Estimating number of fiber directions per voxel for multiple fiber DTI Tractography

C-W. Wong[1], and M. Singh[1]

[1]Radiology and Biomedical Engineering, University of Southern California, Los Angeles, California, United States

Introduction

The objective of this paper is to develop an efficient technique to estimate the number of fibers oriented along distinct directions per voxel. This information is useful in recovering individual fiber directions for diffusion imaging tractography, especially in fiber-crossing regions. It would also be useful to anatomical segmentation methods where eigen vectors are used as one of the features. The approach relies on SPM segmented white matter images as well as diffusion anisotropic values per voxel. K-means segmentation and constrained non-linear optimization techniques are used to classify voxels into one to three fiber directions. Hierarchy of diffusion models [1] are used for optimization.

Method

Diffusion MRI data were acquired using a 3T GE MRI scanner with 25 gradient directions and TR = 8.3s. A white matter (WM) probability map was first created using SPM. Next, T1 images were co-registered to the b0 images of the same subject. K-means segmentation was then conducted on the WM probability, trace, linear anisotropy (CL) and fractional anisotropy (FA) maps respectively to generate clusters. The number of clusters in the segmentation procedure is adjustable. In our study, we segment each map into 10 clusters. We define the top 5 clusters as high clusters and the bottom 2 clusters as low clusters. The middle clusters are left undefined. The number of high and low clusters for each subject can be modified.

As summarized below, the classification procedure follows a sequence in which only those voxels are classified in a particular step that have not been classified in the previous step.

1. High CL clusters are classified as one fiber direction per voxel.
2. In the remaining voxels, clusters with low diffusivity from trace are classified as either two or three fiber directions per voxel.
3. Then clusters corresponding to white matter, low trace and high FA values are classified as two fiber direction per voxel.
4. Then clusters corresponding to white matter, low trace and clusters with lowest FA values are classified as three fiber directions per voxel. These are regions with mixture of white and grey matters.
5. Then clusters corresponding to high trace are classified as zero fiber direction per voxel (or CSF).
6. The remaining unclassified voxels, which are not present in the WM probability map, are classified as grey matter.
7. For the remaining unclassified voxels that are present in the WM probability map, constrained non-linear optimization is used on a hierarchy of diffusion models [2]. Since we are dealing only with 1, 2 or 3 fiber directions per voxel, we set N = 3 and then eliminate the free diffusion term from the model, which can be re-written as follows:

$$S(1000) = S(0)\left(\sum_{i=1}^{N-1} f_i \exp(-bdt_i) + (1-\sum_{i=1}^{N-1} f_i)\exp(-bdt_N)\right)$$

where $S(1000)$ and $S(0)$ is the diffusion signal at $b = 1000$ and $b = 0$, N is the number of fiber directions per voxel

f_i is the fraction of the signal contributed by each fiber direction

$t_i = [\cos^2\varphi_i \cos^2\theta_i \quad \cos^2\varphi_i \sin^2\theta_i \quad \sin^2\varphi_i \quad \cos^2\varphi_i \cos\theta_i \sin\theta_i \quad \cos\varphi_i \cos\theta_i \sin\varphi_i \quad \cos\varphi_i \sin\theta_i \sin\varphi_i]^T$

φ and θ are the two angles defining a fiber direction in polar coordinates, d is the diffusivity coefficient.

The Diffusion MRI data for each voxel is fit into each model and estimation error is obtained.

8. K-means segmentation is performed on the estimation error of all unclassified voxels on each model. Since N = 3, three error maps are generated and the error in each model is segmented into three clusters. If the estimated error using model A is in the lower cluster m, while the error using model B is in the higher cluster n > m, it is concluded that model A is more suitable than model B. If n = m, the model with less number of variables is used.

Results and Discussion

Figures 1a and 1d show the fiber map created from the above procedure showing voxels with 0, 1, 2 or 3 fibers directions. Red, green and light blue correspond to 1, 2 and 3 fiber directions per voxel. Dark blue and grey correspond to grey matter and CSF (zero fiber per voxel). Figures 1b, e and 1c, f show the corresponding CL and FA anisotropy images of two slices respectively. It is observed that the fiber maps are consistent with the underlying brain anatomy. For the voxels with three fibers directions in white matter, it is observed that these voxels actually lie in regions where white and grey matters are likely to be mixed together, and thus are consistent with the high density of fibers expected in gray matter. The advantage of using K-means instead of simple thresholding is that K-means segmentation allows a better clustering of voxels.

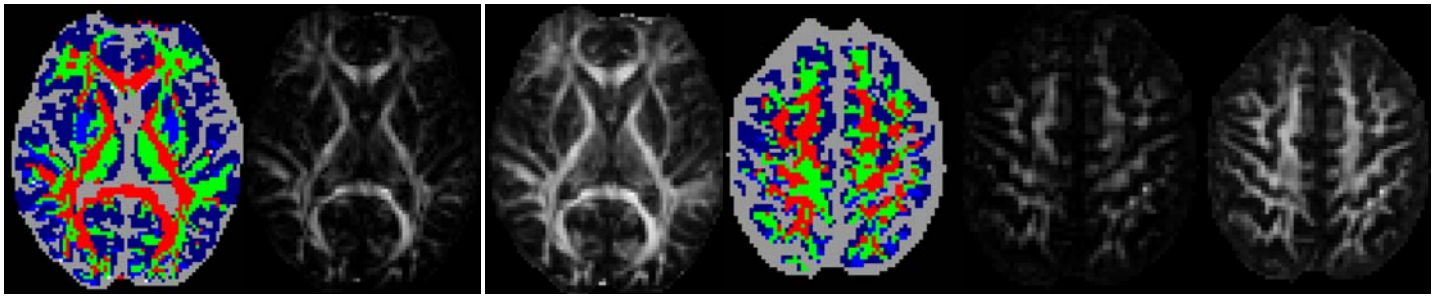

Fig. 1a Fig. 1b Fig. 1c Fig. 1d Fig. 1e Fig. 1f

[1] T. E. J. Behrens et al., "Characterization and Propagation of Uncertainty in Diffusion Weighted MR Imaging." Magn Reson Med 2003; 50: 1077-1088.

[2] S. Nedjati-Gilani, G. J. Parker, and D. C. Alexander, **"Mapping the Number of Fiber Orientations per Voxel in Diffusion MRI", ISMRM 2006.**