

Structure-Specific Statistical Mapping of White Matter Tracts

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Introduction

We present a new model-based framework for the statistical analysis of diffusion imaging data associated with specific white matter tracts. The framework takes advantage of the fact that several of the major white matter tracts are thin sheet-like structures that can be effectively modeled by medial representations. The approach involves segmenting major tracts and fitting them with deformable geometric medial models. The medial representation makes it possible to average tensor-based features along directions locally perpendicular to the tracts, thus reducing data dimensionality and accounting for errors in normalization. The framework enables the analysis of individual white matter structures, and provides a range of possibilities for computing statistics and visualizing differences between cohorts. The framework is demonstrated in a study of white matter differences in pediatric chromosome 22q11.2 deletion syndrome.

Methods and Experimental Results

Tract Segmentation in Atlas Space. Diffusion tensor images of each of the subjects in a study are normalized to a common reference atlas, shown in Figure 1. Normalization uses the Zhang et al. (2006) DT image registration algorithm. Fiber tracking using the FACT algorithm (Mori et al., 2002) is performed in atlas space. Tracked fibers are grouped into white matter tracts (fasciculi) by defining regions of interest through which the fibers in a tract must pass (or must not pass). Fibers belonging to each tract are then rasterized to form a binary image.

Model-Based Tract Representation. Deformable medial models (Yushkevich et al., 2005) are fitted to the binary segmentations of white matter tracts. These models describe the skeleton (medial axis) of each tract as a two-dimensional manifold, and describe the geometric relationship between the skeleton of the tract and its boundary. A medial model fitted to binary segmentation of the corpus callosum is illustrated in Figure 2.

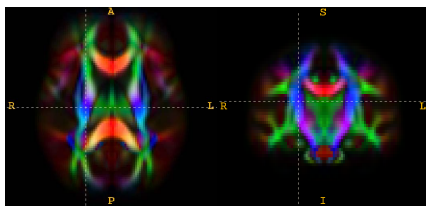


Figure 1. White matter atlas b from 31 DTI datasets from the DS22q11.2 study.

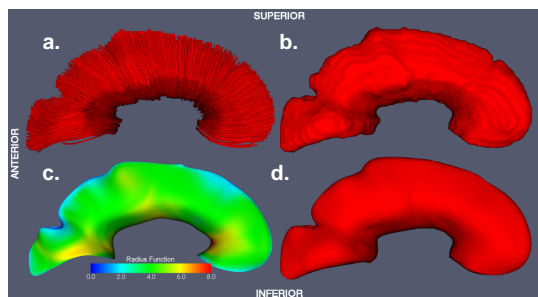


Figure 2. Model-based representation of the corpus callosum (CC). a. The fiber tracks forming the CC. b. binary segmentation. c. fitted medial model, colored by the estimated thickness of the CC. d. boundary surface associated with the medial model.

Dimensionality Reduction. The key feature of our approach is the projection of tensor-derived quantities on the interior of a fasciculus onto its medial manifold. This projection results in a dimensionality reduction along the direction orthogonal to the boundary of the fasciculus. Like smoothing, dimensionality reduction increases sensitivity at the cost of decreased specificity. However, unlike isotropic Gaussian smoothing, data reduction via medial projection respects the boundaries between structures. Furthermore, isotropic Gaussian smoothing causes equal loss of specificity in all directions, while, arguably, dimensionality reduction along the boundary normal causes loss of specificity along the least interesting direction in sheet-like fasciculi.

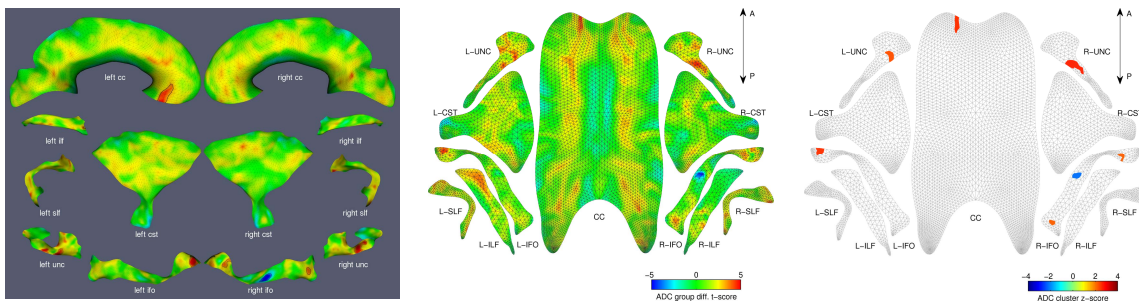


Figure 3. Examples 2D of statistical maps generated by the model-based method. Left: t -maps on manifolds. Middle: t -maps on flattened manifolds. Right: cluster analysis in 2D space.

Statistical Analysis. Projection of tensor data onto the medial manifolds of major tracts enables surface-based analysis of white matter morphology using tools similar to those associated with cortical flattening. As an example, we present results from a chromosome 22q11.2 deletion syndrome study, in which 19 children with DS22q11.2 and 11 typically developing children participated. Fractional anisotropy and apparent diffusion coefficient were compared between groups using surface-based cluster analysis with correction for family-wise error rate. Figures below show the t -maps and significant clusters for the ADC comparison. These maps are generated for fix major fasciculi: corpus callosum (CC), corticospinal tract (CST), inferior longitudinal fasciculus (ILF), superior longitudinal fasciculus (SLF), inferior fronto-occipital fasciculus (IFO) and uncinete fasciculus (UNC).

References

- S Mori et al. Imaging cortical association tracts in the human brain using diffusion-tensor-based axonal tracking. *Magn Res Med*, 47(2):215–223, 2002.
- Zhang, H., et al., Deformable registration of diffusion tensor MR images with explicit orientation optimization. *Med Image Anal*, 2006.
- Yushkevich, P. A., et al. Continuous medial representation for anatomical structures. *IEEE Trans Med Im*, 25(2):1547–1564, 2006.