

Analysis Tool For Diffusion Tensor MRI

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Software Download: <http://midag.cs.unc.edu> *

Abstract. Diffusion Tensor Imaging (DTI) is becoming a routine magnetic resonance technique to study white matter properties and alterations of fiber integrity due to pathology. The advanced MRI technique needs postprocessing by adequate image analysis and visualization tools. Whereas such tools have been developed at various research centers to drive methodological and clinical research, they have not become widely available as software freely distributed to the community. We have developed an integrated software package for efficient processing, fiber tracking, and interactive visualization of DTI data. This allows even non-experts to explore DTI data and to obtain results that so far were exclusive to research teams with strong computer science support. This report describes our effort to combine common, well-established processing methods for DTI data, a recently developed powerful fiber tracking method and a modern image analysis and visualization environment into an integrated tool.

The tool guides a user through the various processing stages including tensor calculation, calculation of fractional anisotropy (FA) and apparent diffusion coefficient (ADC), extraction of fiber bundles between source and target regions of interest, and two-dimensional and three-dimensional visualization of diffusion images and fiber tracts. As a result, we present an open-source, cross-platform software package which runs on various common computer architectures and operating systems and allows efficient analysis and scientific visualization. The tool is fully integrated into ITK and uses commonly used input and output formats to provide a seamless connection to packages like Analyze and SPM.

Tensor Coefficients Calculation The tensor field calculation is based on an analytical solution of the Stejskal and Tanner's diffusion equation system ([1]). The

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current version is designed to use the common directional coding proposed by Basser et al. [2]. The baseline and six directional images are loaded into the program for extraction of the diffusion tensor. The two measures most commonly used in clinical analysis, the “apparent diffusion coefficient” (ADC, trace of tensor) and the “fractional anisotropy” (FA, shape described by tensor), are calculated and can be stored as image data. Non-brain structures are suppressed by a user-defined threshold on the diffusion baseline image. All the images including the original DTI data and tensor measurement can be selected for multi-planar visualization.

Fiber-Tracking Algorithm The vector field defined by the eigenvectors associated with the largest eigenvalues is assumed to represent a good approximation to represent local white matter fiber orientations. The goal of fiber tracking, often called “tractography”, is to find likely paths through the vector field between source and target regions of interest (ROIs). We adapted and extended a previously published method [3]. The parameters for judging local continuity include minimal FA value, local curvature (angle difference between consecutive vectors), and local coherence (regularization over local neighborhood). This method provides traces with sub-voxel precision. We apply this method with a backward tracking scheme instead of a direct tracking. Paths originating from the full brain (target) are traced back to source regions, and only paths passing through these ROIs are finally kept.

We apply this method with a backward tracking scheme instead of a direct tracking. Direct tracking is a forward processing scheme which has the disadvantages that it can provide only one trace per voxel and that it has to make local decisions about path propagation. The backward scheme as used herein is initialized at each voxel of the full brain (target) with FA values larger than a user-selected threshold and traces paths backwards to the source region. Only fiber tracings passing through the user selected ROIs are finally kept. This concept, assuming that the target volume is much larger than the source ROI, makes use of the decrease of the complexity while propagating and results in a significantly improved robustness.

Program Features The DTI processing package includes the following features:

- Loading input DTI data (GIPL, ANALYZE or DICOM-META format).
- Extraction of tensors and calculation of ADC and FA values.
- 2-D orthogonal slice visualization of DTI data and of ADC and FA images.
- Loading label image with user-defined ROIs.
- Fiber tracking from target to source volumes.
- 3-D interactive visualization of fiber bundles, FA isosurface, source and target ROIs, and user-selected image channels.
- Storing of fiber bundles as sets of poly-lines (ITK data format for curvilinear structures) or as binary fiber-tract label images.
- Storing of FA, ADC image data and 3-D renderings.

This software has been developed in ITK (NLM sponsored Insight Toolkit [4]), a powerful C++ library dedicated to medical image processing. Currently, the DTI tool is available for Windows PC (Win2000 and XP), Linux, and UNIX Sun Solaris (download at <http://midag.cs.unc>).

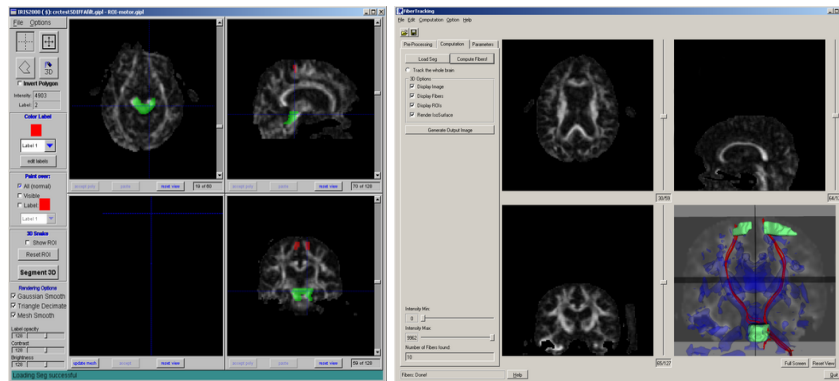


Fig. 1. Left: Definition of the ROIs with IRIS/SNAP. Right: The DTI processing tool GUI showing 2-D and 3-D visualization.

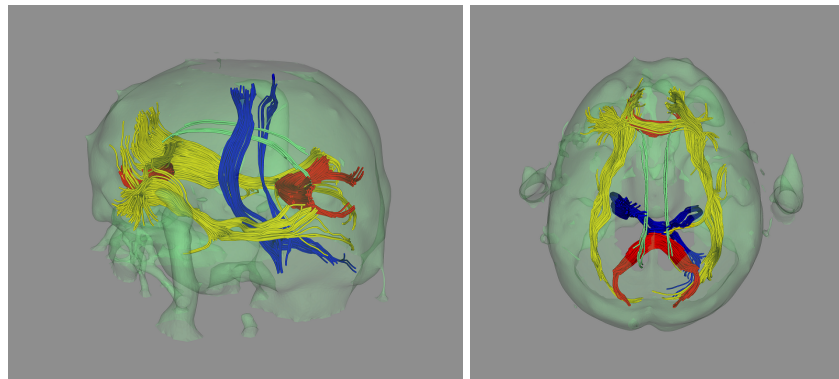


Fig. 2. Result of the reconstruction of 4 major fibers tracts (cortico-spinal tract, transversal tracts through splenium and genu of corpus callosum, cingulate, longitudinal fasciculi, shown with overlay of the intracranial cavity. DTI are acquired on a GE 1.5T scanner with an EPI sequence and 2x2x2mm³ voxel resolution.

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