

A white matter tract atlas based on a diffusion spectrum imaging (DSI) template

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Background Diffusion tractography has raised interests in the neuroscience community for its ability to reveal white matter fiber pathways *in vivo*. However, the procedure of diffusion tractography has been problematic due in part to the necessity of human intervention [1]. To reconstruct a pathway of interest objectively, we proposed a standardized procedure of tractography method for diffusion spectrum imaging (DSI) data. The procedure was performed on a DSI template. We applied a multiple-regions-of-interest (ROIs) strategy to reconstruction white matter tracts on a DSI template. A total of 107 white matter tracts were reconstructed and were categorized into longitudinal, transverse, and vertical tract systems.

Methods DSI data were acquired by a twice-refocused balanced echo diffusion echo planar imaging (EPI) sequence, TR/TE = 9600/130 ms, image matrix size = 80 x 80, spatial resolution = 2.5 x 2.5 mm², and slice thickness = 2.5 mm. 102 diffusion encoding gradients with the maximum diffusion sensitivity $b_{\max} = 4000 \text{ s/mm}^2$ were sampled on the grid points in the 3D q-space with $|q| \leq 3.6$ units [2]. For obtaining the transformation information between individual's DSI coordinates and the DSI template space, we proposed a registration method on DSI dataset by considering the fact that DSI dataset is inherently 6D: 3D image space and 3D q-space. Specifically, we generalized the conventional 3D registration to the 6D scenario by implementing Large Deformation Diffeomorphic Metric Mapping (LDDMM) method [3]. The DSI template was developed from 101 healthy participants' DSI datasets and was coregistered to the Montreal Neurobiology Institute (MNI) space. For DSI tractography, we proposed a multiple ROIs strategy with whole brain seeding. First, we used Wake Forest University (WFU) PickAtlas [4] to define 60 cortical and subcortical regions as ROIs on the MNI space for each targeted tract bundle. Then, a streamline-based fiber tracking algorithm was performed based on the resolved fiber vector fields provided by DSI. Targeted tracts were reconstructed on the DSI template using DSI studio (<http://dsi-studio.labsolver.org>). An atlas of the 107 tract trajectories were created from the DSI template and were incorporated into our image analysis tool for automated tract-specific quantification. A method that projected the generalized fractional anisotropy (GFA) onto a single mean path of a specific white matter tract, called mean path analysis, was used to analyze local changes in structural connectivity along individual tract bundles [5].

Results White matter tracts atlas containing 107 tracts were reconstructed based on 60 pre-defined ROIs. The atlas can be found at the website of Advanced Biomedical MRI Lab at National Taiwan University Hospital (<http://mrlab.mc.ntu.edu.tw/atlas>). The schematic diagram of atlas-guided method procedure was shown as Figure 1.

Discussion In this study, we have developed a white matter tract atlas on a DSI template. There are two potential applications of this atlas. First, the atlas can be used to understand the anatomy of the white matter tracts at a systems level. The atlas is open to the public and is accessible at <http://mrlab.mc.ntu.edu.tw/atlas>. Second, the atlas can be used to implement a template-based approach that enables a high-throughput automated analysis of the microstructural integrity of the tracts identified in the atlas. In this approach, the tract positions determined on the DSI template are transformed to the individual's native DSI data by using the LDDMM DSI algorithm. Once transformed, the tract integrity (e.g., mean GFA and GFA profiles) can be determined along the transformed tract positions automatically. Human intervention is involved only once to determine ROIs suitable for producing tractography of the targeted pathways on the DSI template. The rest of the procedure is virtually automatic. This computationally-efficient approach is potentially useful in the tract-based analysis that involves multiple pathways in a large number of subjects. In conclusion, we have developed a DSI atlas and an automated tract analysis method based on the DSI template. The techniques developed in this study allow us to study tract integrity of the whole brain in a systematic and standardized way, and may facilitate the connectome study in a large cohort.

References [1] Y.C. Lo, *et al.*, Proc ISMRM, 2012 [2] V.J. Wedeen, *et al.*, Magn Reson Med. 2005; 54:1377-86. [3] Y.C. Hsu, *et al.*, Neuroimage. 2012. [4] J.A. Maldjian, *et al.*, Neuroimage 2003; 19(3):1233-9 [5] W.Y. Chiang, *et al.*, Proc ISMRM, 2008.

Figure 1. Schematic diagram of atlas-guided method procedure. A DSI template was established from 101 normal subjects by using the LDDMM-DSI algorithm. A white matter atlas containing 107 tracts was reconstructed on the DSI template by experts with the use of 60 pre-defined ROIs. The atlas could be used to implement a template-based approach method for automated tract-specific analysis of the integrity index over the whole brain.. In this way, a 2D array of tract integrity index is obtained from each individual's DSI data.

