Automatic Tractography Segmentation by Morphological Continuity Clustering

F-C. Yeh[1], and W-Y. I. Tseng[2]

[1]Department of Biomedical Engineering, Carnegie Mellon University, Pittsburgh, PA, United States, [2]Center for Optoelectronic Biomedicine, National Taiwan University College of Medicine, Taipei, Taiwan

Introduction Several tractography segmentation methods have been proposed to cluster the fibers tracts [1-4]. Most of the methods are based on training data provided by experts [3][4], which did not include short or unknown fiber tracts. Another clustering method depends on the assumption of the cluster number [2]. The cluster results may not be correct if the assumption is violated. In this study, we developed a fully automatic method that is unsupervised and without predefining the number of the clusters. It is based on the concept that the fiber tracts in the same cluster share the morphological continuity, which results in a continuous surface of the fiber bundle. This morphological continuity condition is used to construct the clusters that segment the whole brain fiber tracts.

Theory Based on the concept of morphological continuity, we claim that for any two fiber trajectory $t_i(r_i)$ and $t_j(r_j)$, they belong to the same cluster if the following morphological continuity condition is satisfied:

$$\max_{r_i} \min_{r_j} \| t_i(r_i) - t_j(r_j) \| < \delta$$

where δ is a predefined error distance about 1~2 pixel spacing. This condition is used to merge fiber tracts into a cluster or merge two clusters into one. Based this testing condition, the proposed algorithm input fiber tracts sequentially and check the condition with any eligible fiber tracts to determine the current clustering status. Note that the eligible tracts for merging could be reduced by keeping a fiber passing table, thus avoiding a computation complexity of $O(N^2)$, where N is the number of fibers. Moreover, the morphological continuity condition could be transformed into a set inclusion operation without computing the distance metric. This approach could speed up the checking time and improve the efficiency.

Materials and Method A 30-year-old healthy volunteer was scanned on a Siemens 3T TIM scanner by using a 32-channel head coil and single-shot echo planar imaging sequence. The field of view was 200mm x 200mm, matrix size 80x80, slice number 56, slice thickness 2.5mm, resulting in isotropic voxel size of 2.5mm. The maximum b-value was 6500, and a total of 515 diffusion gradient sampling in grid arrangement were used. The TR was 10600ms, TE 148ms, and the scanning time around 1 hour and 40 minutes. The image was reconstructed by generalized q-space imaging (GQI)[5] on DSI studio and tractography generated by streamline tracking algorithm with 100,000 seeding points placed in the white matter area. The generated fibers tracts were then clustered by the proposed MCC method with error distance equal to 1 pixel spacing. The overall computation time for clustering is about 40 minutes on a personal laptop.

Results In Fig. 1, we presented several clusters that correspond to certain well-known fiber tracts, including (a) corpus callosum, (b) corona radiata, (c) inferior longitudinal fasciculus, (d) arcuate fasciculus, (e) cingulum. In Fig. 1a, the cluster only included the middle portion of the corpus callosum, while the anterior and posterior portions were missing. Similarly, in Fig. 1b, the cluster only contained the middle portion of the corona radiata whereas the anterior and posterior portions were not included. The overall clustering result is presented in Fig. 2, where the tracts are painted with the color defined by the cluster. The cluster for corpus callosum (red) and corona radiata (blue) could be observed in the view from the top.

Discussion and Conclusion We demonstrated that the proposed algorithm is able to offer some meaningful clusters that correspond to several well-known fiber tracts. Also, the proposed method could cluster the whole brain fiber tracts automatically without any training data provided by the experts. This feature could further facilitate cortex segmentation for brain connectome study.

In spite of these advantages, we still noted several drawbacks of this method that requires further improvement. First of all, the proposed clustering method requires that the tractography is detail enough to achieve the continuity condition. If the tractography does not have a homogeneous coverage, then in certain areas, the fiber tracts cannot be correctly clustered, resulting in over-segmentation or missing-fiber condition. Better seeding strategy is to be developed to give a homogeneous coverage of the whole brain. Also, we observed that changing the error distance δ results in different segmentation results. Future research will be focused on a better choice of the parameter.

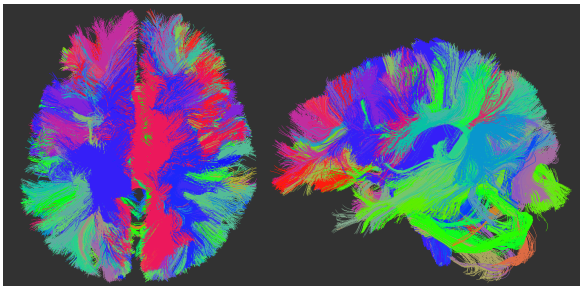

Fig2. The clustering results viewed from the top (right) and from the left side. Fiber tracts are colored according to their clusters.

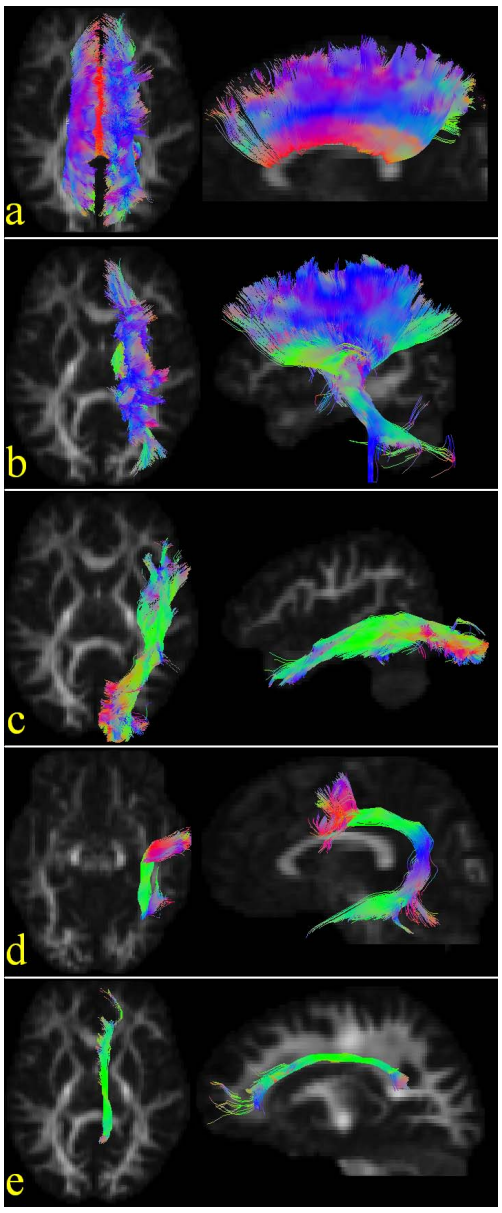

Fig1. Selected clustering results in views from the top side (left) and from the left side (right). The clusters seem to correspond to several well-known anatomical structures.

Reference [1] Hagmann, et al., Neuroimage, 32:665-75, 2006. [2] O'Donnell, et al., AJNR Am J Neuroradiol, 27:1032-6, 2006. [3] O'Donnell and Westin, IEEE Trans Med Imaging, 26:1562-75 2007. [4] Zhang, et al. IEEE Trans Vis Comput Graph, 14:1044-53, 2008. [5] Yeh et al. ISMRM, 2009.