Probabilistic Tract-based Atlas with High Angular Resolution Diffusion Imaging

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Introduction

White matter connectivity in the human brain can be mapped by diffusion MRI. To identify the variability of neural connection from individual subjects is indispensable to the understanding of brain development, functions, and diseases. In order to compare the specific trajectories of neuronal tracts between each subject, methods for spatial normalization have been proposed to realign image datasets, such as the image registration for diffusion weighted images (DWI) [1] and the deformable registration for diffusion tensor images (DTI) that explicitly optimized tensor reorientation [2]. In this study, we proposed a new method to realign the multiple fibers tractography with high angular resolution diffusion imaging (HARDI). We extracted the neural tracts from individual subjects using q-ball imaging (QBI) with MFACT (multiple fiber assignment by continuous tracking) tractography algorithm [3]. Transformation matrices were estimated by mapping T1-weighted image (T1WI) of each subject to MNI152 coordinate using a 12-parameters affine linear registration. These matrices were then applied to the propagated neural bundles. By summarizing individual transferred tracts in the standard MNI152 coordinate, a probabilistic tract-based atlas can be generated to assist clinical studies into the variations of complex connectivity between different subjects.

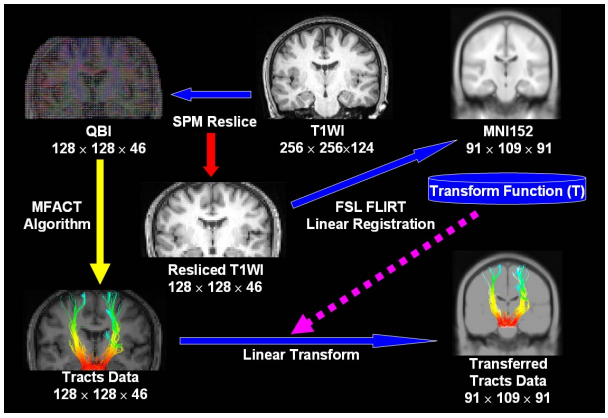
Materials and Methods

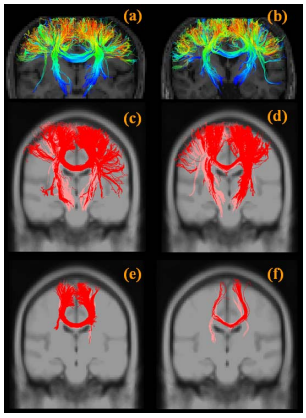
Data Acquisition:

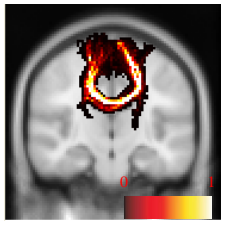
In vivo human brain QBI data (n=6) were acquired in a GE Healthcare Signa 1.5T Excite scanner in Taipei Veterans General Hospital by spin echo EPI sequence with 162 icosahedral diffusion-encoding directions, matrix size=128×128, field of view (FOV)=25.6 cm, voxel size=2.0×2.0×2.2 mm^3, TR/TE = 13600/91.2 ms and b-value=3000 sec mm^{-2}. T1WI were acquired with 3D FSPGE sequence with the same FOV as QBI, matrix size=256×256, and axial slice thickness of 1.5 mm. For each MR voxel, the QBI reconstruction was based on Funk-Radon transformation [4]. The fiber tracking was based on MFACT algorithm with two criteria, tract-turning angle of 60^o and length threshold of orientation distribution function (ODF) of 0.93. After the tracking processing, the extracted complex neural bundles were saved as the tract data files for tract transformation.

Tract transformation:

T1WI were coregistered and resliced to QBI data by SPM2 as the first step. In this way, the resliced T1WI was provided with the same coordinate with tract data. With resliced T1WI as the input image and MNI152 brain image as the reference image, the transformation matrices were obtained using FLIST linear registration (FSL, Oxford). All saved tract data were mapped to MNI152 space by the generated transformation matrices. Finally, the comparison of individual anatomical connectivity in a standard space was implemented by collecting the transferred tract data from each subject. The flowchart about the transformation of fiber tracts was shown in Fig. 1.







◄*Fig.3 The probabilistic map of cortico-cortical connection*

◄◄*Fig. 1 The schematic flowchart of tract-based transformation.*

◄*Fig. 2 The fiber tracts of two subjects propagated from BA4 in individual coordinates (a-b), transferred tracts in MNI152 space(c-d), and the extracted tracts passed through corpus callosum (e-f).*

Results

Fig. 2a-b showed the fiber tracts of two subjects propagated from seed region in individual Brodmann's area 4 (BA4) with the ground image of resliced T1WI. Tracts were color-coded in the range of red to blue according to the distance between the initial seed point and the traced point. The generated fiber bundles were initialed from the primary motor cortex and extended to the opposite hemisphere through corpus callosum and to pons along cortico-spinal tracts. Using the proposed tract-based transformation, the BA4 of MNI152 was applied as the seed region to constrain the transferred tracts of two subjects (Fig. 2c-d). By selecting an additional ROI in midsagittal plane of corpus callosum, the fiber bundles linked the motor areas between two hemispheres could be extracted (Fig. 2e-f). Fig. 3 illustrated the probabilistic map of cortio-cortical connection summarized from transferred and extracted fiber bundles of six subjects.

Discussions

This study proposed a method of tract-based transformation to realign complex neural tracts and presented the preliminary results. Our results showed that neural connectivity derived from QBI with MFACT tracking algorithm could be mapped from each coordinate of different subjects to MNI152 standard space. This method provided a solution to compare the results of multiple fiber tractography from individual subjects. It might facilitate the further observation of the individual variations of anatomical connection within the brain by the assist of MNI152 coordinate and other anatomical templates. This transformation method could be replaced by any other accurate registration transformation to improve the accuracy of tract mapping. In addition, according to this approach, the probabilistic connectivity atlas derived from HARDI could be generated by recruiting more transferred tracts from more normal subjects (Fig. 3).

Acknowledgements

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References

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