

## Fiber statistics in the corpus callosum

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### Introduction

Fiber tractography in diffusion tensor MRI (DT-MRI) provides a powerful tool for the identification of white matter pathways in human brain. Here, a method is proposed that leverages the ability to reliably identify white matter fiber tracts in order to quantitatively analyze structural properties of the underlying tissue. Averaging tissue properties over the length of fiber tracts in the corpus callosum (CC) provides a method for reducing the amount of information into a form that allows for easier identification of relevant features. For inter-subject comparison, continuous medial representation (cmrep) is used to identify shape correspondences. A chromosome 22q11.2 deletion syndrome study is presented to illustrate the proposed methods.

### Methods

#### DT-MRI

DT-MRI data was acquired on a 3T Siemens scanner with a single-shot, spin-echo, diffusion-weighted echo-planar imaging (EPI). The diffusion scheme incorporates one image without diffusion gradients ( $b = 0$  s/mm<sup>2</sup>) and twelve images with non-collinear diffusion encoding directions ( $b = 1000$  s/mm<sup>2</sup>). Each volume is 128 x 128 x 40 with a resolution of 1.72 x 1.72 x 3.0mm. Data was acquired for 19 pediatric patients diagnosed with chromosome 22Q11.2 deletion syndrome and 11 age matched controls. Camino [1] is used to reconstruct tensor values from the diffusion-weighted images.

#### Fiber Tract Evaluation of White Matter

The midsagittal cross-section of the CC is identified in each subject's T1 image. Affine registration provides a means for transforming the CC into the DTI space for each subject. The FACT algorithm identifies all fibers passing through the midsagittal cross-section of the CC. Each arc length parameterized fiber describes a path through the corresponding tensor volume. For each voxel in the CC, the set of all fibers passing through that voxel is determined. These fiber bundles are useful as each approximates the extent of white matter that lies in the same fiber pathway as the voxel being examined. A variety of tensor-derived scalar volumes are calculated to examine properties of the tensor such as: fractional anisotropy (FA), eigenvalues, lattice index, etc. For a given scalar property, an average value along each fiber is calculated and then for each bundle, the average of the fiber-values is used to assign a value to the associated voxel. For each property examined, this provides a 2D map of the CC containing information related to widespread tissue properties.

#### Continuous Medial Representation

The cmrep method [2] provides a continuous description of the geometric relationship between the skeleton and boundary of an object. The centers of all maximally inscribed disks (MIDs) are used to form the skeleton. This imposes a shape-based coordinate system upon the interior of the object with one coordinate along the skeleton and another from the skeleton to the MID tangency on the object boundary. This allows for the values in the 2D CC maps to be projected into a common canonical space in which CC shape differences have been effectively removed. Additionally, this allows for further reduction of dimensionality as the average fiber values may be collapsed onto the skeleton along the traverse coordinate, creating 1D profiles. These profiles are used to identify corresponding locations among subjects.

### Results

Examination of the fiber averaged FA (Figure 1A) suggests that, compared to the controls, the patients have higher FA in the genu. In order to gain further insight into the properties of the tensors, the maximum eigenvalue was examined (Figure 1B), as was the average of the remaining two eigenvalues (Figure 1C). In both cases, patients had higher values in the genu and lower values in the splenium.

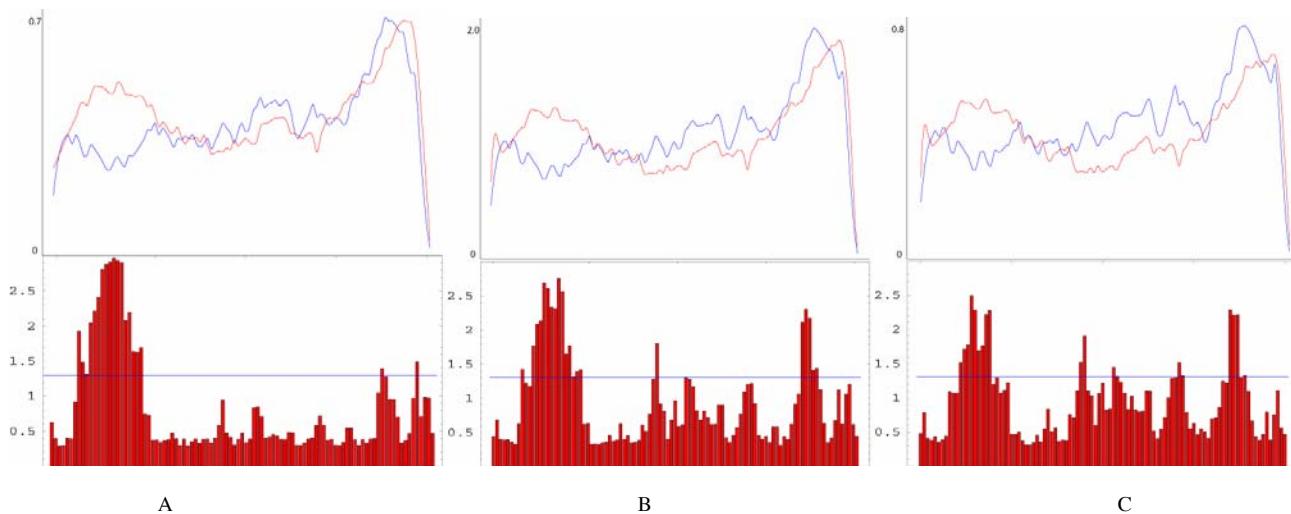


Figure 1) The top row consists of plots showing the fiber averaged values collapsed along the CC skeleton for A) FA B) maximum eigenvalues and C) average of two smallest eigenvalues. Patient values are red while control values are blue. The bottom row shows plots of -Log(adjusted p-values) for multiple point statistical tests on the difference between control group and patient group with p-value adjusted using Benjamini and Hochberg's FDR-controlling procedure [3]. The blue horizontal lines are a significant threshold corresponding to adjusted-p = 0.05.

### References

- 1) PA. Cook, et.al. ISMRM, p. 2759, May 2006. 2) H Sun, et. al. MMBIA, 2006. 3) Y Benjamini, et. al. Royal Statistical Society. Series B (Methodological), 57(1), 1995.