Validation of a template-based approach for quantitative tract-specific analysis of diffusion spectrum imaging data

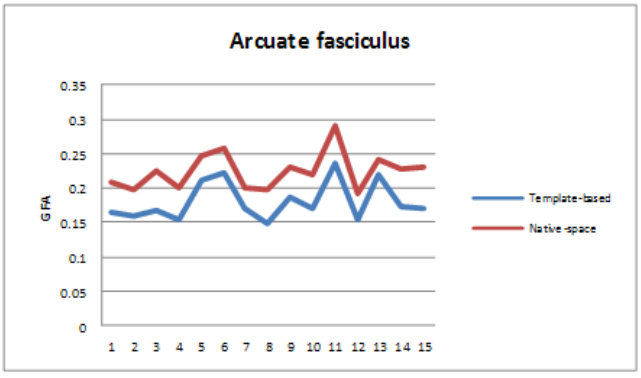
Chieh-En Tseng[1], Yung-Chin Hsu[2], Yu-Chun Lo[3], and Wen-Yih Isaac Tseng[3,4]

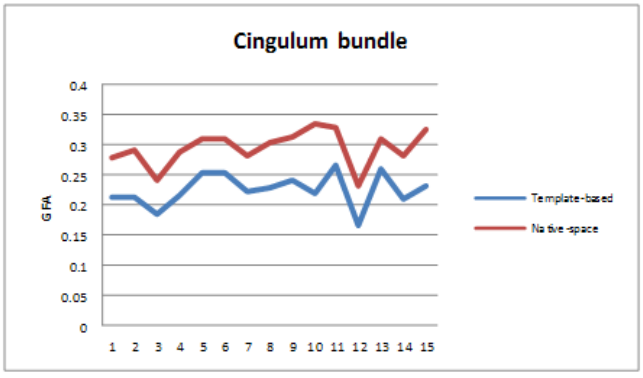
[1]Biomedical Imaging and Radiological Sciences, National Yang-Ming University, Taipei, Taiwan, [2]Institute of Biomedical Engineering, National Taiwan University, Taipei, Taiwan, [3]Center for Optoelectronic Biomedicine, National Taiwan University College of Medicine, Taipei, Taiwan, [4]Department of Medical Imaging, National Taiwan University Hospital, Taipei, Taiwan

Introduction Conventional tract-specific analysis requires substantial manual selection of the tracts, and is time-consuming and prone to subjectivity and poor reproducibility. Recently we have established a template of diffusion spectrum imaging (DSI) using large deformation diffeomorphic metric mapping (LDDMM) [1], and determined tract coordinates of major pathways on this template. Based on the DSI template and tract coordinates, we propose an automatic approach that totally bypasses the manual selection during tractography and overcomes the problems of the conventional approach. This approach, called template-based approach, entails transformation of a native DSI dataset to the template by LDDMM. Tract-specific analysis is then performed on the transformed DSI using the existing tract coordinates provided by the template. The template-based approach, however, inevitably blurs out the DSI data and may lead to errors in quantitative analysis. To evaluate the accuracy of the template-based approach, in this study we compared this approach with a native-space approach. In contrast to the template-based approach, the native-space approach performed transformation of the tract coordinates from the template space to the native DSI space with the transformation provided by LDDMM. Tract-specific analysis was then performed on the native DSI using the transformed tract coordinates.

Materials and methods Fifteen subjects were randomly selected for analysis from the pool of 70 subjects used to establish the DSI template. Images were acquired on a 3T MRI system with a 32-channel head coil (Tim Trio, Siemens, Erlangen, Germany). DSI was performed using 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 mm^2, and slice thickness = 2.5 mm. 102 diffusion encoding gradients with the maximum diffusion sensitivity b_{max} = 4000 s/mm^2 were sampled on the grid points in the 3D q-space with $|q| \leq 3.6$ units [2]. Then, a streamline-based fiber tracking algorithm was performed based on the resolved fiber vector fields provided by DSI. Targeted tracts, namely arcuate fasciculus and cingulum bundle, were tracked on the template. For the template-based approach, DSI dataset was transformed from the native space to the template space through LDDMM. Generalized fractional anisotropy (GFA) of the transformed DSI was then sampled along the tract coordinates in the template space. A method that projected the 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 [3]. As for the native-space approach, tract coordinates in the template space were transformed to the native space through LDDMM, and the GFA values of the native DSI data were sampled along the transformed tract coordinates. Mean GFA values of the arcuate fasciculus and cingulum bundle obtained by these two approaches were compared by 2-tailed Pearson's correlation test.

Results As expected, the mean GFA values estimated by the template-based approach were lower than those estimated by the native space approach. However, significant correlation between the two methods was seen in both tracts (arcuate fasciculus: r=0.92; p= 0.00, cingulum bundle: r=0.825; p= 0.00).





Discussion Although the template-based approach presents lower GFA value due to the smoothing of the transformed DSI dataset, it maintains the same trend of GFA values as those estimated from the native DSI. The results provide supportive evidence for the use of the template-based approach in the tract-specific analysis. This automatic approach allows high-throughput quantitative analysis of all the fiber tracts in the brain over a large number of samples, and will be potentially useful in connectome research.

References [1] Y.C. Hsu, *et al.*, Peoc ISMRM, 2010. [2] V.J. Wedeen, et al., Magn Reson Med. 2005; 54:1377-86. [3] W.Y. Chiang, et al., Proc ISMRM, 2008