Diffusion Tensor Image Segmentation and Classification: Project Interim Report

Dan Merget, Fiona Loke, Daniel Russakoff

Abstract

Diffusion tensor imaging (DTI), which measures the diffusion characteristics of water molecules in the brain, is an important technique for inferring the structure of the white matter tracts. However, DTI data is often underexploited in current techniques for segmentation and classification of these tracts. By incorporating not only scalar measures of diffusion such as fractional anisotropy, but also the diffusion directions, proximity to similarly oriented points, and a priori information about the location of major fiber bundles, this project aims to develop more effective segmentation and classification algorithms.

Introduction

Diffusion tensor imaging is a relatively recent technique which measures the probability distribution of water molecules' positions in a fixed time period to infer the anatomy of the surrounding tissues. One popular application is the identification and examination of the white matter tracts in the brain. DTI is currently one of the only noninvasive, in vivo imaging techniques that reflects white matter anatomy [Wiegell, Larsson, and Wedeen]. One recent study has established links between white matter structure and reading ability in children [Deutsch, Siok, Dougherty, Bammer, Gabrieli and Wandell]. Other studies have used DTI data in assessing neurodegenerative diseases such as multiple sclerosis and amyotrophic lateral sclerosis [Wiegell, Larsson, Wedeen], as well as brain ischemia in cats [Le Bihan].

The field of DTI is still relatively new, having emerged only in the mid-1980s as a type of magnetic resonance imaging procedure. Thus, finding techniques for segmentation and identification of white matter tracts is still a goal of active research. DTI is currently being used to identify some major white matter tracts, namely the corpus callosum and callosal projections, the corona radiata, and the superior longitudinal fasciculus, whose characteristics are believed to be important to ongoing investigations of reading ability [Dougherty and Wandell, personal communications].

We have a three-stage approach:

1. Preprocess the image, using fractional anisotropy (FA) to separate the white matter from the grey matter and fluid.
2. Segment the white matter with a graph-cutting technique, such as n-cuts or a modified k-means. The edge weights are computed from the entire DTI tensor and the relative positions of the voxels.

3. Classify the corpus callosum and if possible, the corona radiata and superior longitudinal fasciculus of the segmented image, by identifying prominent features of each cluster such as position and fiber orientation, and using an atlas or adaboost algorithm.

This approach is promising because it combines and extends several successful techniques. FA is a well-established method for separating the white matter from grey matter and ventricles, and from FA images alone, major white matter tracts may already be visually identified, as shown in the Results section. Graph-cutting algorithms have been used successfully in segmenting 2D images, and it tends to avoid the cumulative error of techniques that start from a single “seed” point and then progressively expand to a few neighboring voxels at a time (e.g. fiber-tracing and simulated diffusion algorithms).

Our preliminary fractional anisotropy-based threshold procedure yielded most of the white matter tracts and removed the grey matter, air, and fluid filled ventricles. The thresholding procedure also scaled the intensity of the resulting image according to a simple dot product-based similarity measure between each voxel and its six closest non-diagonal neighbors. This resulted in high intensity in one major region of interest, the corpus callosum, as compared to the surrounding ventricles and thalamus. The results suggest that the FA thresholding procedure is suitable for reducing the size of the data set and still retaining the white matter regions of interest. We hope to achieve a reasonable trade off between heavy computation and the easier O(n) thresholding algorithm followed by heavier but more accurate computation on a smaller subset of data.

Background

A diffusion tensor is a 3x3 matrix in which each element expresses a diffusion coefficient in the direction given by the subscript as shown below.

$$\mathbf{D} = \begin{bmatrix} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{bmatrix}$$

Thus, DTI data consists of a MxNxPx6 matrix containing the six independent diffusion tensors D_{xx}, D_{yy}, D_{zz}, D_{xy}, D_{xz}, D_{yz}. The principal diffusion direction is the eigenvector of **D** with the greatest eigenvalue. In addition, a number of rotationally invariant scalar-valued metrics have been defined. These are the fractional anisotropy (FA) and relative anisotropy (RA):

$$\text{RA}=\sqrt{(\lambda_1- <\lambda>)^2+(\lambda_2- <\lambda>)^2+(\lambda_3- <\lambda>)^2}\,/\sqrt{3}<\lambda>$$

$$\text{FA}=\sqrt{3\{(\lambda_1- <\lambda>)^2+(\lambda_2- <\lambda>)^2+(\lambda_3- <\lambda>)^2\}}\,/\sqrt{2(\lambda_1^2+\lambda_3^{\,2}+\lambda_3^{\,2})}$$

$$<\lambda>=(\lambda_1+\lambda_2+\lambda_3)/3$$

To date, techniques for segmentation and identification of white matter tracts have included fiber tracking algorithms as well as direct thresholding based on the principal diffusion direction or scalar measures of diffusion. These methods, however, have proven suboptimal for several reasons. The fiber tracking algorithm, for instance, fails at nerve fiber crossings and tends to be misled by other fiber bundles in close proximity to the one being traced [Fillard, Gilmore, Piven, Lin, Gerig]. In addition, referencing each tracking step to the one before leads to cumulative error [Dougherty, personal communications].

Several methods use only the principal diffusion direction or fractional anisotropy, a scalar index of the dominance of the principal diffusion direction, but no directional information. Others use measures computed from the lengths of the x-, y- and z-diffusion vectors, but this is dependent on the coordinate axes of the imaging equipment and does not reflect an actual physical parameter or quantity [Le Bihan]

The difficulty of the problem is exacerbated by the lack of a gold standard, because white matter tracts are still not fully characterized in terms of anatomical location, structure and function. [Dougherty, personal communications] Indeed, some researchers have focused on building a statistical model of the white matter tracts [Alexander, Gee, Bajcsy].

Detailed Approach

We are using a three-stage approach that consists of preprocessing, graph-cutting, and classification. In the first step, the data is thresholded at an FA of 0.15, eliminating voxels that are too isotropic to be part of fiber bundles. With the data space reduced, a more computationally intensive method may be applied for the subsequent steps. Our approach is set out as follows:

Preprocessing

In the preprocessing stage of our approach, we use the FA to separate the white matter from the grey matter and fluid. Grey matter and fluid have a low FA, because water tends to diffuse equally in all directions. Even within the white matter, the FA tends to be higher in some regions than others. For example, the corpus callosum has a very high FA near the center of the brain, and gradually disperses as it nears the occipital lobe, with an arbitrary boundary at about FA = 0.1-0.2. [Dougherty, personal communications]

FA thresholding is a very fast algorithm, and can be used without any further enhancement to obtain a reasonably good model of the brain's structure, but fails to separate one fiber bundle from a nearby bundle with a similar FA. In this project, it is used primarily as a preprocessing step for the graph-cutting algorithm, which is very memory intensive and computationally expensive by comparison.