Template-based Automatic DTI Fiber Bundle Labeling

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Introduction – We developed a template-based method for automatic labeling of white matter fiber bundles within whole-brain tractography models derived from diffusion-tensor imaging (DTI). The results show that the automatic labeling algorithm is able to correctly label six specific fiber bundles in two new subjects. We first ran automatic fiber clustering on DTI datasets of four healthy control subjects, then developed a template by manually labeling fiber-bundles-of-interest according to their shapes and locations, and finally automatically labeled the same fiber bundles from two new subjects using this template.

This method aims to provide accurate white-matter tracts-of-interest (TOIs) for quantitative assessment of white matter. DTI tractography methods trace sufficiently large coherent neural pathways based on diffusion characteristics in cerebral white matter [1]. These pathways can be grouped into spatially related bundles that appear to represent underlying white matter anatomy. These DTI fiber bundles provide a potentially important research tool for improving our understanding white matter development or injury and its cognitive and behavioral correlates. However, to realize this potential, efficient and accurate automated methods are needed to reliably cluster, match, and label TOIs across individuals. We present an initial attempt at automatically matching and labeling the fiber bundles.

Methods – Six healthy volunteers were imaged on a Siemens Symphony 1.5T scanner. For each, three slice packets of DWIs were acquired sagittally and interleaved to acquire a data volume of 128×128×90 with a voxel size of 1.7×1.7×1.7 mm. The Siemens MDDW protocol was used, with two b values (0, 1000) in 12 directions. Diffusion tensor images were calculated from the DWIs.

Streamtube models were generated by uniformly seeding in the data volume with a high seeding density of one seed per 0.85 mm^3 in order to cover the entire data volume. Each seeding point was jittered to avoid aliasing artifacts. The resulting streamtubes were culled, in order to remove those that were too similar to others (distance threshold = 0.85mm, minimum distance threshold = 0.475mm) [2]. The streamtubes for each subject were clustered using minimum distance clustering [3] with a distance threshold of 3.0mm. Only clusters with more than 10 streamtubes were retained.

We built a fiber bundle template by matching the clustering results on 4 data sets (S1, S2, S3, and S4) using the expert-defined optimal proximity threshold. First, we registered the non-diffusion-weighted image from every data set to one randomly selected data set using FLIRT [4]. The registration was constrained to translation, rotation, and scaling operations only. We then used the transformation matrices to register all the cluster models. For each integral curve cluster, the centroids of the starting points C_s, middle points C_m, and end points C_e were calculated. Integral curve clusters from the two subjects were then aligned and grouped according to the sum of the distances between these centroids $d_M(A,B) = \| C_s(A) - C_s(B) \| + \| C_m(A) - C_m(B) \| + \| C_e(A) - C_e(B) \|$.

To be matched together, clusters are required to be mutually closest in the feature space as well as nearer than 40 mm.

These matched clusters are then used to construct a color-labeled fiber-bundle template by picking six fiber bundle structures that are matched well across all four data sets. The six fiber bundles include left and right cingulum bundles, left and right uncinate fasciculi, forceps major, and forceps minor. A cluster, *A*, from a new subject can be matched to one of the fiber bundles, *B,* in the template by a matching score of $M(A,B) = \min_{i \in S}(d_M(A,B_i)/|A|)$, where $|A|$ is the number of curves in *A*. S is the set of subjects we used for building the template. B_i is the cluster in subject *i* that is labeled as *B*. $M(A,B)$ is designed to favor big clusters in *A* that are close to *B*. $M(A,B)$ is set to a large number if there is a non-match. The algorithm then searches for a proximity threshold on the new subject that minimizes the sum of the matching scores for all the clusters from the new subject that are matched to one of the fiber bundles in the template. We then match the automatically-thresholded clustering result to the fiber bundle template. For validation, an expert examined the resulting labeled bundles and rated them for accuracy on a 4-point Likert scale ranging from "not labeled correctly" to "very likely" labeled correctly. All six automatically rated bundles were labeled "likely" or "very likely" labeled correctly.

Results and Discussion –Fig. 1 shows the matched bundles for S5 and S6. The ratings for these bundles were all "likely" or "very likely," which we construe as correct labeling. We also experimented with other fiber bundles besides the six we chose. The ability to label them correctly across subjects varied according to the size, coherence, and context of the fiber bundles, indicating the need to improve the accuracy in the fiber bundling and labeling algorithms [5].

Conclusions – We built a labeled fiber bundle template from the automatic fiber clustering results of four subjects and automatically identified and registered six fiber bundles from two new subjects to the template. The results show that our labeling method is able to correctly identify the fiber bundles in the template for the new subjects. The method has the potential to automatically identify anatomically-related fiber tracts for quantitative study.

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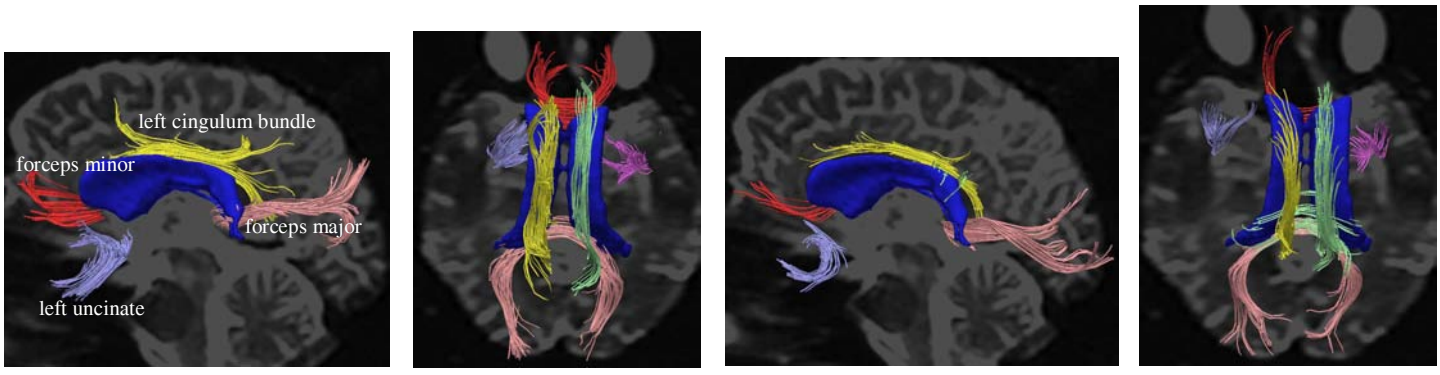
References – [1] Basser et al. 2000 MRM [2] Zhang et al. 2003 IEEE TVCG [3] Zhang et al. 2005 ISMRM [4] Jenkinson et al. 2001 Medical Image Analysis [5] Zhang 2006 Ph.D. Thesis



(a) S5 sagittal (b) S5 coronal (c) S6 sagittal (d) S6 coronal

Figure 1: Automatically labeled fiber bundles for two subjects, S5 and S6. Color is fixed on each label. Each image shows the 3D fiber bundles as well as a t2-weighted section behind them. Blue surface represents the ventricles. Note the correspondence between the same bundles across the two subjects.