A Spatial Model of White Matter Fiber Tracts

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Introduction: Real-time visualization of fiber tracts is crucial for neurosurgical application to minimize post-operative neurological deficits while maximizing tumor removal [1]. Pathways of the fiber tracts obtained from DTMRI data using a tractography method are being visualized along with anatomical data for this purpose. Although this provides a viable representation of the underlying connectivity between the functional regions, the complexity of the structure limits the usefulness of the method for surgical application. From a surgical point of view, only the spatial extent of the fiber tracts would suffice in order to prevent damages during operation. A hull that surrounds all fibers of a certain tract has been proposed to represent the extent of the tract for this purpose [2,3]. However, information enclosed by individual trajectories is lost when constructing the hull. Such information is valuable when registering pre-operative data onto intra-operative acquisitions or when performing quantitative analyses during the post-operative course. To preserve an aggregate of the information for each fiber tract requires that the point correspondence between individual trajectories belonging to that tract is obtained. Finding the point correspondence of 3-D curves in a large dataset is not trivial and that is why this task has not been rigorously tackled in the past.

Method: We applied the method on DT-MR data acquired from healthy volunteers with b-factors of 5 and 750 s/mm^2 for baseline image and six gradient directions, respectively. The spatial resolution of the images, acquired in the axial direction was 1.054×1.054×2 mm^3. Trajectories are initiated from a region of interest in the white matter and traced through the streamline tractography. Expectation maximization is used to cluster these trajectories into bundles with user-defined initial centers. Point correspondence is readily obtained at each EM iteration by building a 3-D distance map and a label map for each cluster centers (Fig. 1). The label map consists of regions, each composed of all points in the space that have their minimum distance to a specific point on the cluster center. Therefore, projecting any curve on this label map determines the point correspondence of each of its samples to the center based on the region that sample is located in. A gamma mixture model is used to describe the distribution of the distance between trajectories and cluster centers. The output of the algorithm is the probabilistic assignment of the trajectories to each cluster and their point correspondence. A spatial model of the tract is easily and accurately calculated as the average trajectory (cluster center) and the standard deviation of its position at each point. With the intra-cluster point correspondence known, calculation of other quantitative parameters averaged over all trajectories that belong to a specific tract is also straightforward.

Results: Clustered white matter trajectories for corpus callosum (CC) and middle cerebellar peduncle (MCP) are shown in Fig. 2(a) with their spatial model as the average trajectory and isosurfaces defined as the average plus/minus the standard deviation in Fig. 2(b). Results of clustering roughly 3000 trajectories into 25 groups and their associated spatial model are illustrated in Fig. 2(c) and (d). As an example of quantitative analysis, the average curvature and fractional anisotropy (FA) along the cluster center for MCP are shown in Fig. 3. Therefore, building such models for the fiber tracts is not only beneficial for the neurosurgical applications but also maintains enough information to perform a quantitative analysis.

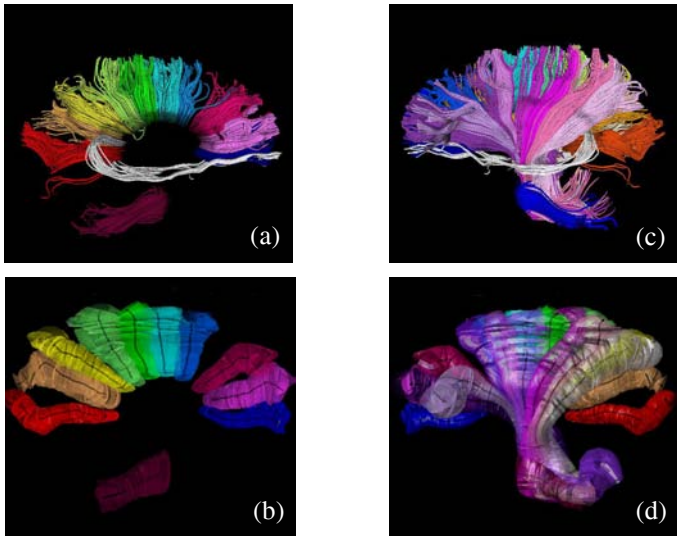

Fig. 2 Trajectories of (CC) and (MCP) tracts clustered into bundles (a) and their corresponding spatial models (b). Each model is represented by the average trajectory and the isosurfaces defined by the point-wise standard deviations. Similar results are shown for roughly 3000 trajectories from major white matter fiber tracts in (c) and (d).

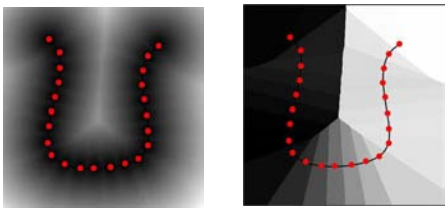

Fig. 1 Distance map and label map generated for a sample 2-D curve.

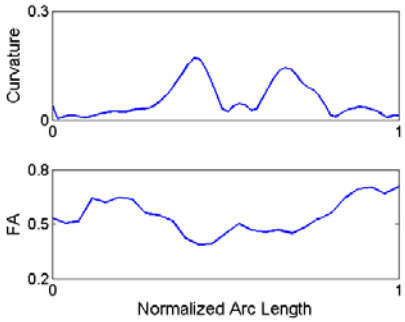

Fig. 3 Example of quantitative analysis results for MCP tract. With point-correspondence determined by the algorithm, accurate averaging of the quantities is possible.

Conclusion: A method was presented to construct a model of fiber tracts defined as the average trajectory and its spatial variation for each bundle. Knowledge of point correspondence between the trajectories in each fiber tract is essential for building this model as well as for accurate quantitative analysis. This is achieved by constructing a distance map and a label map for each cluster and at each iteration of the EM algorithm. The proposed model provides a viable approach for visualizing fiber tracts for neurosurgery applications and for quantitative analyses during post-operative course.

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References:

[1] I.-F. Talos, et al. Diffusion tensor and functional MRI fusion with anatomical MRI for image-guided neurosurgery, MICAAI, 407–415, 2003.
[2] Z. Ding, et al. Case study: reconstruction, visualization and quantification of neuronal fiber pathways. IEEE Visualization, 453–456, 2001.
[3] F. Enders, et al. Visualization of white matter tracts with wrapped streamlines, IEEE Visualization, 51–58, 2005.