A Quantitative DTI Fiber Tract Analysis Suite

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Abstract. Diffusion tensor imaging (DTI) allows a quantitative study of the underlying geometry and architecture of white matter. We have developed a suite of open source tools for quantitative analysis of DTI suitable for use in clinical research studies. We have leveraged open source tools for file IO, image processing, visualization, and user interface. The tools are designed to provide several interconnected modules to perform quantitative analysis of DTI data based on fiber tracts generated from tractography.

1 Introduction

Diffusion tensor imaging (DTI) provides quantitative measurements of the localized diffusion of water in the brain. Since water tends to diffuse more easily along axons, rather than perpendicular to them, localized diffusion measurements can give insight into the structure of the white matter in the brain. For each voxel in the image we can model the local diffusion properties of the tissue by a 3x3 symmetric matrix with positive eigenvalues. The largest eigenmode of the tensor estimates the principal direction of diffusion locally, and the relative values of the eigenvalues estimates the anisotropy of the diffusion. Tractography extracts streamlines along the principal diffusion directions as fiber tracts [1].

We have developed a prototype suite of tools suitable for use in clinical research studies to implement tract oriented statistics of DTI. As part of a modular design, we have developed two separate tools FiberTracking and FiberViewer. FiberTracking computes tensor fields from diffusion weighted images and performs tractography to analyze the architecture of white matter. FiberViewer analyzes the geometry and diffusion properties of fiber tracts produced by the FiberTracking tool with a tensor statistics analysis package. Together these tools provide an integrated package for analysis of DTI data [2]. Open source libraries are used as a base for processing, IO, and visualization. ITK provides the basis of image and object processing, while VTK and SOViewer provide the basis of visualization [3], [4], [5]. The tools described in this paper are a prototype environment for algorithm developments that can be contributed back to the open source community as ITK modules.
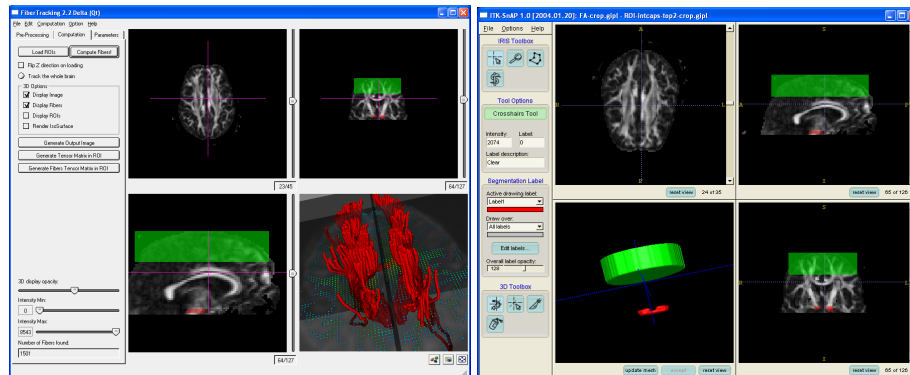
Fig. 1. a) Interface of FiberTracking program showing 3 orthogonal views of the Fractional Anisotropy (FA) image as well as a 3D view of the image and the fibers which have been generated. **b)** Interface of SNAP tool which is used for ROI specification.

2 Prototype Tools for Quantitative Analysis

2.1 FiberTracking: Tensor Estimation and Tractography

FiberTracking is a program for tensor estimation and tractography. An early version of FiberTracking was developed by Pierre Fillard and described in [6]. The purpose of this tool is (1) estimation of the tensor field from diffusion weighted images and (2) generation of fiber tracts for exploration of the architecture of the white matter. Fibers generated by the program are streamlines through the diffusion tensor field and serve as a coordinate system for understanding the geometry and connectivity of the white matter.

The full diffusion tensor field is recovered from seven diffusion weighted images by solving the Stejskal and Tanner equation using the method described in [7]. Currently the software uses the directional coding scheme defined by Basser. Data with other direction coding schemes can be processed by using an external tool, and loading the estimated tensor field directly in the FiberTracking tool. Once tensors have been estimated for each voxel, tractography can be performed to extract probable fiber bundles in the white matter. Tractography is implemented by following streamlines according to the principal diffusion directions defined by the largest eigenvector of the diffusion tensor as described in [8]. Our software uses backward tracking in order to improve stability. Seed points are generated in a destination ROI and tracked backwards. The tracts are rejected if they do not pass through the source ROI. The analysis suite uses the ITK-provided DTITubeSpatialObject data structure for representing fibers and associated traits along the fibers. The user interface for the FiberTracking program is shown in Fig. 1. ROI specification is accomplished by using Insight-SNAP which is distributed as part of the InsightApplications [9].
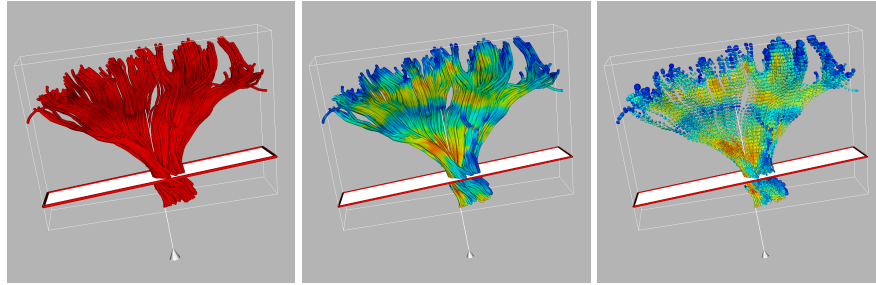
Fig. 2. Examples of fiber visualization **a)** Visualization of streamlines generated from tractography. **b)** Visualization of FA value plotted along streamlines. **c)** Visualization of the tensors representing diffusion properties along the streamlines colored by FA value.

2.2   FiberViewer: Fiber clustering and analysis

FiberViewer is a program for performing quantitative statistical analysis of streamlines generated using the FiberTracking program. The major components of FiberViewer are visualizing the geometry of fiber tracts, clustering fibers into bundles representing anatomically significant tracts, visualizing properties along the fibers, and performing quantitative statistics along bundles. Furthermore, several manual tools are provided for tasks such as cropping fibers.

Visualization of fiber tracts relies on the VTK and SOViewer libraries. The geometry of fibers can be visualized as a solid tube, or a sequence of tensors. Furthermore, various properties can be visualized as colors along the fiber. For example, users can see the fractional anisotropy, mean diffusivity, or one of the the eigenvalues of the tensor volume plotted along the fiber bundle as shown in Fig. 2.

Fibers are clustered into bundles with the normalized cut algorithm [10]. The clustering requires a pairwise distance matrix between all fibers. The distance between fibers is defined as the mean of the closest points distances of all points along each fiber. Figure 3 shows an example of the clustering. The module for performing normalized cut is a generic clustering module and is in the process of being integrated into ITK.

Fiber bundles are used as the coordinate system for quantitative statistical studies. There are two primary aspects to the statistical analysis of fiber bundles. First the geometry of the fiber bundles can be analyzed to give a shape model of the fiber tracts as developed in [11]. Each bundle is modeled by a mean 3D curve attributed with tensors which represent average tensors calculated within cross-sections. Secondly, the averaged tensors can be analyzed along fibers to show derived measures such as fractional anisotropy (FA), mean diffusivity (MD), or any of the three eigenvalues of the tensors as a function of arc-length. Tensor averaging is computed using a non-linear framework based on Riemannian symmetric spaces [12]. The tensor statistics modules are being
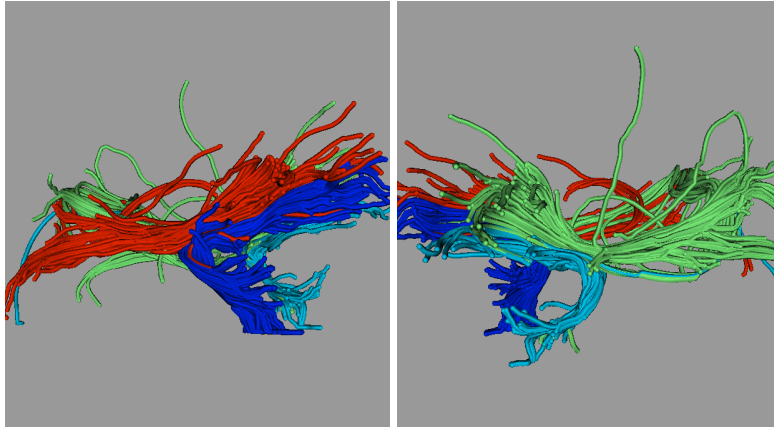
Fig. 3. Automatic clustering of sets of streamlines into four main groups which characterize left and right uncinate and longitudinal fasciculi using the normalized cut algorithm.

developed for contribution back into ITK. Figure 4 shows a model of the final result of the statistical analysis.

3 Discussion

When used in combination the FiberTracking, FiberViewer, and associated tools form an open platform for quantitative analysis of DTI data. Validation tests have been done on a single individual scanned 6 times with slightly different orientations. Results from this study have shown reproducible results for the geometry and diffusion properties along fiber tracts [13]. Currently the fiber analysis package is being used in clinical neuroimaging studies of neonates at risk for schizophrenia and of autistic pediatric subjects. The software is freely available as part of the NeuroLib software library at `http://www.ia.unc.edu/dev/`.

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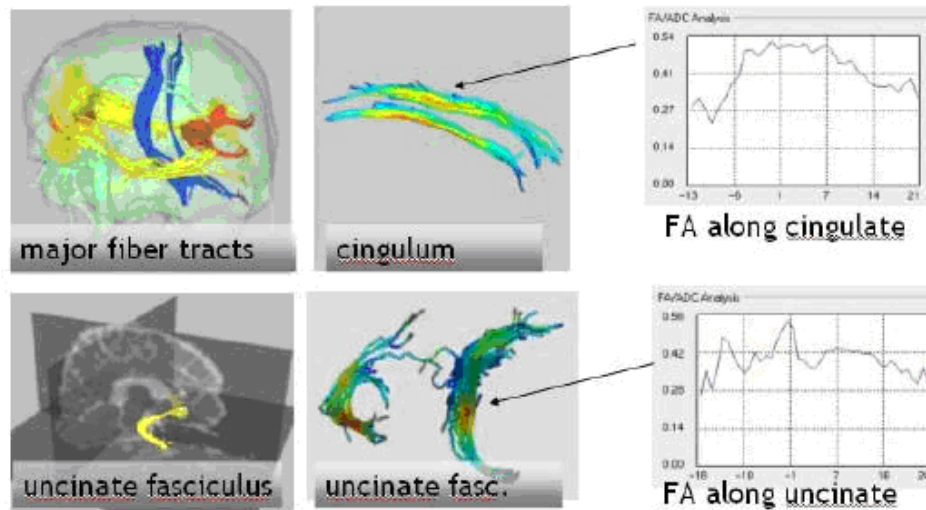
Fig. 4. Illustration of the statistical analysis pipeline. First, fibers are generated from the diffusion tensor field. Secondly, fibers are clustered into anatomically significant bundles. Finally, statistical measurement such as FA, MD, etc. are made along the fiber bundles.

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