Validation of a tract-based automatic analysis by comparison with manual tractography

Yu-Jen Chen[1], Yun-Chin Hsu[1], Yu-Chun Lo[1], and Wen-Yih Isaac Tseng[1]
[1]*Center for Optoelectronic Medicine, National Taiwan University College of Medicine, Taipei, Taipei, Taiwan*

Objectives: Manual tractography is time consuming, subjected to intra-/inter-rater's variability, and so it is not suitable for analyzing tract-specific white matter (WM) property of the whole brain tracts. In this study, we proposed a new method to perform tract-specific analysis over the whole brain, named tract-based automatic analysis (TBAA), using a diffusion spectrum imaging (DSI) template and tract atlas. To validate this method, geometric overlap (VO) and functional difference (FD) of manual tractography and TBAA were assessed and compared.

Methods: *Method of TBAA*: The TBAA method requires two important pieces of information, a high quality DSI template and whole brain WM tract atlas. The DSI template was constructed by coregistering 122 healthy participants' DSI datasets (Male: Female = 63:59) in the Montreal Neurobiology Institute (MNI) space using the Large Deformation Diffeomorphic Metric Mapping (LDDMM) method [1]. Whole brain WM tracts were reconstructed on the DSI template by an expert using multiple regions of interest (ROIs) and whole brain seeding [2]. A total of 117 tracts were reconstructed from 60 ROIs defined in the Automatic Anatomical Labeling system. Each reconstructed tract was subdivided into multiple steps with even spacing [3] and the step coordinates along tract bundles were saved as sampling coordinates. The procedures of TBAA method were as follow. 1) Study subjects were coregistered to create a study specific template (SST) using LDDMM. 2) The SST was coregistered to the DSI template. 3) Sampling coordinates were transformed from the DSI template to individual DSI datasets via the transformation matrix between DSI template and SST as well as the matrix between SST and individual DSI. 4) The generalized fractional anisotropy (GFA) values were sampled in the native space using the transformed sampling coordinates and a 2D array of GFA profiles was created for each subject.

Validation of TBAA: A SST was created from 54 healthy adults' DSI datasets. Fifteen DSI datasets were randomly chosen from the 54 subjects. On each subject's DSI dataset, an expert performed manual tractography using the same approach as that used to reconstruct 117 tracts in the DSI template. Arcuate fasciculous (AF), cingulum bundle (CB), corticospinal tract (CST), genu, and splenium were reconstructed in the native space of each individual subject. VO and FD between two different tracts were calculated. VO was defined as $(V_a \cap V_b)/(V_a \cup V_b)$, where V_a and V_b are voxels contained in tract a and tract b, respectively. FD was defined as $\left(\frac{1}{n}\right)\int_{t1}^{tn}|fa(t)-fb(t)|dt$, where *fa*(t) and *fb*(t) are the GFA values in steps (t) of tract a and tract b, respectively. [4]. Figure 1 shows the diagram of the comparisons. VO comparison was performed in the SST space, as shown in the upper panel of figure 1. All the reconstructed tracts including the template tracts and those made in the native space were transformed to SST. FD comparison was performed in the native space, as shown in the lower panel of figure 1. GFA values were sampled in the native space using either transformed sampling coordinates or coordinates of manual tracts. VO and FD were calculated to assess the geometric similarity and functional variability of TBAA method and manual tractography.

Results: Figure 2 shows the VO between template tracts and individual tracts (TBAA method, blue) and the VO among individual tracts of 15 subjects (manual method, red). TBAA method showed significantly higher overlap than the manual method in AF, genu, and splenium ($p<0.001$). Figure 3 shows the FD in GFA values between each two samplings of TBAA method (blue) and the FD in GFA values between each two samplings of manual tracts (red). TBAA method showed significantly lower FD values than the manual method in AF, CB, CST, and splenium ($p=0.02$, 0.004, 0.001, and 0.041, respectively).

Conclusions: In this study, we proposed a whole brain tract-specific analysis using a high quality DSI template, predetermined tracts in the template, and LDDMM coregistration method. Compared to manual approach, TBAA showed higher overlap of tract positions and smaller variability of the sampled GFA values. In conclusion, TBAA overcomes the problem of variability in manual tractography on individual DSI, and is potentially useful in high-throughput tract-specific analysis of the whole brain.

References: [1] Hsu, Y. C. et al. (2012). A large deformation diffeomorphic metric mapping solution for diffusion spectrum imaging datasets. Neuroimage. [2] Lo, Y. C. et al. (2011). The loss of asymmetry and reduced interhemispheric connectivity in adolescents with autism: a study using diffusion spectrum imaging tractography. Psychiatry Res. [3] Chiang, W. Y. et al. (2007). Tract-Specific Analysis of Human White Matter: Mean-path Based Method. Proc 16th ISMAR. [4] Gouttard, S. et al. (2012)Measures for validation of DTI tractography. Medical Imaging.

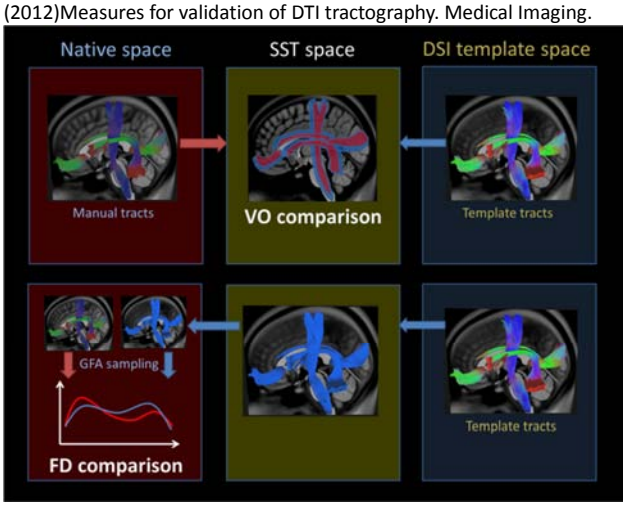

Figure 1. Comparison between TBAA and manual tractography.

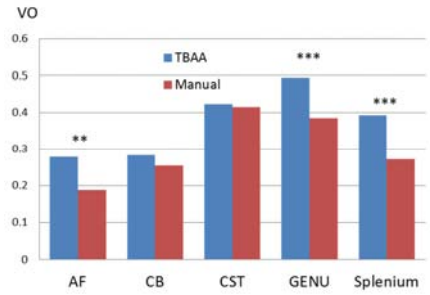

Figure 2. The volumetric overlaps of TBAA method and manual method.

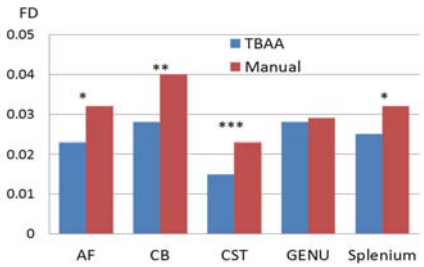

Figure 3. The functional difference of GFA in TBAA tracts and manual tractography on individual DSI.