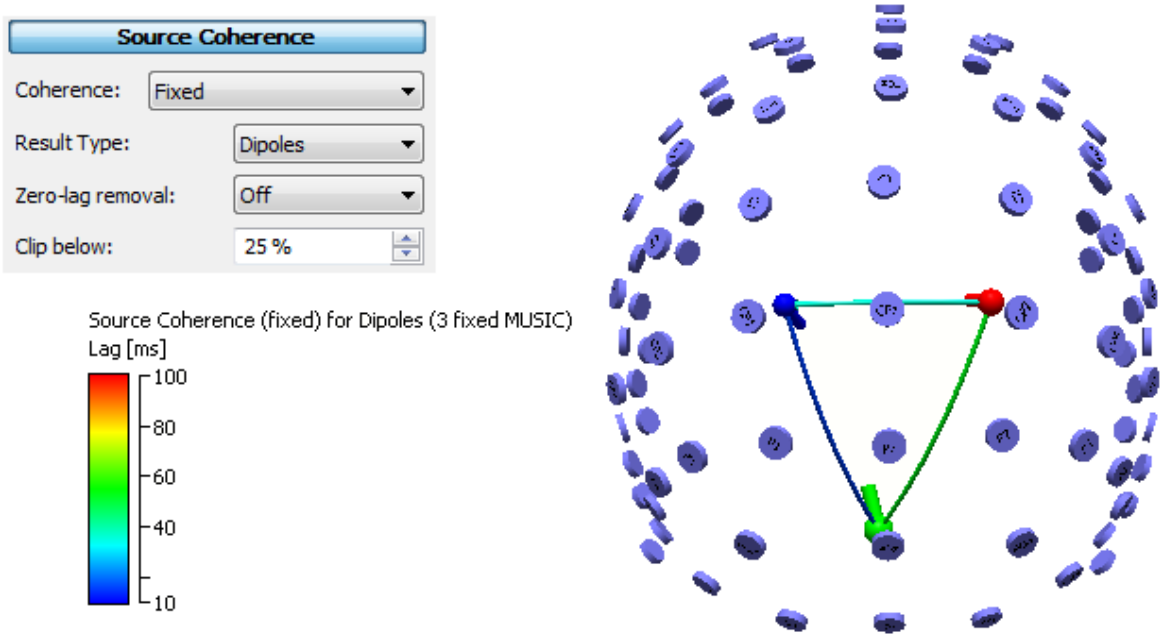
4. Select the FD, Maps, 3D View view. Click the **Dipole Strengths** icon on the Maps Toolbar.



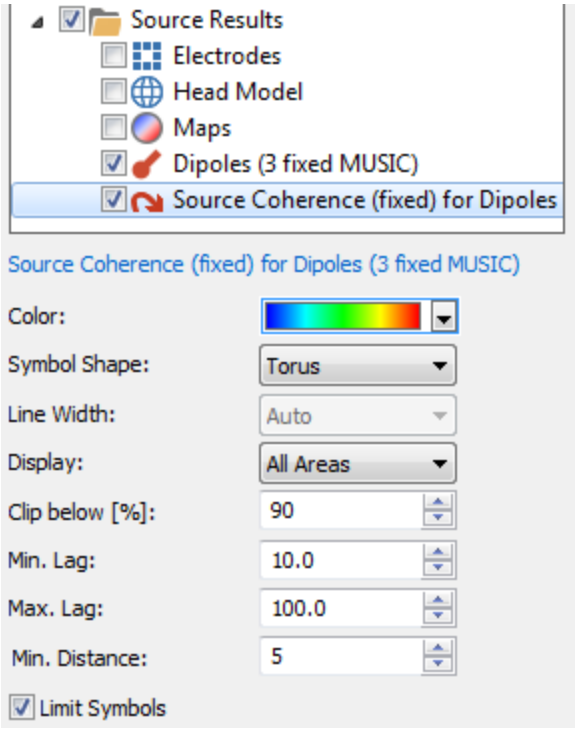
You now see the 3 dipole strengths, color coded to the 3 dipoles. Red comes first in time, then blue, then green. Then enable the **Time Range Display Mode** icon (on the 3D View toolbar) to see all three at one time.



5. Expand the **Source Coherence** panel and select **Fixed** for **Coherence** (verify the remaining parameters). You see that three links now appear, connecting the three dipoles. Coherence values greater than 25% (.25 x 100) are present. The colors of the links represent the time lags, or phase relationship. (Realize also that coherence is being computed for all frequencies. To explore specific frequency bands, filter the data accordingly first).

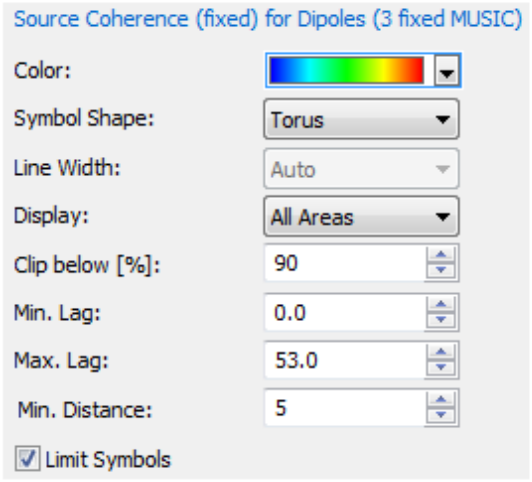


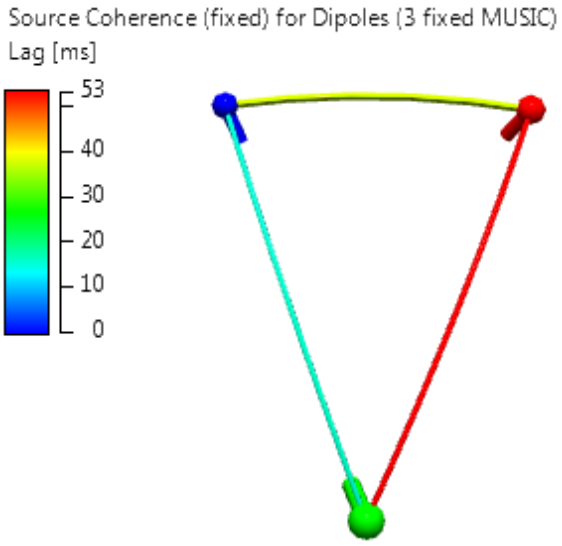
6. Remove the **Electrodes** in the display (if desired) to reduce the clutter. Now examine the **Source Coherence Properties**.



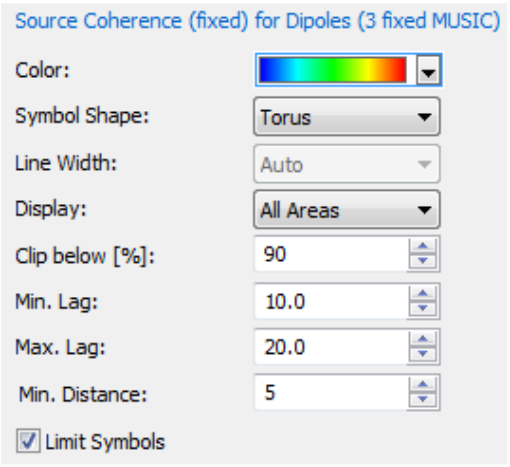
7. Slowly increase the **Clip below** parameter. At **92%**, one of the links drops out. At **98%**, the other two drop out. Coherence varies between 0 and 1.0, or, 0 and 100% in this case. The waveforms are very coherent. Return **Clip below** to **90%**.

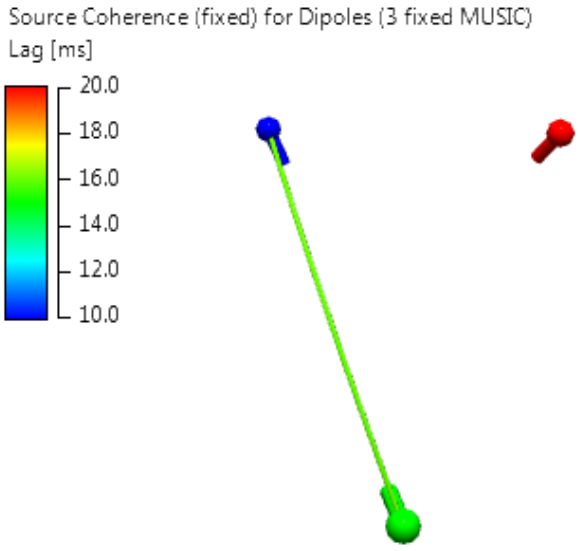
8. Set **Min. Lag** and **Max. Lag** both to **0.0**. The links disappear. There are no links that do not have at least some lag. Now slowly increase **Max. Lag** and see the link between Dipole 3 and dipole 2 appear at 16ms. There is just the one link that has a phase lag between 0 and 16ms. If you measure the latency difference between the dipole Strengths at the peaks for dipoles 2 and 3, the distance is 16ms. At 37ms, the link between dipole 1 and dipole 2 appears (the distance between their peaks), and the final link appears at 53ms, between dipole 1 and dipole 3. As you increase the Max. Lag time, the scale for Source Coherence Lag changes accordingly, and the colors of the links change to match the scale.





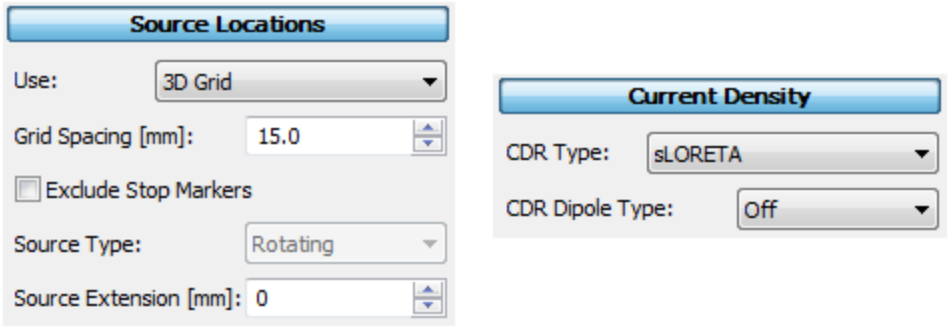
9. Now, if you are only interested in links with lags of at least 10 ms and not more than 20, enter those values for Min. and Max. Lag. As you would expect, there is only the one link that falls within that range.



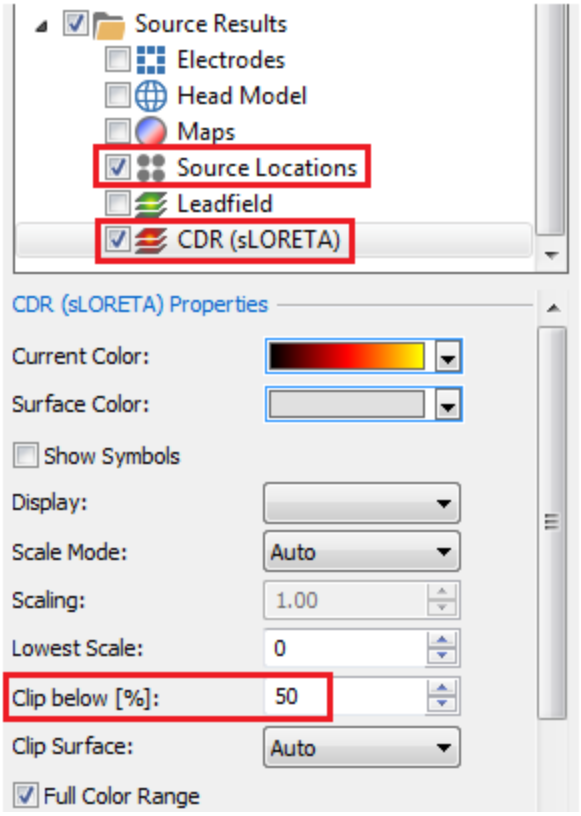


10. Set the **Dipole Fit** to **Off** to remove the **Fixed MUSIC** dipoles. Set **Source Coherence** to **Off** also.

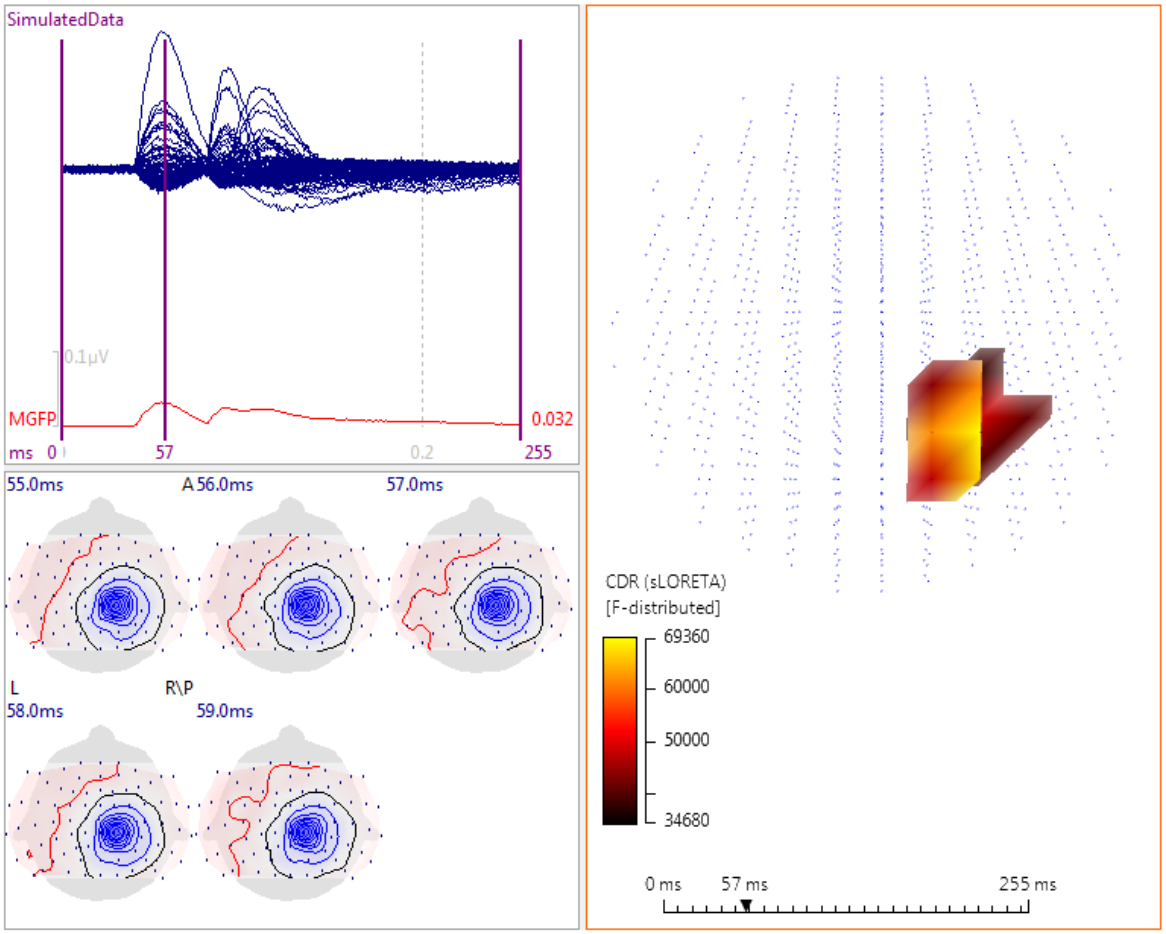
Expand **Source Locations**. Use the 3D Grid option. Coherence will be computed for all of the points in the grid, which can result in a large number of coherence links. We can reduce this by setting **Grid Spacing** to, for example, **15**mm. Expand the **Current Density** panel and select **sLORETA** for the **CDR Type**.



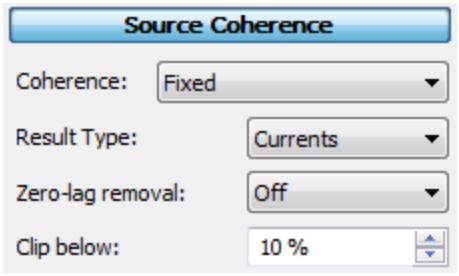
In the **CDR Properties**, set **Clip below** to **50**%. Enable the display of the **Source Locations**.



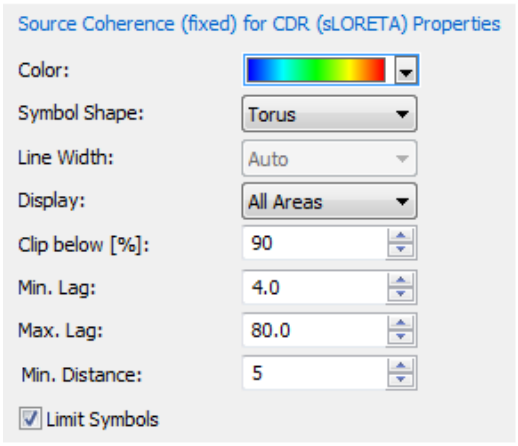
Toggle off the **Time Range Display Mode**. Move the time cursor to see the CDR results for each peak in the waveforms (**Top View** selected).

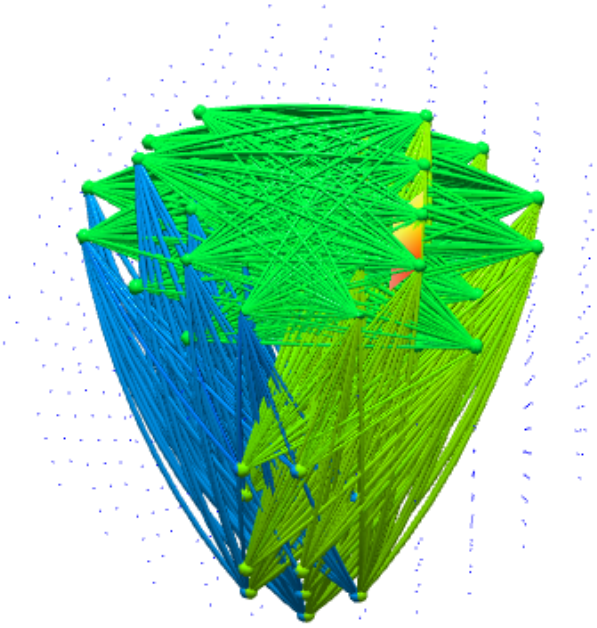


11. Expand **Source Coherence** set **Coherence** to **Fixed**, **Result Type** to **Currents**, and **Clip below** to **10**%.



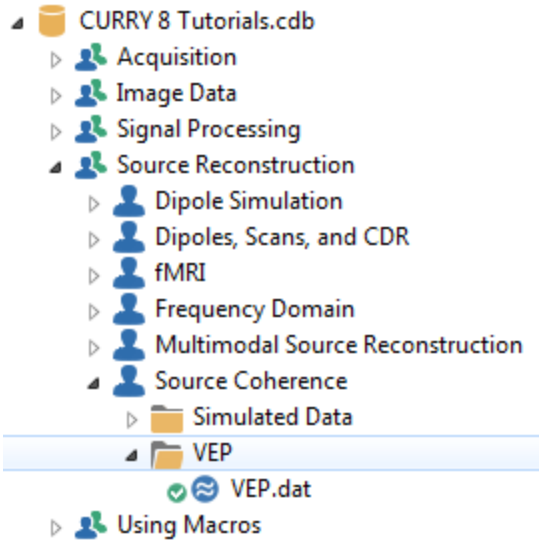
In the **Source Coherence Properties**, set **Clip below** to **90**%, **Min. Lag** to **4**ms, **Max. Lag** to **80**ms, with **Limit symbols** enabled. With these parameters there are multiple links among the three dipole sources. With different parameters, you can narrow down the number of links, focusing in on only the most robust ones (Rear View selected). You can also use the **Display** options to select links between different regions.





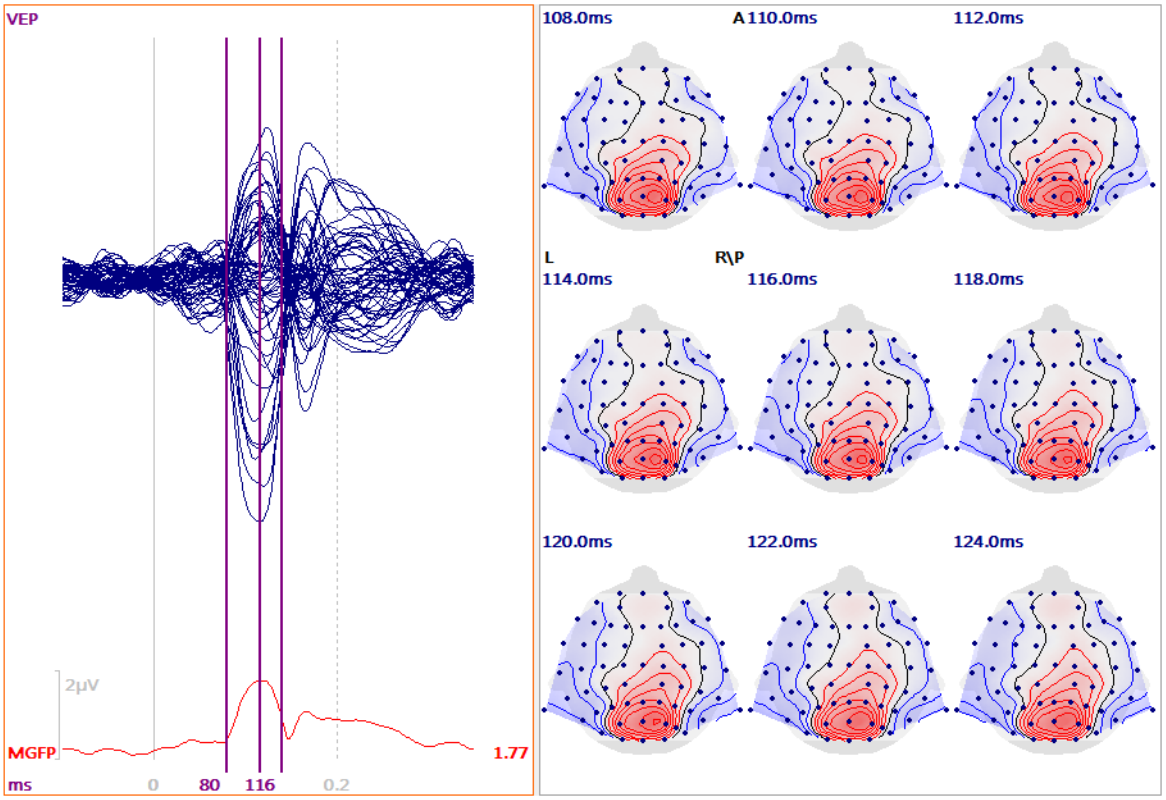
Thus far, we have been using simulated data. We will now switch to a real data file. Close this study without saving any of the results.

In this example, we will explore source coherence in a basic VEP. The file is found in the Study shown below. (It is assumed that you have already acquired familiarity with some of the operations that will be used).

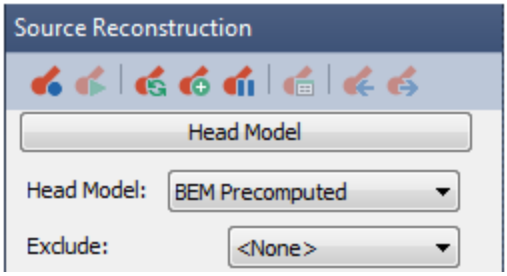


1. Open the Study, perform **Baseline Correction** (**Pretrigger**), and note that **Noise Estimation** has been computed automatically for the prestimulus interval.

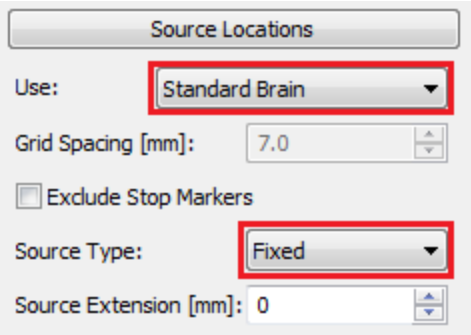
2. Set the **Timerange**. As always, the Timerange you select depends on the question you are asking. If we want to explore source coherence throughout all of the VEP components, we would set the Timerange to encompass them. In this case, we want to examine just the P100 component. We therefore selected a Timerange of 80-140 ms.



3. We do not have MRI data for this subject, so we will use the **BEM Precomputed** head model.



4. The next step is to compute the CDR solutions. We first need to select the **Source Locations**, and select the **Standard Brain** to **Use**. Set **Source Type** to **Fixed**. The "fixed" options in Source Locations (only available with cortical CDR) determine whether cortical normals are used. For coherence analysis, if "fixed" is selected anywhere in the chain of operations, fixed is used throughout.

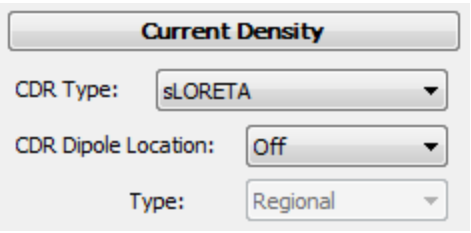


Source coherence, for numerical reasons, does not like more than a few thousand source locations. When computing CDR-based coherences, one should either:

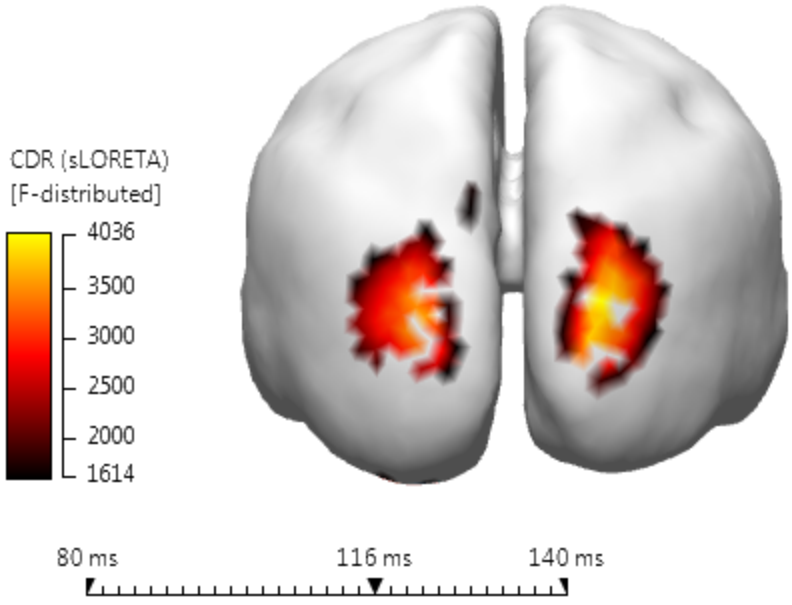
- compute CDR on a low-res grid (defined in Source locations), e.g., a 13mm grid, or

- compute a high-res CDR and use CDR dipoles in Localize mode based on a low-res grid created in Localize (e.g., a 13mm grid created in Grid Setup) as a means of data reduction/location subsampling.

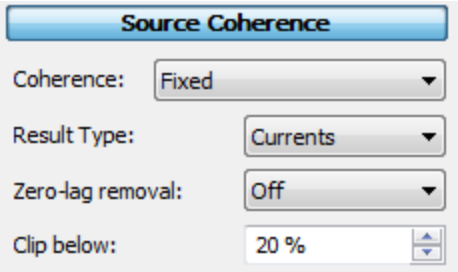
5. Select **sLORETA** (for example) for **Current Density**. (This will take a few moments).



The CDR results are seen in the **3D View** (**Clip below** at **40**).



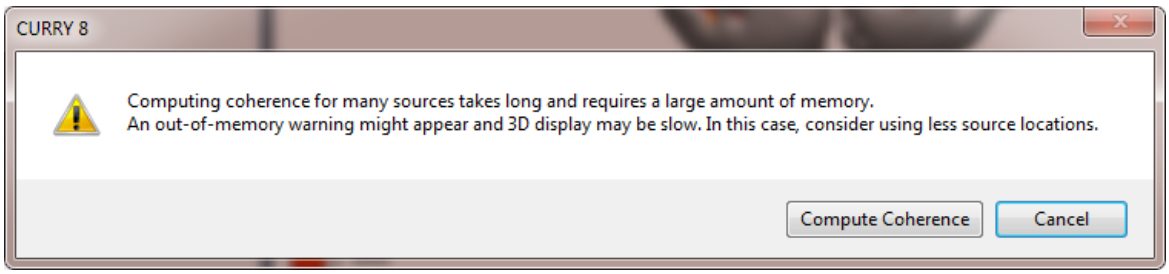
6. Compute **Source Coherence** using **Fixed**, **Currents**, and **20**%.



Sources with strengths below the 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.

If you compute coherence for **Rotating** sources (with all-positive waveforms), the quality of the results is reduced and the coherence values are generally very high. 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 as one of the CDR dipole options, **Cursor** and **Localize**.

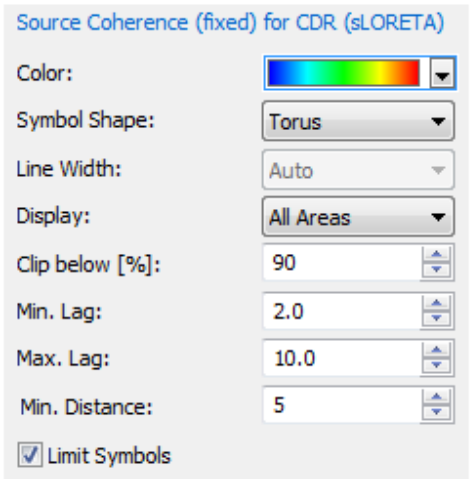
You may see the following message. Click **OK**.

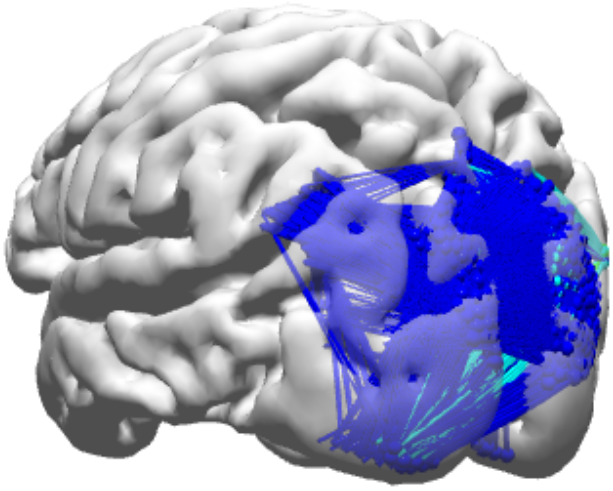


If you compute using too many source locations, 3D performance will go down and coherence computation times will go up (both quadratically, with the number of sources). As a general guideline, you should compute coherence directly for CDR results if you have less than 3000 locations. This is generally the case with a 10mm grid. If you use the **Clip below** parameter for **Source Coherence**, you can extend these performance limits, but not dramatically so.

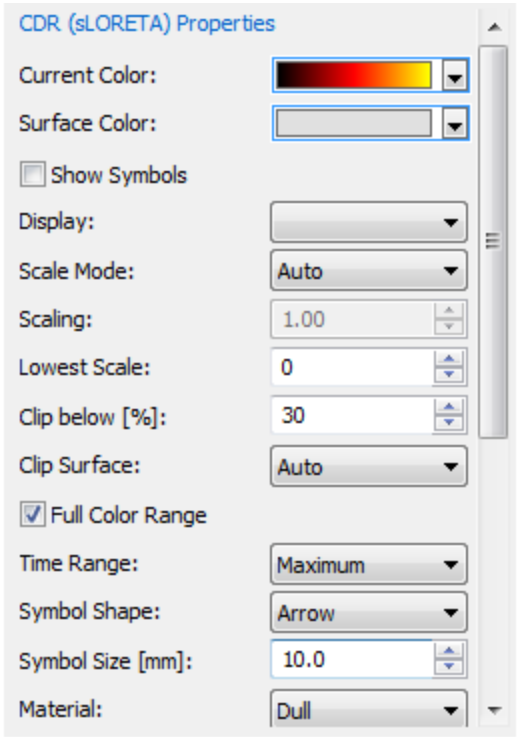
If you have substantially more source locations than 3000 (as may occur with the cortical CDR case), you need to use CDR dipoles in the "Localize" mode to subsample the many CDR locations onto a 3D grid. You can easily create such a "3D grid" as one of the options in Localize's grid setup. You will see blue crosses and brown arrows that document what you did to enable this subsampling. Coherence must then be used for the "CDR dipole" result type. (Other Localize subsampling options than a 3D grid are of course possible, e.g., by thinned-out Points created in Image Data based on the segmented cortex and then imported to Localize).

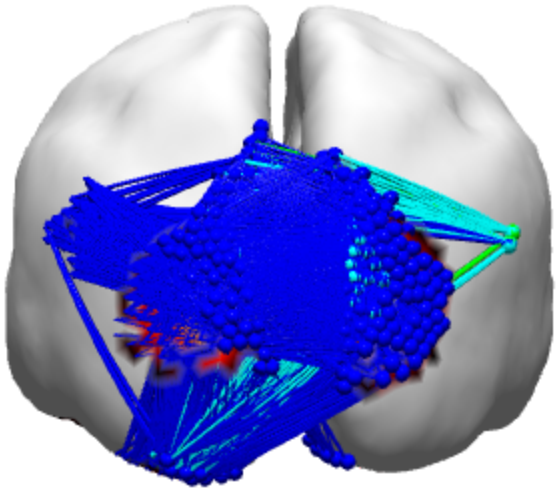
7. In the **Source Coherence Properties**, increase **Clip below** to **90%**, and set **Min.** and **Max. Lag** to **2** and **10 ms**. The Source Coherence links are seen as shown below. (**CDR** was turned off, and the **Cortex** was turned on, with its **Transparency** increased).





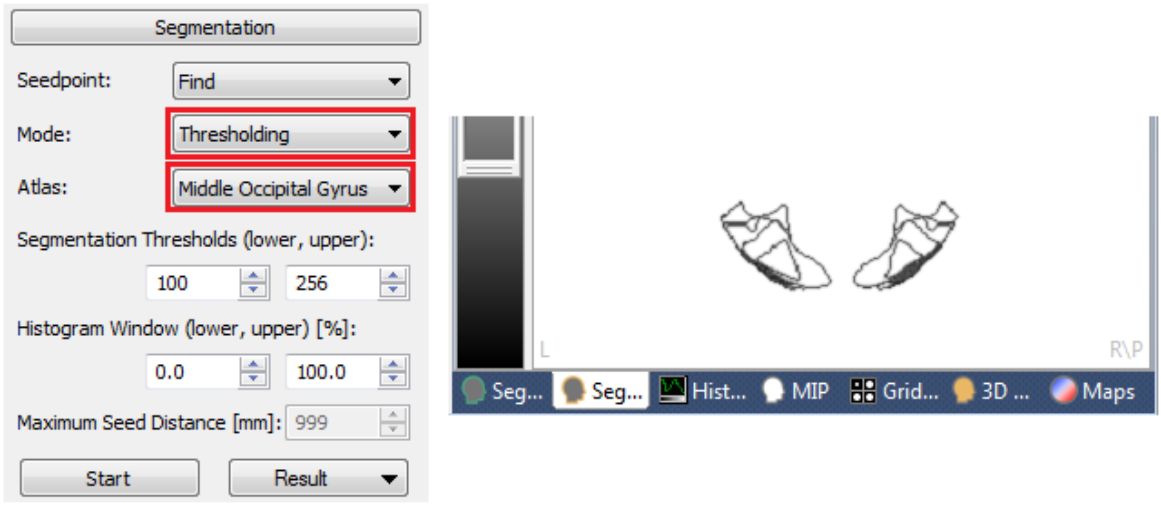
9. Enable the CDR results to see both sets of results (cortex turned off, **Clip below** reduced to 30%; increase the CDR **Transparency**).





10. You can segment structures and display only those links that connect those structures. Let's say we would like to see the links from the bilateral middle occipital gyri only.

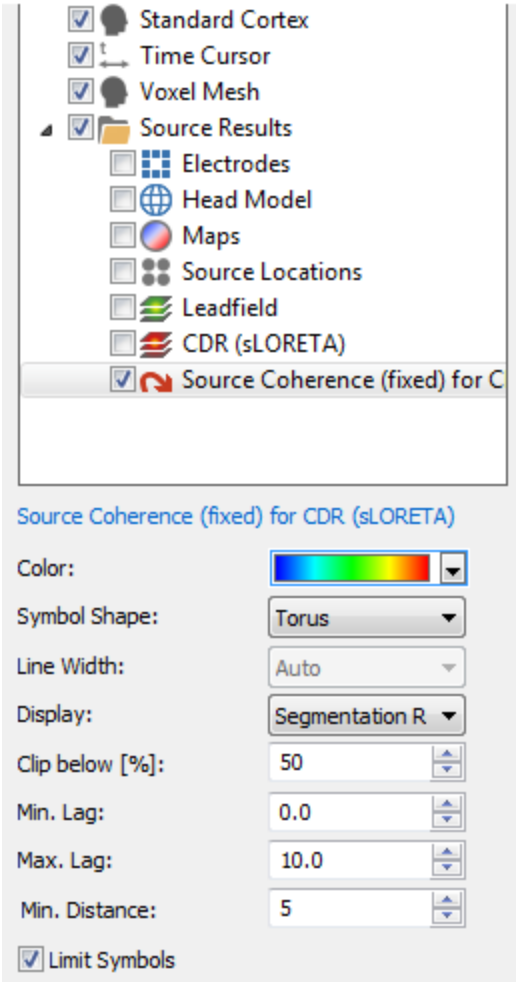
Select the **Image Data** display. In the **Segmentation** panel, set **Mode** to **Thresholding**, and in the **Atlas** list, select **Middle Occipital Gyrus**. Click **Start**. You will see the segmented structures in the **Segmentation Results** display (**Top View** selected).



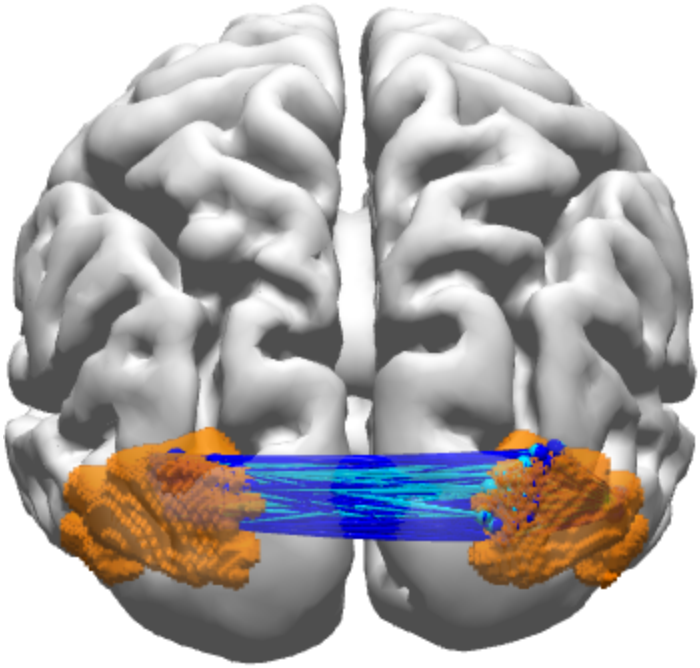
In the **Morphology** panel, select **Smoothing** for the **Mode**, with **Dilation** set to **2.0mm**.

Right click in the **Segmentation Results** display and select **Create Voxel Mesh**. Select the **3D View**. You will then see the **Voxel Mesh** in the **Objects** list. Set its **Transparency** to **30%**. Enable the newest **Cortex** and set its **Transparency** to **70%**.

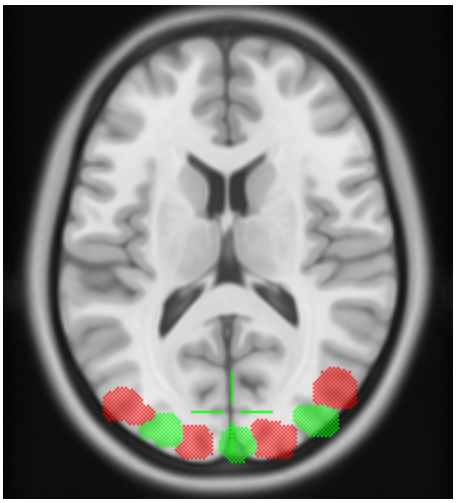
In the **Source Coherence Properties** list, set **Display** to **Segmentation Result**, **Clip below** to **50%**, **Min. Lag** to **0 ms**, and **Max. Lag** to **10 ms**.



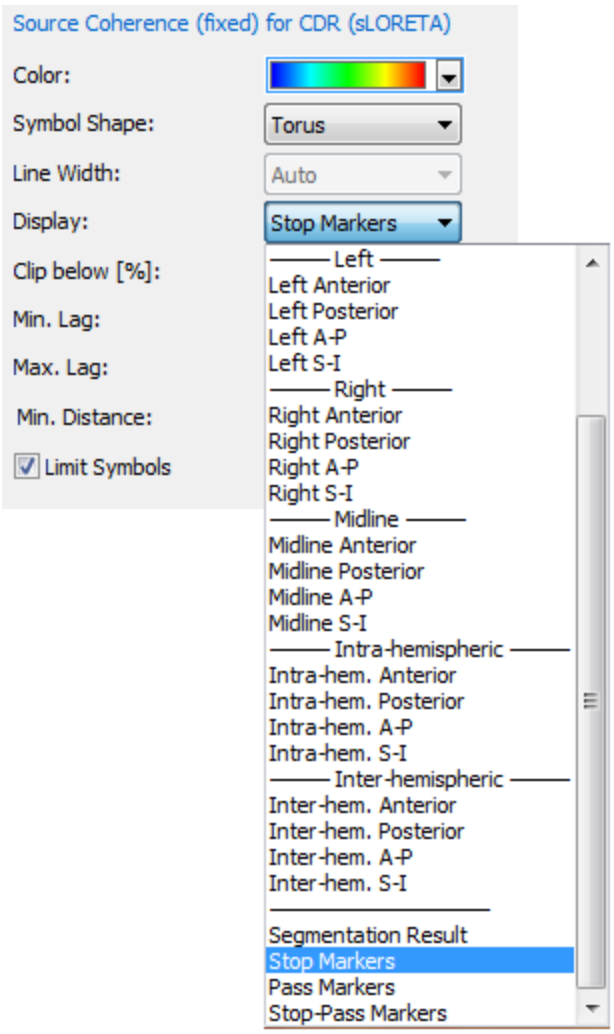
Now you see only the coherence links between the middle occipital gyri that have lags between 0 and 10 ms.

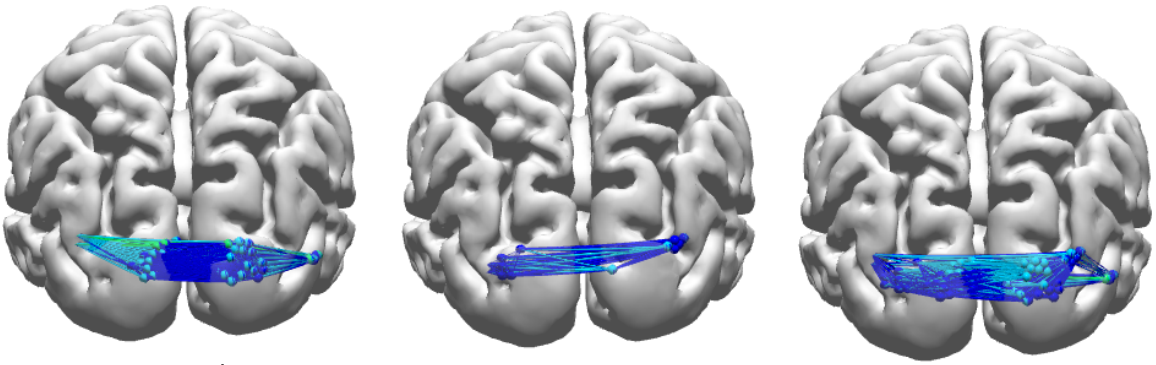


12. Alternatively, you can use **Stop** and/or **Pass Markers** to define regions of interest. In this case we added Stop and Pass Markers in several slices to define regions on both sides.



By selecting **Stop Markers**, **Pass Markers**, or **Stop-Pass Markers**, you can display the links among these regions independently.





Stop Markers

Pass Markers

Stop-Pass Markers

2.6.7 Statistical Comparisons - Dipoles, CDRs

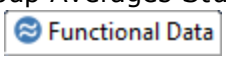
In the earlier **Statistical Comparisons - Maps** tutorial, we illustrated how to use the statistical section of CURRY to analyze functional data or "Maps". In this part, we will look at the types of analyses that can be performed with dipole and CDR results.

We will use the same mock data files as in a previous Tutorial. These are from a sham study in which there were two groups of subjects (males and females, M and F), with VEPs recorded in two conditions (fast stimulation rate - Fast, and slow stimulation rate - Slow). For the dipole analyses, all male subjects were combined (All Male), all female subjects were combined (All Female), all fast condition recordings were combined (All Fast), and all slow condition recordings were combined (All Slow).

We will compute Moving Dipoles for each group, throughout the Timerange of interest (85-115 ms), and compare the results.

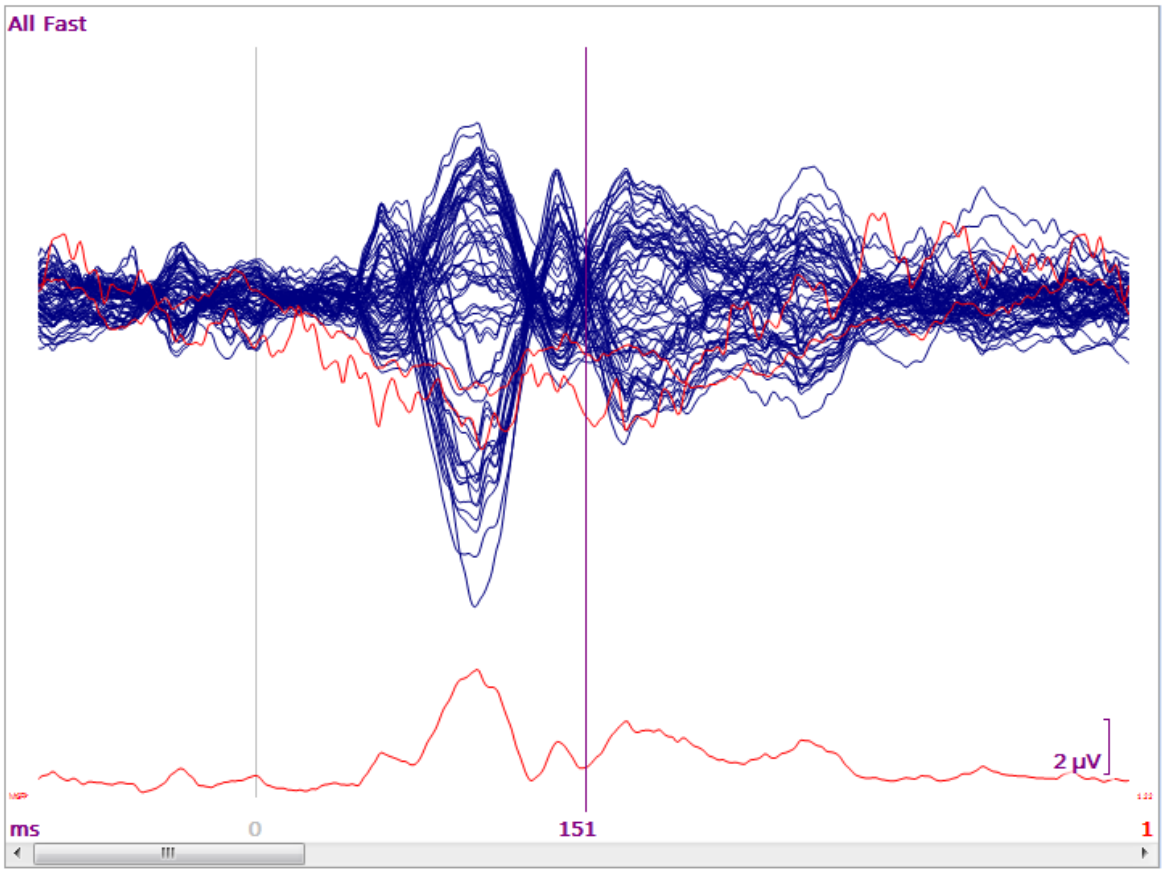
The four group averages were loaded into a single Study.

Dipole Statistics

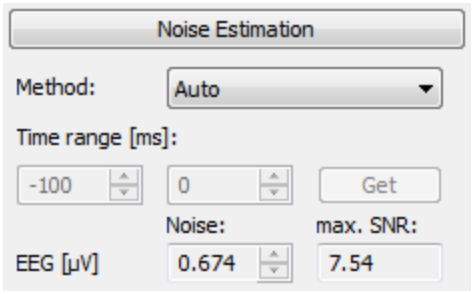
1. After opening the Group Averages Study, the 4 group averages are seen as separate epochs in the 

display. Drag the sliding bar at the bottom to see the individual data files, or use the Toolbar icons .

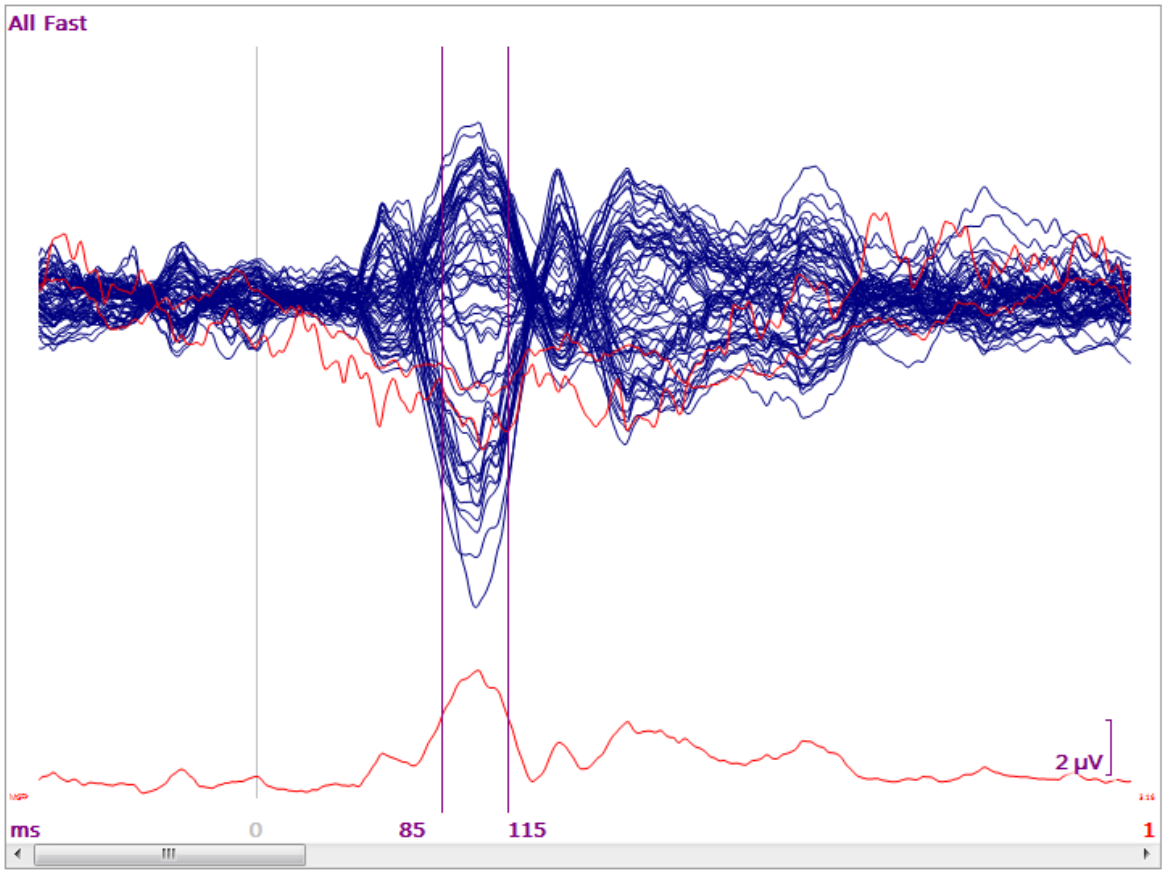
The HEO and VEO channels are seen as regular EEG channels in this file. Click on their labels to deselect them; we do not want to include them in the analyses. The color of the deselected channels was changed to Red to make them easier to see. Select the **Butterfly Plot**.



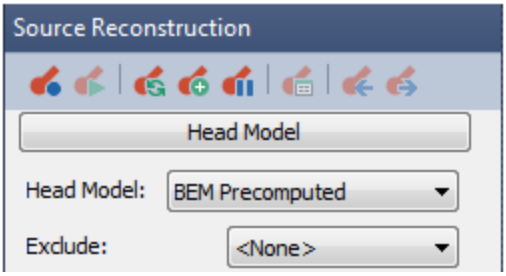
2. A noise estimate must be obtained prior to the dipole analyses, and CURRY will compute this automatically. Go to Noise Estimation (**Functional Data**) and verify that **Auto** has been selected (this will use the pretrigger interval, -100 to 0 ms). Separate noise estimations will be obtained for each data file.



3. Select the Timerange of interest using the two outer cursors (85-115 ms).

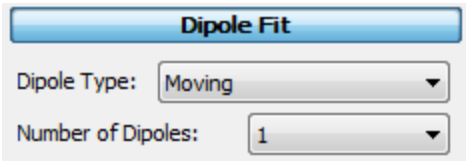


4. In this case we do not have MR data for the subjects, and instead we will use the precomputed **BEM Precomputed** model for the Head Model (in the **Source Reconstruction** parameters).

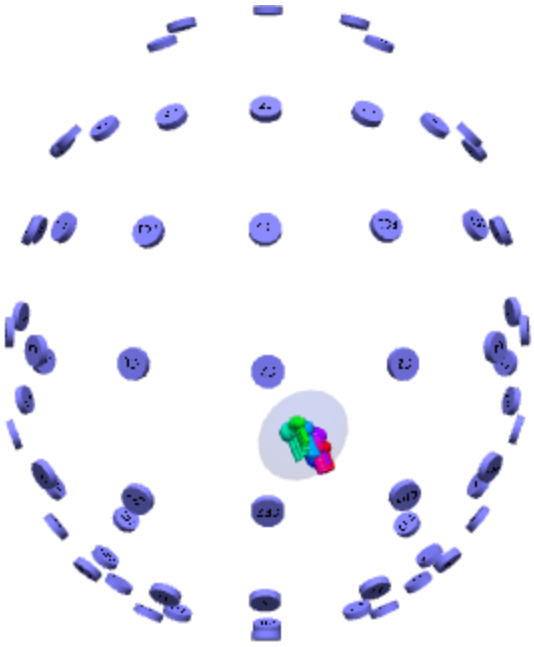


5. Display the *first group averaged data file* in the **Functional Data**. Select the FD, 3D View display option (for convenience).

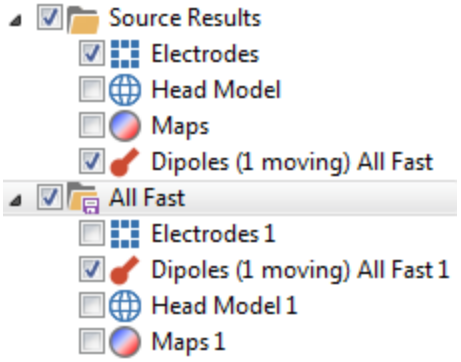
6. In the **Dipole Fit** panel (under **Source Reconstruction**), select **Moving** for the **Dipole Type**.



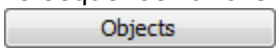
7. The dipole results are seen in the 3D View. Enable the **Timerange Display Mode** , if needed, to see all results.



8. Select **Source Results** → **Keep Results**, or click the icon on the **Source Reconstruction** Toolbar. The Kept Results are added to the Objects list under **3D View**. If desired, you can rename Kept Results (*All Fast*) using the *F2* key.

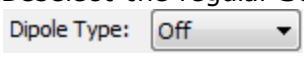


9. Click the **Next Epoch** button on the **Functional Data** Toolbar to display the second group averaged data file. The moving dipole results are seen in the

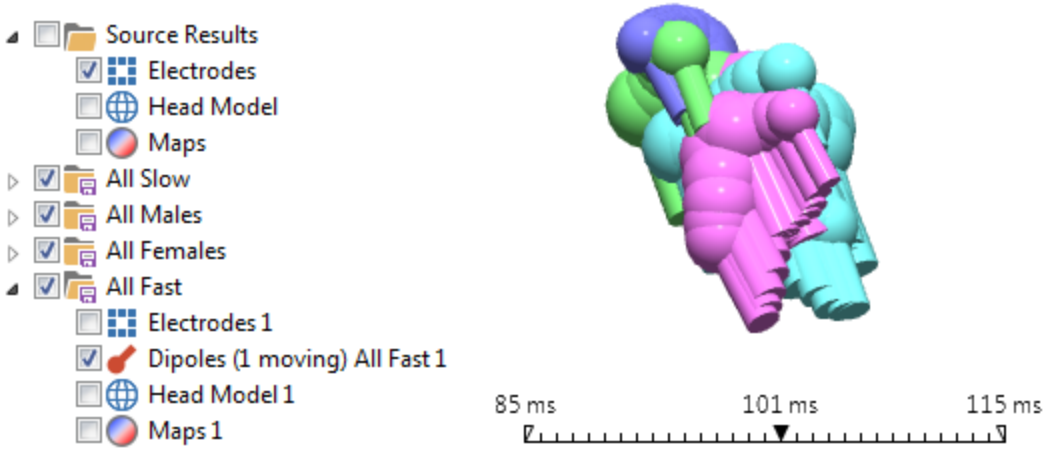
. Click **Source Results** → **Keep Results** again to keep the new results (change the label). Repeat this sequence for the remaining groups. The four sets of Kept Results are seen in the 

list, and the four sets of moving dipoles are seen in the

.

Deselect the regular **Source Results** item in the list, and also set **Dipole Type** to **Off** 

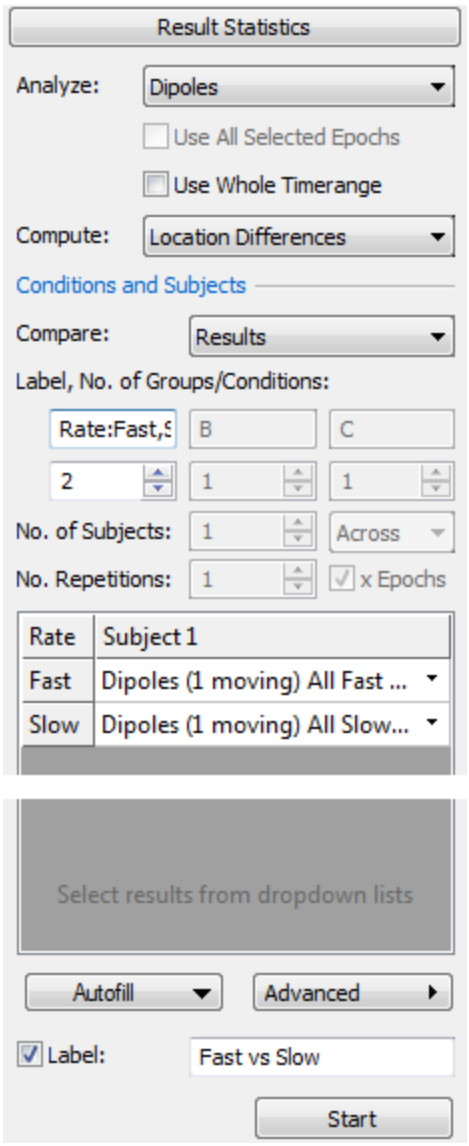
(so that they will not be added to the analysis matrix later on). (The display of the **Confidence Ellipsoids** was disabled).



10. What matters here is the order in which the results were Kept. The cells in the data matrix will be filled in the same order - 1 through N. It is necessary to keep track of which kept dipole results go with which data file. If you relabel the Kept Results, you will see the labels below and it will be obvious which ones to select.

Now go to the

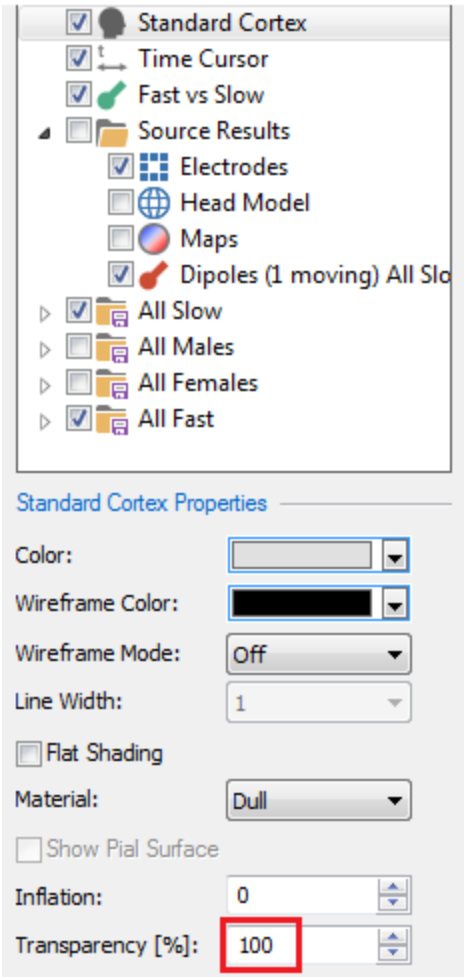
panel under **Results**. We will compare two sets of results at a time. Set the parameters as shown. The Condition Label is "Rate:Fast,Slow". Use the drop-down lists in the cells to select the desired kept results. In this case, we are comparing the Fast and Slow conditions, as there were the ones that showed the differences in the Maps analyses in an earlier Tutorial. Enable **Label** and enter text that will allow you to keep track of the results (Fast vs Slow).



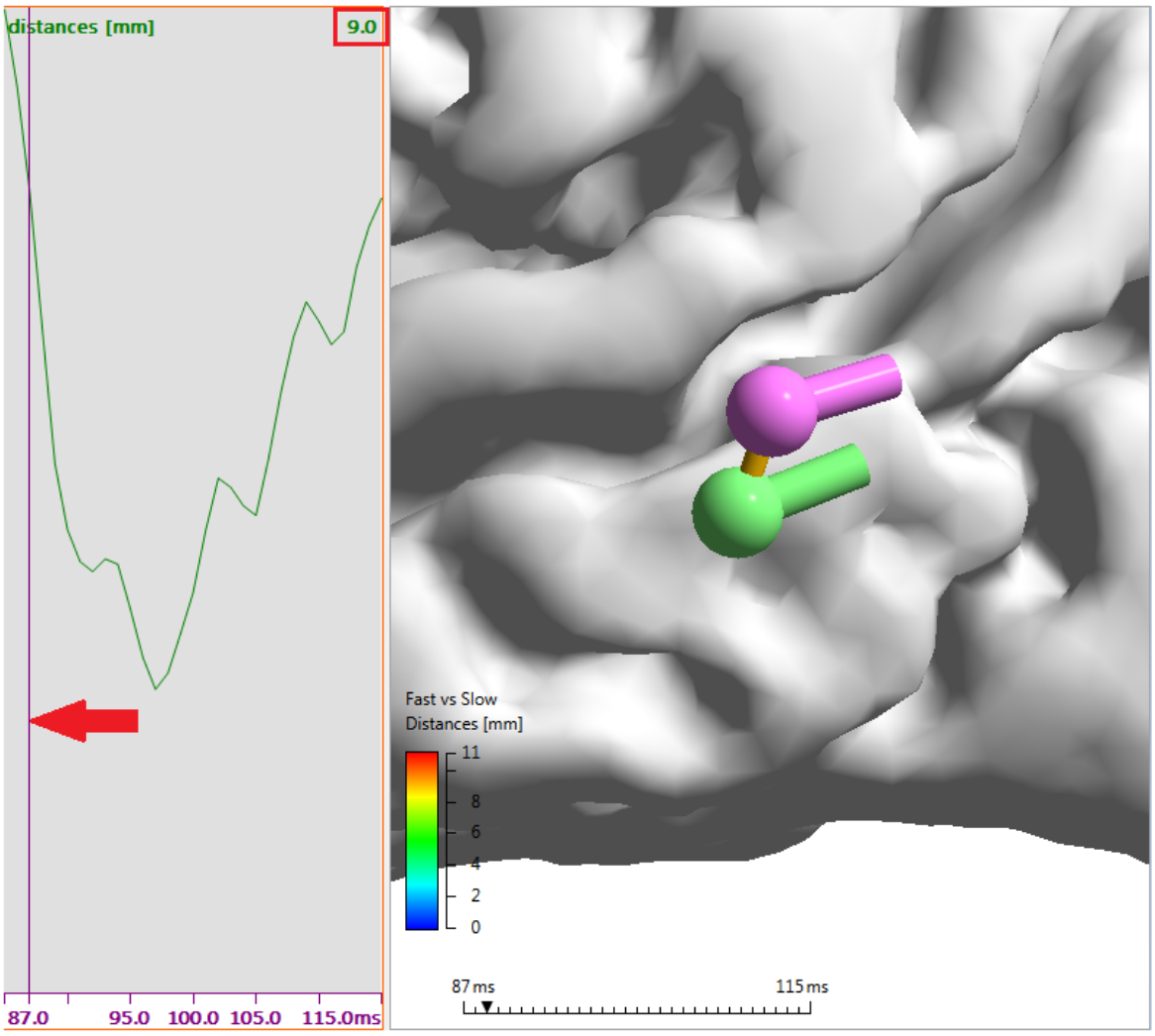
11. Click

. To make the results easier to see, deselect the **Time Range Display Mode** so that you can see the changes as you move the cursor in the Time Scale. Be sure to display only the Kept Results that are being analyzed (1 and 4).

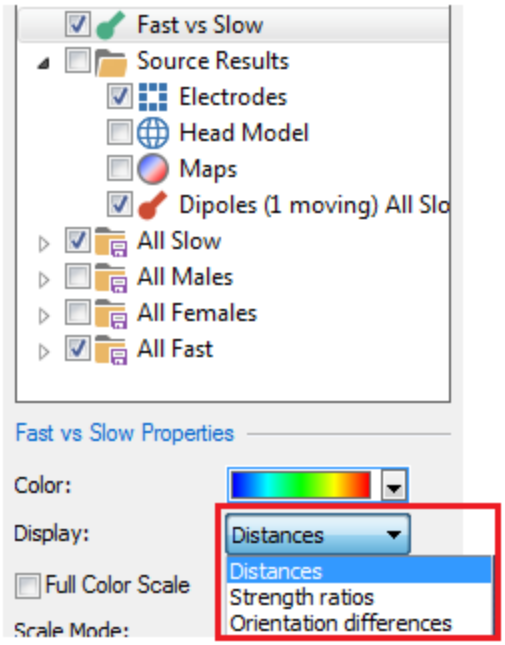
To have a frame of reference for the results, enable the **Standard Cortex**, and set its **Transparency** to **100**%.



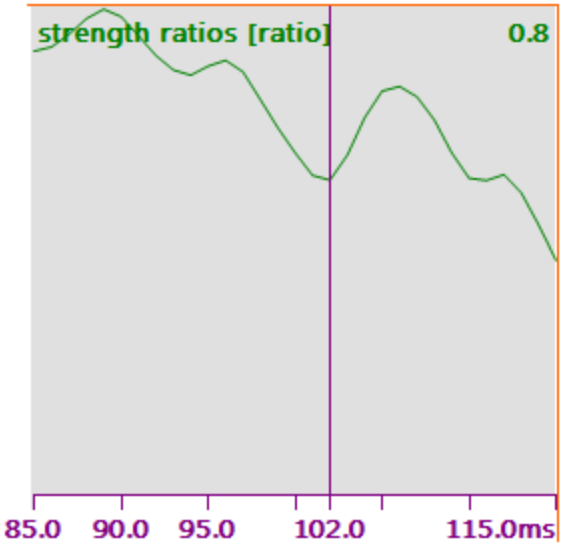
You will then see the results on the cortical surface. Reposition the display as desired. The function in the Maps display shows the Distances (mm) across time. Move the time cursor to see these change for each time point in the Timerange. The color of the line will change as the distance changes, in accordance with the colors on the scale.

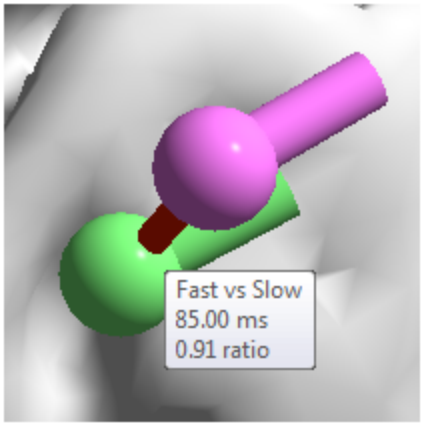


12. Now look at the Properties for the Statistics results, which we labeled *Fast vs Slow*. The **Display** parameter has options for **Distances**, **Strength ratios**, and **Orientation differences**.

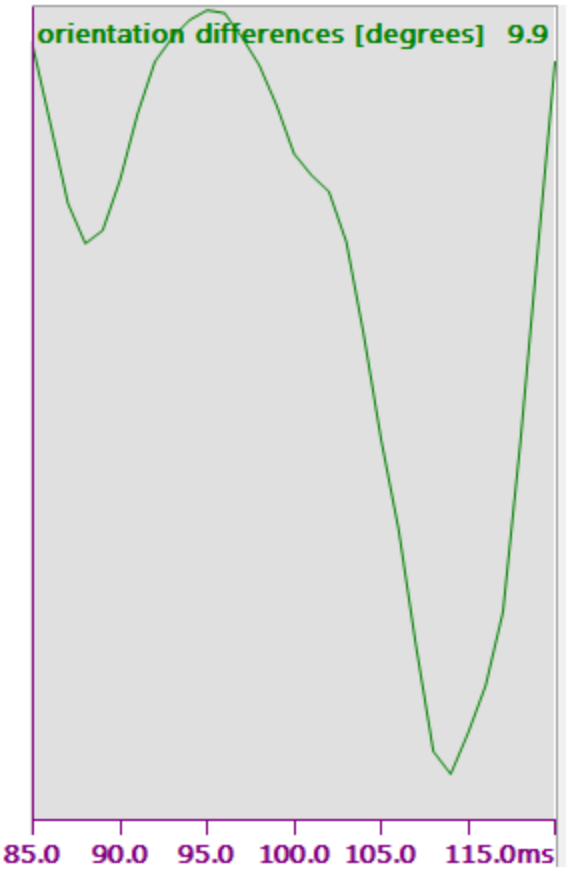


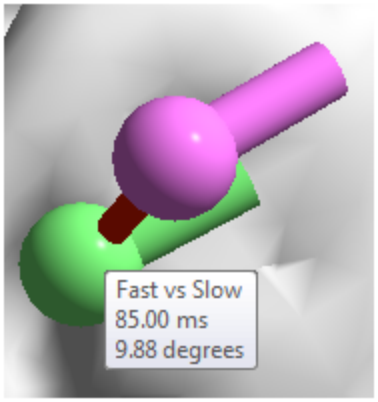
Select **Strength ratios**. This is the ratio in dipole strength (Fast/Slow, or Kept Results 1 / Kept Results 4). Position the cursor over the dipoles to see the Strength ratios for them. The **Maps** display shows the ratios over time.





Select **Orientation differences**. This shows the difference in degrees in the orientation of the dipoles. Position the cursor over the connecting line to see the Orientation difference.





13. Hard copies of all of the results are found in the **Output** display.

Displacements [mm]: sample size 31, mean 10.0536, standard deviation of the sample 2.32459, sample standard deviation 2.36301
Displacements [mm] quartiles: Q0 (minimum) 7.12037, Q1 8.90615, Q2 (median) 9.42888, Q3 10.6516, Q4 (maximum) 17.0865
Displacements [mm] deciles: D0 7.12037, D1 7.60984, D2 8.62501, D3 9.067, D4 9.33883, D5 9.42888, D6 9.83293, D7 10.5361, D8 10.9331, D9 12.5354, D10 17.0865

Distances [mm]: sample size 31, mean 10.0536, standard deviation of the sample 2.32459, sample standard deviation 2.36301
Distances [mm] quartiles: Q0 (minimum) 7.12037, Q1 8.90615, Q2 (median) 9.42888, Q3 10.6516, Q4 (maximum) 17.0865
Distances [mm] deciles: D0 7.12037, D1 7.60984, D2 8.62501, D3 9.067, D4 9.33883, D5 9.42888, D6 9.83293, D7 10.5361, D8 10.9331, D9 12.5354, D10 17.0865

Strength ratios [ratio]: sample size 31, mean 0.855339, standard deviation of the sample 0.0466171, sample standard deviation 0.0473877
Strength ratios [ratio] quartiles: Q0 (minimum) 0.753134, Q1 0.815056, Q2 (median) 0.861468, Q3 0.891716, Q4 (maximum) 0.929025
Strength ratios [ratio] deciles: D0 0.753134, D1 0.799844, D2 0.805353, D3 0.821378, D4 0.843525, D5 0.861468, D6 0.878252, D7 0.88584, D8 0.90168, D9 0.912308, D10 0.929025

Orientation differences [degrees]: sample size 31, mean 9.43587, standard deviation of the sample 1.90246, sample standard deviation 1.9339
Orientation differences [degrees] quartiles: Q0 (minimum) 5.55678, Q1 8.16431, Q2 (median) 10.1646, Q3 11.0381, Q4 (maximum) 11.4246
Orientation differences [degrees] deciles: D0 5.55678, D1 6.16852, D2 7.44498, D3 8.93941, D4 9.75019, D5 10.1646, D6 10.3062, D7 10.7352, D8 11.1717, D9 11.2733, D10 11.4246

14. Saving the results is essentially the same as described in the **Statistical Comparisons - Maps** tutorial.

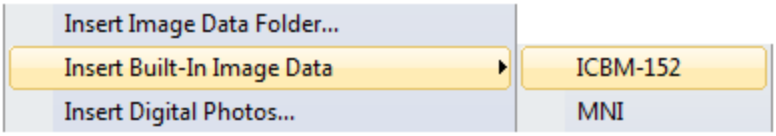
Close the Study without saving the results. Now we will do the same operations using CDRs.

CDR Statistics

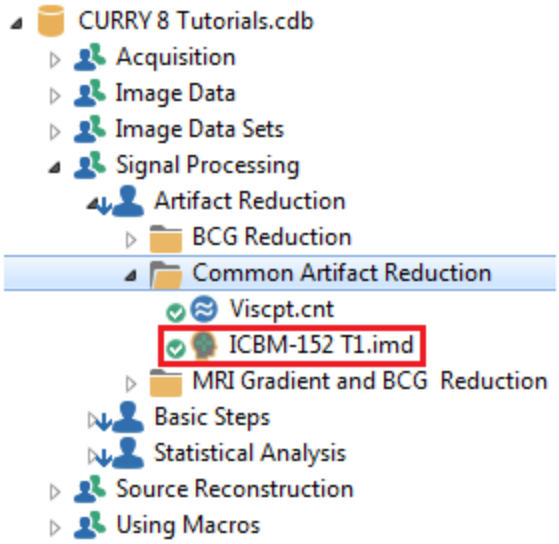
CDRs are more analogous to statistics using Maps, in that you need the individual data (a simple group-to-group comparison of averages does not work with this type of statistics). For this example, we will use the Study shown below.

CDR statistics require large amounts of memory. Memory demands are contingent on the number of epochs, number of channels, the sampling rate, and the Timerange. If you encounter a shortage of memory, you should try reducing the width of the Timerange, or reduce the number of epochs using Interleave

, under Epochs (to use every other epoch, every third epoch, etc., if feasible). For this example, right click on **Common Artifact Reduction** and select **Insert Built-In Image Data**, and then select **ICBM 152**.



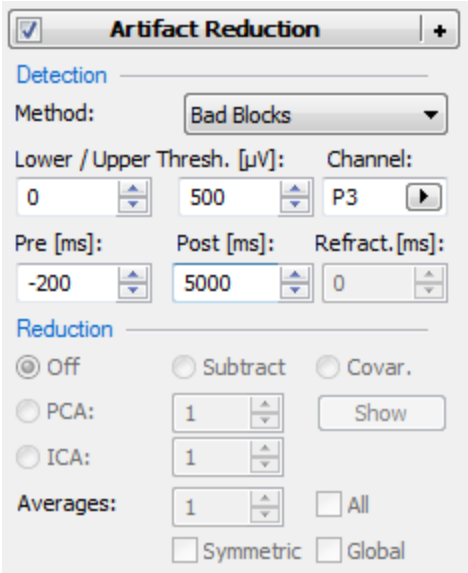
You will see that file in the Database.



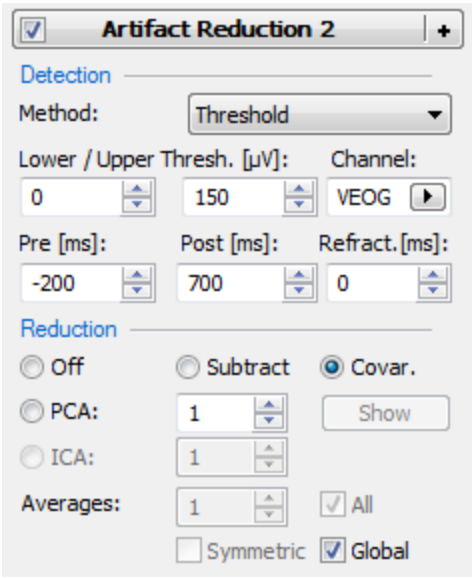
We will need to do some clean up with this file before doing statistics in order to maximize the chances of finding any differences.

1. Open the Study. This is similar to a visual P300 study, where there are targets (type 1) and distractors (type 2).

2. There are a couple of types of artifact: an electrode popping at P3 and occasional eye blinks. Add an **Artifact Reduction** panel and enter the parameters as shown. Don't click the **Scan** button just yet.

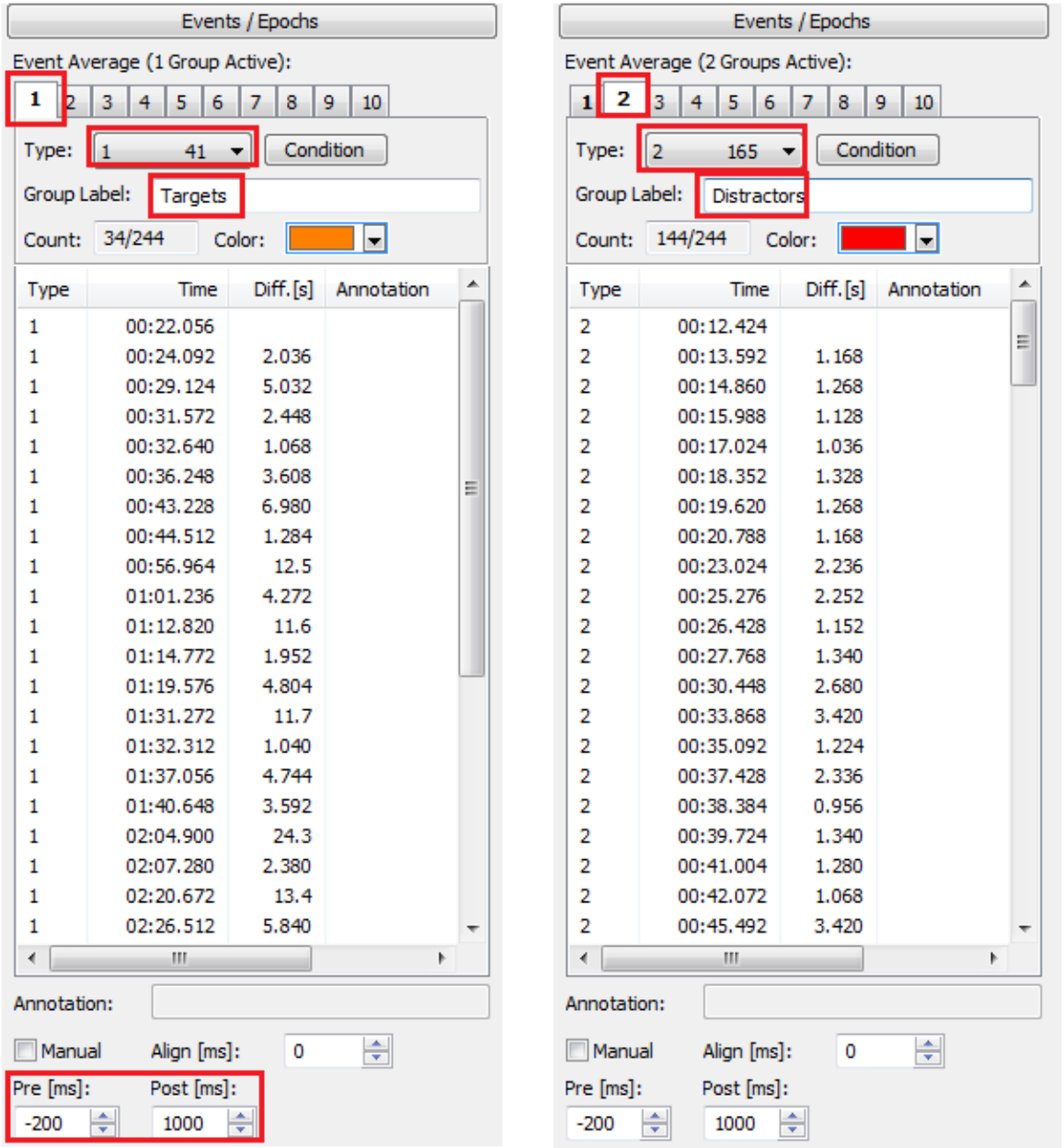


Add a second **Artifact Reduction** panel and enter the parameters as shown.

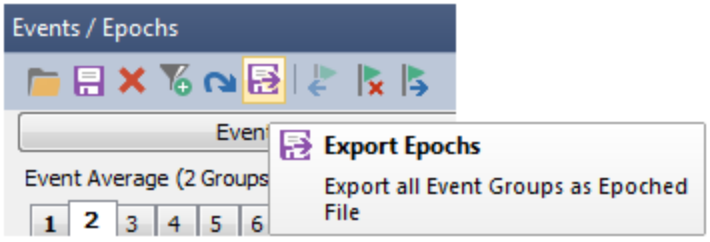


Now click the blinking **Scan Artifact** button. The file will be scanned twice to reduce both types of artifact.

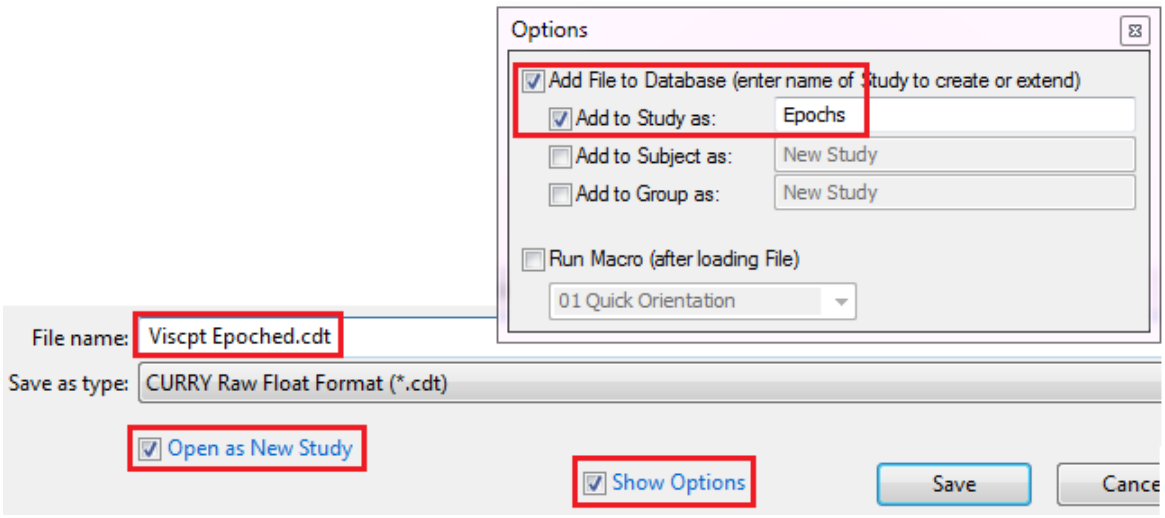
3. Click the **Open Events** button to access the **Events / Epochs** panel. Enter the parameters as shown to select the two event Types and Labels. Entering Labels here will facilitate the statistical operation.



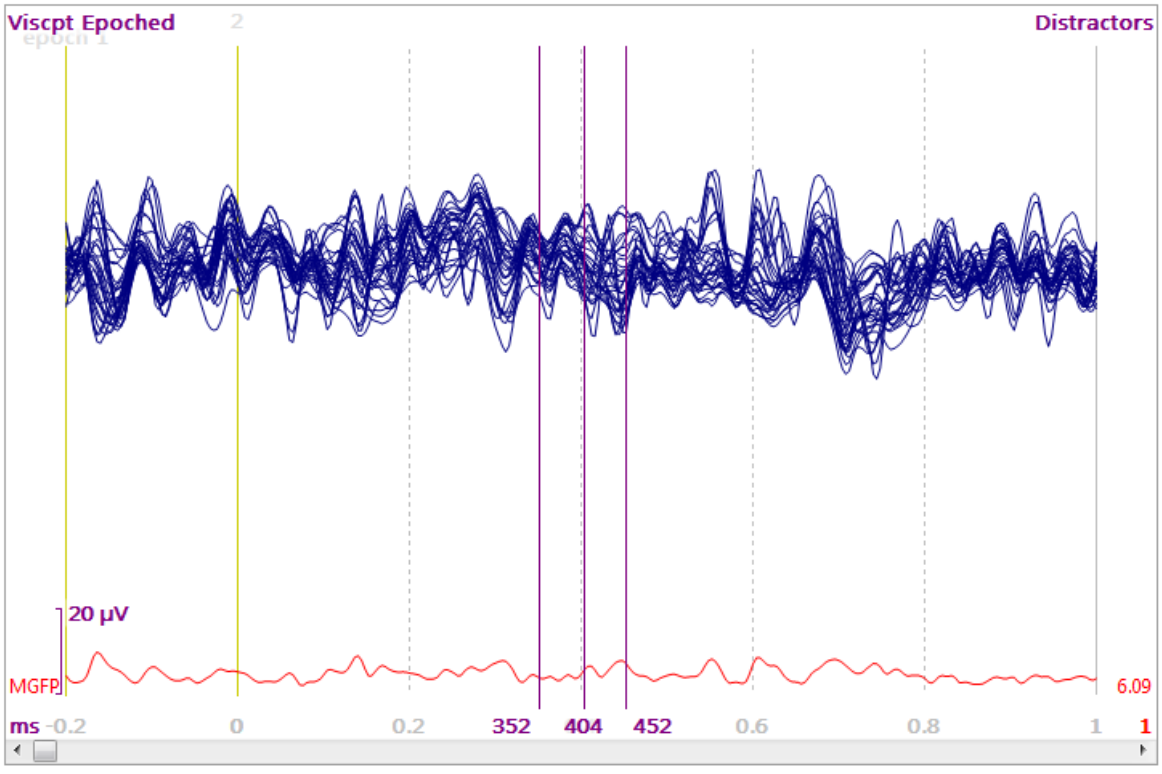
4. Click the **Export Epochs** icon to create the epoched file containing all epochs.



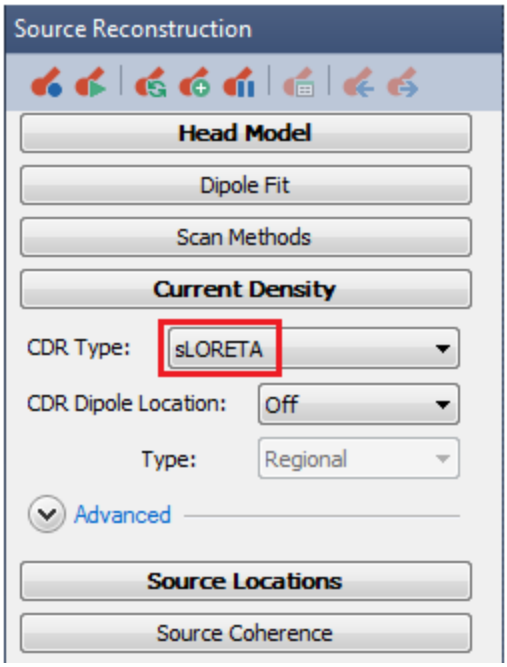
Enter a file name (*Viscpt Epoched*) and create a new Study in the Database called *Epochs*. Enable the **Open as New Study** option, Then click **Save**.



5. Select the **Butterfly Plot**. Set a Timerange from **352-452ms**. Again, we are constricting the Timerange to make the demonstration run faster and to avoid possible memory issues.

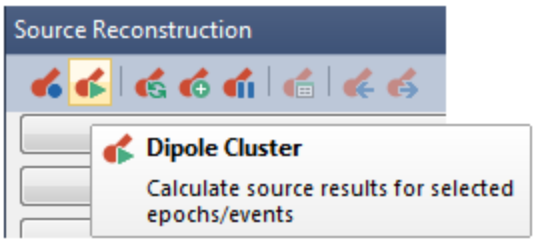


6. Go to the **Source Reconstruction** panel and select **sLORETA** for **Current Density**. Note that **Head Model** and **Source Locations** become bold. When you select the **CDR Type**, it automatically uses the default Head Model (**3 Spherical Shells**) and **Use** parameter (**3D Grid**). You may wish to use realistic models and the actual cortical surface with your own analyses.

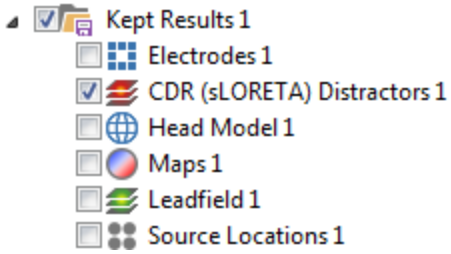


Then click the

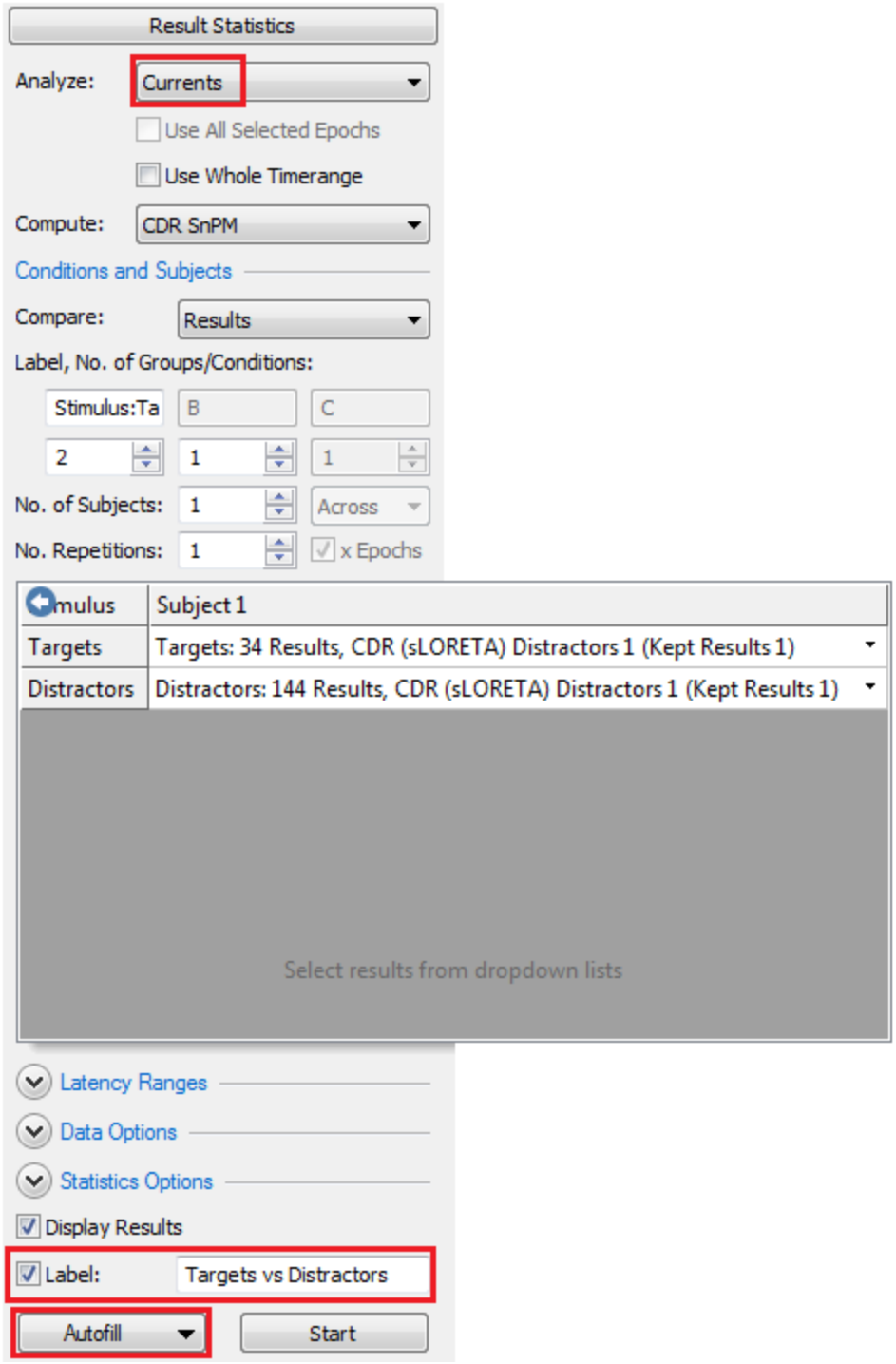
display, and then click the **Dipole Cluster** option at the top of the **Source Reconstruction** panel. This will take a few minutes.



When it is finished, you will see the **Kept Results** in the **3D View Objects** window.



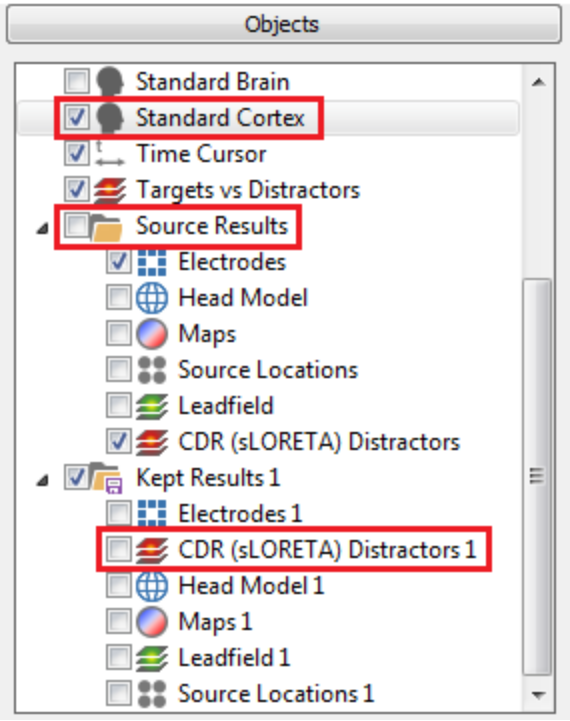
7. Go to **Results Statistics**. Enter **Currents** for **Analyze**. This will automatically set **Compute** to **CDR SnPM**. Under **Autofill**, select **Columnwise** to fill the **Labels** and matrix. Enter a **Label** for the results. Then click **Start**. This will take a few minutes.



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

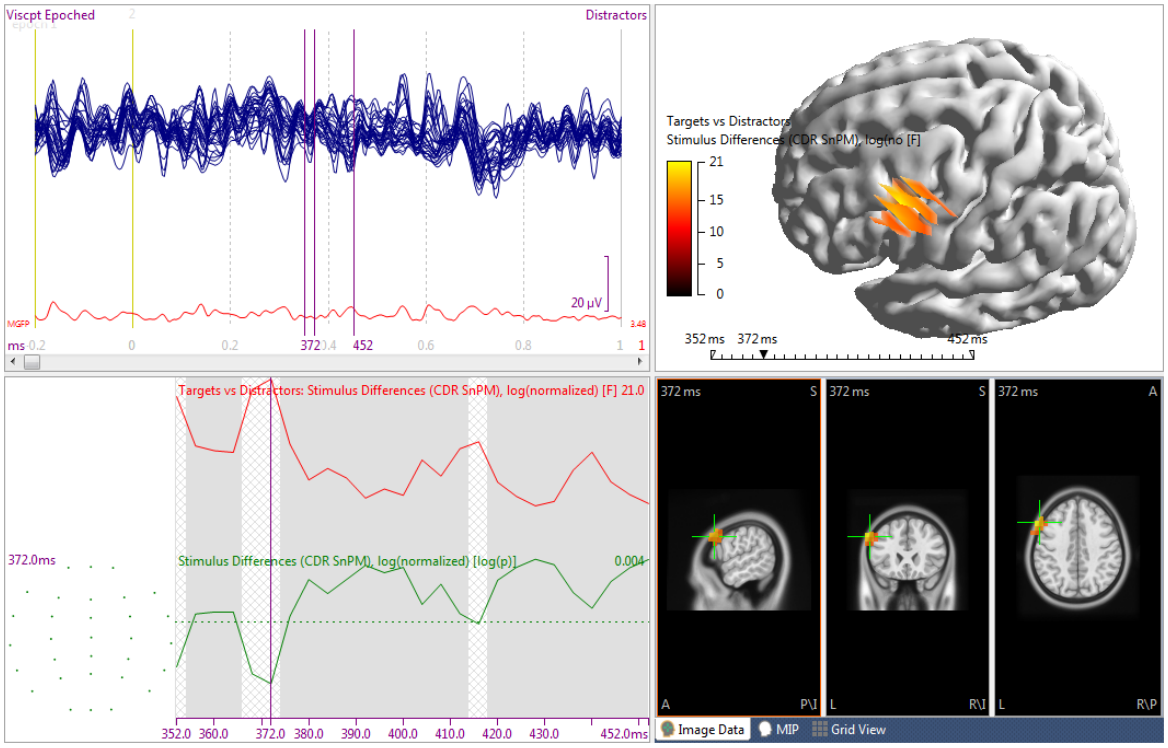
favorable properties that make it a more suitable candidate for CDR SnPM than e.g., MNLS; see the reference below) and the desired timerange (typically the complete timerange-of-interest or just everything as is usually done for TANOVA), and, in Threshold Criteria, "Keep Source Reconstruction Results" 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.

8. When it is finished, enable the **Standard Cortex**, disable the **Source Results**, and disable the **CDR (sLORETA) Distractors 1** results.



9. You should now the significant differences between the Targets and Distractors. Position the middle cursor in a white section in the **Maps** display (red arrow). In the Maps display, the upper line shows the F values (red) and the lower line shows the p-values (green). You may see regions that have white backgrounds or cross-hatched backgrounds. The white regions are where the differences were significant (<0.05). The cross-hatched regions are where p is below the significance threshold, but that the *number* of consecutive significant samples might be due to chance (see the

output, where these occurrences are mentioned). The gray areas are where the differences were not significant. The differences are seen in the 3D View as well in on the MR images. (Your results may vary slightly; this is due to the randomization procedure).



10. A summary of the CDR statistics is found in the Output field (the section for the main effects is shown below).

Targets vs Distractors Differences (CDR SnPM), log(normalized): testing if the total number of significant samples and the length of conti

Stimulus: 10 samples with $p < 0.05$; this number of samples is significant (with $p = 0$); 1 samples with $p < 0.05$ should be expected due to ra
Stimulus: contiguous segment with $p < 0.05$ from 352.0 to 376.0 ms (7 samples); this segment length is significant (with $p = 0$)
Stimulus: contiguous segment with $p < 0.05$ from 412.0 to 416.0 ms (2 samples); this segment length is significant (with $p = 0.0446$)
Stimulus: contiguous segments with $p < 0.05$ of 1 sample (4.0 ms) are to be expected; this segment length is not significant (with $p = 1$)

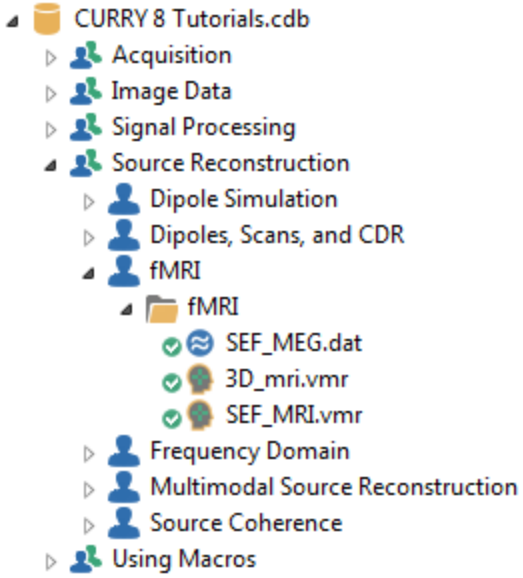
11. Saving the results is similar to that described in the **Statistical Comparisons - Maps** tutorial. In this case, the results will appear under Statistics (in Results).

Right click and select **Save As** (.std extension). When you reopen the Study, *right click* on **Statistics** and select **Load From**. Then select the file that you had saved.

2.6.8 fMRI Weighting

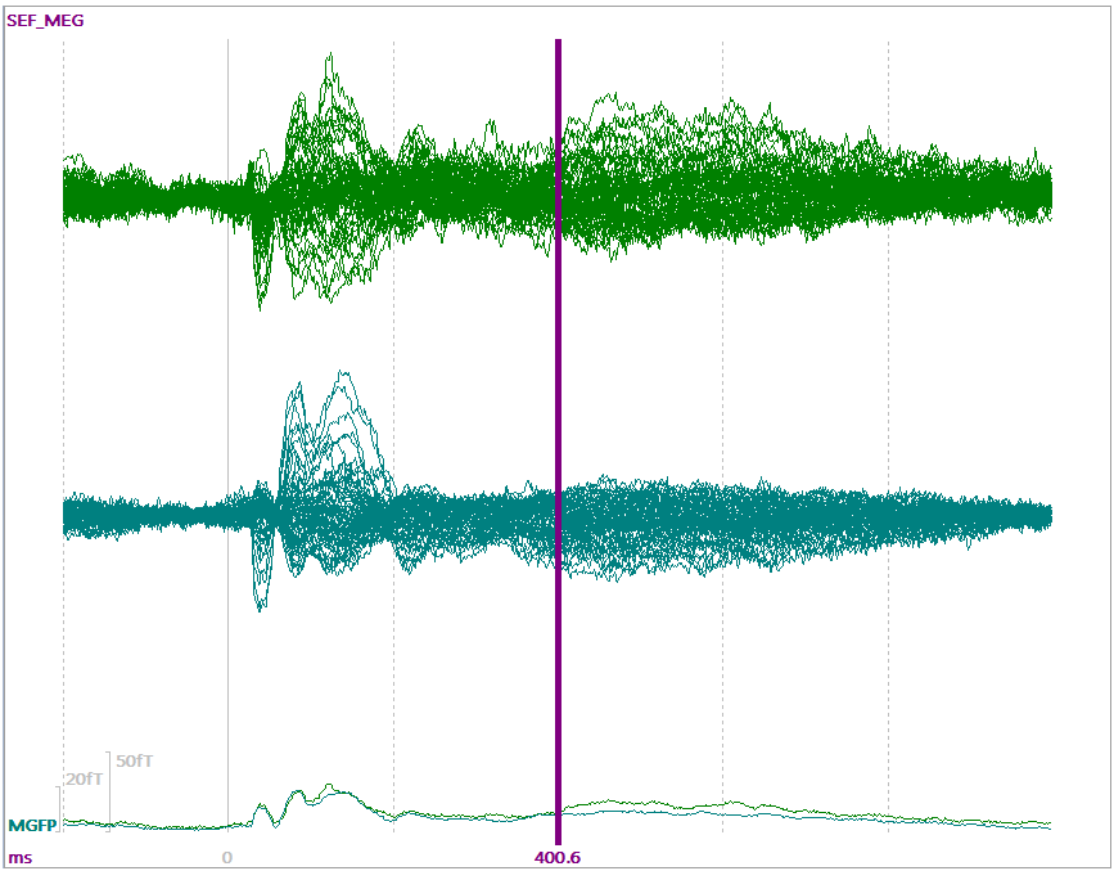
In this Tutorial, two image datasets (MRI and the results of an fMRI analysis) and an MEG dataset are used to perform fMRI-constrained source reconstruction. The 3D fMRI statistical map is stored in a second image data file that has previously been coregistered with the structural MRI.

1. Locate the fMRI Study in the *CURRY 8 Tutorials* Database and open it.

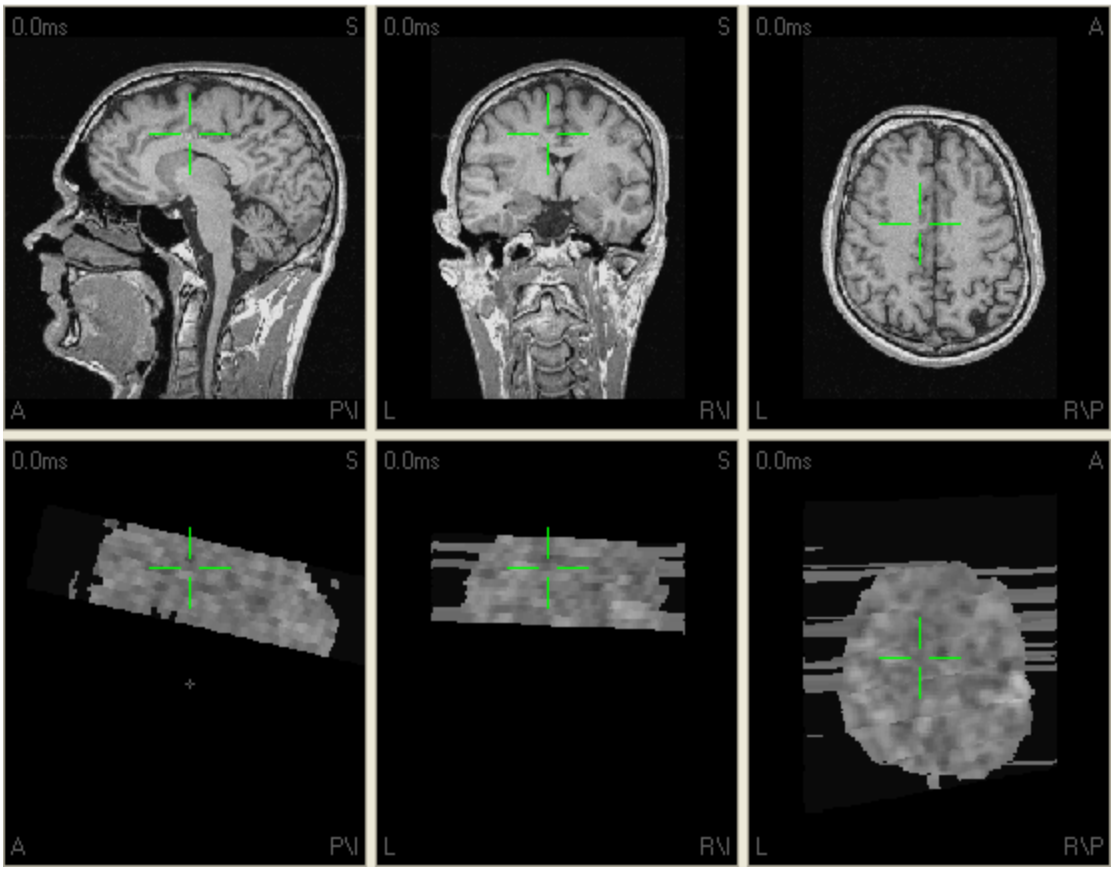


Note
The 3D statistical maps that are a result of fMRI analysis software are typically already coregistered and image data landmarks from the structural MRI can be used.

2. The MEG data are shown in the Functional Data display. Select the **Butterfly Plot** and see that there are 2 MEG devices.

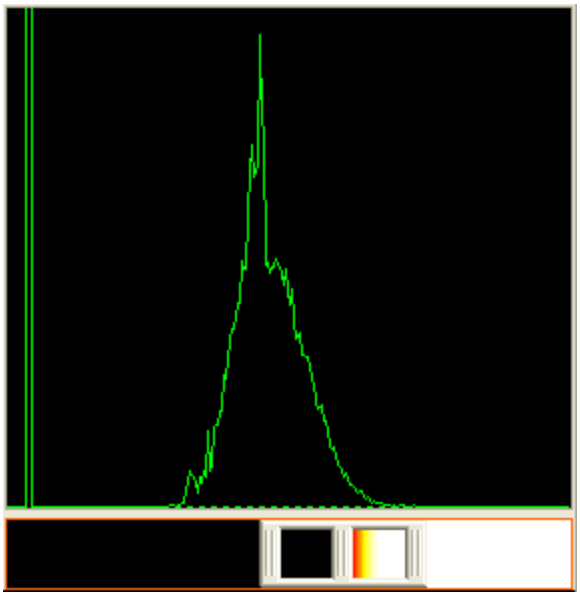


3. Click ID 1, 2 to see both image data sets.

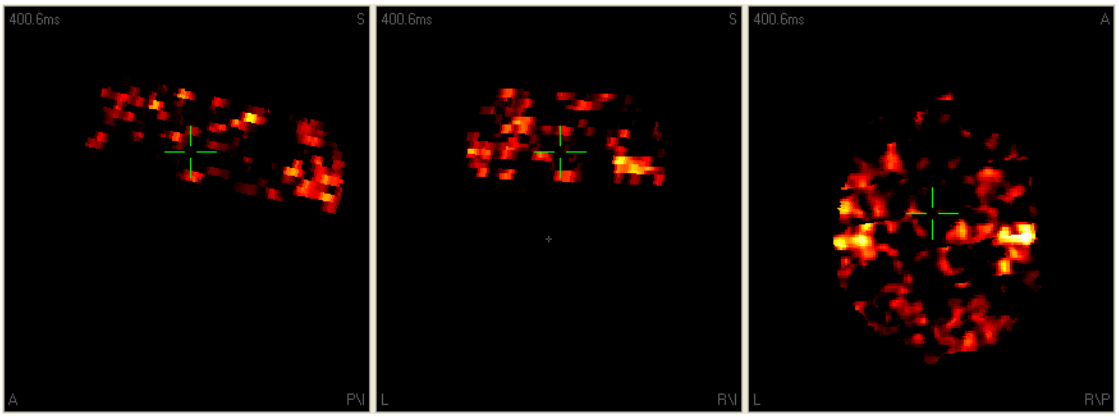


4. To change the color scale of the fMRI data, click in Image Data 2 to select this data set. In the Colors panel, change the **Slices** color scale to, for example, *Black..Red..Yellow..White* Slices: .

In the fourth image display view, select **Histogram** and adjust the colorscale as desired using the mouse and the sliding tab below the Histogram. For example, drag the left edge of the slider to about the middle of the intensity peak, and drag the right edge to about where the peak ends.



Then adjust the middle slider to give a few similar to that shown below.

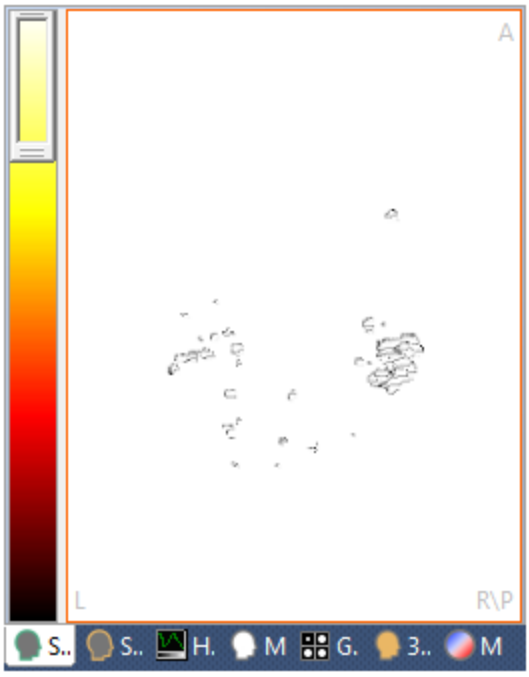


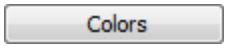
Press the icon or **File** → **Parameters** → **Save Study Parameters** to save these color settings (optional).

Note
Saving the color scale settings to the Study parameters will apply them whenever you open this Study.

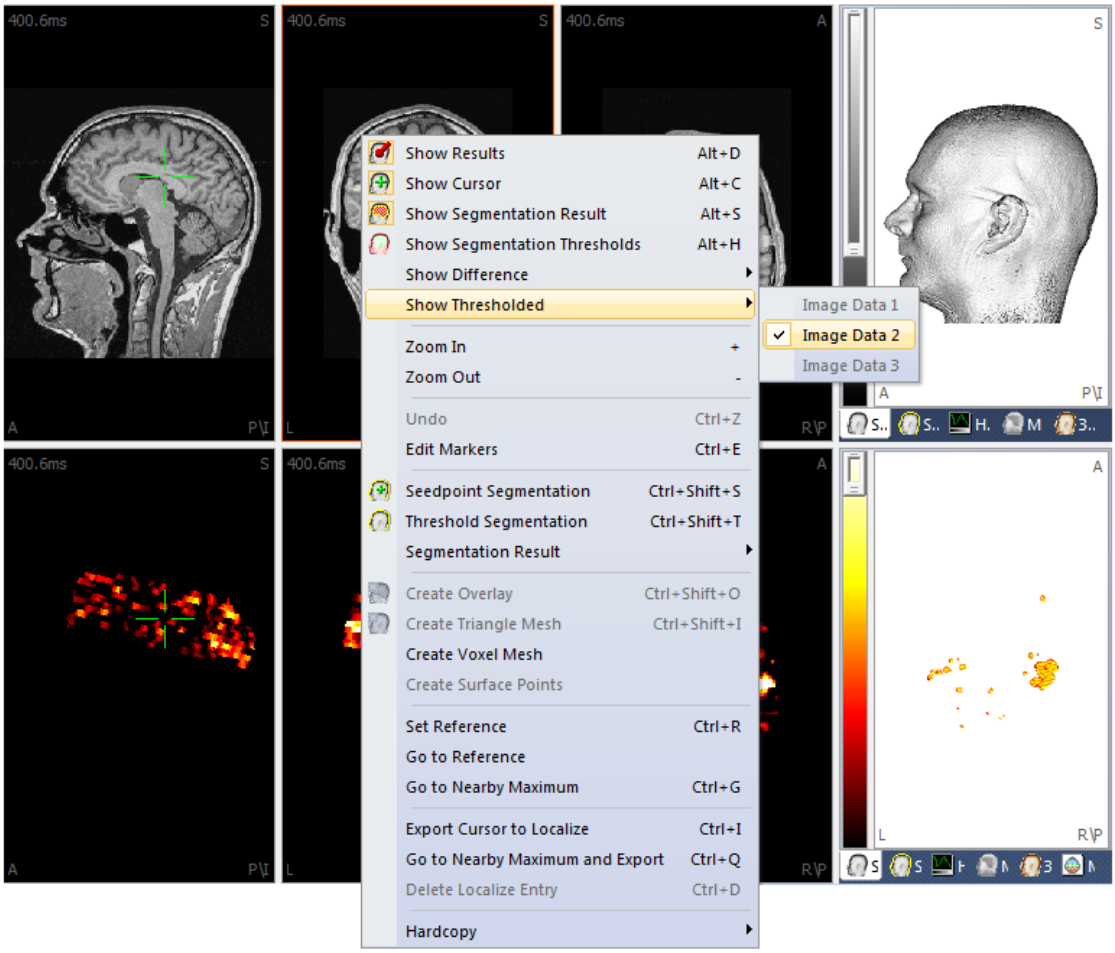
Overlay of MRI and fMRI (optional)

5. In the fourth display view, select **Segmentation Preview** and from the context menu, select **Top View**. Adjust the segmentation threshold using the *mouse wheel*, or by dragging the slider on the left up and down. We want just the hot spots to remain.



6. In the  panel, change the **Surfaces** color scale to *Black..Red..Yellow* .

7. If you want to see the fMRI hotspots in the MRI data, then in Image Data 1, click the *right mouse* button and select **Show Thresholded → Image Data 2** in order to overlay the two image data sets.



Note
Overlay of image data sets is based on the segmentation threshold for the data set that is added to the display.

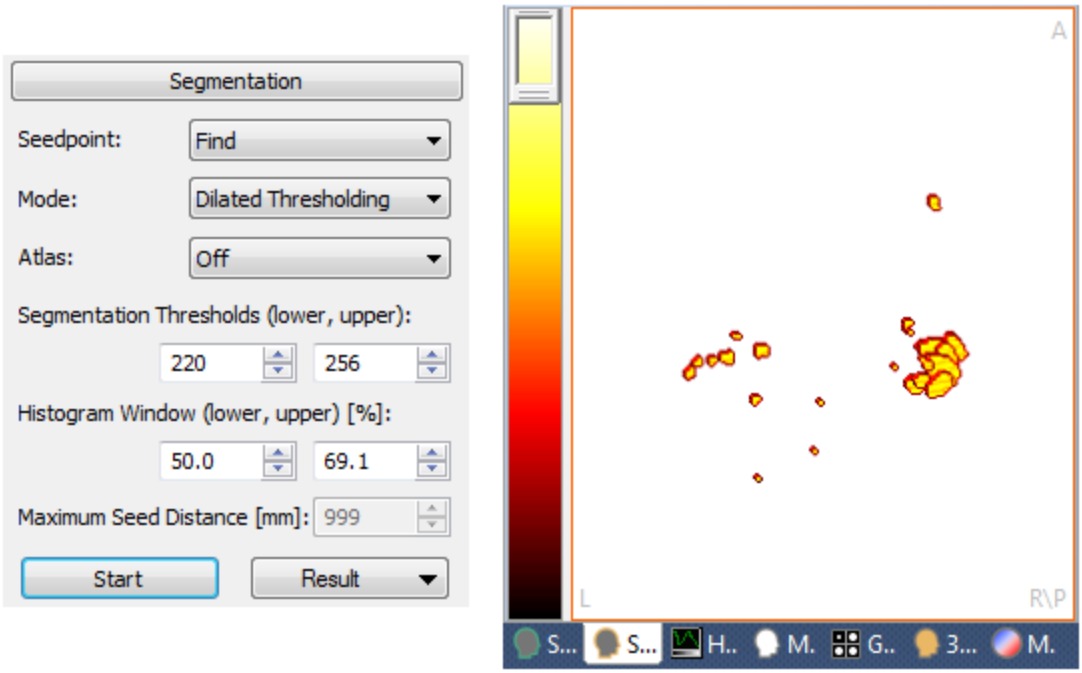
Segmentation, Overlay of MRI and fMRI in 3D View

8. Click in Image Data 1 to select this data set.

9. In the **BEM/FEM Geometry** panel, set **Create** to **BEM Head Model**, and set **Resolution** to **High**. Click **Start**. This will take a few moments to create the BEM Model.

10. Click in Image Data 2 to select this data set.

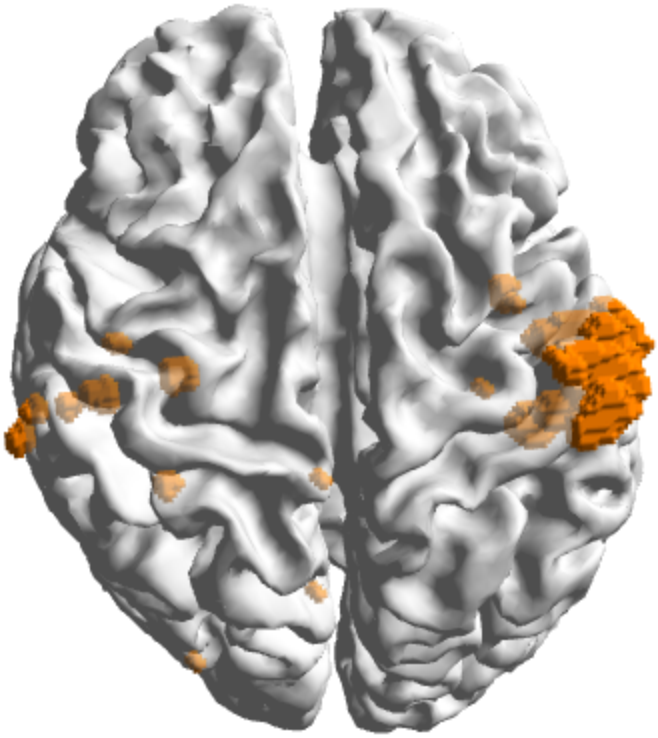
11. In the **Segmentation** panel, set **Mode** to **Dilated Thresholding**, and the **Lower Threshold** to a suitable level (approximately **220** in this case). Press **Start**. Select the **Segmentation Results** display to see the segmented areas.



12. *Right click* in the **Segmentation Result** and select **Create Voxel Mesh**.

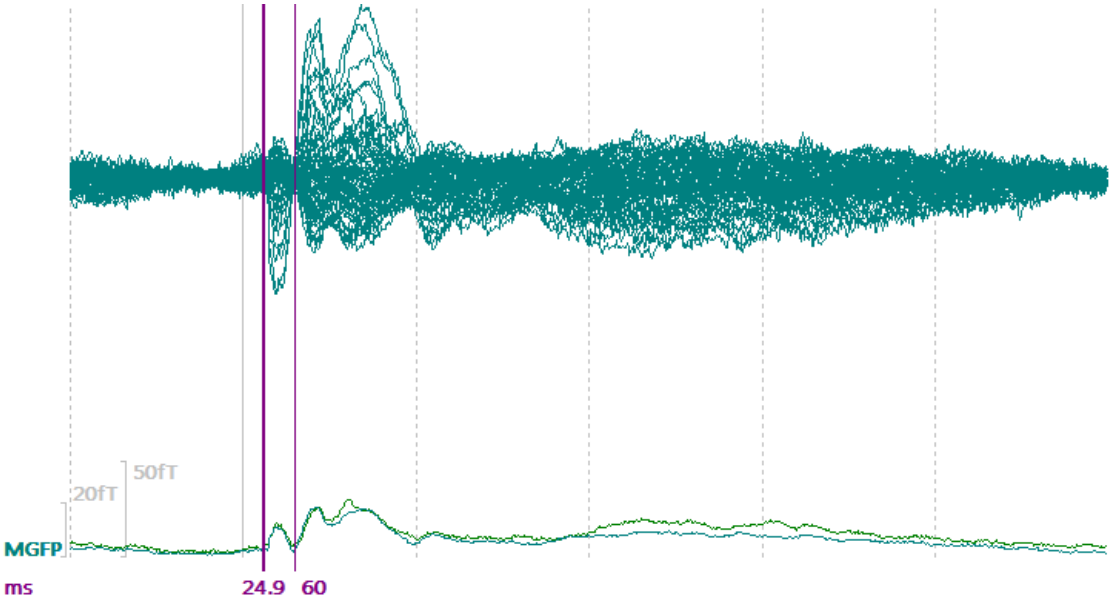
13. Switch to the **3D View**. In the context menu, select **Top View** (if needed).

14. Select the Cortex, and increase its Transparency to **50%**, if desired. The fMRI hotspots are then seen with the MR data (**Coils** were deselected). A higher value for the **Lower Threshold** would remove more of the weaker hotspots.



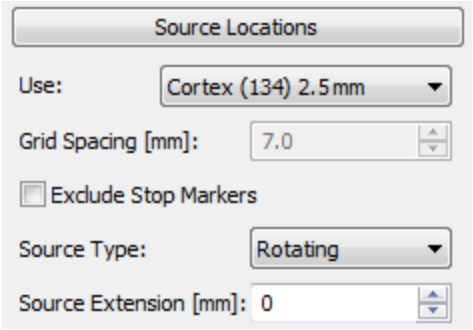
For fMRI-constrained CDR

15. First select a Timerange of interest for the CDR analysis, such as 25-60 ms.



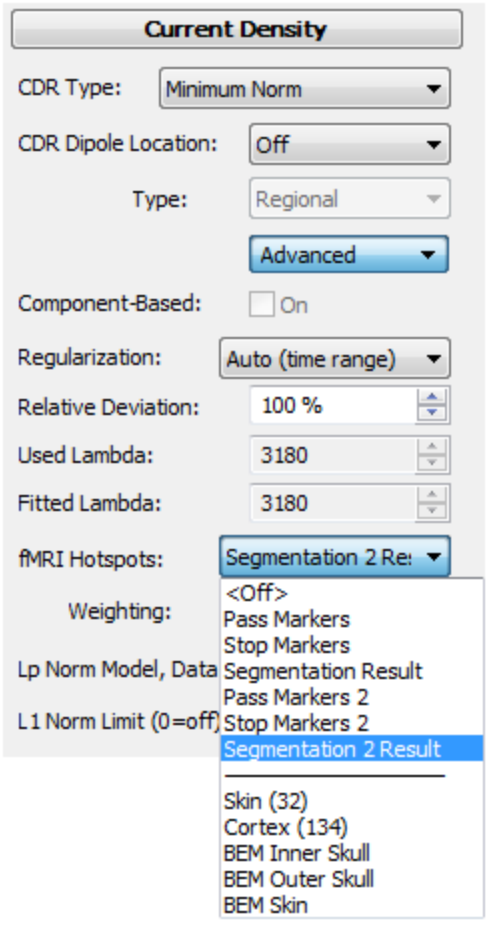
16. Switch back to the ID 1, 2 display. In the Morphology panel (**Image Data 2**), select **Dilation** for the **Mode**, with **Dilation** of **5**mm. This is because we want to have source locations (which are, on the cortex, around 3mm apart) to lie within the segmented hotspots. Click **Start**.

17. In the Source Locations panel, select the **Cortex** for **Use** (constrains results to the segmented cortex surface).

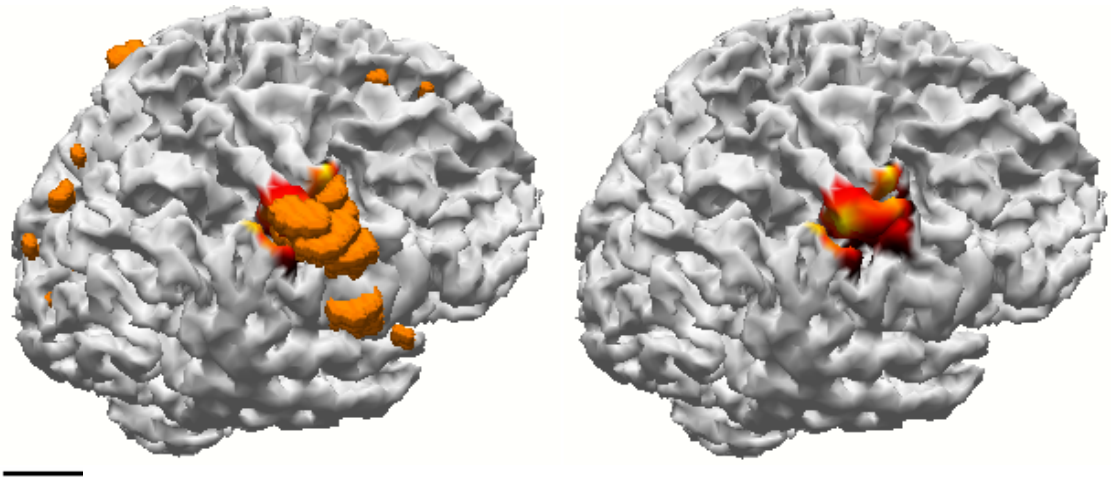


In the Current Density panel, select **Minimum Norm** for the **CDR Type** (MNLS is suggested because with sLORETA, fMRI weighting has very little effect). The results are seen in the **3D View**.

18. To do the fMRI CDR, set **fMRI Hotspots** to **Segmentation 2 Result** (the dilated hotspots), with **Weighting** at **140%** (default).



Turn **Voxel Mesh X** (in the **Objects** list) on and off to see the CDR results (**Right View** selected, **Transparency** increased). Change the 140% to a higher value in order to perform a more stringent hotspot constraint, and between 100 and 140% to impose a weaker constraint. Values below 100% are also possible, and these can be used to keep sources away from those regions.



2.6.9 MEG and EEG Source Reconstruction

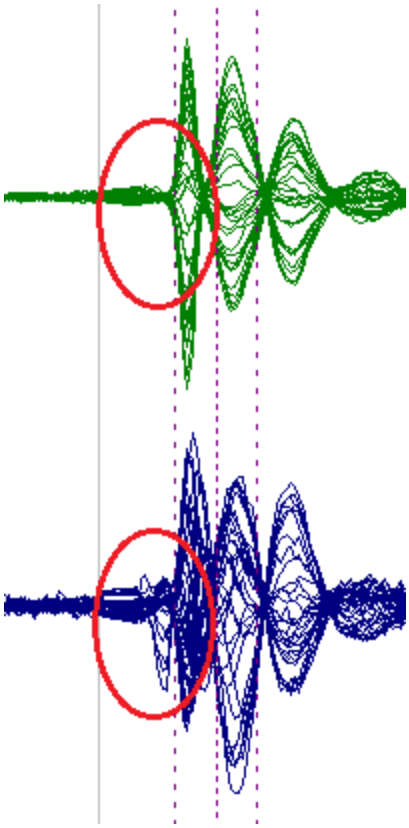
This tour demonstrates how to use combined EEG and MEG data for source reconstruction. It is completed independent from the other tutorials. It does not rely on previous steps, nor does it create any results worth saving. It does assume familiarity with the operations covered in prior tutorials.

The MEG file used below is an older recording with only 31 magnetometer channels. Newer MEG system can easily have several hundred magnetometer channels, as well as Groups of gradiometer channels. The placement and configuration of gradiometers (planar or radial) varies across MEG manufacturers. The simple file below is good for illustrating the basics of MEG, EEG and source reconstruction. The following general facts and guidelines are relevant with all files.

- A realistic head model is needed for source reconstruction using EEG; whereas, a simple spherical or single shell model may be sufficient for MEG. When using both MEG and EEG, a realistic head model is needed. For MEG alone, start with a sphere, and a better model would be a single shell BEM with the inside of the skull (brain compartment).

- Due to volume conduction, a radial current does not produce a magnetic field in a spherical volume conductor. This means that radially oriented dipoles are not seen with MEG, while they are with EEG. Tangential components produce a magnetic field, and so tangential dipoles are seen with MEG (and EEG). The SNR (signal to noise ratio), however, is better with MEG since there are no radial noise sources, so the confidence ellipsoids will be smaller for superficial tangential sources. Again, the EEG will see both tangential and radial sources, while the SNR will be somewhat less.

An example is seen in the data files below, where an early peak is seen in the EEG (bottom waveforms) that is not seen in the MEG (top waveforms). This means the peak is likely a radial source. Note also the decreased noise in the MEG recording, which will result in the better SNRs.



- MEG is not as sensitive for deeper sources compared to EEG because the deeper the sources are, the more radial they are. EEG is therefore more sensitive to deeper sources.

- The best source results are obtained by combining MEG and EEG, using a common volume conductor model that includes the skin and skull as well as brain compartments.

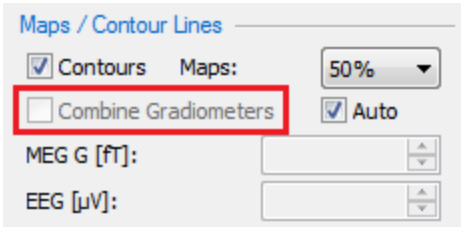
- Magnetometers measure the magnetic fields; gradiometers measure magnetic field differences (similar to bipolar EEG recordings). Homogeneous magnetic fields will tend to cancel out with gradiometers, leaving only nearby sources that produce a field gradient.

- There is no difference between MEG and EEG in terms of the source models that you use (Moving, sLORETA, etc.). Again, radial components will not be seen in the MEG, so there will be no sources for them.

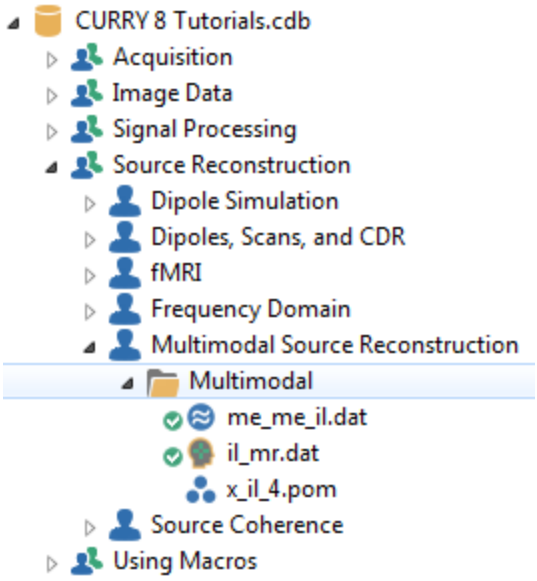
- The EEG signals strongly depend on the brain, skull and scalp conductivities, and these are normally not well known. MEG depends only very slightly on the conductivities, or not at all with a sphere modal. This finding lets CURRY "calibrate" the conductivities. If you are combining MEG and EEG, you may select

a time point where a tangential source dominates, and "fit" the conductivities, using the **Conductivity Factor Fit** button under **Head Model**. (The Factor should range normally between 0.5 and 2.0; larger values may give incorrect results). This will modify the conductivities for EEG only (the MEG is not affected by the conductivities).

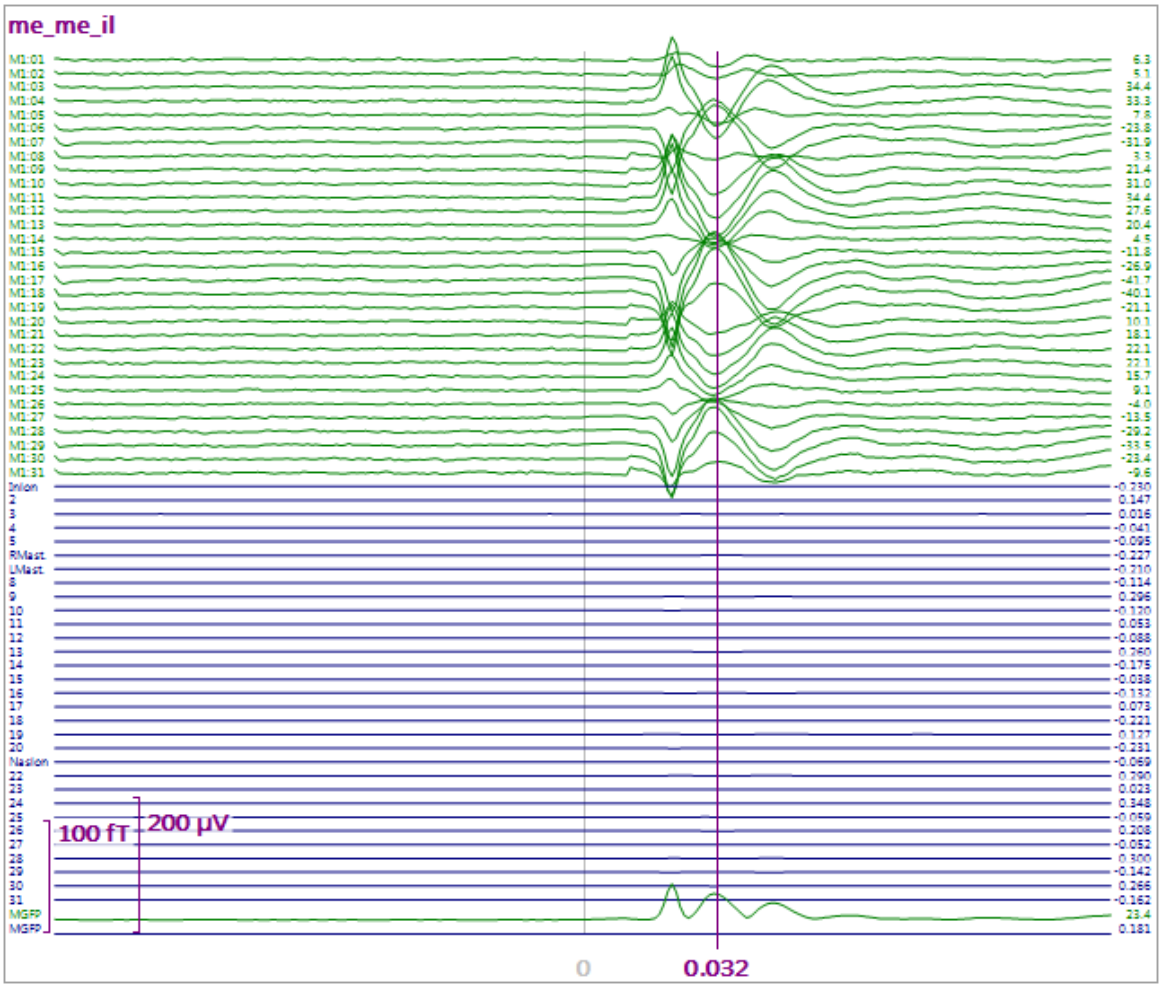
- Note also that gradiometers may be combined or not, using the **Combine Gradiometers** option in the **Parameters** panel under **Maps**.



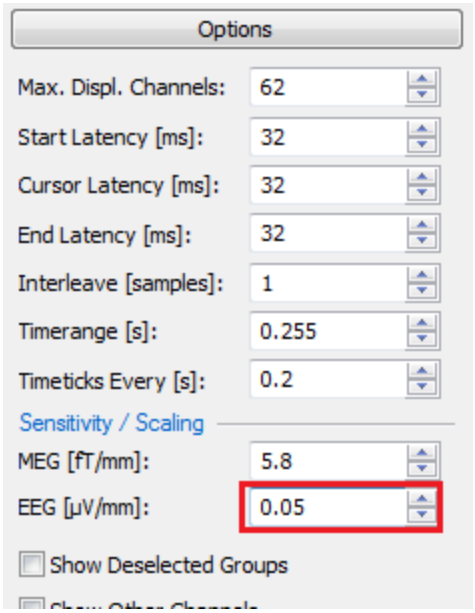
1. This demonstration uses the *Multimodal* tutorial in the *CURRY 8 Tutorials* Database. The functional data file has the magnetic and electrical recordings to left median nerve stimulation.



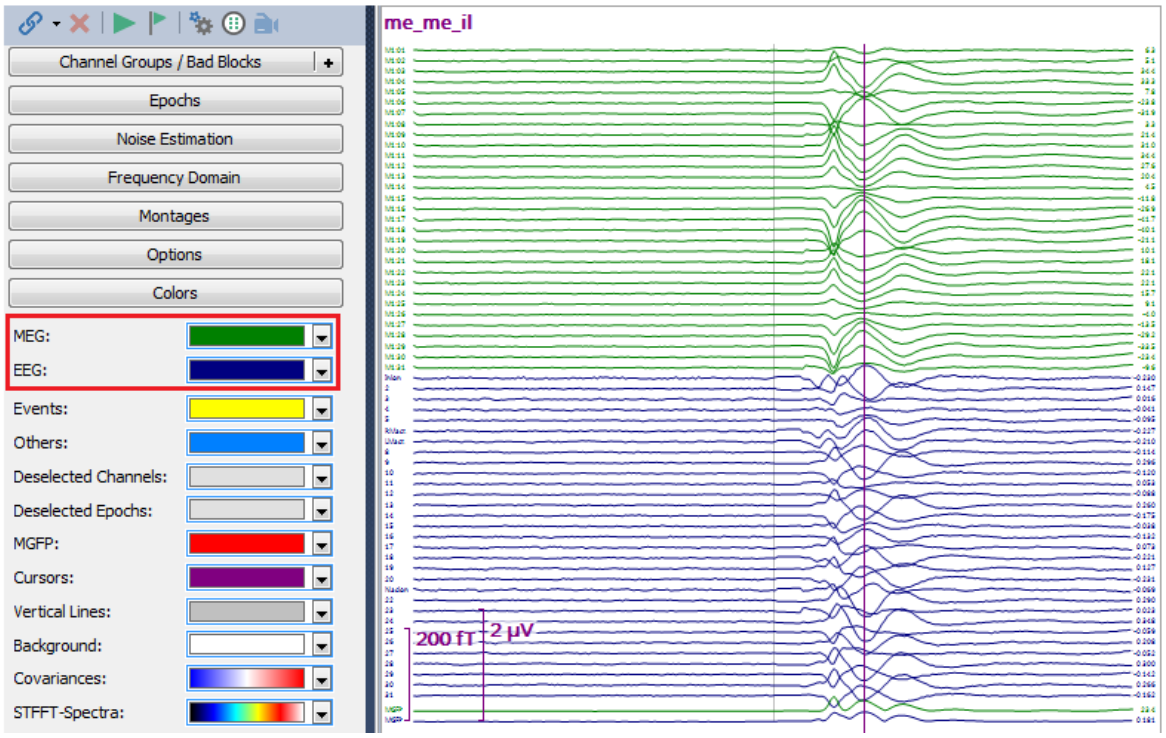
2. Open the Study and note that it contains both MEG data as well as EEG data. The file may open with essentially flat looking EEG channels.



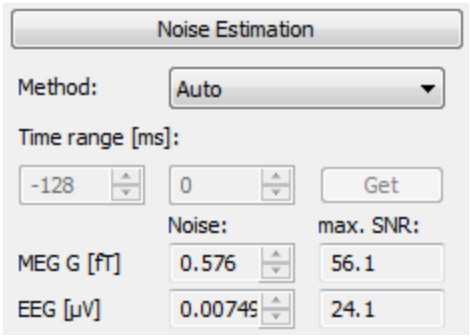
In that case, go to **Options**, and set the **EEG Scaling** to **0.05**.



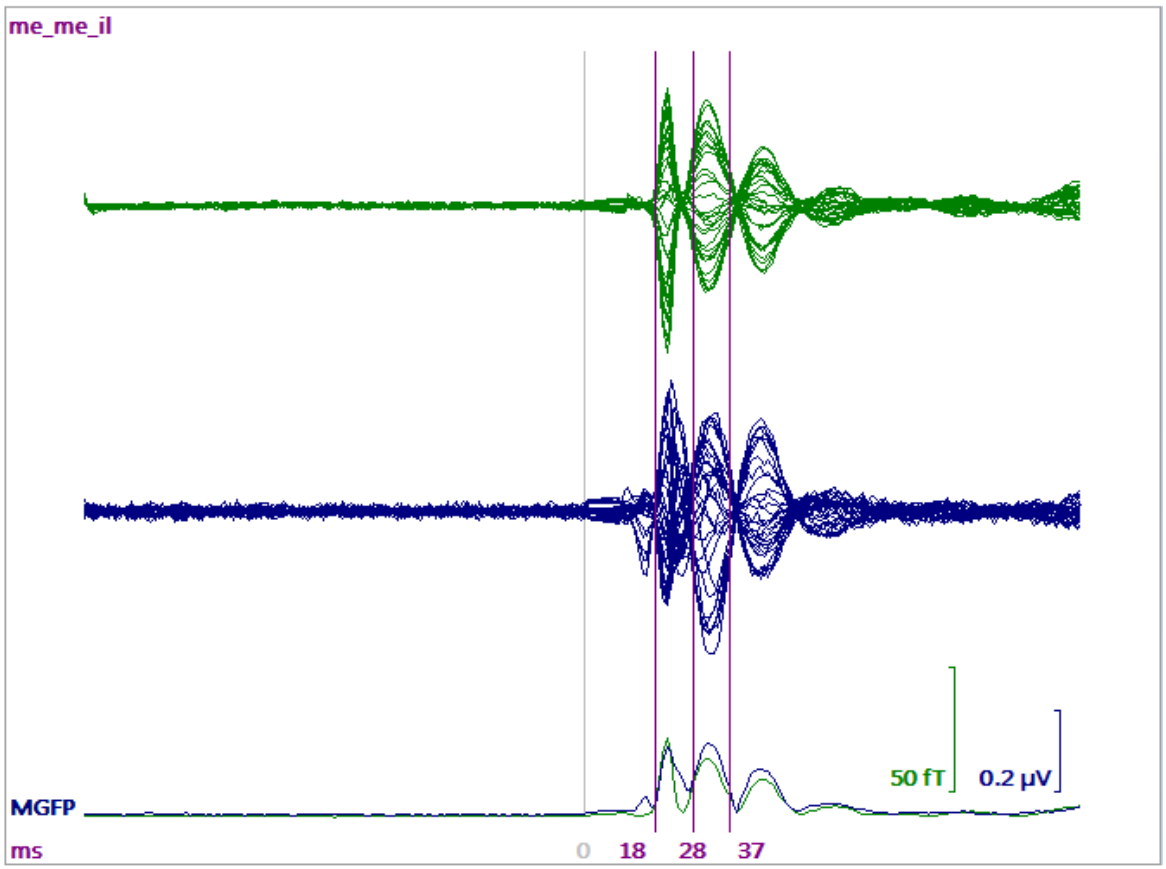
The channels are in different colors, as determined in the Colors panel under **Functional Data**.



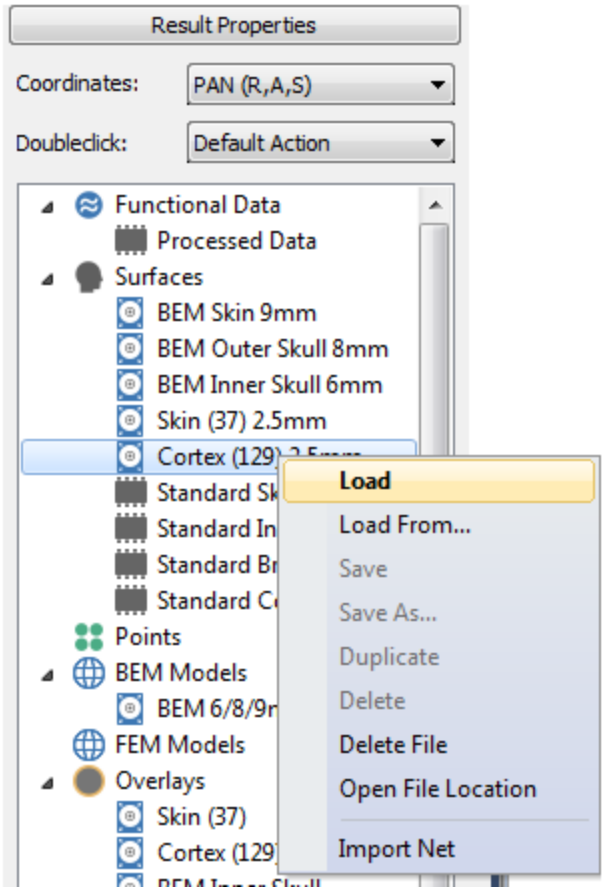
3. Expand Noise Estimation and note that **Auto** has been selected. The prestimulus interval is used for the averaged data. Notice that the Noise is computed separately for the MEG and EEG data. As stated at the beginning of this tutorial, the SNR is much greater for the MEG data.



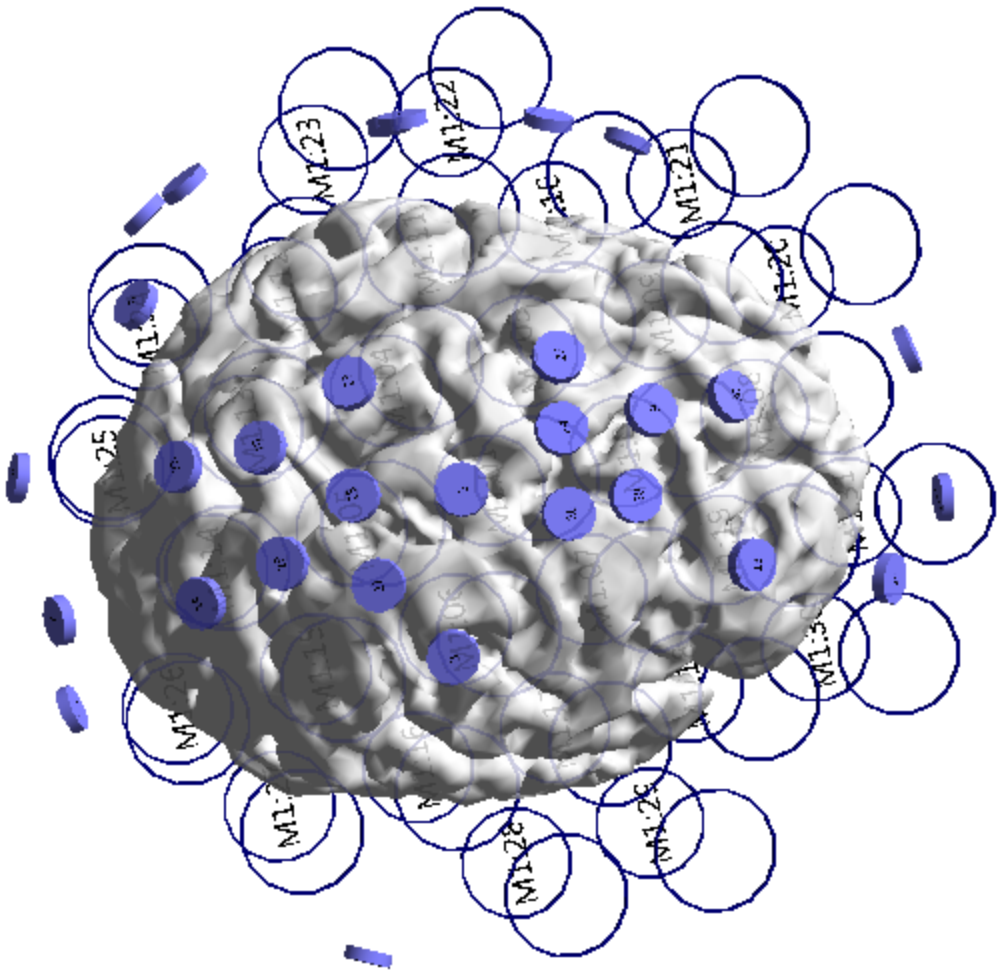
4. Select the interval from **18-37**ms (**Butterfly Plot** shown).



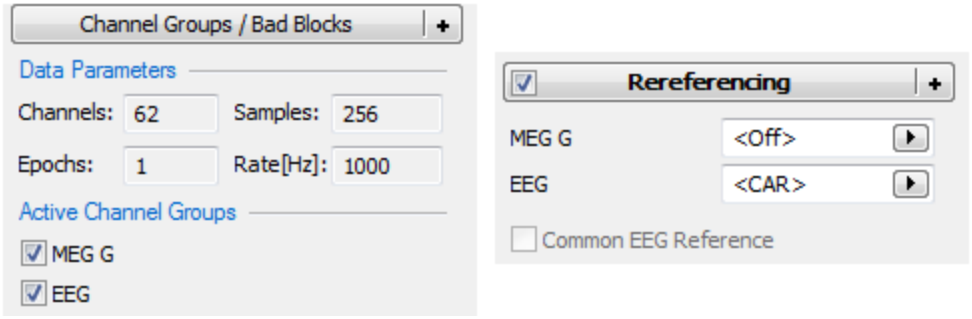
5. Go to the Results parameters, in the Results panel, and *right click* on the **Cortex (129) 2.5mm** Surface (this is from a previously computed BEM Model). Select **Load** to make available the previously created cortex surface.



Then go to the 3D View. You will see the MEG coils, the electrodes, and the segmented cortex (enabled and **Right View** selected and rotated). The Coils **Transparency** was set to **80%**. In the **Coils** properties, enable Show Labels.



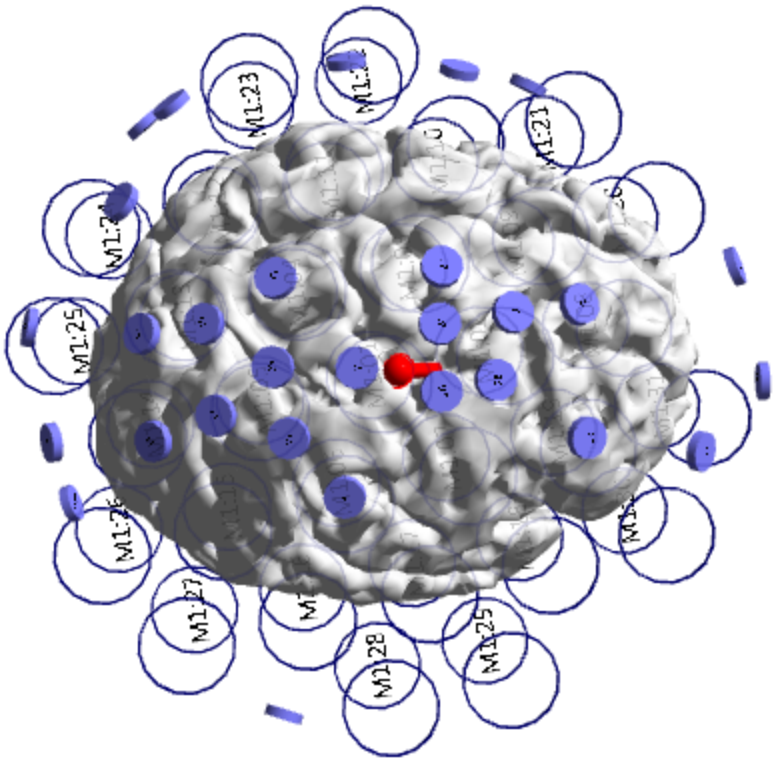
6. For source reconstruction, we can compute a solution using just the MEG data, just the EEG data, or both. Select the data that you want to use in the **Active Channel Groups** section in the Channel Groups / Bad Blocks panel under the Functional Data parameters. Select either MEG, EEG, or both. In the Rereferencing panel, set the EEG reference to **CAR**.



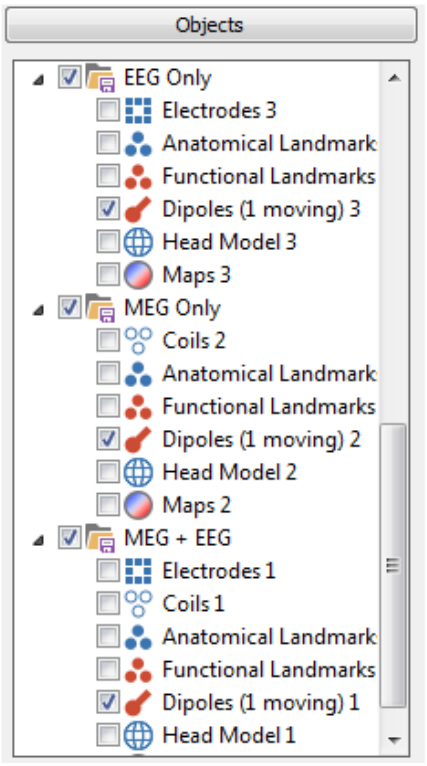
Then select the head model and type of source reconstruction that you wish to compute (from Source Reconstruction). In the figure below, **MEG** and **EEG** were selected, with the **BEM 6/8/9** head model, and a single **Moving** dipole (in red). The

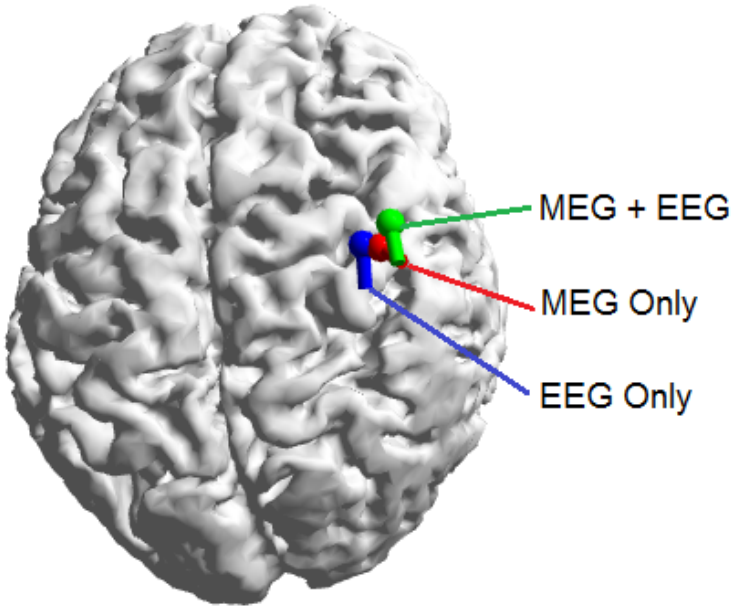
results are seen, with either the electrodes, coils, or both types of sensors in the **3D View**, along with the dipole results (you can select/deselect the devices and the dipoles will be recomputed automatically; use **Keep Results** to save the results).

Deselect the **Time Range Mode** , and play a **Movie** for each to see the results across the Timerange.



7. In the example below, a single time point **Moving** solution was computed with the BEM head model. (Increase the Cortex **Transparency** to see the solutions). There are very small differences in the solutions (21ms point shown; colors changed).



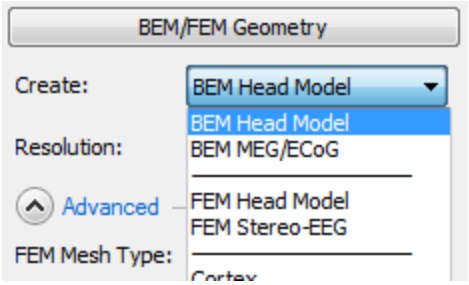


2.7 Stereo-EEG Tutorials

The following tutorials are designed primarily for stereo-EEG recordings. You will see how to create a FEM model using Isotropic and Anisotropic properties, perform source localization with depth electrodes, perform source localization with focally increased resolution of the FEM model, and how to use Oblique perspectives to better see the tracks of the depth electrodes.

2.7.1 FEM Models with Anisotropic Skulls

When you create a BEM or FEM Head Model, there are several choices.



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 Head 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 Head Model** has nodes throughout the inner compartment, and is used with Intracranial-EEG recordings (depth electrodes).

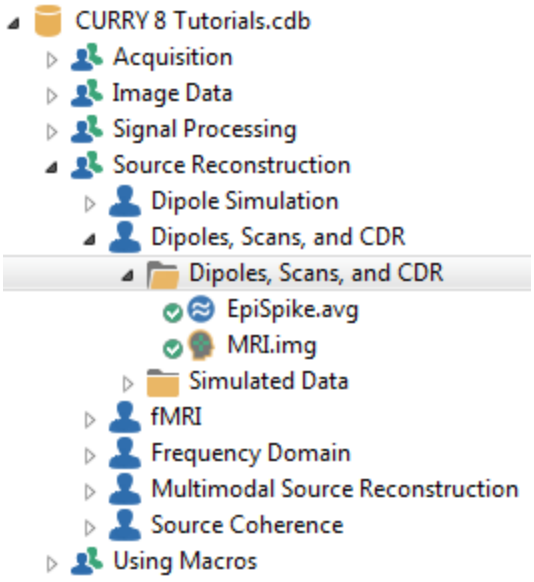
The **BEM MEG/ECoG** model creates the same head model and segmented skin and cortex as the BEM model. Additionally, it creates an inner skull compartment using a higher resolution, and a BEM Realistic Head Model containing the single compartment. This is used with ECoG recordings, where a single component 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.

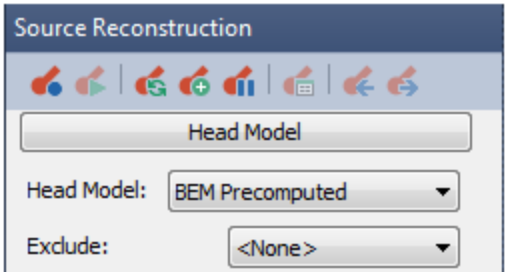
In the previous tutorials, we have replied primarily on BEM Models. In this example, we will use a FEM Model where we will take the skull anisotropy into account.

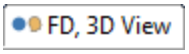
Open the indicated Study. It is assumed in the steps below that you already have a basic understanding of head model creation and source analysis.

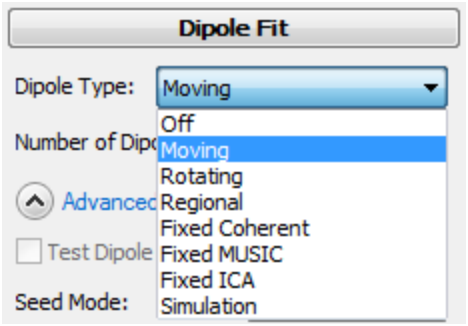


1. Select the **Butterfly Plot** and position the cursor at **20 ms**. If you see three vertical cursors, *double-click* in the Functional Data to enter **Tracking Mode**, where there is the single cursor.

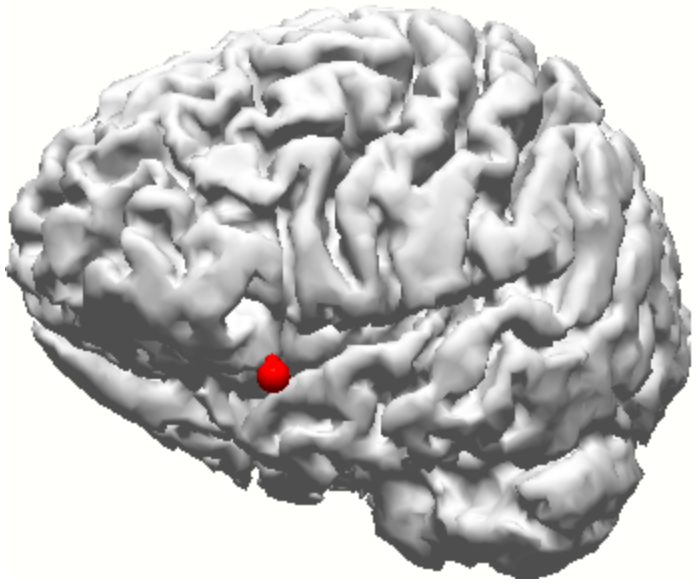
2. First, for comparison sake, select the **BEM Precomputed** Head Model.



3. Select a **Moving Dipole**, and select the  view.



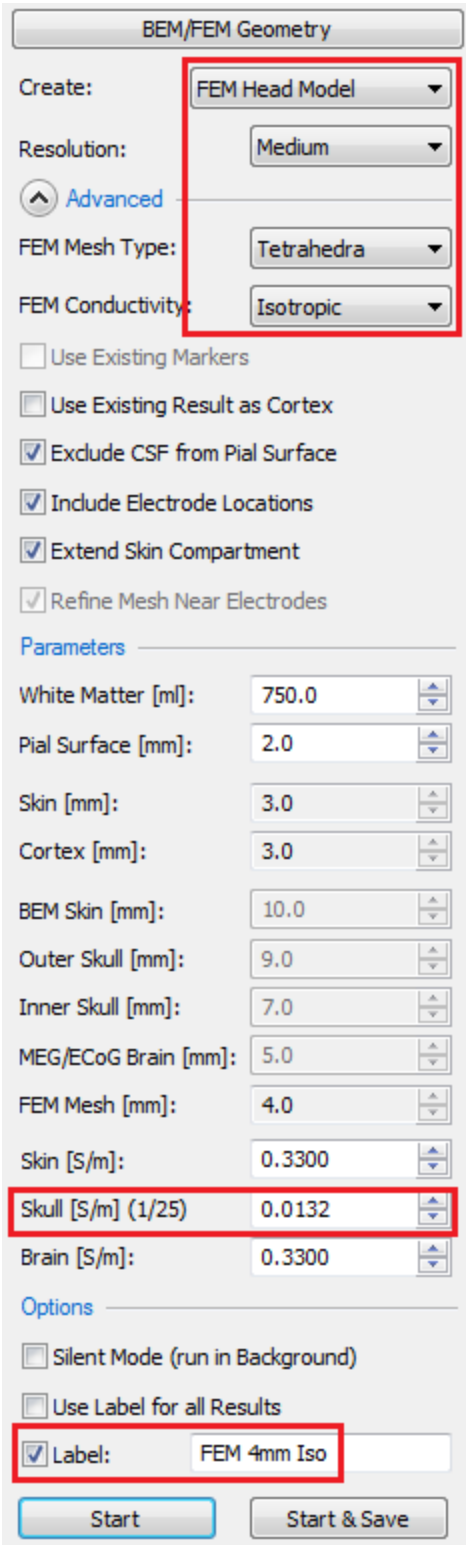
4. In the **3D View**, select the **Left View**, turn off the **Electrodes**, turn off the **Confidence Ellipsoids**, and enable the **Cortex (56)** surface. Set the cortical **Transparency** to **100%**. You should see the single dipole result. Click the **Keep Results** button .



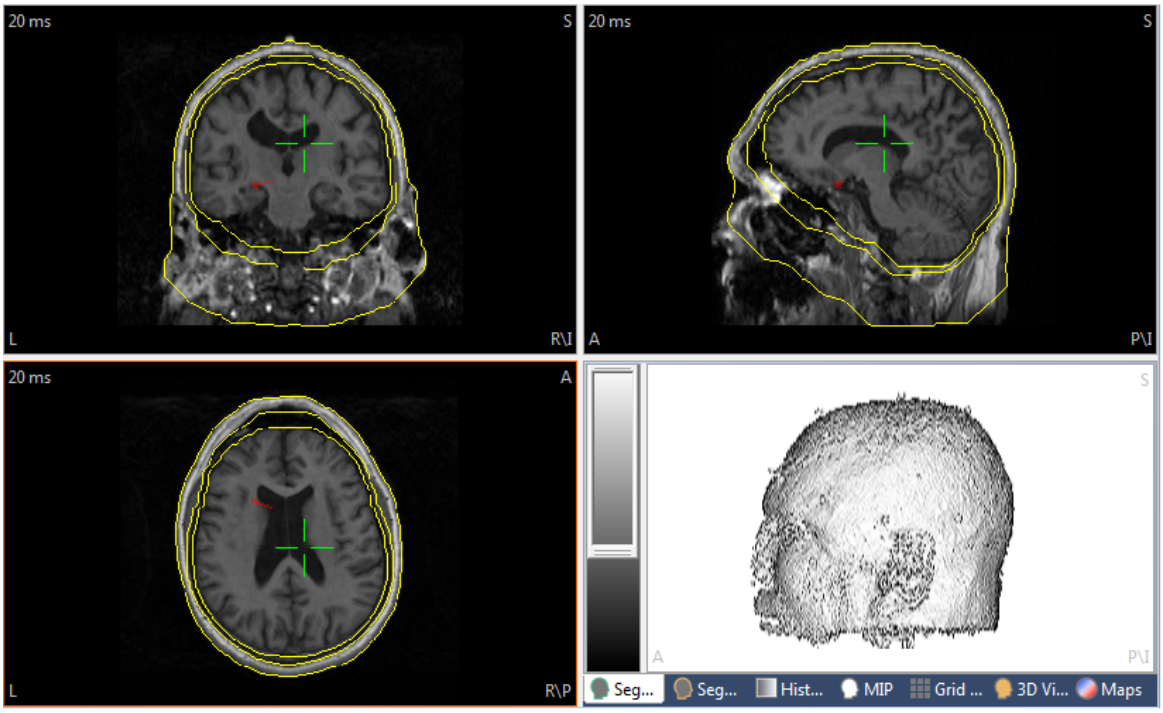
5. Now we have the results using the basic BEM Head Model. Select the

display. In the **BEM/FEM Geometry** panel, verify, select or enter the parameters as shown, and click **Start**. This will create an isotropic **FEM Head Model** that we will use for comparison. Reducing the **Resolution** will save time and memory.

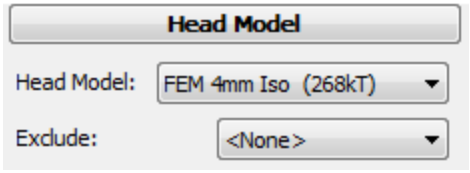
Incidentally, when you compute an Isotropic model, the **Tangential/Radial Conductivity Ratio** is always 1.0. We will return to this value when we use an Anisotropic Skull.



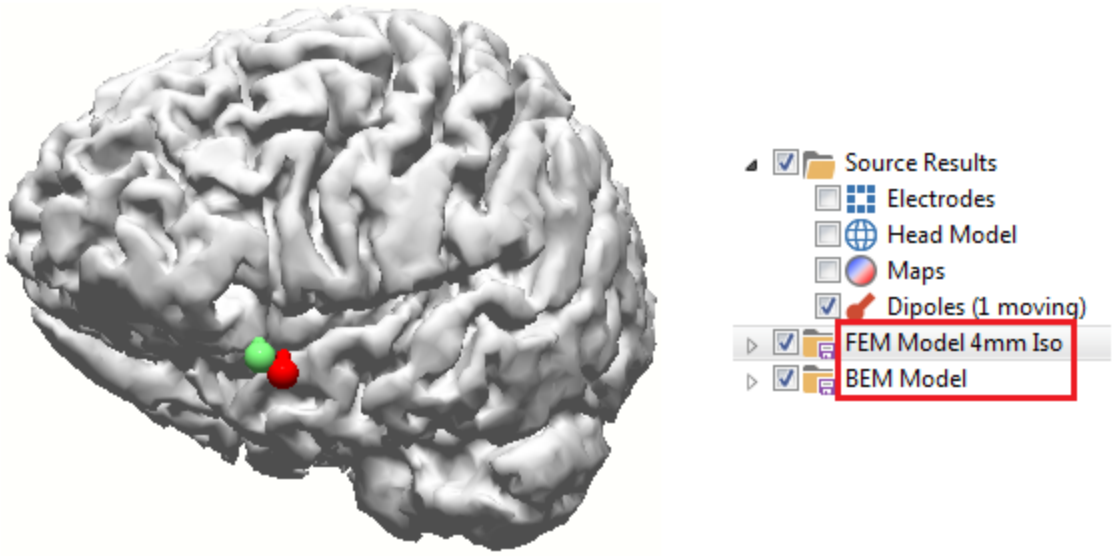
The FEM model is seen on completion.



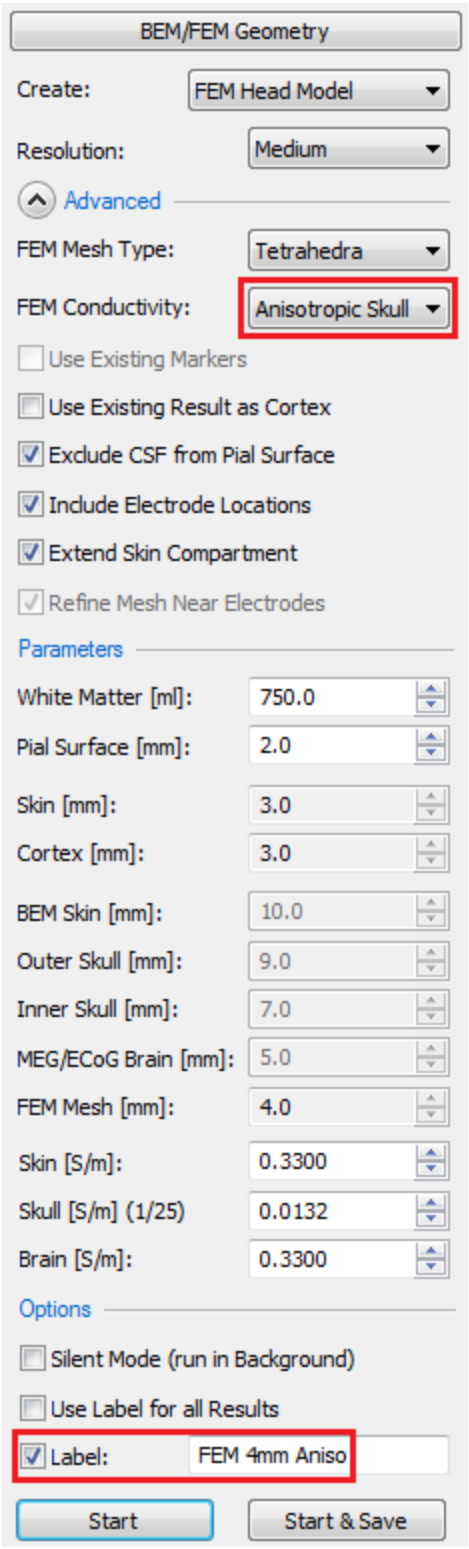
6. Now select that Head Model, and CURRY will recompute the moving dipole with that head model. Whenever you create a new Head Model, do not forget to select it as the Head Model.



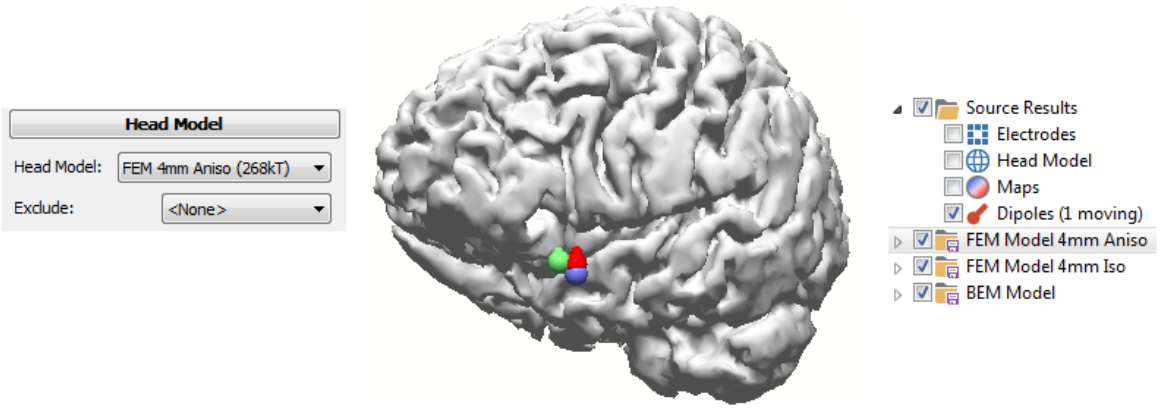
7. Go to 3D View to see those results. Click **Keep Results** again. In the **Object** list, rename the Kept Results so it will be easier to keep track of them (highlight and click *F2*).



8. Next, we will create a FEM Model using an anisotropic skull. Go back to **BEM/FEM Geometry** and enter the parameters as shown. Click **Start**.

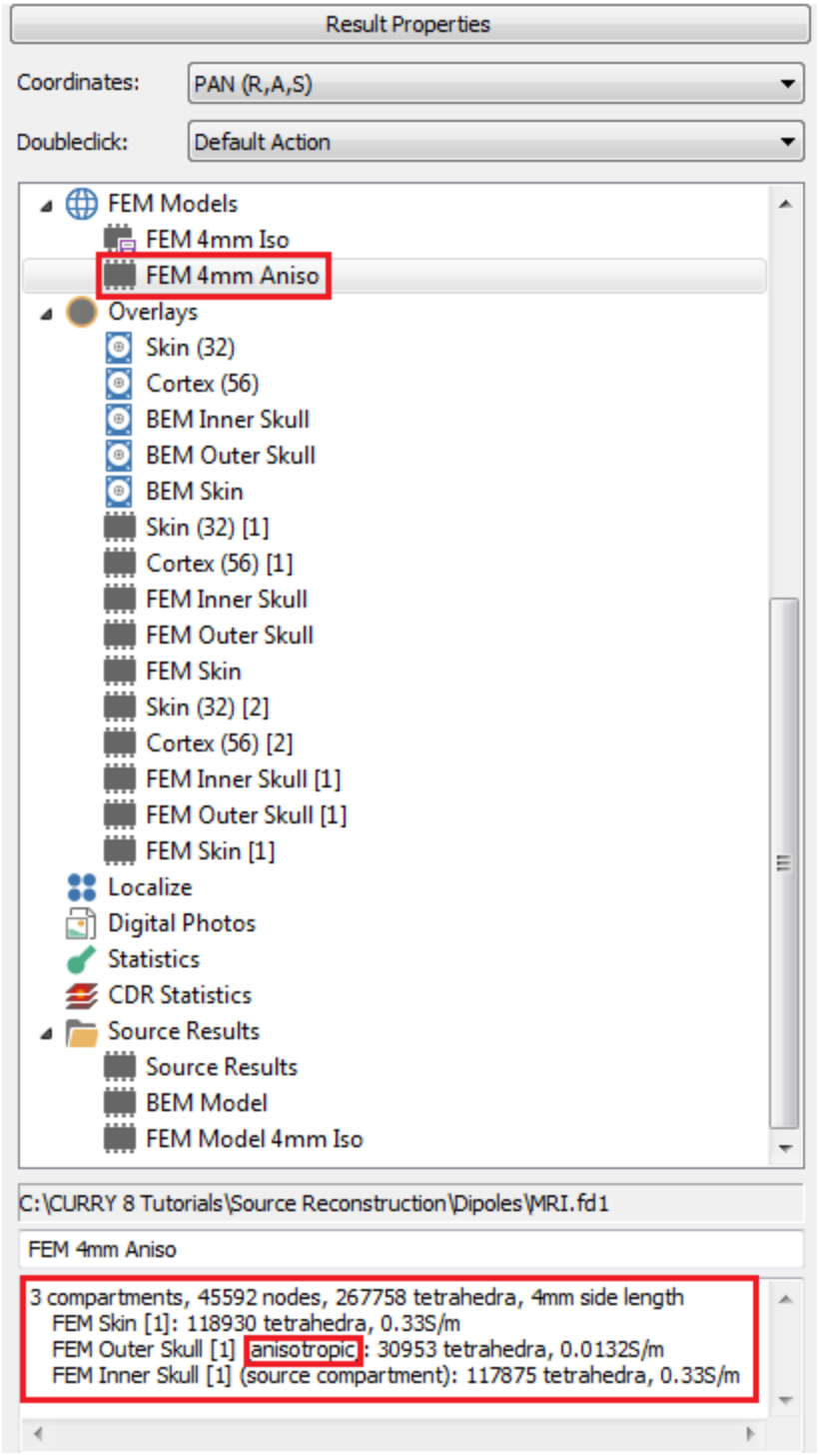


9. Select that Head Model, and CURRY will automatically recompute the results. Keep the results, renaming them as desired.



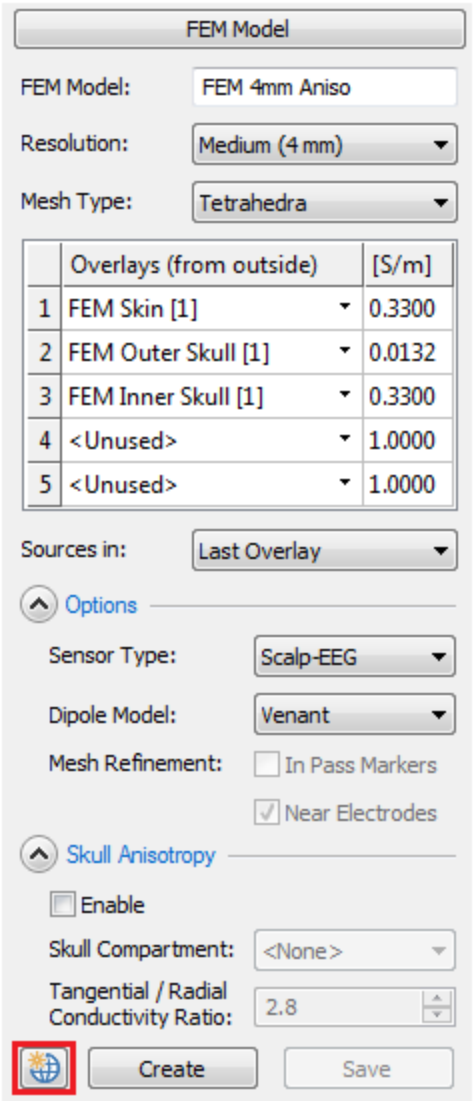
10. The results are all fairly close, as one would hope. We created a Medium Resolution FEM Model; the results may be a little closer if we used a higher resolution.

If you want to see the details of the FEM Model, highlight it in the Results list for FEM Models and see the details below, including the fact that outer skull conductance was anisotropic.

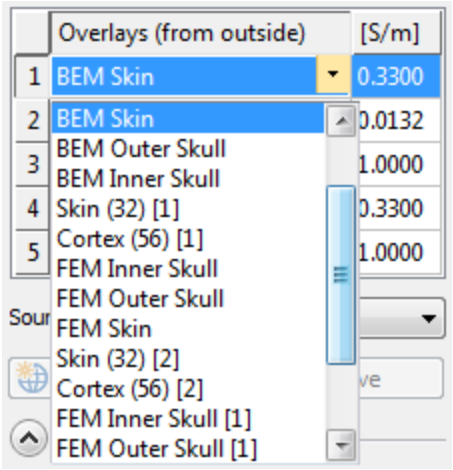


11. So far we have been using the automatically created BEM and FEM Models. In some cases you may have customized cortical or other segmentation that you want to use (due, for example, to some abnormality that is better captured with manual segmentation), and/or you may also wish to vary the skull compartment properties.

First we want to set up a new FEM Model. Click the button in the FEM Model panel.

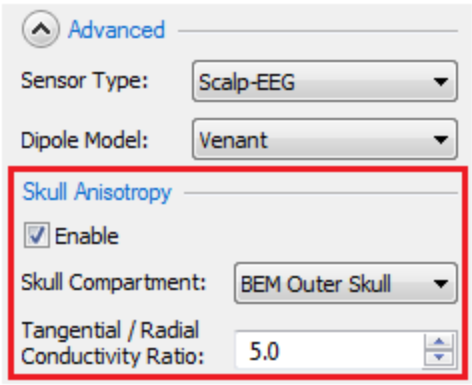


The surfaces are seen in the list. It is not important that these show BEM overlays - the segmentations from BEM and FEM are the same. Should you want to change one, the drop down list shows all of the available overlays. You can use up to 5 overlays (for example, if you have an overlay for the cortex or the CSF, you can add it here).

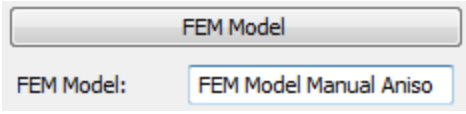


12. Enable the **Skull Anisotropy** section at the bottom. The **Sensor Type** of course should be **Scalp-EEG** in this case, as opposed to stereotaxic recordings. Use **Venant** for the **Dipole Type** as it is faster and also best when the sources are relatively more distant to the sensors. If you are not sure which to use, use the default options.

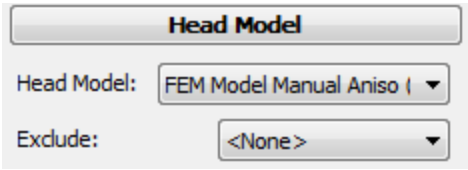
Select a Skull Compartment, which is typically the **BEM Outer Skull** although others may be selected. If you do not select a compartment, you will receive a Warning to select one. Here you can also vary the **Tangential/Radial Conductivity Ratio**, if desired (1.0 is an invalid value, as it implies isotropic conductivity). If we use 2.8, we will get the identical result as with the previous dipole solution, since the automated anisotropic FEM Model also uses the Ratio of 2.8. So in this case, set the **Ratio** to **5.0**.



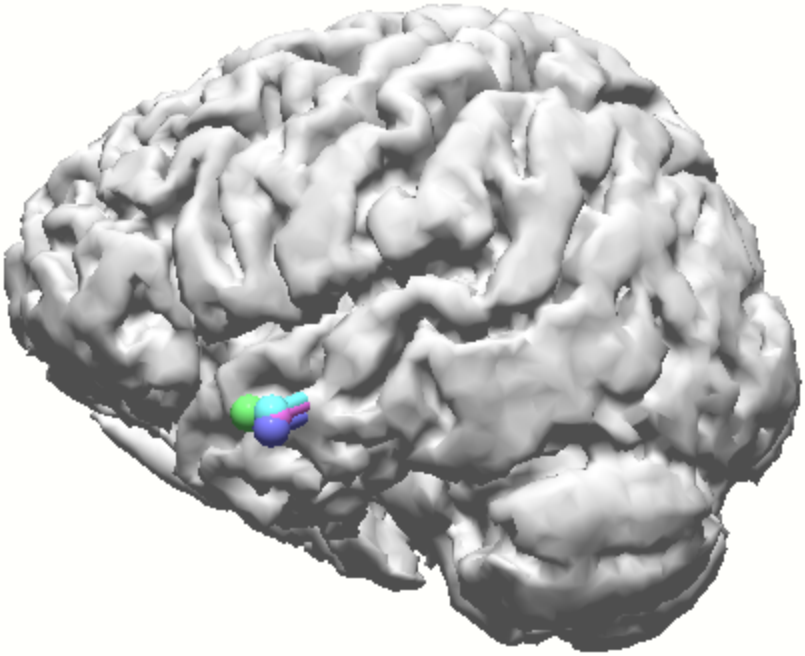
13. Then click the Create button (this will take a few moments). When it is finished, you may enter a file name and then click the Save button.



14. Go back to **Source Reconstruction** and select the **Head Model** you just created.



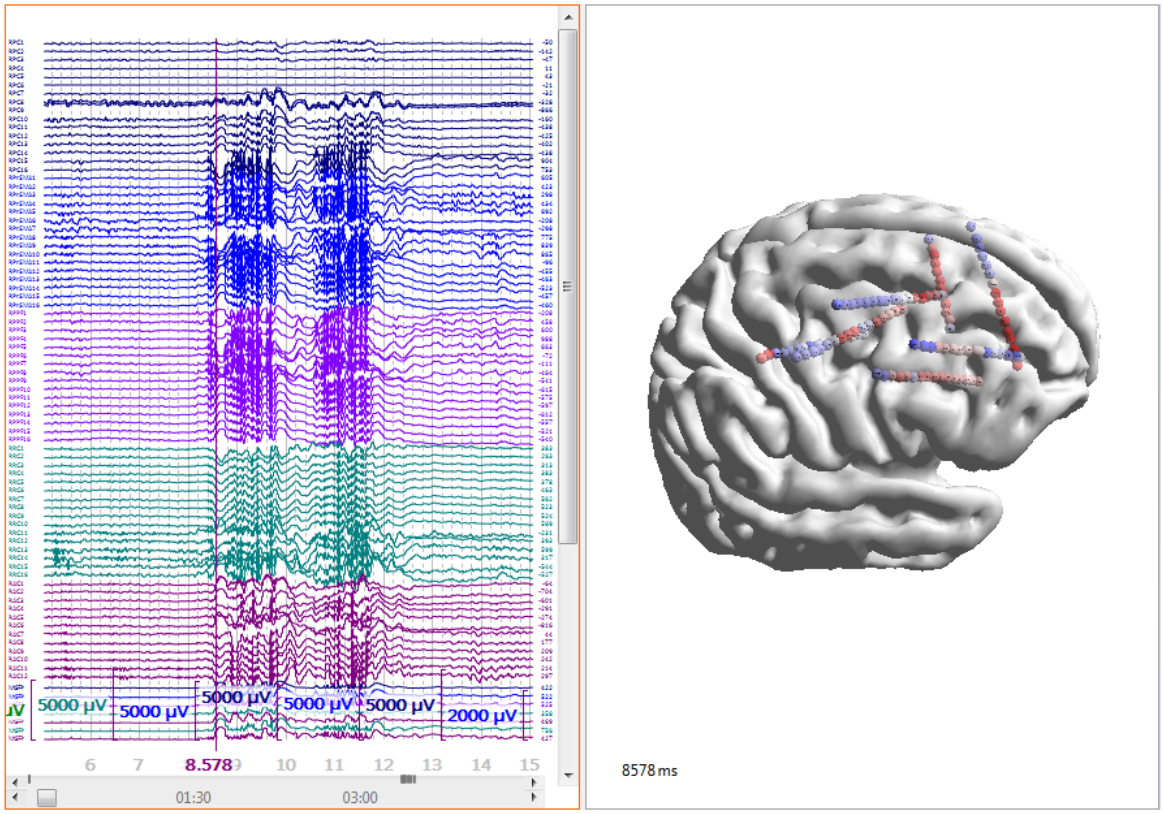
15. The source results will be computed automatically. Keep the results, as before. Now you can see all of the results together. There are only very slight differences in this case.



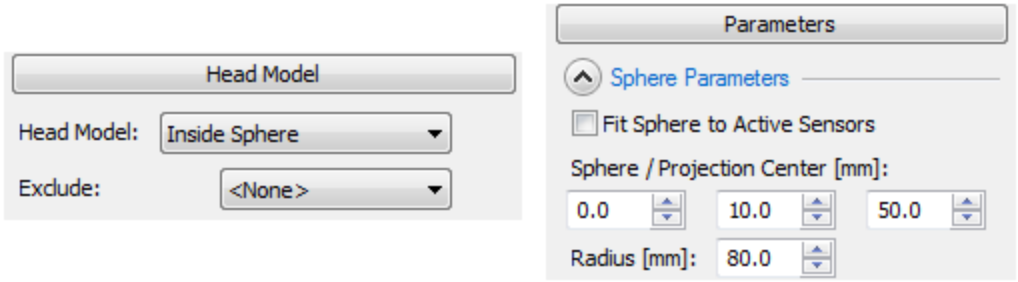
2.7.2 Stereo-EEG Source Localization

In this example we will demonstrate how to perform CDR analyses with stereotaxic recordings. The file we are using is not found in the Tutorial Database, so please just follow along with the steps. They will be similar to those used with your data files.

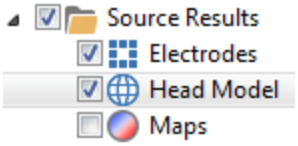
In this case we have data from 7 depth electrodes. Their positions have already been located from the CT, as described in the **MRI and CT Grid Merging** tutorial. We have selected a time point near the peak of a spike. Actually, in this particular file, the obtained results are not particularly meaningful, so we will focus on the steps, rather than the results.

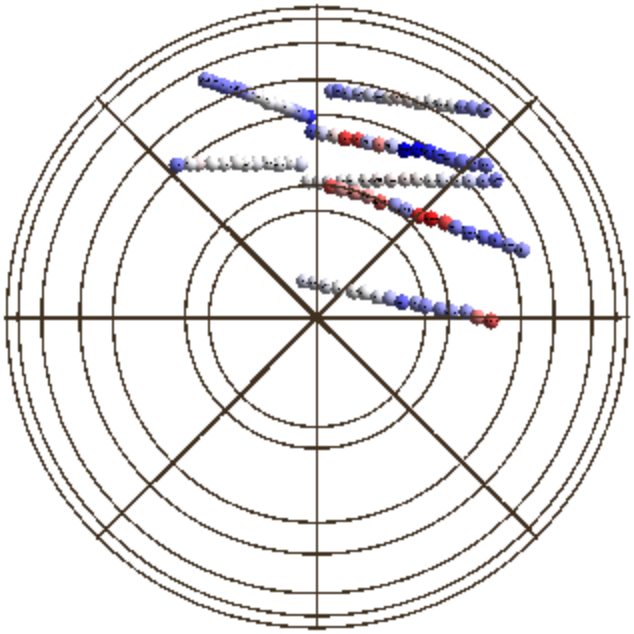


1. Typically you will use the **Inside Sphere** Head Model. The dimensions for that are seen in the **Parameters** panel for **Maps**.

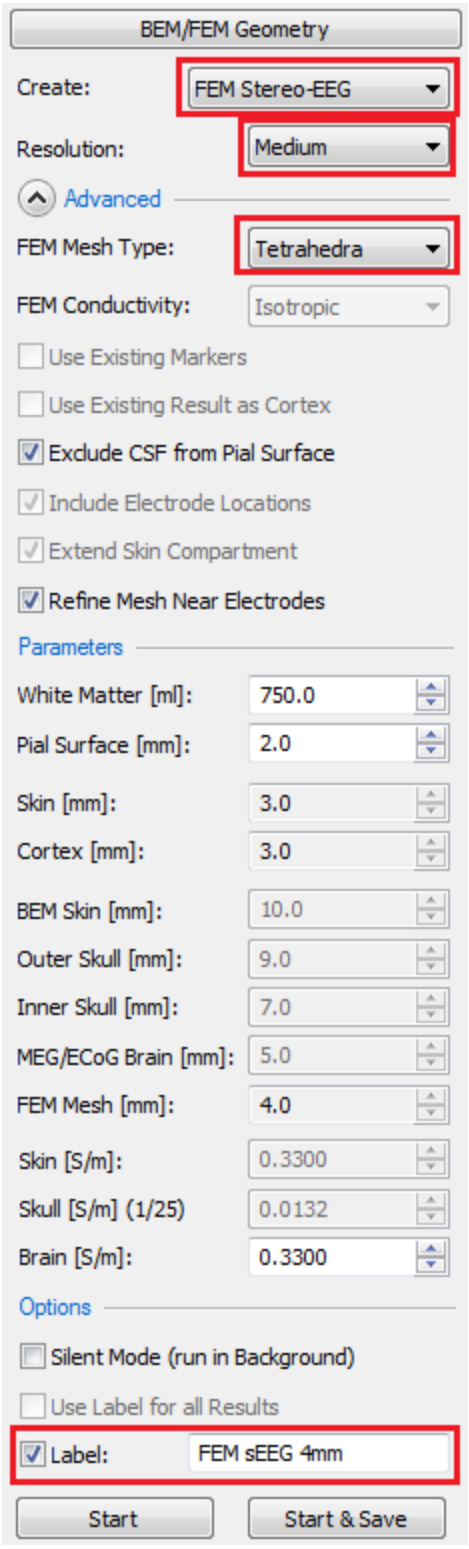


The **Inside Sphere Head Model** can be displayed in the **3D View**.

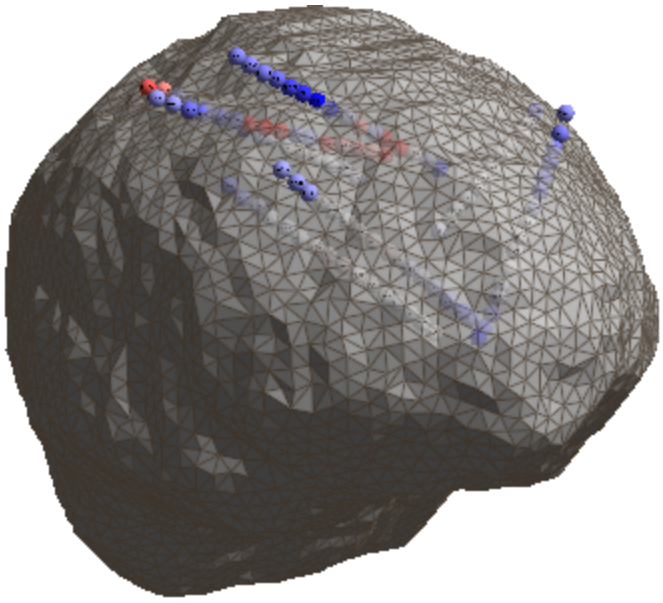




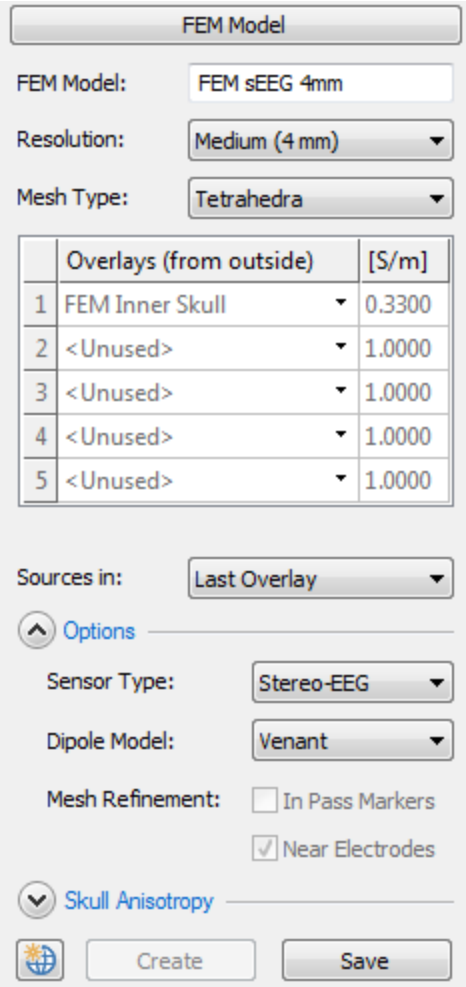
2. In this case we have the MRI data so we can create a realistic head model. We selected the FEM Intracranial-EEG model, with Medium resolution to make it go faster. We accept the default **Tetrahedra Mesh Type**, and the default **Label**. The Skin and Skull have been grayed out, as they are not included here.



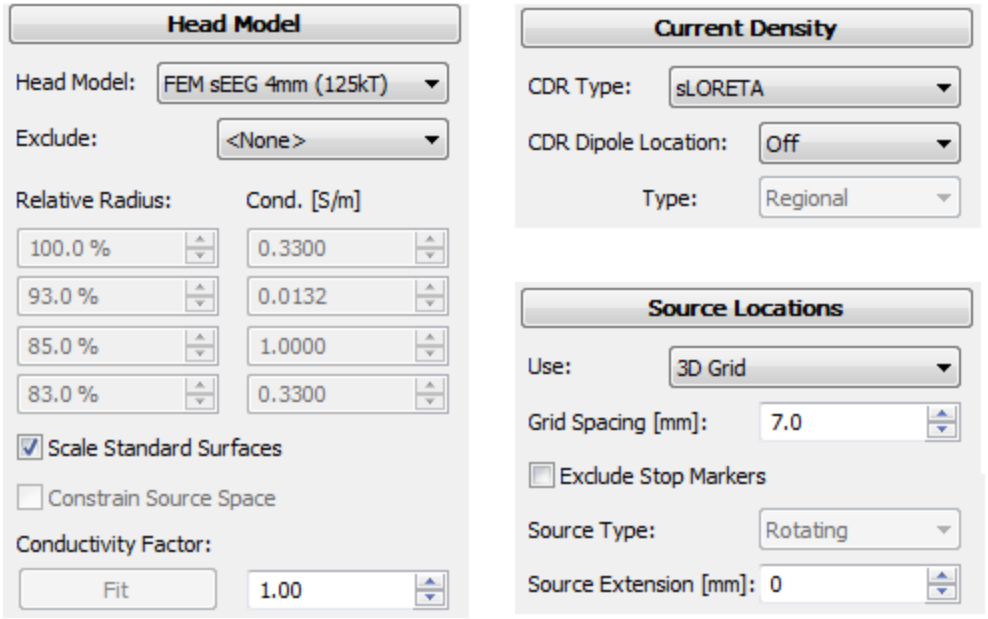
Now we can see the realistic FEM Head Model with the electrodes. Note that some of the electrodes extend beyond the head model. These will be removed shortly.



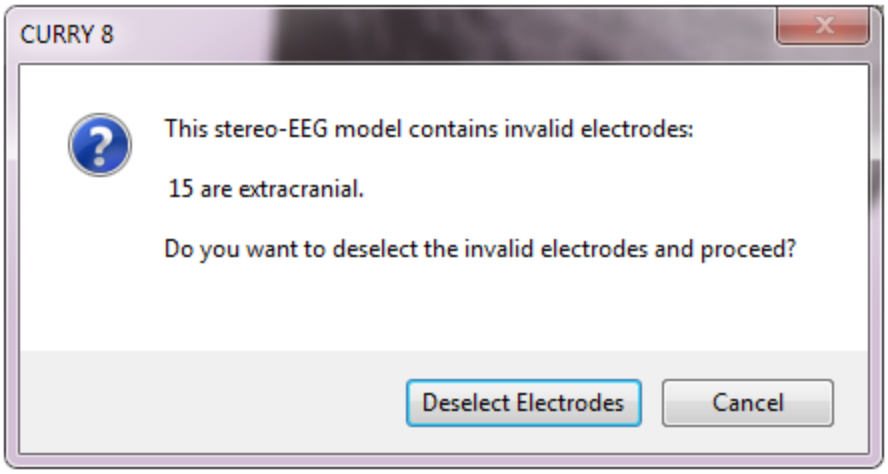
3. If we go to the **FEM Model** panel under **Results**, we can review the model that was created. The only parameter you might want to change is the Dipole Model. The Skull Anisotropy does not really come into play with depth recordings.



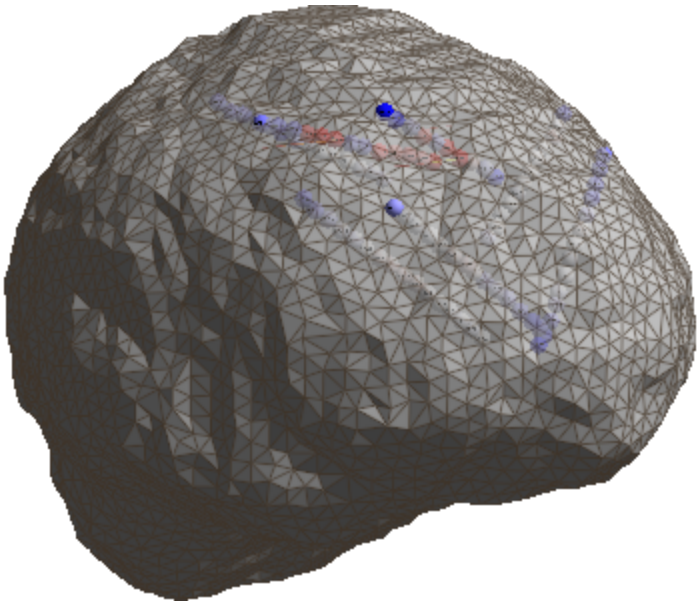
4. For source solutions a CDR makes more sense than a moving dipole, for example, because the CDR will make full use of the source space. First we selected the FEM model we just created, then selected the **3D Grid** for **Source Locations**, and then selected **sLORETA** as the **CDR Type**.



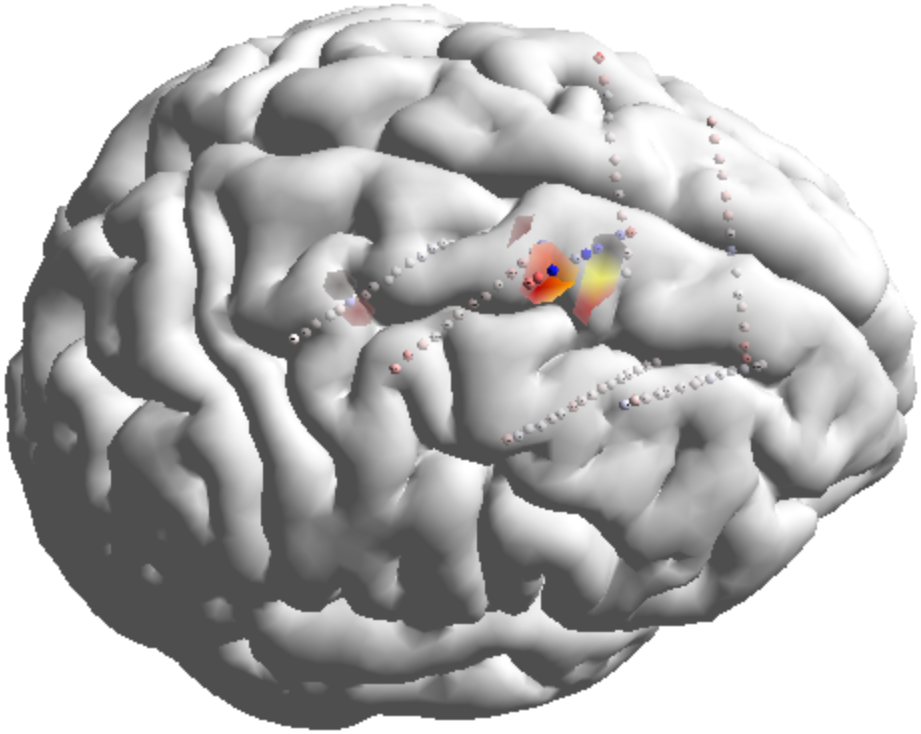
At this point we see the message that there are 15 extracranial electrodes that are invalid. Click **Deselect Electrodes**.



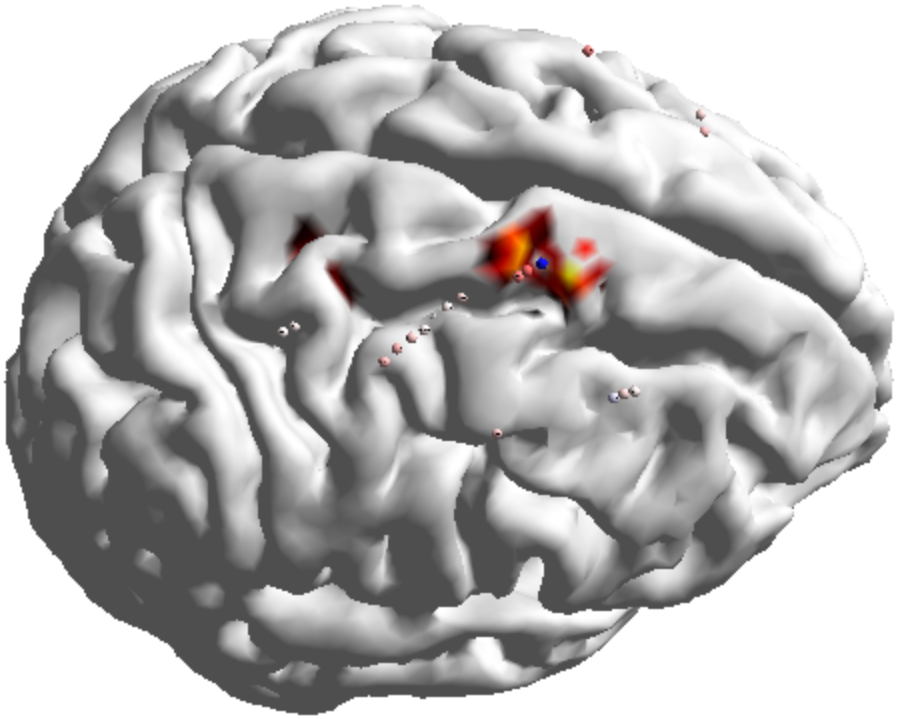
Now we can see that the extracranial electrodes have been removed. Should you need to remove individual electrodes manually, you may do so by using *Ctrl+Shift+click* on the electrode.



5. The CDR results can be seen with the cortex (**Pial Surface** on).



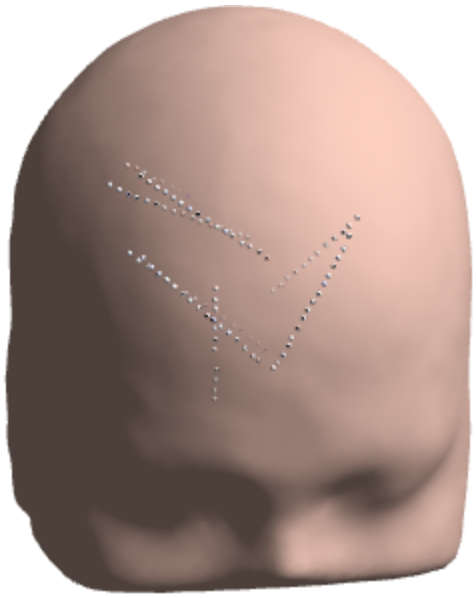
6. Instead of using the **3D Grid** for **Source Locations** you can use the **Cortex** that was created in the FEM model.



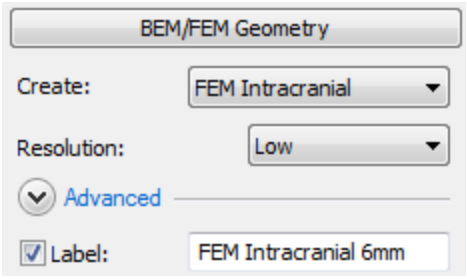
2.7.3 Focal High Resolution Localization

FEM Models, used with stereo-EEG localization, can be time consuming to create in high resolution. In CURRY, it is possible to create a low resolution FEM Model that has higher resolution only in those areas of interest (such as, near the electrodes). It is also possible to create focally high resolution areas manually. The file we are using is not found in the Tutorial Database, so please just follow along with the steps. They will be similar to those used with your data files.

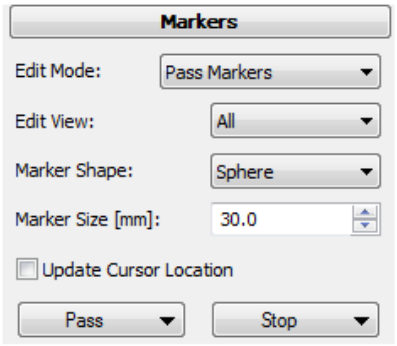
There are a number of depth electrodes, and we have a recording plus the patient's MRI and CT images. We want to create a low resolution FEM Model that has high resolution areas near the electrodes.

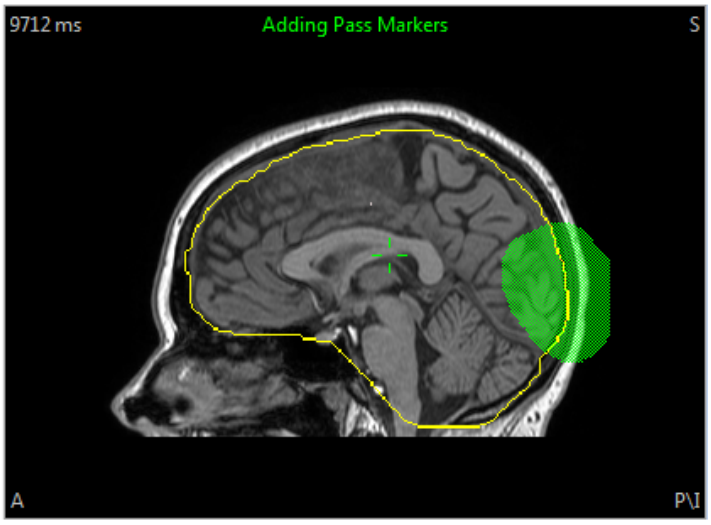


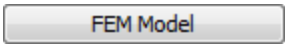
1. First, we will need an overlay to work with. We will use a FEM Intracranial model, with low resolution. All other options were the defaults.



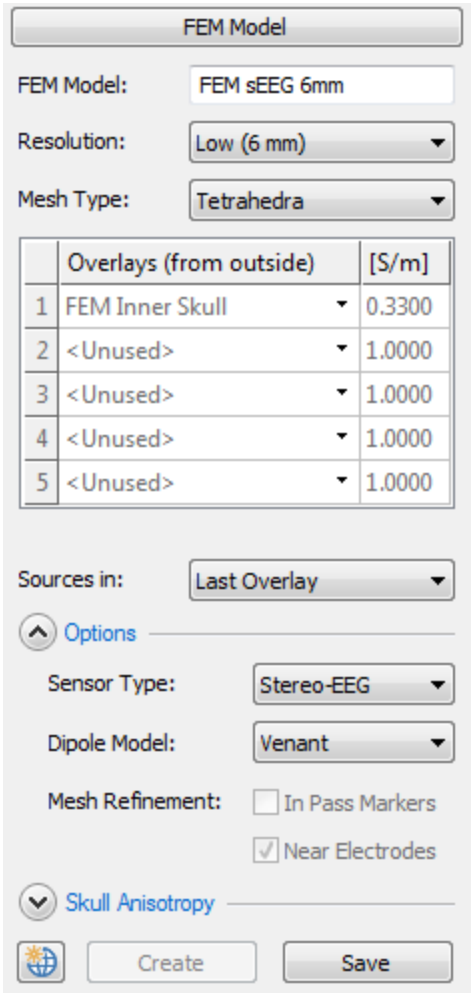
2. For demonstration purposes, we will add a high resolution area manually. This is done by adding Pass Markers in the area of interest. Just to make it easier to see, we will add the Pass Markers to the back of the head. To make it easier, we increased the Marker Size to 30 mm.





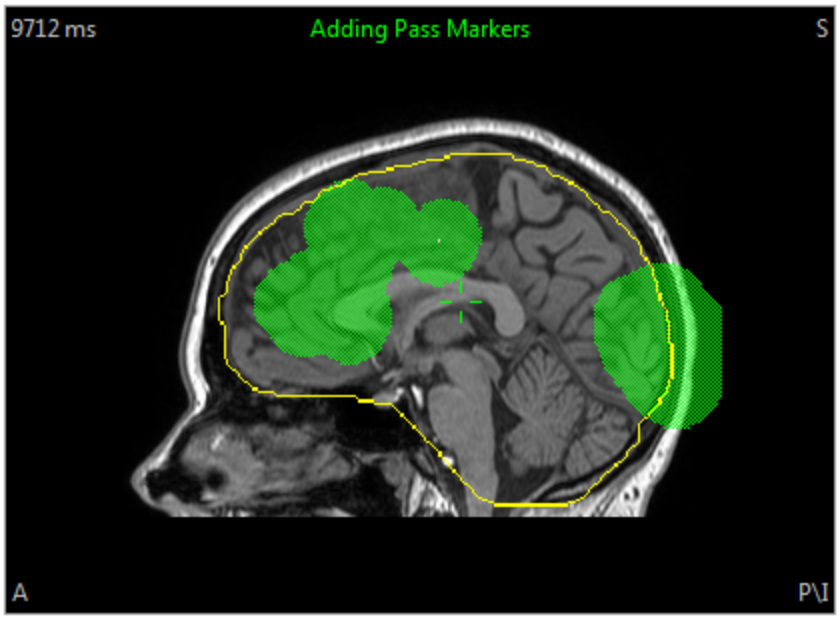
3. Next, go to the 

panel. Note that we now have an Overlay. Note also that the **Mesh Refinement** options - **In Pass Markers** and **Near Electrodes** - are grayed out. The In Pass Markers option will create higher resolution in the area where we added the pass markers manually. The Near Electrodes option will increase the resolution (triangle size is decreased to 70% of the original) by adding pass markers automatically, having 30 mm diameters (hard wired). Note that **Low Resolution** was selected - this saves time and space. You must use **Tetrahedra** for the **Mesh Type**.

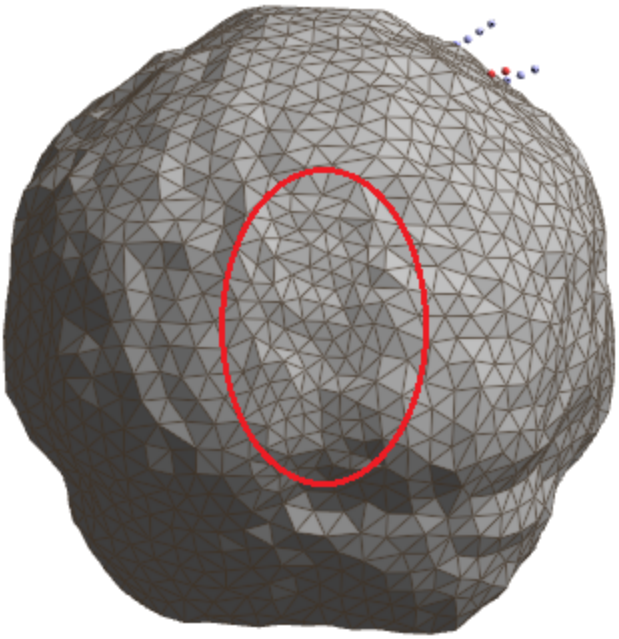


Click the Setup new FEM Model button , and the **Mesh Refinement** options and **Create** button will become active. Enable both options and click **Create**.

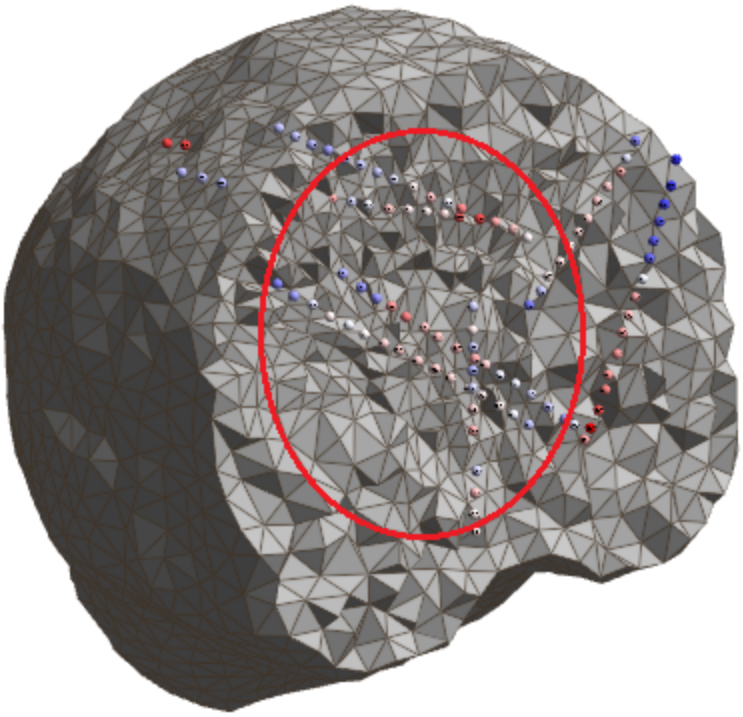
In the process of creating the model, you will see Pass Markers being added to the back of the head (the manual ones) and along the electrode tracks (the automatic ones).



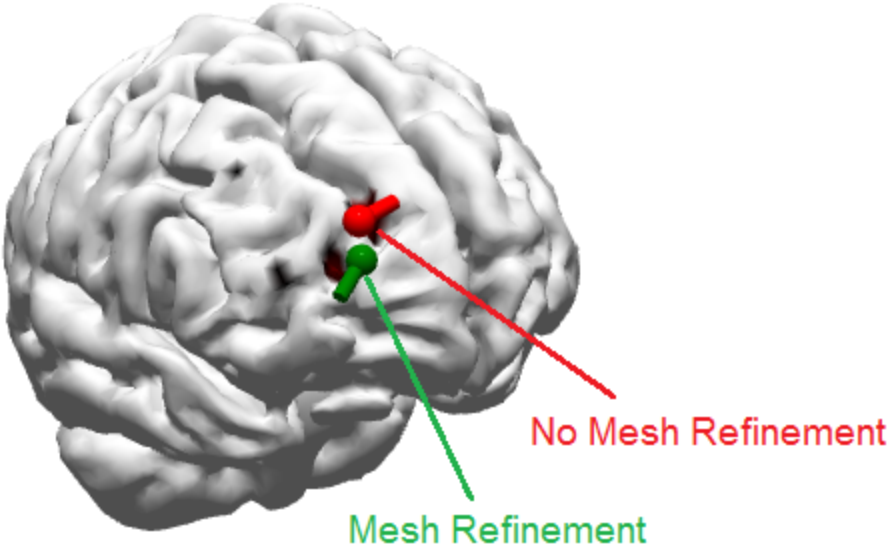
4. If you look at the back of the head in the 3D View, with the FEM Model selected, you will see the areas with finer resolution.



5. By using Cut Planes, we can see into the FEM Model, and see the finer mesh in the vicinity of the electrode tracks. Additional viewing options are described in the **Electrode Track Viewing** tutorial.



6. Now the question is, what difference does it make to refine the resolution along the tracks? In this file, at this time point, there was a small but possibly significant difference in the location.

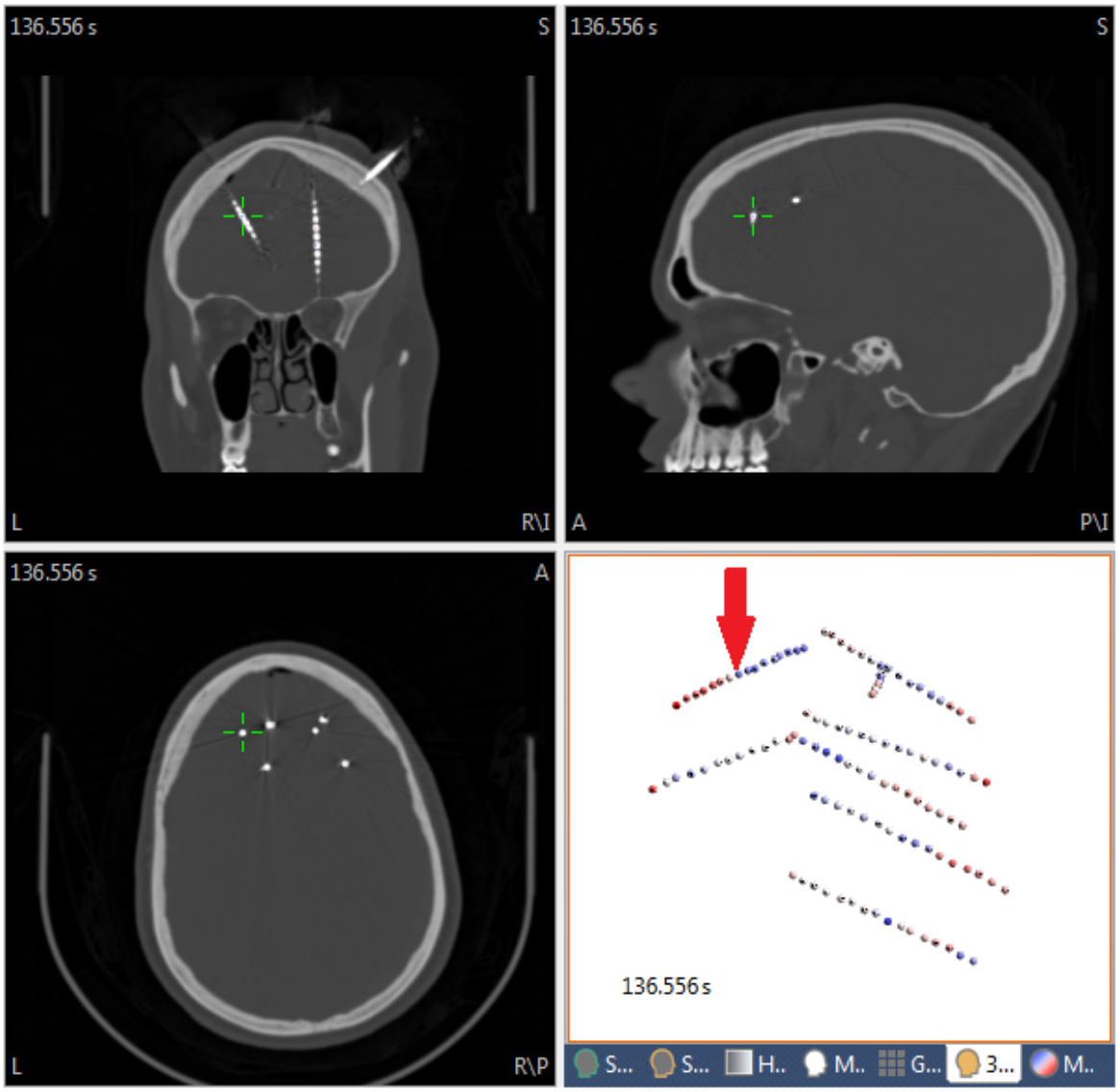


2.7.4 Electrode Track Viewing

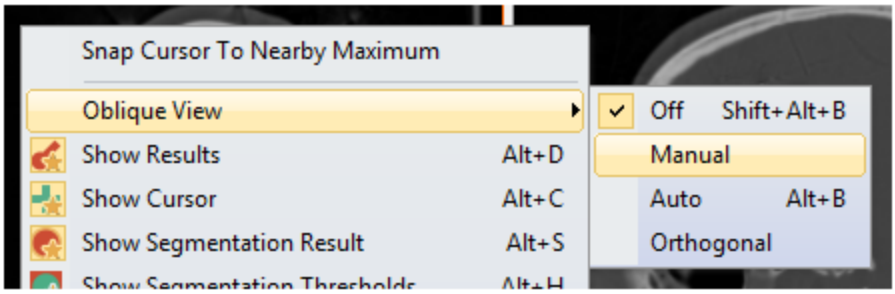
It is helpful to view the depth electrodes with whatever oblique perspective that best reveals the track of the electrodes. Again, the file we are using is not found in the Tutorial Database, so please just follow along with the steps. They will be similar to those used with your data files. There are a number of depth electrodes, and we have

a recording plus the patient's MRI and CT images. The electrodes have already been segmented, and are shown here with the CT images. The **3D View** was selected in the lower right display.

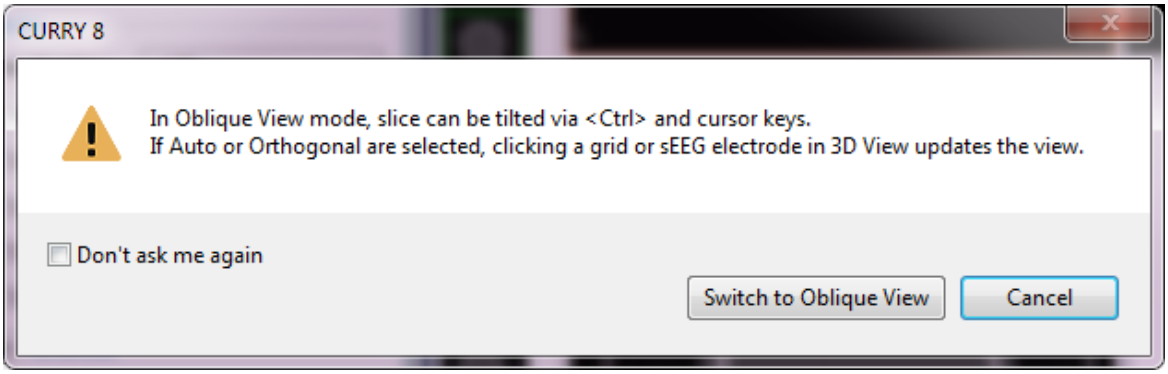
1. In the simplest case, you can click on an electrode in the **3D View**, and that electrode will be shown in all three views.



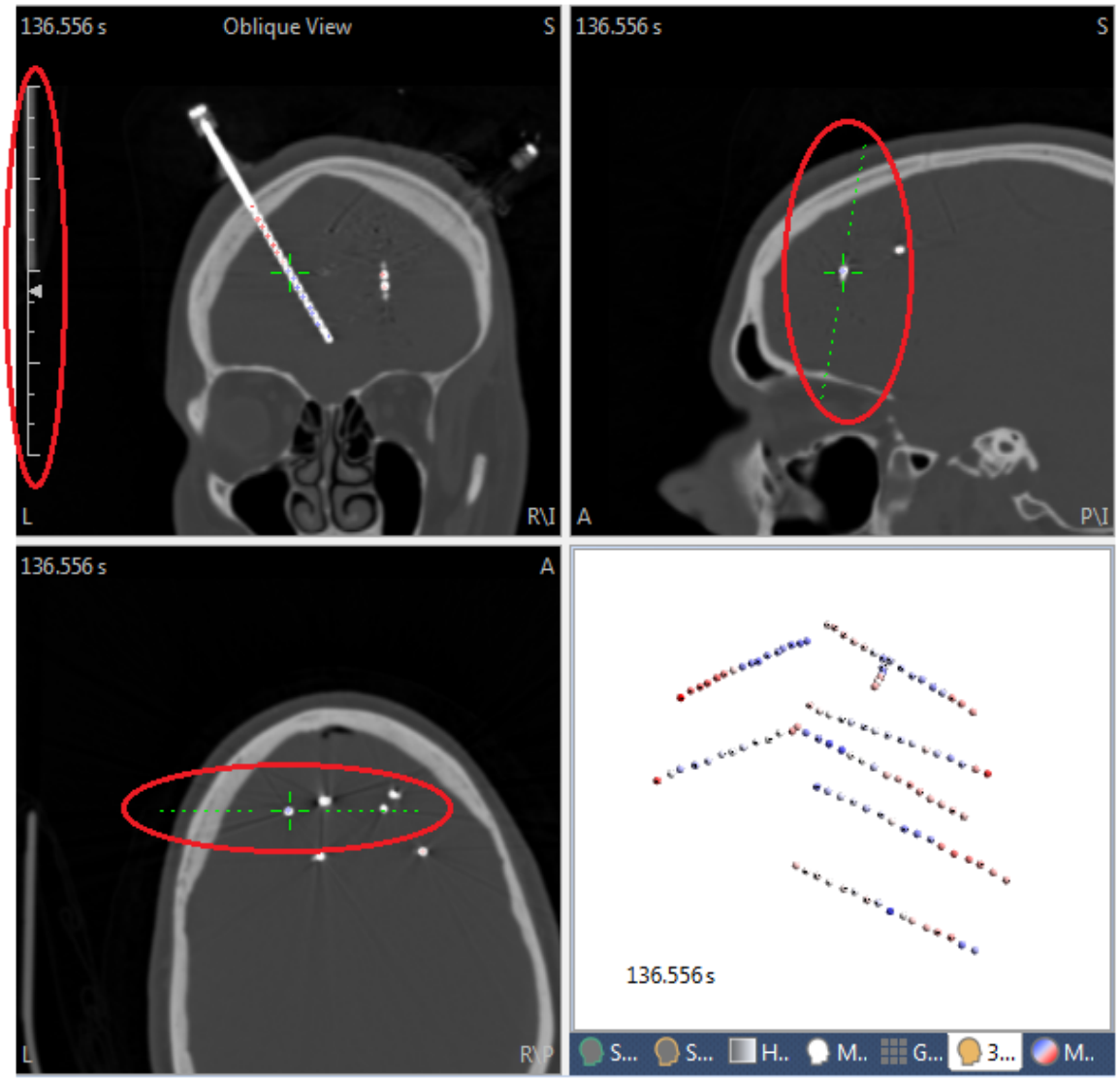
2. *Right click* in the Coronal display, for example, and select **Oblique View** and **Manual**.



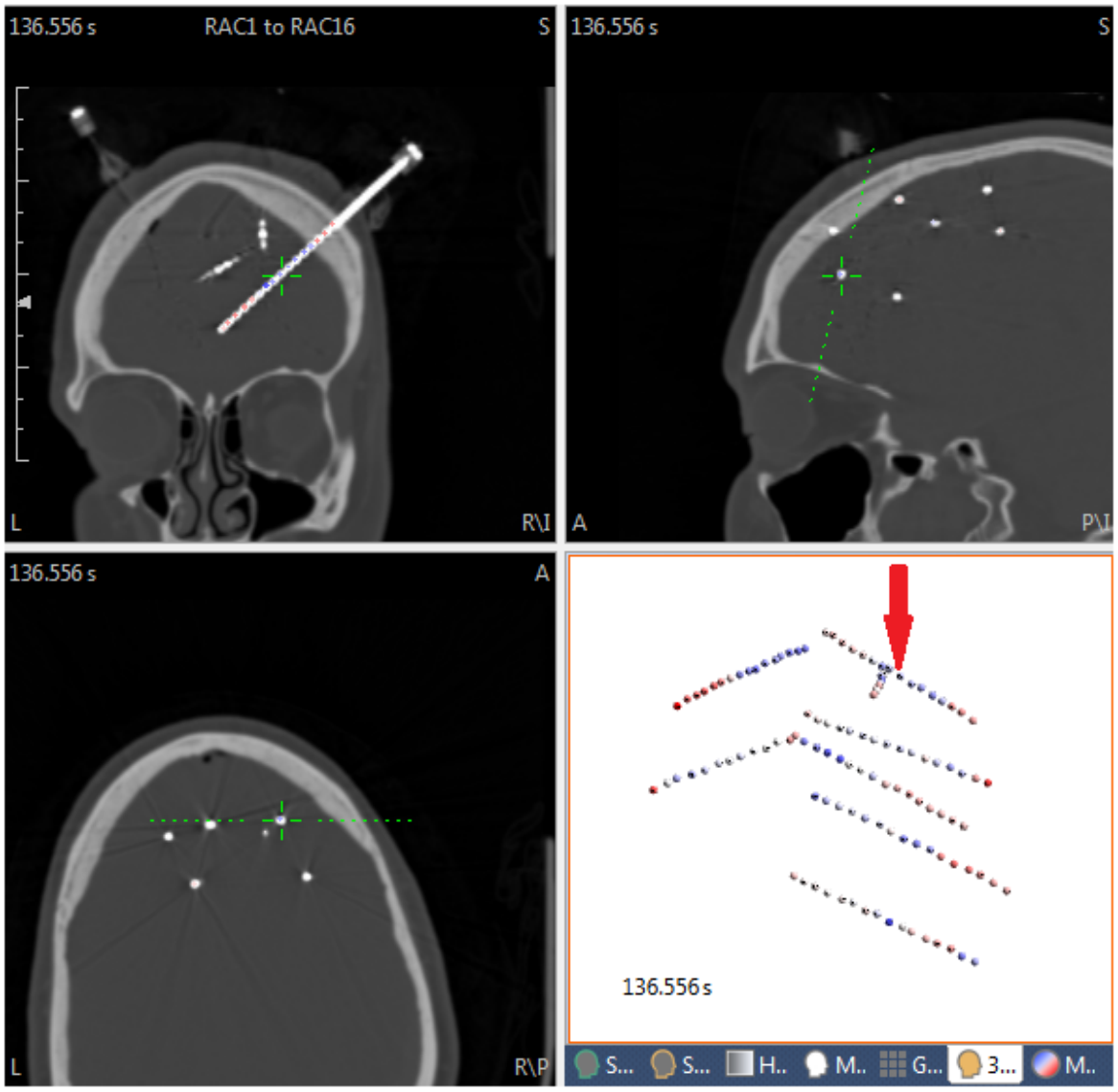
3. A message appears with reminders for which keyboard keys are used to modify the perspective.



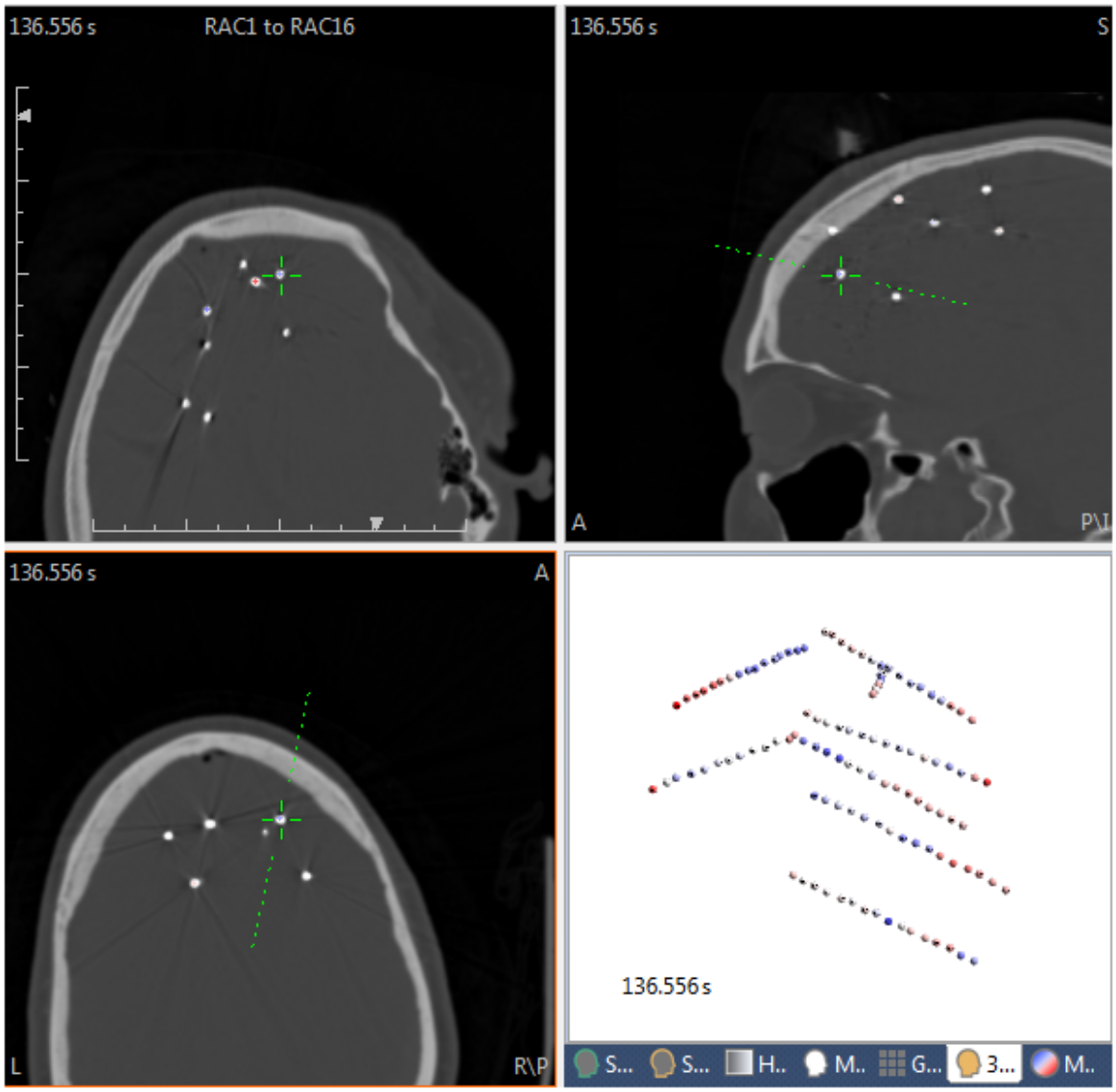
When you use *Ctrl + arrow* keys you will see a scale appear on the left (or at the bottom if you are using the left and right arrow keys). (You will need to have the mouse cursor positioned in the selected pane). You will see green dotted lines in the other displays, showing what the degree of angulation is. You can also use the arrows by themselves to move the contents of the displays.



4. Manual allows you to make changes as desired. *Right click* again, and select **Oblique**, then **Auto**. Now when you click on an electrode in the 3D View, you will see that complete track. In this case, we selected Auto from the coronal view, and that is where you see the whole electrode, using whatever oblique angulation is needed. Notice also at the top that the actual electrode labels are displayed - RAC1 to RAC16.

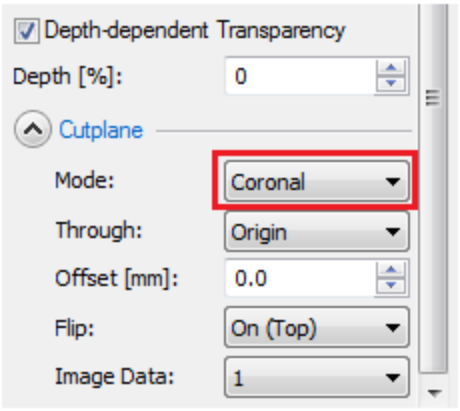


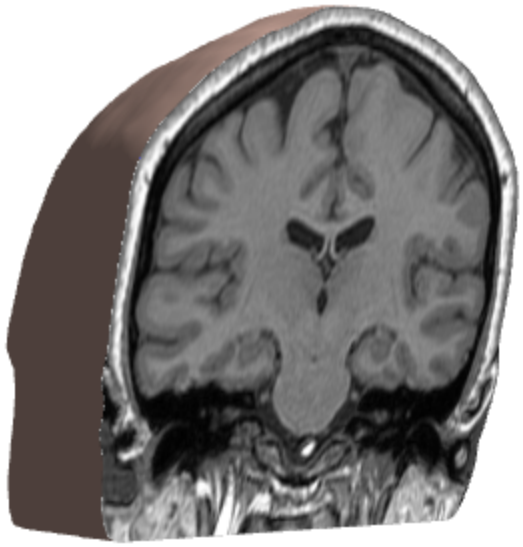
5. Instead of **Auto**, select **Orthogonal**. Now the view is perpendicular to the selected electrode.



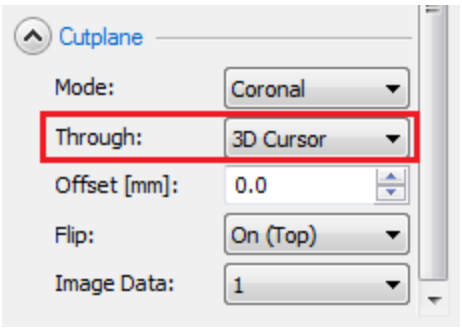
6. You also have control over what is seen in the **3D View**. We started with the digitized electrode positions, as above, and created a BEM Model to get the segmented Skin surface. In the Skin Properties, we set **Depth [%]** to **0**, and dragged the display to a posterior view.

We then selected a **Coronal Cutplane**, and repositioned the display.

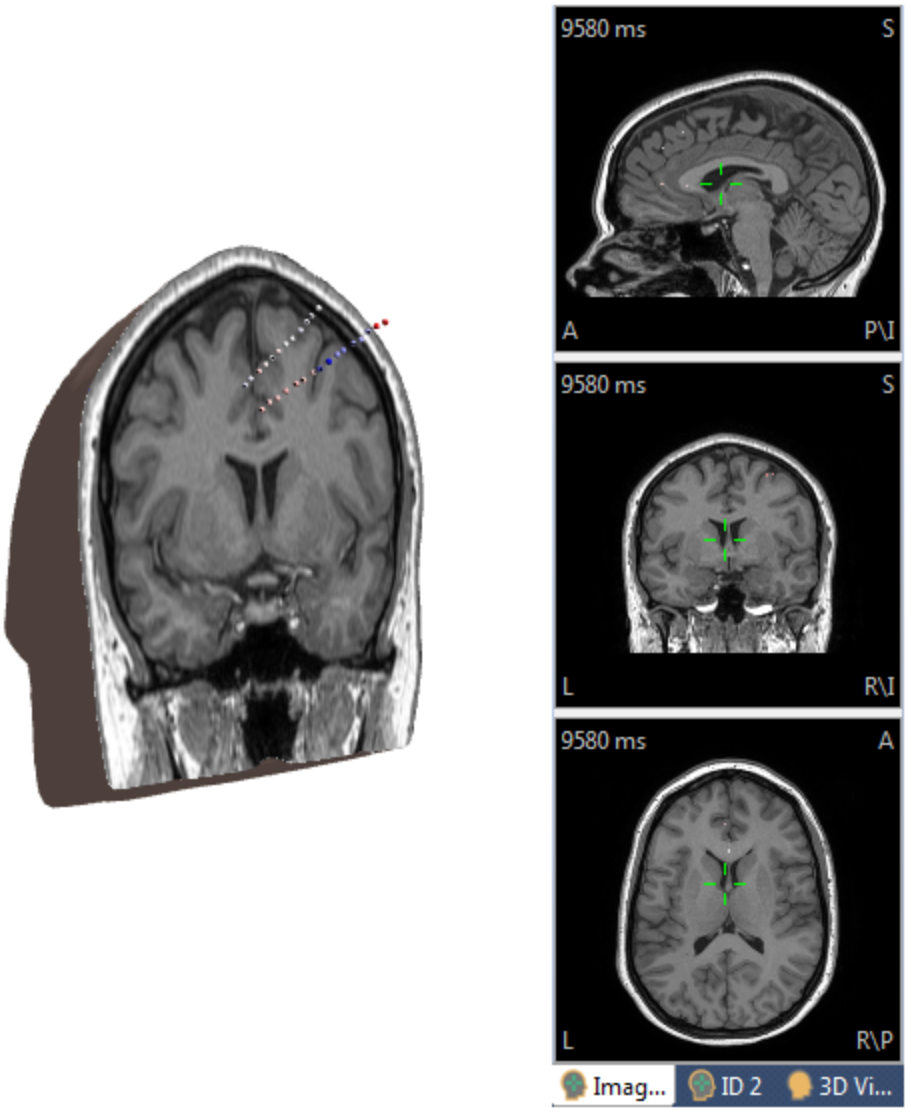




Next, select the 3D Cursor for the Through option.

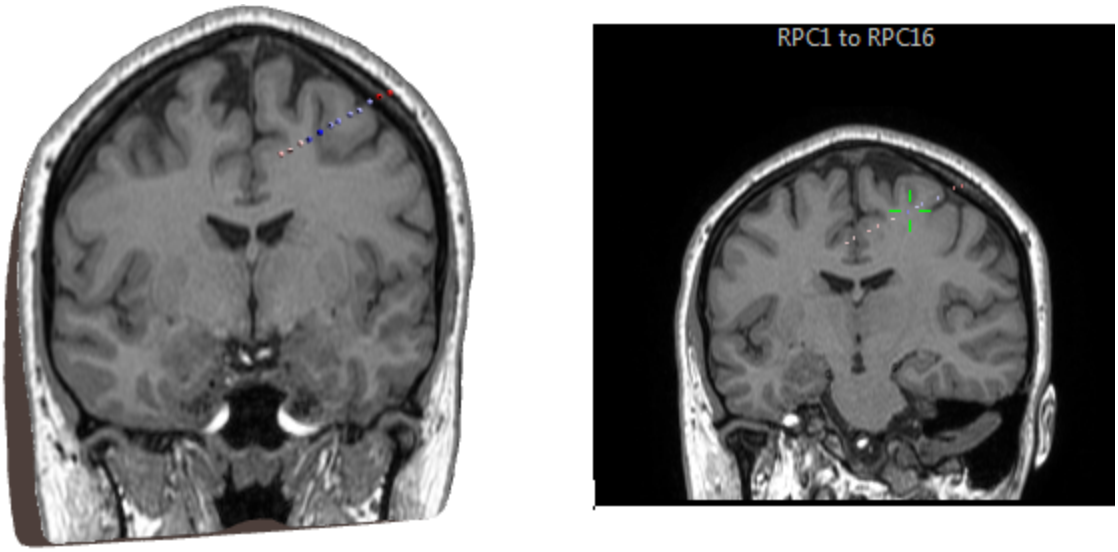


Now when you move the mouse in the MR images, the **3D View** will change accordingly.



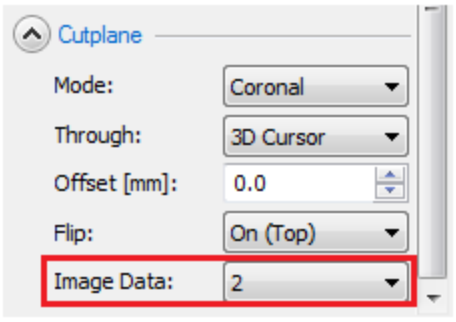
In the Coronal image data display, *right click*, select **Oblique View**, and select one of the options, such as **Auto**. Now when you click on an electrode, in the 3D View or

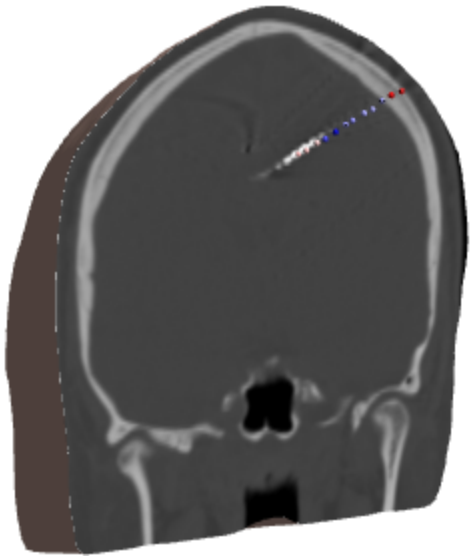
image data, the two views are linked. What you see in the 3D View is the same as what you see in the image data.



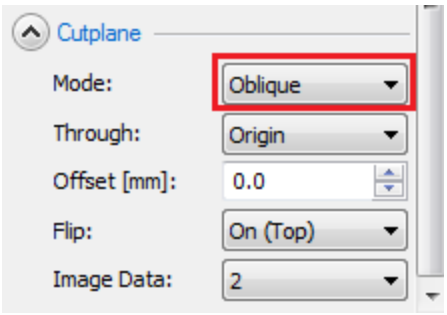
If you want to see the CT images instead of the MRI images, go to the Skin Properties and, under **Cutplanes**, set **Image Data** to 2 (assuming you have the image data and that it is seen under

).

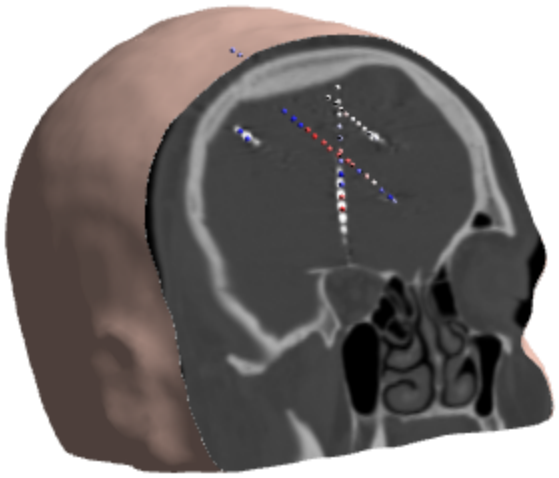




7. Lastly, experiment with the Oblique option under **Cutplane Modes**.



When you find a view you like, switch the Mode to Locked, to save that position. You can then rotate the view to any perspective without losing the information.



These are just a few of the visualization options. Feel free to experiment with other ones to get the perspective and content you want.

2.8 Macro Recorder

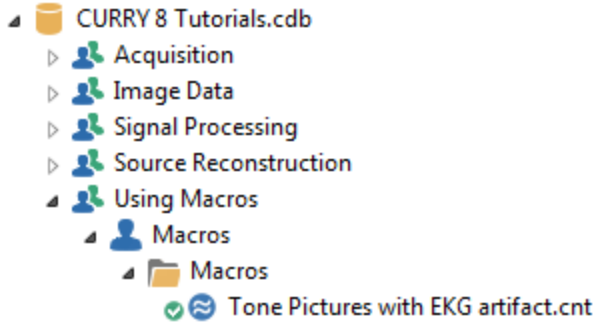
The Macro Recorder records a series of operations you perform on a data file. When you open the same or similar data file and run the macro, the same operations will be repeated. This allows you to duplicate an analysis sequence and apply it across multiple data files. You can select the files one at a time and then run the macro, or you can select multiple files and the macro will process all of them.

Within the macro, there is a naming convention that allows you to create new files that will have unique file names. You can pause the macro at defined places, and make changes to the parameters. You can insert a variety of dialogs into the macro at defined locations, explaining what is happening or directing others to perform some action during the macro.

When you record a macro, plan in advance what you want to do, including where you want to insert Pauses, Text Dialogs, etc. You can edit the macros, but it is easier if you include as many operations as you can at the time you make the recording.

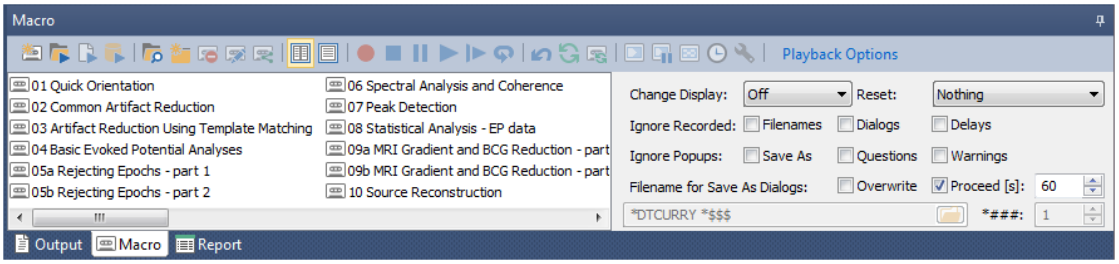
We'll start with a simple example in which we take a continuous data file, mark some bad blocks, remove blink artifact, average evoked responses to two different type codes, and save the final averages.

For this demonstration, use the Study shown below, in the *CURRY 8 Tutorials* Database.

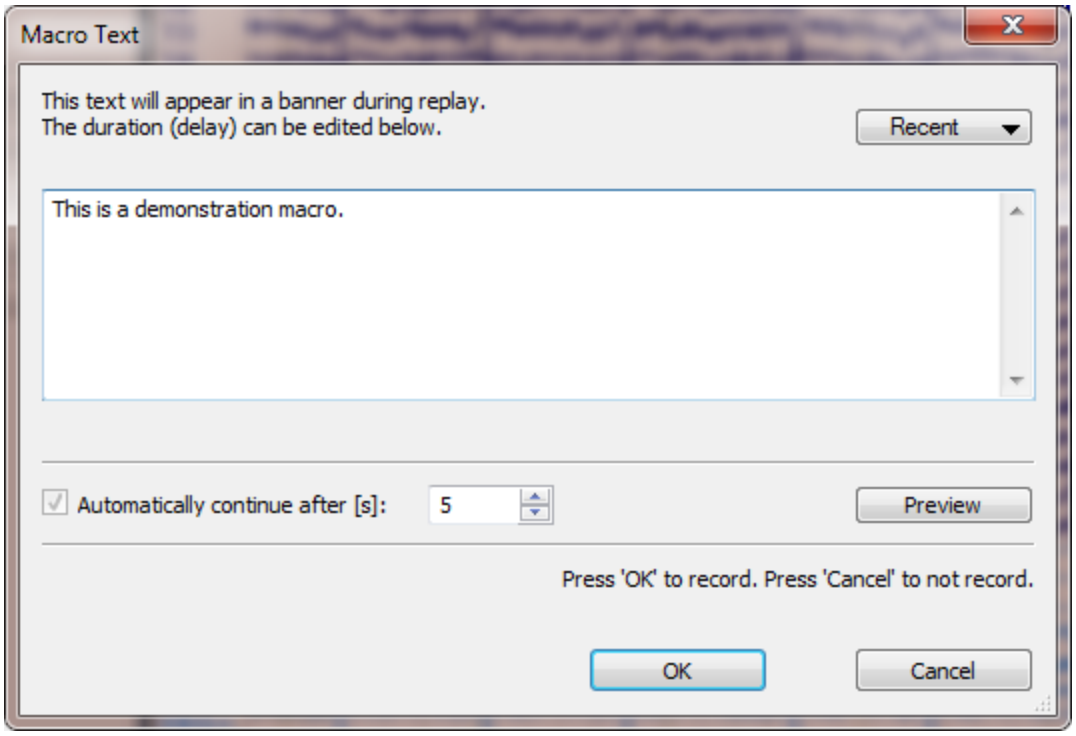


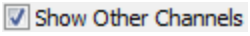
1. Start by opening the Study. (If you have saved any **Study Parameters** with a file, it may be a good idea to remove that .cfg file from the Database before opening the Study if you want the macro to record all of the operations you wish to perform on this file or others in the same research project).

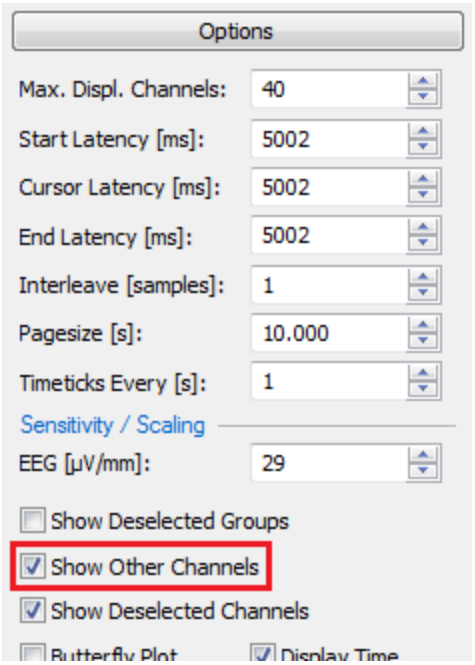
2. Select the Macro tab below the data display. Select the **New Macro** icon , and enter a file name when prompted (*Tutorial.mac*). Using the default folder is recommended - those are the macros that will be displayed in the list. The macro has now begun to record. When the macro is recording, you will see a red ball beside the mouse cursor.



3. We'll start with a "banner" stating that this is a demonstration macro. Click the **Show Banner** icon from the Toolbar. Enter text as desired. Click the **Preview** button to see the banner. The banner is set to display for **5** seconds and then disappear. Click **OK**.

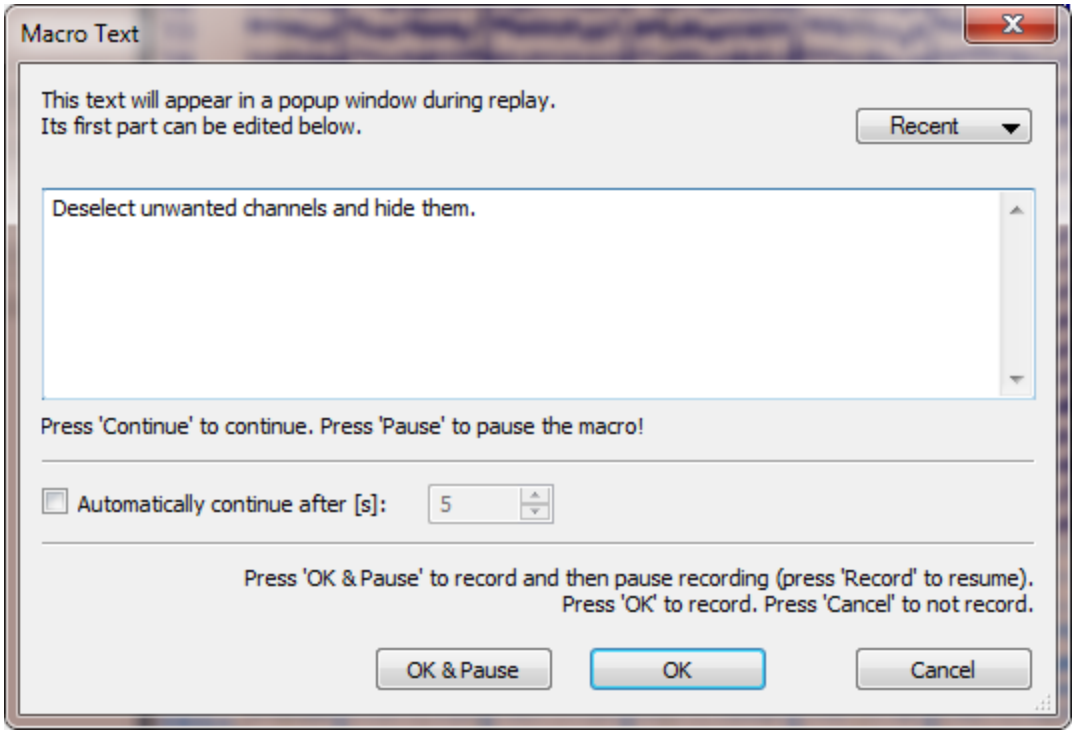


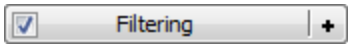
4. There are actually some additional channels that are not seen unless you select  under **Options** (enable the option).



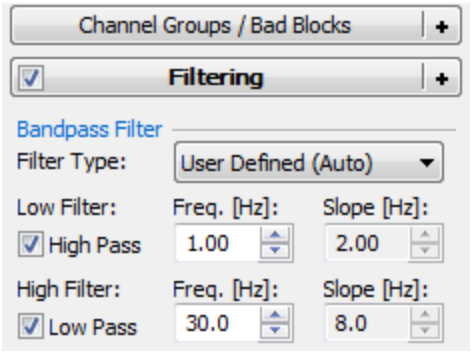
Looking at the data file, there are a number of bad channels that we want to exclude. We could do it automatically within the macro, but instead, for demonstration purposes, we will pause the macro so they can be excluded manually. We will add a message to that effect, and pause until the action is

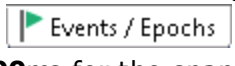
completed. Click the **Show Popup Window and Pause or Continue** option, found on the Toolbar. The Macro Text window will appear again. Enter text and click **OK**. If we clicked **OK & Pause**, the macro will stop, allowing us to deselect the channels now. After doing so, we would click the **Record** button to continue with the macro. By clicking **OK**, we will be able to deselect the channels during the replay.



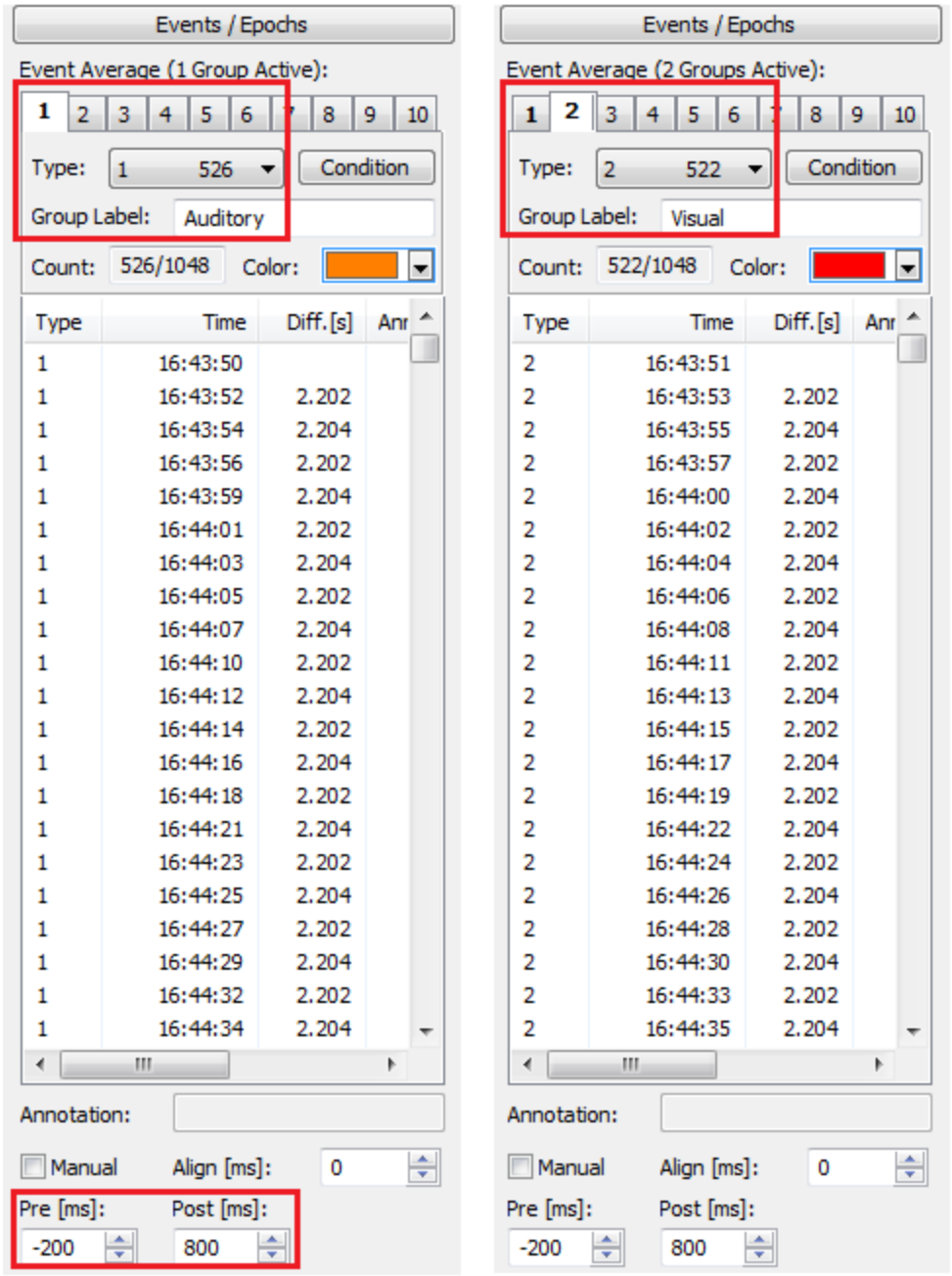
5. Next, we will Filter the data. Go to 

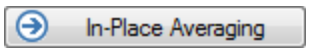
and enter the settings as shown.



6. We will create Averages for the two file types. We want to keep the averages separate, so we will need to define two event groups. Go to the event list in the **Events/Epochs** panel under 

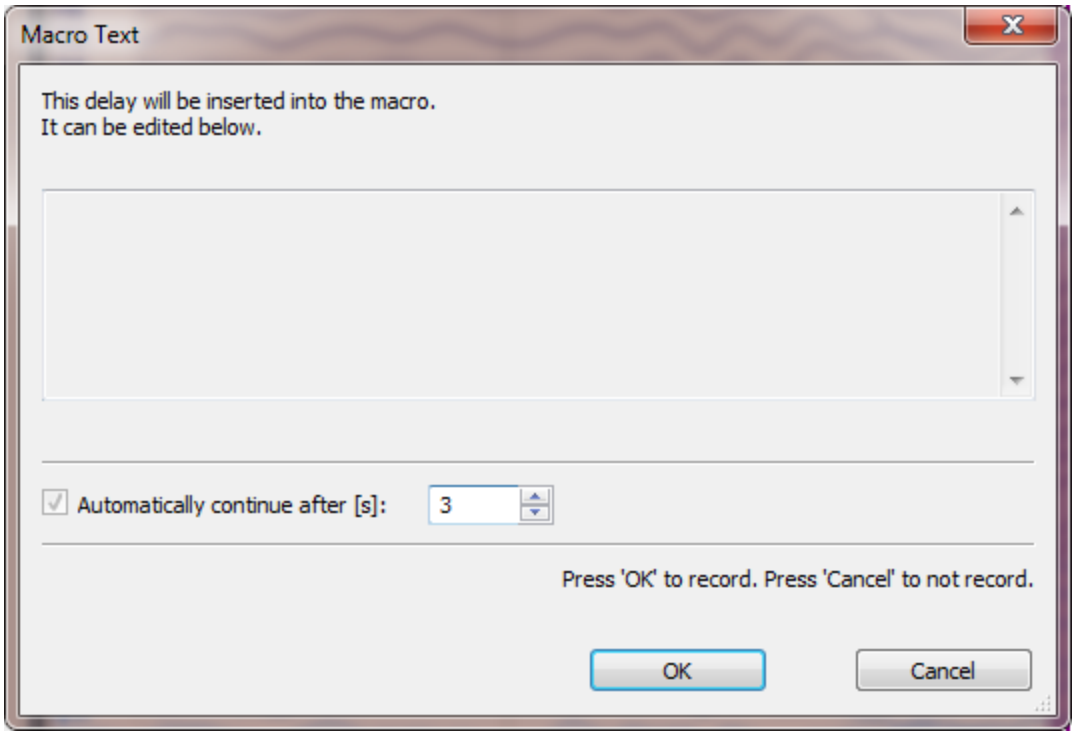
. For the first one, select **1** for the **Type**, and enter **-200** and **800**ms for the span of the epochs. Select the second tab and select **2** for the **Type** and verify or enter -200 and 800 ms. Enter "Auditory" and "Visual" for the **Group Labels**.



7. Click the 

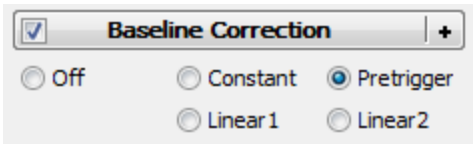
button. It will take just a few moments to average the epochs.

9. Insert a 3 second Delay by clicking the **Delay** icon . Set the **Automatically continue after** field to **3**, and click **OK**.

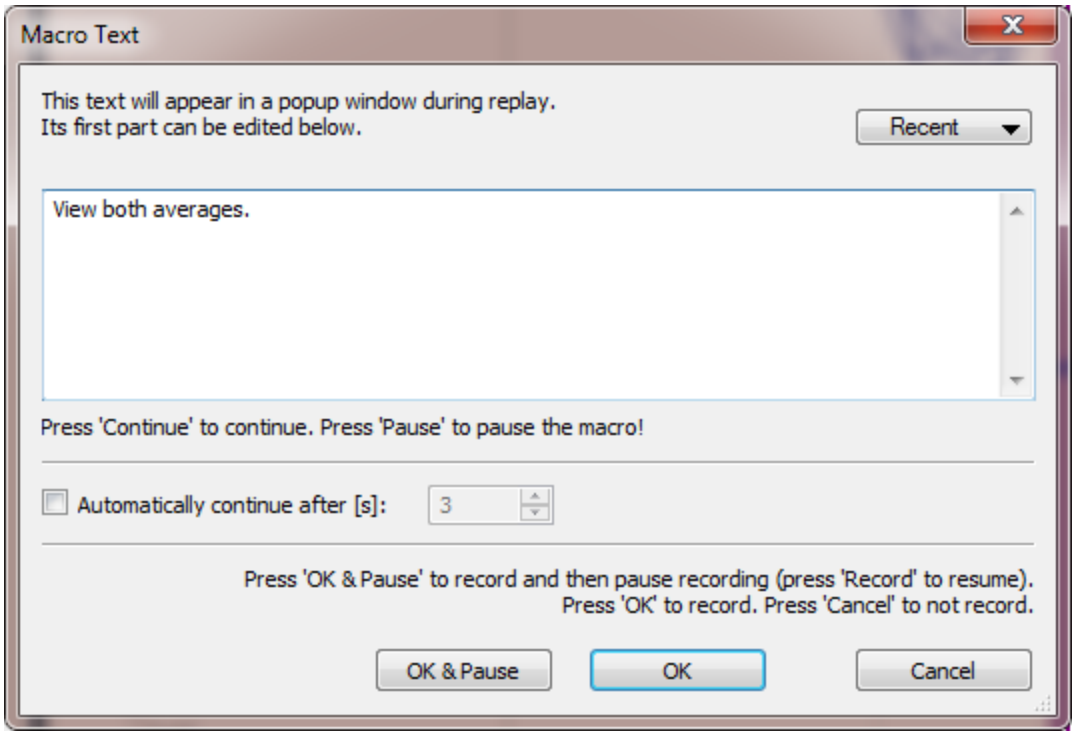


This is just to let you verify the operations to this point.

10. Select the **Butterfly Plot** and perform a **Baseline Correction** (**Pretrigger**).

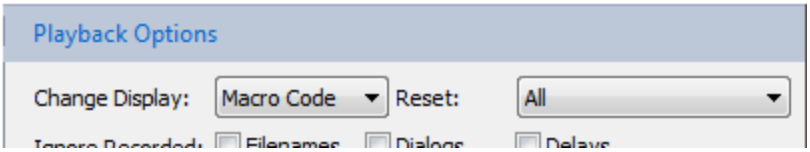


Click the **Show Popup Window and Pause or Continue** option, and enter the text. Click **OK**. This will let us view the results.



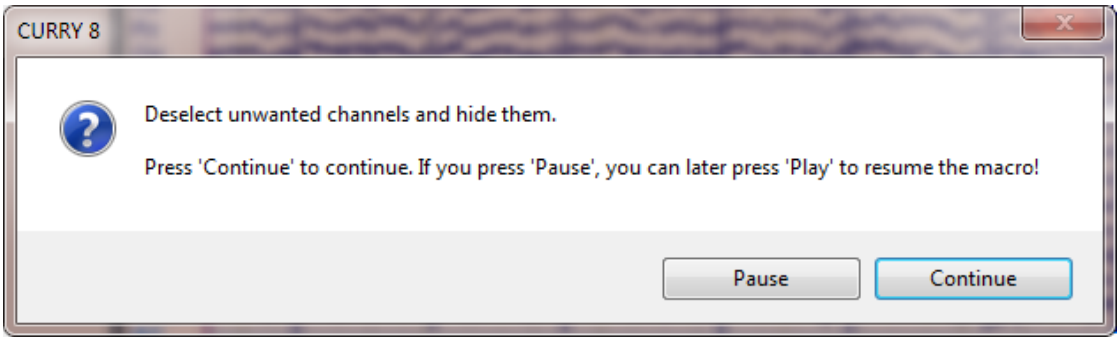
11. Click the **Stop Macro** icon on the Toolbar. Close the Study and reopen it.

12. Before replaying the Macro, note the **Playback Options**. **Change Display** lets you view different things during the playback. In this case, we will select the **Macro Code** option. This will display the macro code in the main macro window (for illustration purposes). When you stop recording a macro, the program will often be in a different state than when the macro was started. To return the program to its original state, select **All** for **Reset**.



Then click the **Play Macro** icon to start the replay. A green arrow will appear by the mouse cursor to let you know the macro is replaying.

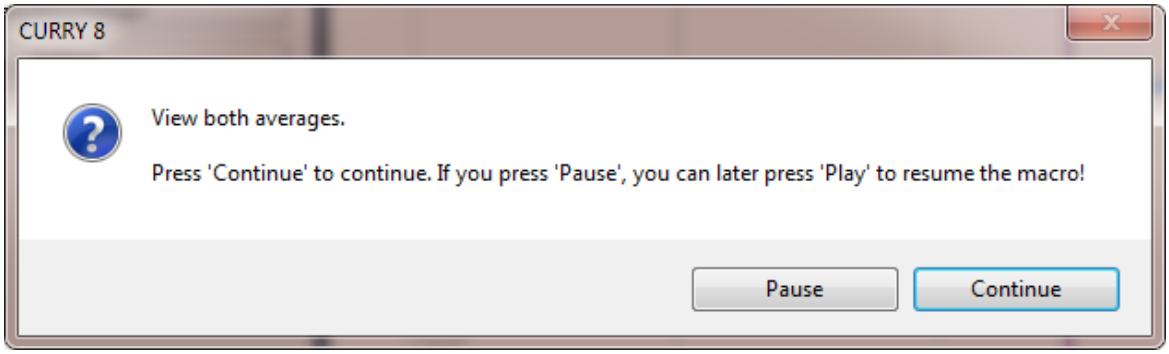
As the macro replays, you will first see the Banner, and then the macro will pause, giving you will have the opportunity to click on the labels for A2, X1, X2, H+, H-, V+, V-, EKG+, and EKG-. Click **Pause** to pause the macro. If you click **Continue**, the macro will continue without pausing. *Right click* on the indicated channel labels and select **Deselect Channel** for each.



Then go to **Options** (under **Functional Data**) and deselect Show Deselected Channels. The deselected channels will disappear. Click the **Play Macro** icon to continue. (Again, you could do this within the macro - we did it manually just for demonstration).

Lastly, you will be directed to view the final averages - click **Pause**. You may now rescale the averages, and move from one to the other using the slider at the bottom.

The macro will end when you click the **Play Macro** icon one last time.



The above is an example of a simple macro. Obviously you can develop the macro to a much fuller degree, including, for example, source reconstruction. If we were analyzing the file fully, we would have also removed the blinks and pulse artifact. The steps will be very similar.

Editing Macros

One question that arises is: how can I edit a macro? Below is a section of a simple macro. It starts off by inverting the polarity, then a baseline correction was performed. The blink artifact was reduced and selected type codes were averaged. A Pause was inserted at that point, followed by a Butterfly Plot and Baseline Correction. Finally, the Revert to Continuous button was pressed.

Click the **Edit** icon to see the macro code in Notepad. Without getting lost in the code, you can see with a little scrutinization where the commands are encoded. Note that each step ends with a STEP END line. Note also that the Noise Level estimation is updated automatically for each step.

```
FunctionalData.Action      = FdScanArtifacts
FunctionalData.ThresholdChannels = VEOG| <Off>| <Off>| <Off>| <Off>
FunctionalData.ProcessDataMode =  6
FunctionalData.DataPlusUp =  1
FunctionalData.BaselineCorrectionMethod =  1
FunctionalData.ThresholdType = 2 0 ...
FunctionalData.UserDefinedNoiseLevel = 3.1456 1 ...
FunctionalData.LowerThresholdValue = 0 -200 ...
FunctionalData.ThresholdPre = -200 -100 ...
FunctionalData.ThresholdPost = 500 100 ...
STEP END
FunctionalData.Action      = FdFirstEpoch
STEP END
FunctionalData.Action      = FdAverageEvents
FunctionalData.SelectedEventAverage =  1
FunctionalData.NoiseStartSample =  25
FunctionalData.NoiseEndSample =  35
FunctionalData.SignalStartSample =  25
FunctionalData.SignalEndSample =  25
FunctionalData.EventPreLatency = -200
FunctionalData.EventPostLatency =  1000
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 1 2 0 ...
FunctionalData.ThresholdProj = 1 -1 ...
FunctionalData.ThresholdAverages = -1 1 ...
FunctionalData.ThresholdGlobalReduction = 1 0 ...
FunctionalData.UserDefinedNoiseLevel = 3.0575 1 ...
STEP END
FunctionalData.Action      = FdRevertOrg
FunctionalData.DataPlotMode =  1
FunctionalData.BaselineCorrectionMethod =  1
FunctionalData.BaselineEndSample1 =  50
FunctionalData.DataAmplitude = 1.84 0 ...
FunctionalData.UserDefinedNoiseLevel = 0.5398 1 ...
Study.Action               = MacroDelay
Study.Action               = MacroUpdate
STEP END
```

Now, let's say that we meant to perform Filtering between Baseline Correction and Artifact Reduction near the beginning. The easiest way to do this is to create a second macro that contains only the Filter parameters. When you record the macro, record the setting of the filter parameters only, then *click the **UI Update** button on the macro Toolbar* . This forces the operation(s) to be written to the macro file; otherwise, the macro will be empty (until a process such as Scanning occurs). Looking at the content of that macro, we see the following:

```
Study.Action               = MacroUpdate
FunctionalData.FilterType =  61
FunctionalData.LowPassFilter =  1
FunctionalData.HighPassFilter =  1
FunctionalData.FilterTypes = 61 ...
```

```
FunctionalData.LowPassFilters = 1 ...
FunctionalData.HighPassFilters = 1 ...
FunctionalData.DataAmplitude = 370 0 ...
FunctionalData.UserDefinedNoiseLevel = 3.051 1 ...
STEP END
```

Now it is just a matter of copying the relevant text (in red) from the filter macro into the desired location in the initial macro. Save the modified macro.

```
FunctionalData.Action      = FdScanArtifacts
FunctionalData.ThresholdChannels = VEOG| <Off>| <Off>| <Off>| <Off>
FunctionalData.ProcessDataMode =  6
FunctionalData.DataPlusUp =  1
FunctionalData.BaselineCorrectionMethod =  1
FunctionalData.FilterType =  61
FunctionalData.LowPassFilter =  1
FunctionalData.HighPassFilter =  1
FunctionalData.FilterTypes = 61 ...
FunctionalData.LowPassFilters = 1 ...
FunctionalData.HighPassFilters = 1 ...
FunctionalData.DataAmplitude = 370 0 ...
FunctionalData.UserDefinedNoiseLevel = 3.051 1 ...
FunctionalData.ThresholdType = 2 0 ...
FunctionalData.UserDefinedNoiseLevel = 3.1456 1 ...
FunctionalData.LowerThresholdValue = 0 -200 ...
FunctionalData.ThresholdPre = -200 -100 ...
FunctionalData.ThresholdPost = 500 100 ...
STEP END
FunctionalData.Action      = FdFirstEpoch
STEP END
FunctionalData.Action      = FdAverageEvents
FunctionalData.SelectedEventAverage =  1
FunctionalData.NoiseStartSample =  25
FunctionalData.NoiseEndSample =  35
FunctionalData.SignalStartSample =  25
FunctionalData.SignalEndSample =  25
FunctionalData.EventPreLatency = -200
FunctionalData.EventPostLatency =  1000
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 1 2 0 ...
FunctionalData.ThresholdProj = 1 -1 ...
FunctionalData.ThresholdAverages = -1 1 ...
FunctionalData.ThresholdGlobalReduction = 1 0 ...
FunctionalData.UserDefinedNoiseLevel = 3.0575 1 ...
STEP END
FunctionalData.Action      = FdRevertOrg
FunctionalData.DataPlotMode =  1
FunctionalData.BaselineCorrectionMethod =  1
FunctionalData.BaselineEndSample1 =  50
FunctionalData.DataAmplitude = 1.84 0 ...
FunctionalData.UserDefinedNoiseLevel = 0.5398 1 ...
```

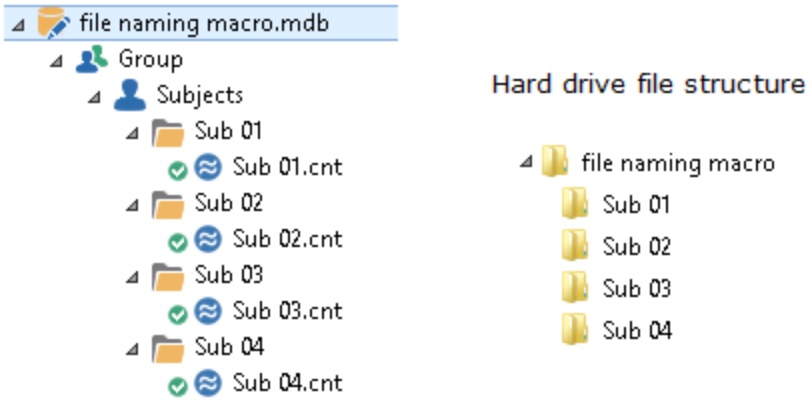
```
Study.Action          = MacroDelay
Study.Action          = MacroUpdate
STEP END
```

In a similar way, you can see how to add text dialogs, change the order of operations, or change the specific parameters for an operation. You do not need to know how to write code to make these modifications. It takes only a little studying of the existing code.

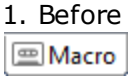
In another example, say you have saved the final data files and the final images to the same folder. Then you decide that you want the figures to be in a separate folder. If you Edit the macro, you will see separate paths for the data files and figures. Change the target folder for the figures, save the macro file, and then run it as normal.

File Naming Convention
Another question that comes up frequently has to do with applying a macro across a group of subjects. In most macros of this type, there are results files that are saved, and the created files need unique file names. At the same time, you want the macro to run continuously without stopping to input the unique file names. An automatic file naming strategy is needed.

Below is a Database with four Subjects (left). Each has a continuous data file, and from it we want to create an averaged file. We want to do that in a macro, and then we want to apply that macro across subjects, where each averaged file has a unique file name. The Database structure is similar to that seen on the hard drive (right). Recall that a Database does not contain the files, but rather points to the files on the hard drive. When you save a data file that you create during processing, you are saving it to the hard drive. You are pointing to it from the Database.

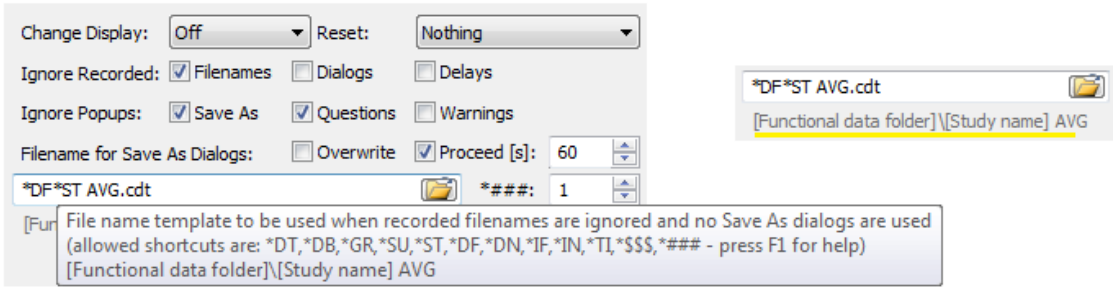


In this case, we will record a macro, resulting in an averaged data file, and then apply that macro to the continuous data in the other subjects.

1. Before recording the macro, note the Playback Options displayed in the 

window. Enable the **Filenames** option for **Ignore Recorded**, and the **Save As** option for **Ignore Popups**. This tells the program to ignore the recorded Filenames and the Save As dialogs that would otherwise appear, and instead use the **Filename for Save As Dialogs** naming convention. The first line in the Tooltip

reminds you to enable these options. We entered **DF*ST AVG.cdt* for the filename. (If you are re-running a macro, after the files already exist on the hard drive, and you want to avoid being asked if you wish to overwrite them, then enable the Questions field as well to overwrite the files automatically). The current path will be seen below the Filename string.



Position the cursor in the naming field to see the Tooltip, which we will examine in more detail. The shortcuts are:

*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 **Shortcut *###** field)

For example, suppose the Filename is **DTCURRY 7 *TI*. *DT is the path for the desktop (which in this case is the D drive), and the file name starts with "CURRY 7". Then there is a space, followed by *TI, which is the program generated code based on the date and time. These substitutions result in the full path shown at the bottom of the Tooltip D:\Documents and Settings\<user>\Desktop\Curry 7 20100514092534. Whenever a file is saved, it will be saved to the Desktop, using a file name ending in a unique code.

What we want in this case is a file name that uses the Study name, followed by "AVG". We want to save the files in the data folder where the continuous data came from. Therefore, we will use *DF for the path to the data folder, followed by *ST, the Study name. We will add "AVG" to the file name. The entry becomes: *DF*ST AVG, as shown in the figure above. The Tooltip now displays the path and name for confirmation [Functional data folder]\[Study name] AVG.

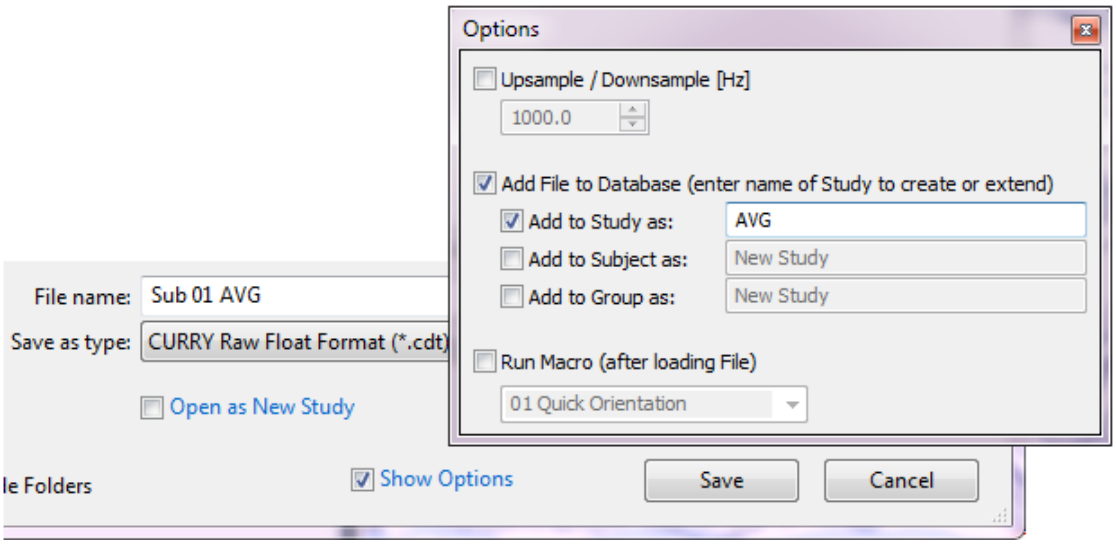
If you want to use a totally different path, not derived from the Database at all, you can do that simply by typing in the desired path (or by using the Browse button):

c:\My Data\My Folder*ST AVG.

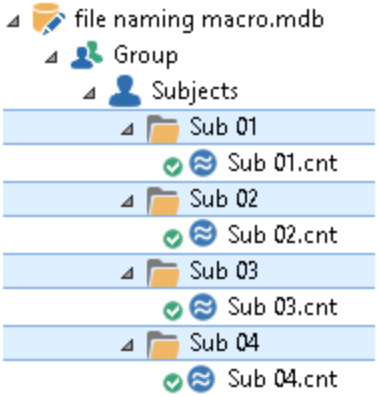
The file name remains Sub 01 AVG (where the 01 changes with the Study), and the path is whatever you type in.

You do not have to enter the file information before recording the macro; this was done to clarify the reasons why the particular file names were chosen when the macro was recorded.

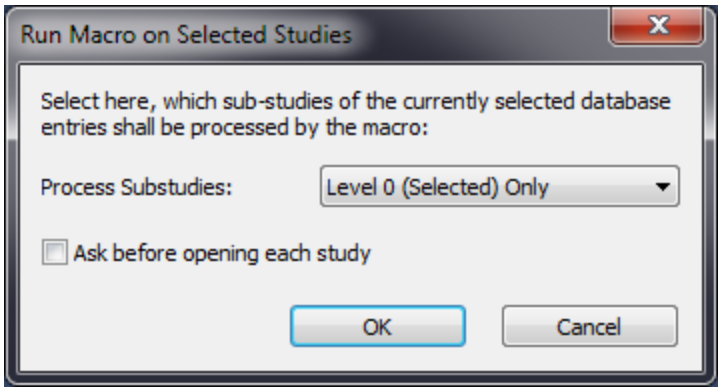
2. Now we can create the macro for analyzing the initial data file. In this case we will only average the epochs for a selected type code, and save the averaged data. When we get to the point where the averaged file is to be saved, we will save it normally. In this case we are creating a derived Study, under the original Study, called "AVG". After saving the average, we stopped recording the macro and closed the Study.



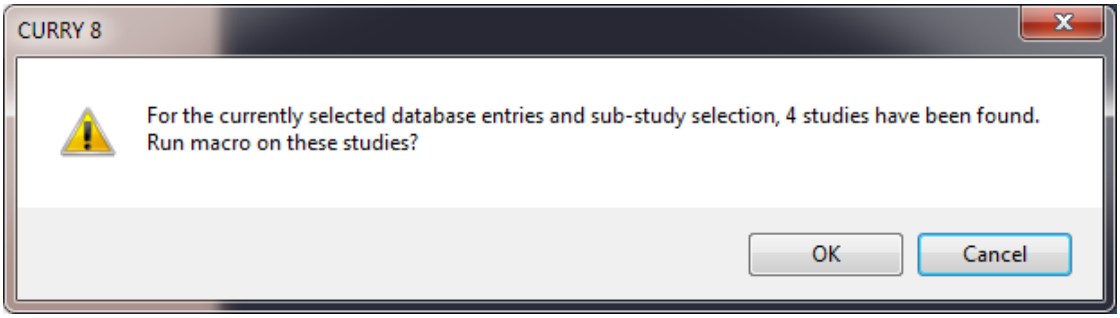
3. We want to loop the macro over several Studies. At this point, no Studies are open, but the Macro field is partially functional. We highlighted (*Ctrl+click*) the Studies in the Databaseto indicate which studies we want to be looped.



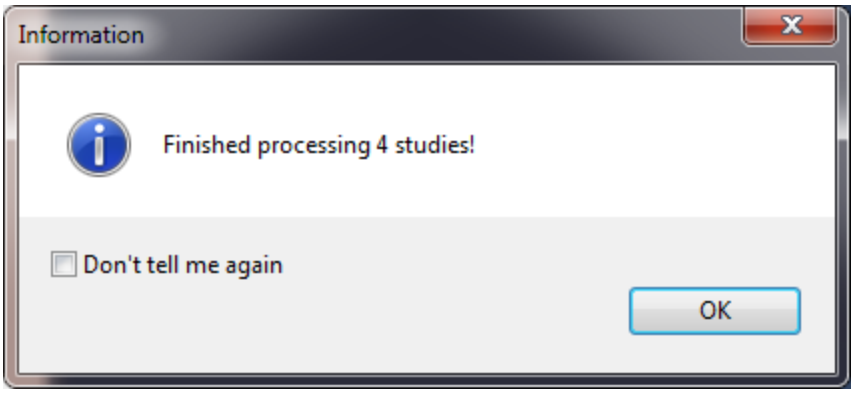
Make sure the desired macro is highlighted, then click the **Loop Over Studies** icon . A window appears allowing us to select which Studies or substudies we want to include. In this case we want only to include the studies we have selected - the **Level 0** studies.



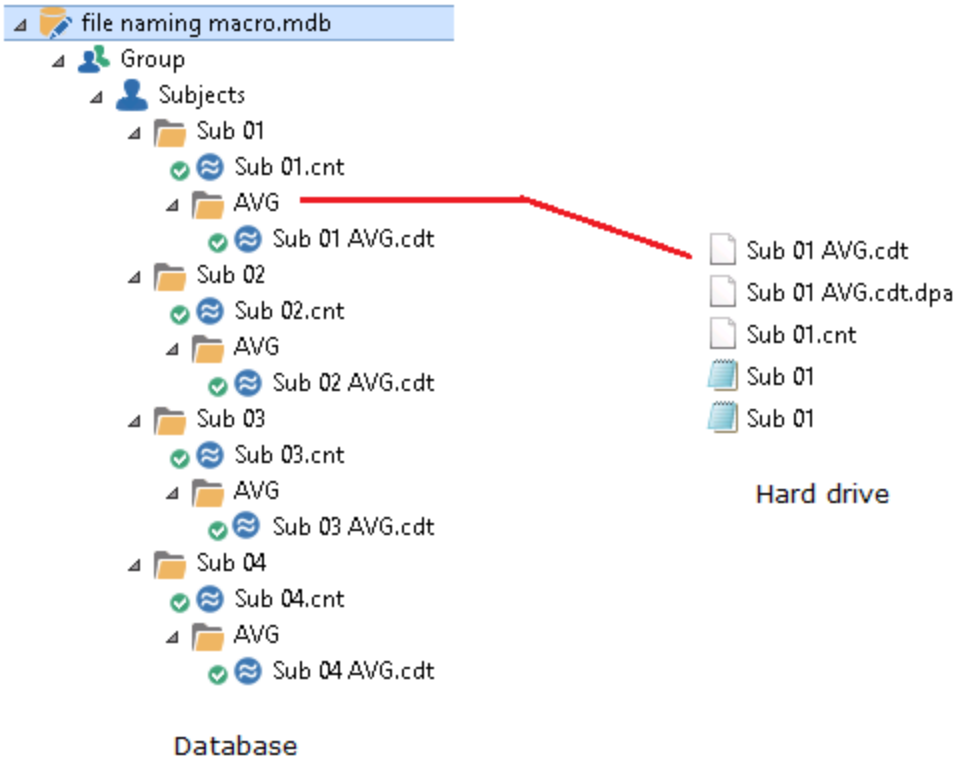
After clicking **OK**, a message appears, stating that 4 Studies were found, and asking if we wish to run the macro on these studies (confirmation). Click **OK**.



At the end of the process, you will see a message saying that the cycling has been concluded.



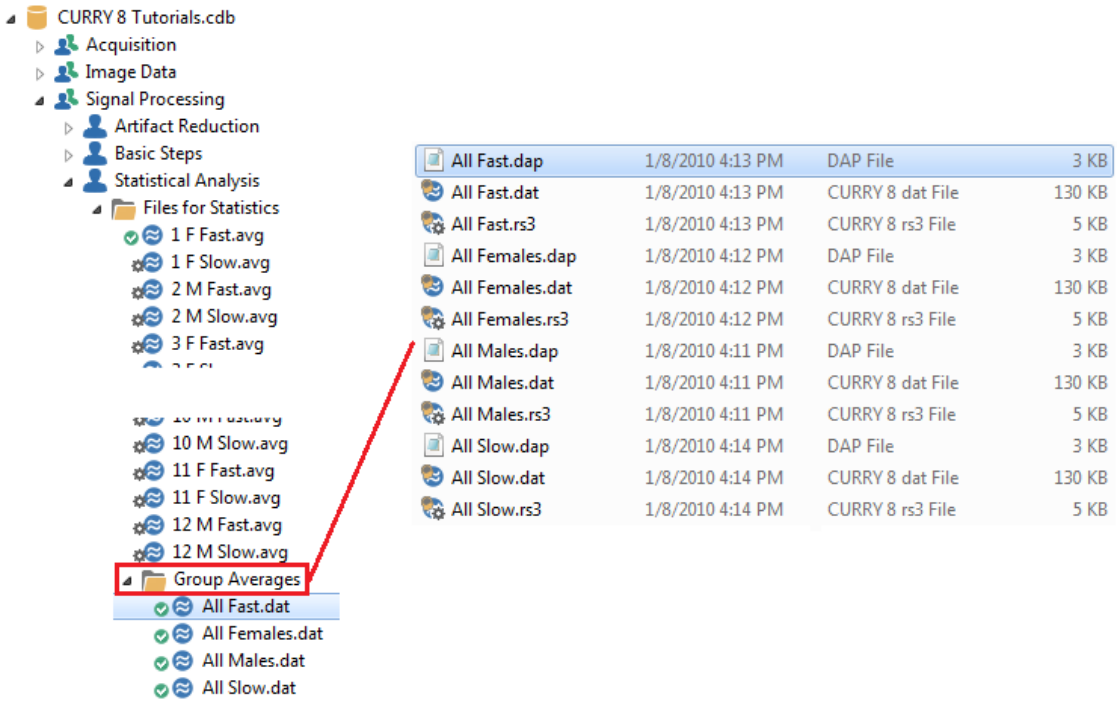
4. If you look at the Database, you will see the derived folders that have been created. If you look on the hard drive, you will see the data files and parameter files that have been saved in their corresponding folders.



Looping Over Files

You do not have to use a Database in order to use macros. For example, you might have several averaged data files, and you want to perform source reconstruction with them. You can use the **Loop Over Files** option. The files do not have to appear in the Database, but they do need to be in the same folder on the hard drive. If they are in the Database, they need to be in the same Study.

For this example, we will be using the averaged data files in the Group Averages folder, and as shown on the hard drive.



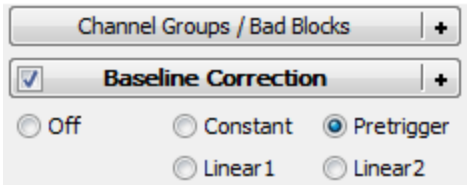
We will open the first file, create a macro containing the steps, and end with saving the source reconstruction results. Then we will apply the macro to all of the files in the folder.

1. Start with (**Open**) one file (e.g., All Fast.dat) to record the macro. Use **Open File** to open the first data file.

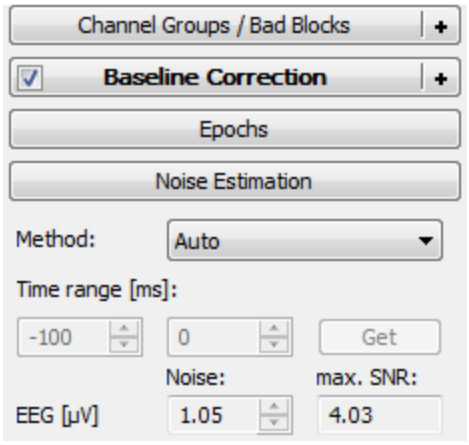
Create a **New Macro** (*Loop over files.mac*).

2. Select the **Butterfly Plot** option. In this case, we will invert the polarity (**Plus is up** icon on the Toolbar).

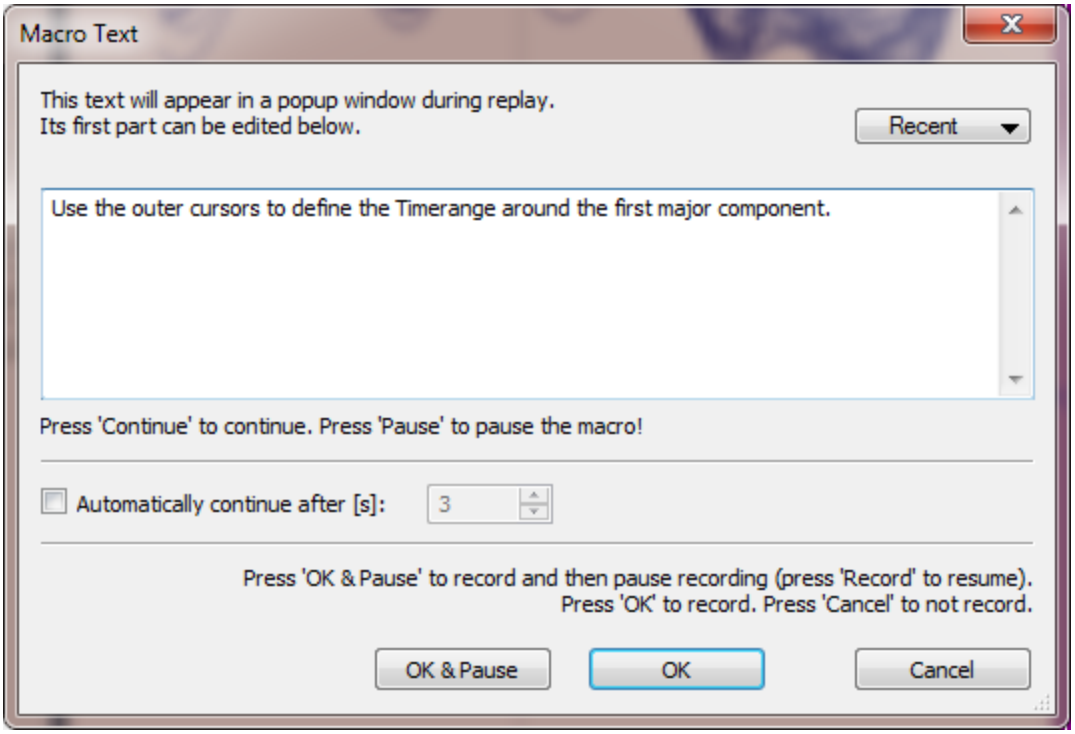
3. Perform **Baseline Correction**. In this example, we are using evoked potential data, so we selected the **Pretrigger** options.



4. Perform **Noise Estimation** using the **Auto** option (default). (This happens automatically, but it is good to get in the habit of checking).

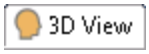


5. The next step is to select the Timerange. Since this is something that could vary from file to file, we will insert a pause with directions to set the Timerange manually. Select the **Show Popup Window and Pause or Continue** option (from the Toolbar). Enter directions to set the Timerange and click **OK**.

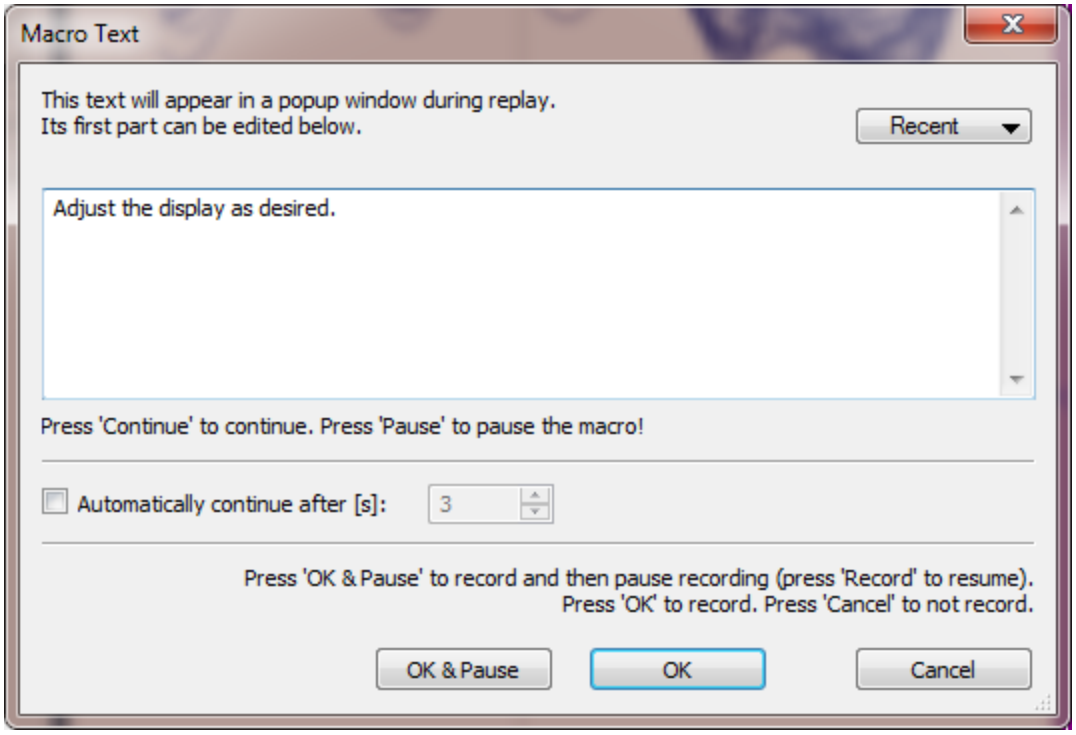


If we were to go on and set the cursors now, while the macro is recording, we would click **OK & Pause**, and the positions would be set but not recorded. In this case, just leave the cursors in whatever position they are in, knowing that the results will be affected.

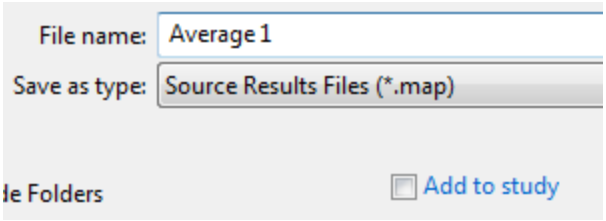
6. Select the Head Model (in this case we are using the **Standardized BEM** model). Select the type of Dipole Fit (**Fixed MUSIC**).

7. Select the **3D View** 

display. At this point we could record the exact operations that we want performed (not everything may be recorded), or we could pause the macro and set the display however we like. We will do the latter. Again select the **Show Popup Window and Pause or Continue** option. Enter directions and click **OK**.

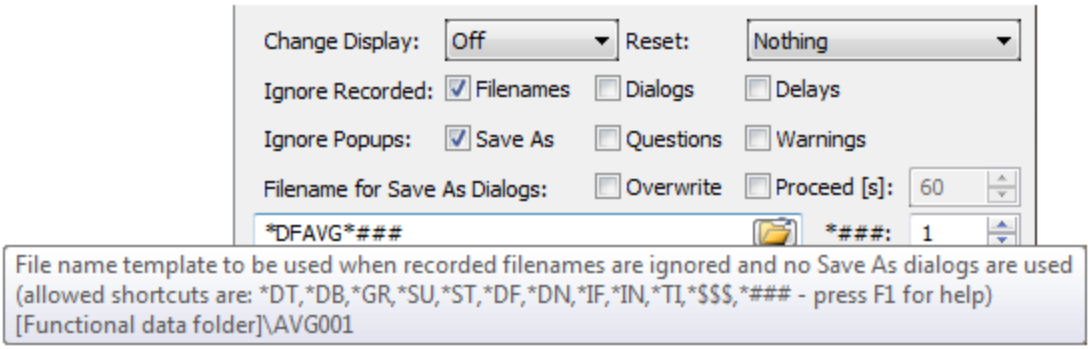


8. The last step is to save the results as a .map file. When we replay the macro, we will set it to save the filenames automatically, but for now, go to **Source Results → Save Results As**. We will be doing this without a Database, so we will not enable **Add to study**. Click **Save**.



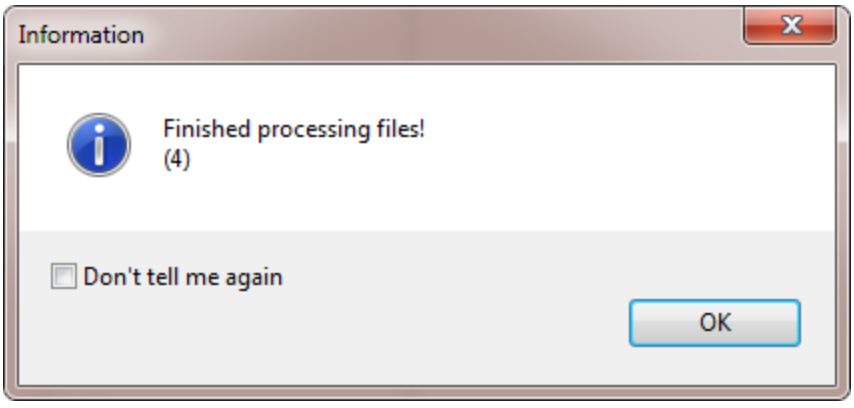
9. Stop recording the macro. Close the Study. Click No to the message, if one appears.

10. When we play back the macro, we will select the files we want to use from the [single] folder on the hard drive. We want the .map files to be saved in the same folder, using unique file names, in this case AVG001, AVG002, etc. In the **Playback** section, enable the **Filenames** option for **Ignore Recorded**, and the **Save As** option for **Ignore Popups**. For the Filename, we will use *DF (functional data folder directory), followed by "AVG" and a sequential number (*###) beginning with 1. A Tooltip appears to facilitate your selections.

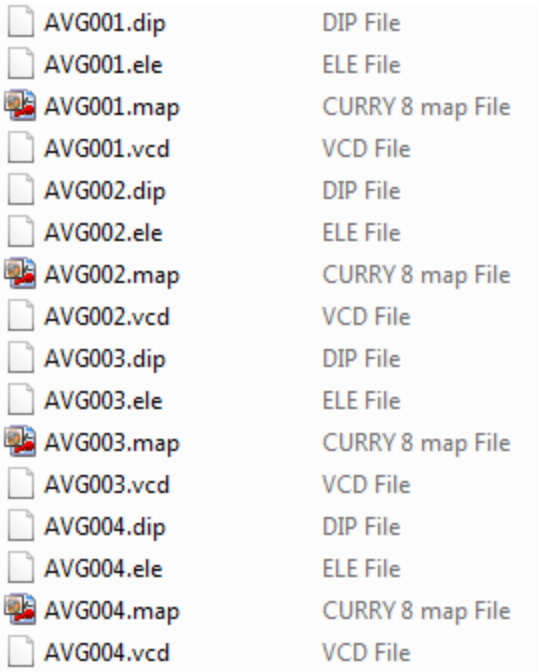


11. Now we will replay the macro (when the macro is replaying, you will see a small green arrow beside the mouse cursor). Highlight the macro file in the list, and select the **Loop Over Files** option from the Toolbar. In the Open File dialog, select the files you wish to include (use *Ctrl+click*), and click **Open**.

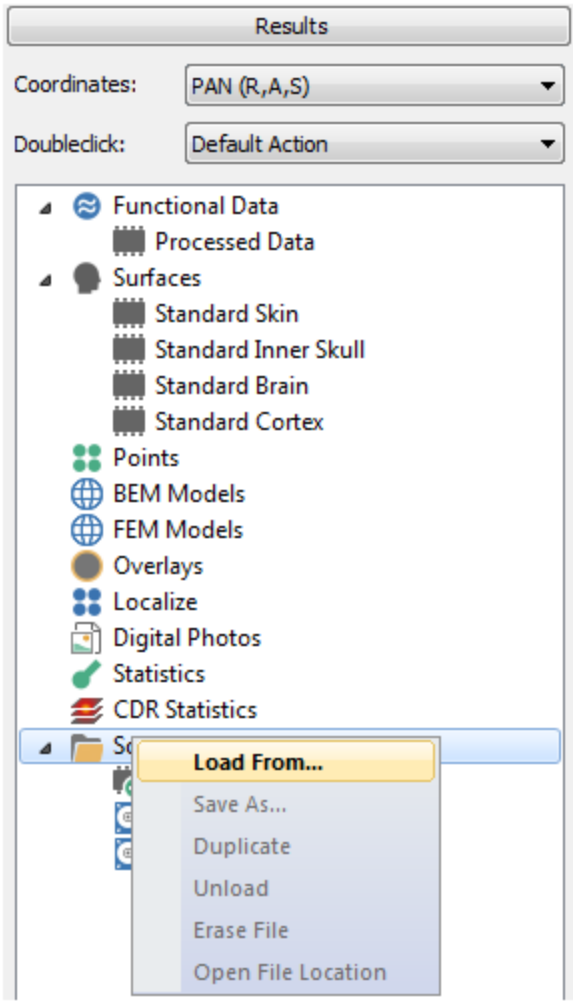
12. As the macro replays, you will have the opportunity to set the Timerange and create the final display. (These steps could have been saved as part of the macro instead). When the macro finishes cycling through the files, you will see the following message.



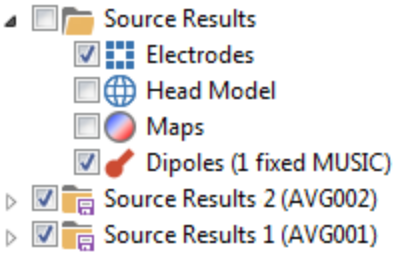
13. The sets of files that were created are seen on the hard drive.



The .dip files are the dipoles that were saved. The .ele files are the electrode positions. Vcd files are the head models. The .map files are the results that were saved, and these may be loaded back into CURRY from the Results panel. *Right click* on **Source Results** and select **Load From**.



The results are then seen in the 3D View in the Objects list, and are then treated as any other objects in the list.



Linking and Automating Macros

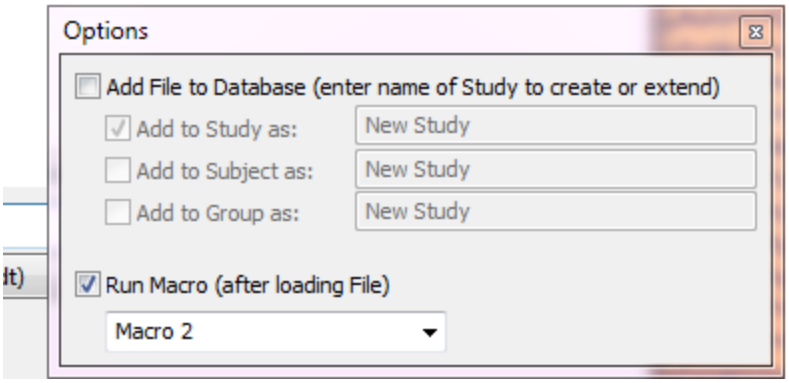
One of the realities of macros in CURRY 8 is that you cannot start a macro in one Study, and then have it continue on with additional operations in a different Study. For example, if you start with continuous data, and you then create a file containing the epochs, you may have that file open in a new 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, as described above, 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, some 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 **Save As** dialog (when you click the **Export Epochs** button).

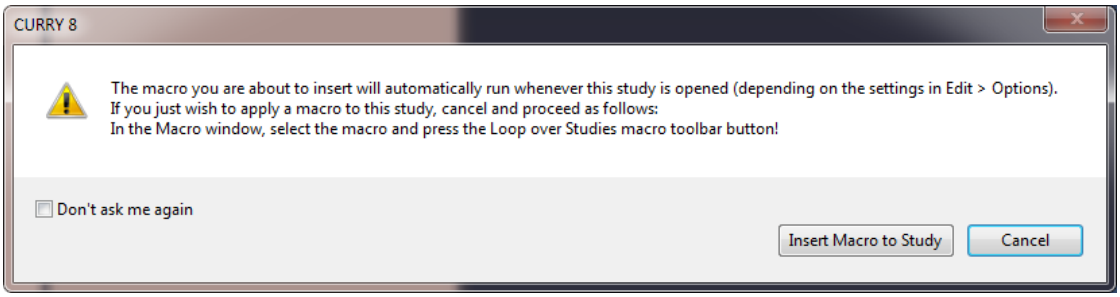


3. Enter the name of the second macro. At this point you have not created the second macro - enter the name that you will use. (If the macro already exists, you may select it from the drop-down list).

4. Record the second macro using that name, starting with the epoched data file.

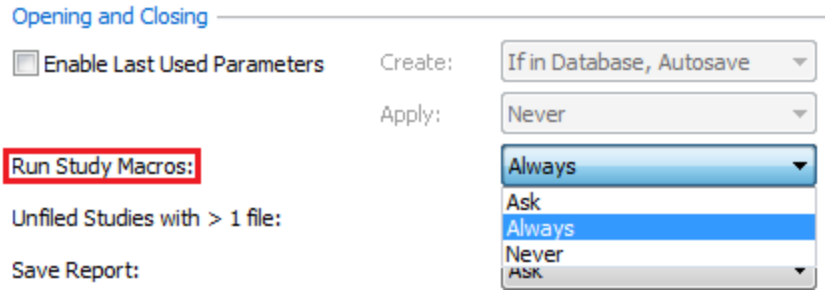
5. When you loop over the files or studies, the second macro will be called automatically.

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 Group/Subject/Study and select **Insert Study Macro**. You will see a confirmation message.



To continue, click **Insert Macro to Study** 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 demonstrations in this Tutorial have touched on the types of things that can be performed with macros. Please see the *CURRY User Guide* for more information.

2.9 Report Generation

The Report part of CURRY allows you to create a heading for the report that can be used in all reports. You can then add images or text (such as dipole solutions) to the report. There are options for copying and pasting to the report, automatically placing images in the report, and printing the report.

The first step is to create a template for the Report, which consists of the heading (the information at the top of the report that will appear on all reports). The Report is saved as an .rtf file. You can create it completely within CURRY, or you can create it in another text editor, such as Word or Wordpad. Since it is saved as an .rtf file, some formatting may be lost if you create it in Word. For example, if you wrap the text in the header around a facility logo, the wrapping will be lost in the .rtf file.

1. With a Study loaded in the working area of CURRY, select the

tab below the data display. Drag the top of it upward so that you have room to work in the display.

2. If anything is displayed already, delete it (using standard options, such as highlight and use *Ctrl+X*, or the icon on the Toolbar).

3. With an empty display, enter the text information you want to include. You can copy graphics from other sources, and paste them into the Report. A simple example appears as follows.

CURRY Source Analysis

Compumedics/Neuroscan
6605 West W. T. Harris Blvd.
Charlotte, NC 28269

Name: Date:
Gender: Age:

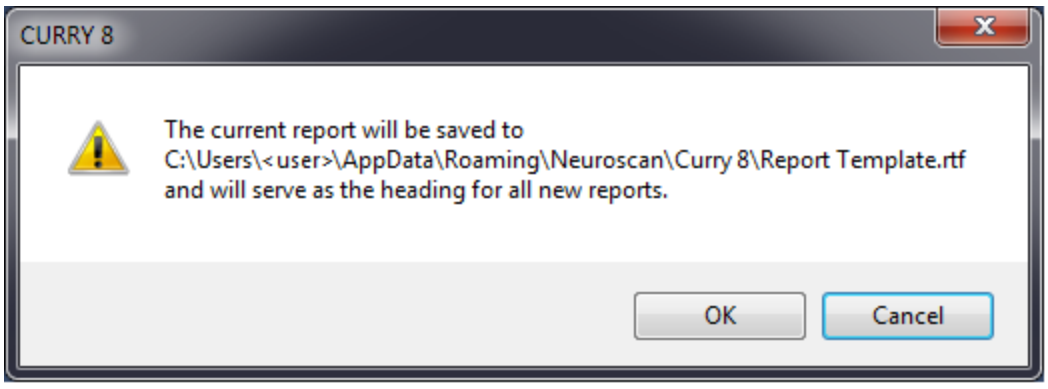
Medications:

Diagnosis:

Reason for referral:

Results

4. When you have the heading created, click (Save As Report Heading). You will see the message below, saying where the file will be saved. It will be called *Template.rtf*. That is the file (and the location) that CURRY will use for the Report template.



When you click the New Report icon , the heading will appear.

5. You can then enter the text into the heading, and add the Results as desired. There are several places in CURRY where results can be added to the Report.

From the Standard Toolbar:

copies the complete data display to the Report.

pastes whatever is in the Windows Clipboard to the Report.

From the Context Menus:

Right clicking in most displays will have an option called either **Append Image to Report**, or else **Hardcopy → Append Image to Report** (*Ctrl+Shift+R*). This typically transfers on the section of the display in which you clicked the *right mouse* button, as opposed to the Toolbar icons that transfer the entire display.

From the Report Toolbar (same as the Standard Toolbar):

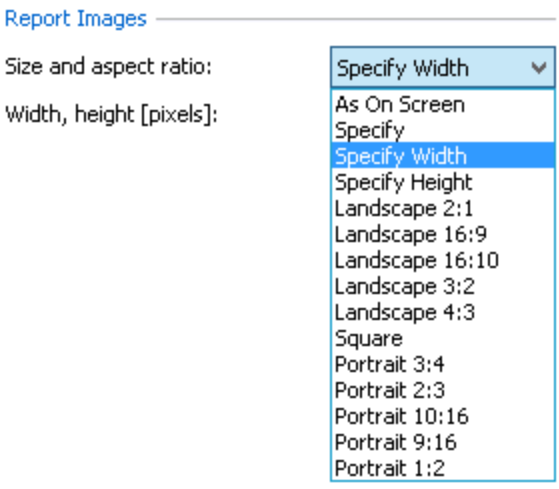
copies the complete data display to the Report.

pastes whatever is in the Windows Clipboard to the Report.

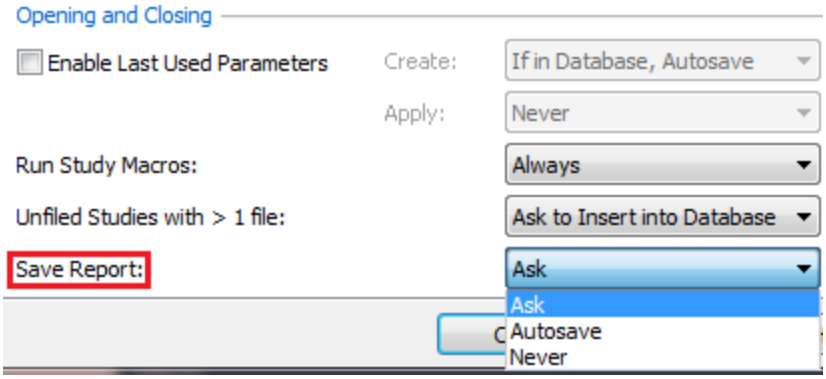
adds the dipole results to the Report (text results).

The graphics and dipole results will be placed at the next open place of the Report below the heading.

Graphics can be resized and the aspect ratio can be changed. Go to **Edit → Options → Hardcopies** and see the options for **Report Images**.



6. When you have completed the Report, click the icon on the **Report** Toolbar (or other places, such as **File → Save Report As**) to save the Report. You can control when or if the report is saved when you exit CURRY. Under **Edit → Options → Settings**, you can have the program **Ask** if you want to save the report, **Autosave** it, or **Never** save it (you would need to do it manually).



You can open the Report at a later time using the icon on the **Report** Toolbar.

Print the Report using the icon on either Toolbar.