Automated Registration, Segmentation and Labeling of White Matter Fiber Tracts

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Introduction

Magnetic resonance diffusion tensor imaging (DTI) has been widely used as a non-invasive tool for studying neuronal fiber pathways in the brain white matter (WM) (1). Exploitation of diffusion tensors allows a collection of open curves that represent the WM neuronal pathways to be reconstructed (2). To further characterize these pathways, those with similar geometry and locations are typically clustered into fiber bundles (3). Comparisons of corresponding WM bundles in subjects from two or more studies often reveal brain anatomical differences among different patients or patient groups, or between different stages of disease progression. To facilitate such comparisons, a registration algorithm is proposed to robustly align whole-brain fiber sets with a constructed reference bundle model, so that fibers from different datasets can be transformed into a common coordinate system and further segmented and labeled automatically using the reference bundle.

Methods

(1)Imaging: DTI of eight healthy human subjects was performed *in vivo* using a 3T Philips Achieva MR scanner with 32 non-collinear weighting directions (b = 1000 s/mm^2), which generated a volume of 256×256×120 mm^3 at an isotropic resolution of 2×2×2 mm^3 for each subject.

(2)Fiber reconstruction: Whole-brain fiber sets for the eight DTI data volumes were reconstructed by using a first order Euler tracking method with step size of 2 mm. Each curve was then resampled uniformly to N=30 points for further processing.

(3)Construction of reference bundles: By referring to the known anatomy, nine specific reference WM fiber bundles were manually segmented for one arbitrarily chosen fiber set. These bundles are left and right corticospinal tracts (CST), left and right medial lemniscus (ML), left and right superior cerebella peduncle (SCP), middle cerebella peduncle (MCP) and the lower half of genu (GCC) and splenium bundle (SCC) respectively. Assuming that the distribution of fibers in the whole brain is modeled with a Gaussian mixture model, a reference bundle model was constructed by computing $\pi_{x,k}, \mu_{x,k}, \sigma_{x,k} (k = 1,2,...,9)$, which are the mixture proportion, central fiber and covariance matrices for each bundle (x) respectively.

(4)Registration algorithm: The goal of the registration is to compute a transformation T that warps target fibers to optimally match the reference bundle model. The degree of match is measured by the conditional probability as follows:

$$p(y \mid \pi_x, \mu_x, \sigma_x, T) = \prod_{j=1}^{M} p(y_j \mid \pi_x, \mu_x, \sigma_x, T) = \prod_{j=1}^{M} \sum_{k=1}^{K} \pi_{x,k} \prod_{i=1}^{N} \frac{1}{(2\pi)^{3/2} \mid \sigma_{x,k,i} \mid^{1/2}} \exp(-(T(y_{j,i}) - \mu_{x,k,i}) \sigma_{x,k,i}^{-1} (T(y_{j,i}) - \mu_{x,k,i})^T), \quad (1)$$

where $y_{j,i}$ represents the ith point on the jth fiber (y_j), $\mu_{x,k,i}$ the mean coordinate of all the ith points on the fibers in the kth reference bundle, and $\sigma_{x,k,i}$ their covariance matrices. In this work, T was chosen to be Thin-Plate Spline (TPS) due to its smoothness in deformation fields and closed-form solution for warping and parameter estimation. Taking the prior distribution $p(T)$ of TPS into account, we convert the fiber registration problem into a Bayesian maximum a posteriori (MAP) problem, which aims to estimate a transformation $\hat{T}$ that maximizes a posteriori $p(y \mid \pi_x, \mu_x, \sigma_x, T) p(T)$. Such an optimization problem was solved by using an Expectation Maximization (EM) algorithm. Given the resulting $\hat{T}$, the target fibers can be transformed into the reference coordinate system, and thus can be automatically labeled using the reference bundles.

(5)Evaluation: With the reference bundle model, the proposed registration algorithm was applied to the other seven target fiber sets and then automatically labeled the fibers. First, the post-registered target bundles were visually compared with the reference. Second, the automatically labeled bundles were mapped back to their native spaces and then quantitatively compared with manually labeled target bundles (regarded as "ground truth"). Their differences were measured by mean square root errors (MSE) as follows:

$$MSE_k = \sqrt{\sum_{i=1}^{N} (\mu_{k,i}^{true} - \mu_{k,i}^{estimated})^2 / N}, \quad (2)$$

where $\mu_k^{estimated}$ and $\mu_k^{true} (k = 1,2,...9)$ denote the central fibers of estimated target bundles and the ground truth respectively.

Results

It can be appreciated from Figure 1 that the post-registered target bundles show the locations and courses that are quite consistent with the reference (left panel), which indicates the algorithm is capable of registering target fibers to the reference bundles non-rigidly. Table 1 summarizes the mean and standard deviation of the MSE over seven target data sets for each type of bundle. The mean MSEs are below one voxel for all bundles except ML and SCP (Left), whose mean MSE is slightly larger. These results show that the algorithm automatically generated bundles that are consistent with the ground truth at a sub-voxel accuracy for most of the bundles studied. The relative larger mean MSE in ML and SCP (Left) may be caused by overlap of significant portions of the two bundles.

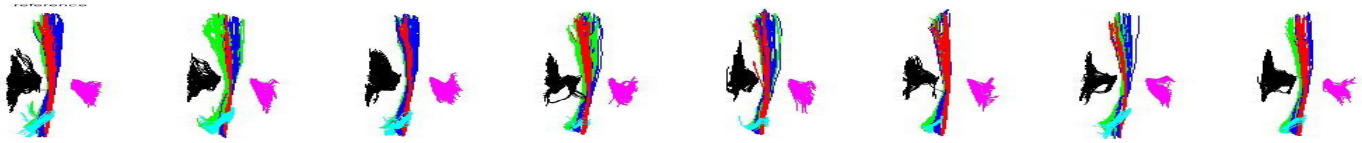

Figure 1 Sagittal view of reference (1st) and seven post-registered target bundle sets (the rest). Different fiber bundles were plotted with different colors. (red: CST, blue: ML, green: SCP, cyan: MCP, SCC: black, GCC: magenta)

	CST(Left)	CST(Right)	ML(Left)	ML(Right)	SCP(Left)	SCP(Right)	MCP	SCC	GCC
Mean	0.5265	0.5717	1.1431	1.3629	1.4364	0.9247	0.3770	0.8139	0.5834
Std	0.4160	0.2821	0.8351	0.8839	1.1779	0.6181	0.2241	0.2363	0.2530

Table 1 Mean and standard deviation of MSE with the ground truth (unit: voxel)

Conclusion

To conclude, a novel algorithm is proposed to align a whole-brain WM fiber set to a reference bundle model. The proposed algorithm also offers an automated tool for consistently segmenting and labeling WM fiber bundles, thus allowing homologous bundles to be compared in a common reference space. Experiments with DTI data from eight human brains have shown good similarity of the reference to the post-registered target bundles, and high consistency with manually segmented ground truth.

References

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