Unsupervised fiber reconstruction of distinct anatomical structure using diffusion tensor MRI

W. Li[1], J. Tian[1], J. Dai[2]

[1]Institute of Automation, Chinese Academy of Sciences, Beijing, China, People's Republic of, [2]Department of Neuroradiology, Beijing Tiantan Hospital, Beijing, China, People's Republic of

Introduction

Determination of neuronal fiber pathways with distinct anatomical structure in vivo is of significant neurological and clinical interest [1]. It can uncover different fiber bundles, analyze the connectivity of different brain functional regions, and potentially guide brain surgery. Most current methods generate fibers with distinct anatomical structures by manual selecting specified brain regions and tracing fibers initiated from them[2,3]. Another strategy starts by seeding large regions of the brain, followed by selecting tract groups that cross a specified region of interest[4]. The two method are both laborious and time consuming. In this study, we propose an unsupervised method to reconstruct fiber pathways with distinct anatomical structure while tracing fiber pathways simultaneously.

Material and Method

The images used for this study were acquired with a 3.0T clinical MRI scanner (General Electric Medical Systems, Milwaukee, WI, USA). Diffusion tensor imaging was performed using a single-shot SE-EPI pulse sequence with 24cm×24cm field of view, TE/TR 87/8499ms, b value of 1000mm-2s, 13 directions (voxel size: 0.9×0.9×3.5mm). The diffusion tensor eigenvalues and eigenvectors were calculated from DTI data, and fractional anisotropy (*FA*) maps were generated using locally written software. The automatic fiber reconstruction approach consists of 3 main steps:

(1)*Selecting starting points.* We select the seed points on the 2D FA maps with high anisotropy (*FA*>0.5) within the distinct anatomical structure that we interested in.

(2)*Fiber tracking.* White matter tractography of fiber assignment by continuous tracking (FACT) method is adopted[5]. Initiated from the starting points, the anatomical fibers are bidirectionally traced. If the traced fiber pathway originates from the seed points, it will be accepted; if it originates from other starting points, it will be accepted only when it has higher similarity *SI* with the accepted fiber pathway than the similarity threshold T_{si} ($SI > T_{si}$). Two fibers are considered high similarity when they have similar direction of fiber propagation, similar shape, and are separated by a small distance[6]. *SI* between two fiber pathways F_i and F_j is defined as follows:

$$SI_{i,j} = V_{i,j} \cdot \exp\left(-D/C\right)$$

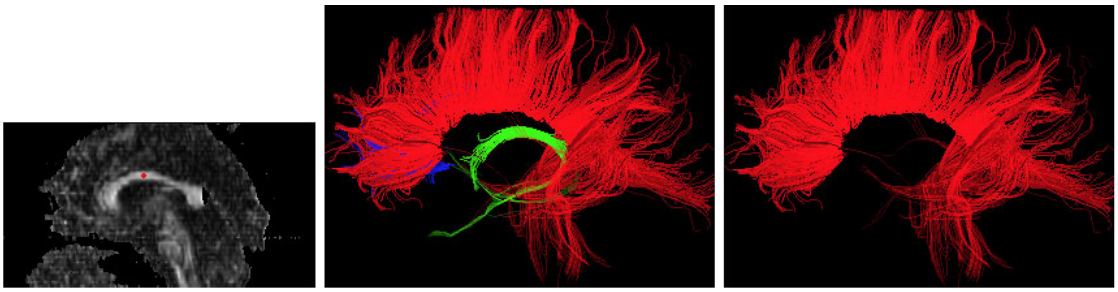
where $V_{i,j}$ is the corresponding direction difference of the two fiber; *D* is the mean Euclidean distance between the two fibers; *C* is the coefficient for *D*, which regulates a trade-off between *D* and $V_{i,j}$.

(3)*Detecting other starting points.* If the neighboring point of the starting point in the 2D FA map satisfies certain conditions, such as the difference of *FA* of the two neighboring points higher than threshold T_{fa}, it will be the new starting point.

Step 2 and step 3 interactively proceed until no other point is selected as the new starting point.

Results

Figure 1 shows the unsupervised reconstructed fibers of corpus callosum. Initialized from the selected seed points, fibers of corpus callosum are automatically reconstruction. To validate the importance of the limitation of *SI*, Fig. 1(b) shows the reconstructed fibers without *SI* limitation. Without *SI* limitation, some fiber pathways which don't belong to corpus callosum are erroneously traced (colored in blue and green), which is almost orthogonal to correctly traced fibers of corpus callosum (colored in red). The fibers reconstructed by our method (Fig. 1c), with the limitation of *FA* and *SI*, are comparable with the fibers reconstructed by manual selecting specified brain regions and just tracing fibers initiated from them.



(a) (b) (c)

Figure 1. Fiber reconstruction of corpus callosum. (a) FA map and user selected seed points (in red). (b) The reconstructed fibers without *SI* limitation. (c) The reconstructed fibers with limitation of *FA* and *SI*. In (b) and (c), red indicats the corrected traced fibers of corpus callosum; blue and green indicate the erroneously traced fibers.

Discussion and Conclusion

Initiated from the selected seed points and the detected starting points, all possible fibers are automatically reconstructed; new starting points are automatically detected using the values of *FA;* with the limitation of *SI*, erroneous fiber pathways, cause by noise, partial volume effect, and the overlapping of *FA* value, are successfully excluded. Although in our method fiber tracking is based on FACT method, other more robust fiber-tracking algorithm will be used in our future study. In summary, we have developed a new approach to reconstruct neuronal fiber pathways with distinct anatomical structure in vivo using DTI. Results demonstrate that the unsupervised method is convenient, accurate and reproducible. Fibers reconstruction is a useful tool for analyzing the connectivity of brain regions and studying disease.

References

[1] Ding ZH et al, Magn Reson Med. 2003; 49:716-721. [2] Basser PJ et al, Magn Reson Med. 2000; 44:625-632. [3] Mori S et al, Magn Reson Med. 2002; 47:215-223. [4] Hagmann P et al, NeuroImage 2003; 19:545-554. [5] Mori S et al, Ann Neurol 1999; 45:265-269. [6] Lazar M et al, Human Brain Mapping 2003; 18:306-321.