Group Analysis of Human Brain White Matter Using Mean Path Analysis Method

W-Y. Chiang[1], V. J. Wedeen[2], and W-Y. I. Tseng[1]

[1]Center for Optoelectronic Biomedicine, National Taiwan University College of Medicine, Taipei, Taiwan, [2]MGH Martinos Center for Biomedical Imaging, Charlestown, MA, United States

Abstract

One way to perform group analysis of human white matter is to transform all the brain images onto a template and build up the atlas. While globally optimized normalization was achieved, the performance of alignment for local structure, empirically, was not always guaranteed. Recently we developed one technique to transform the 3-D structure information onto a mean path (MP), thus simplifying the freeform white matter structure onto a 1D coordinate. In this study, we proposed a simple and effective strategy for group analysis of human white matter via co-registration of inter-subject mean paths of the tract bundles. In addition to obtaining the averaged structural information, we can also analyze the change along the tract bundle in a robust and efficient way.

Introduction

Tractography has become a well-established neuroimaging tool to analyze the white matter structure of a single subject, and various kinds of normalization methods of diffusion tensor image (DTI) [1-3] have been proposed to perform group analysis. Two possible approaches can be performed to analyze multiple-subject tractography: (1) tracking on an averaged tensor field and (2) tracking on individual DTI then overlaying the individual tractography results [2-4]. Thus, the normalization of inter-subject human brains is essential for both approaches. However, the inter-subject variability is inevitable so that both approaches are subject to normalization error, which may result in inaccurate estimation of diffusion tensor for the first approach and pseudo white matter structure for the second approach respectively. Instead of estimating global normalization of the whole-brain white matter structure, our goal is to normalize individual white matter to avoid the propagation error of the global normalization. In this study, we aimed to use mean path analysis (MPA) [5] on diffusion spectrum imaging (DSI) tractography and incorporate a combined normalization strategy of mean path (MP) to analyze inter-subject white matter structure.

Materials and Methods

Twelve normal Chinese volunteers classified as left handers by the Edinburgh Handedness Inventory and without neurological and psychiatric diseases were studied. DSI data was acquired on a 3T MRI system (Trio, Siemens, Erlangen, Germany) using twice-refocused balanced echo diffusion EPI sequence. A total of 203 diffusion-encodings on the homogeneous Cartesian lattice points over the q-space were acquired with maximum b-value = 6000 s/mm^2, TR/TE = 9100/142 ms and 45 slices comprising whole brain with isotropic voxel size of 2.93×2.93×2.93 mm^3. DSI was reconstructed based on the 3D Fourier relationship between diffusion signal and probability density function [6].

MPA, which effectively analyzes the subtle change along a tract bundle, is one way to project the 3D structure information such as generalized fractional anisotropy (GFA) [6] onto a single mean passage of the specific white matter structure (Fig. (a)). In this paper, we choose the analysis of arcuate fasciculus (AF) as a demonstration. We used MARINA software (Bender Institute of Neuroimaging, University of Giessen, Germany) to select opercular and triangular parts of inferior frontal gyrus on MNI coordinate as the seeding area, and transformed it to the B0 images of individual participants using the normalization information generated by SPM5. Tracts generated from this seeding area and marched toward temporal lobe were selected as AF (Fig. (b)). We applied MPA [2] to calculate the MPs of both sides of AFs of individual participants and the GFA along the MPs. Since simply normalizing the lengths of individual MPs for group analysis suffers inconsistent brain sizes and orientations, it is better to normalize the MPs inhomogeneously along each individual MP. We first used SPM5 to estimate the 3D affine transform matrix of B0 images between source and reference one, and applied it to the MP that to be co-registered to correct the variation of sizes and orientations of the brains. Furthermore, we incorporated a line co-registration method to fine-tune the position of each MP to obtain a better coregistration result.

$$\vec{G} = \sum_i \sum_j \frac{\vec{r}_i - \vec{r}_j}{\left|\vec{r}_i - \vec{r}_j\right|^2}$$

Where $\vec{r}_i$ denotes coordinates of MP of template, and $\vec{r}_j$ denotes coordinates of source MP. This function, without the prior knowledge of correspondent points between the two MPs, conceptually calculates the gravity force between two MPs as the direction of translation of the source MP. Finally, we applied MPA over all the MPs again to analyze the structural property along the AFs of these 12 volunteers.

Results

Fig. (a) and (b) show that the 3D affine transformation is capable of compensating the size variations of the brains and correcting the orientations of the individual original brain images. After applying a gravity-force algorithm to the co-registered MPs (Fig. (c)), MPs were co-registered with less inter-subject difference as shown in Fig. (d). Mean co-registered MP is shown in Fig. (e), and the according GFA change along the fiber bundle is shown in Fig. (f). The average standard error of the mean (SEM) of the GFA values is 0.0137±0.0033, suggesting that the MPA approach can promisingly improve the inter-subject co-registration of individual fiber bundle.

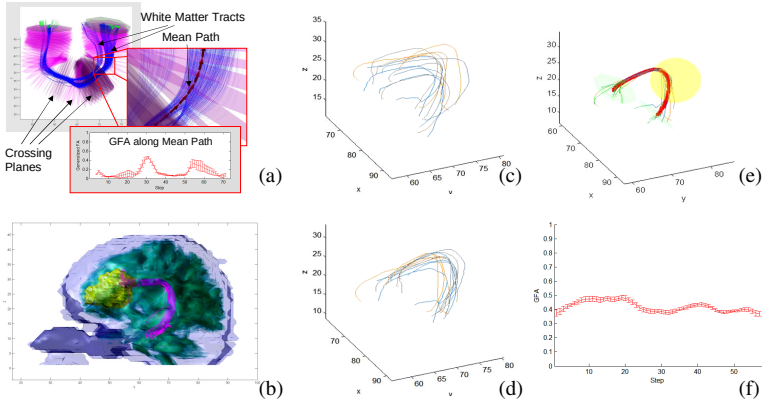

Fig (a-f) (a) Mean Path Analysis of part of corpus callosum seeding on Witelson's Area II (1989); (b) Yellow region: seeding area / Magenta lines: Arcuate fasciculus (left side); (c) 12 Mean Paths of arcuate fasciculus of 12 volunteers. (d) 12 Mean Paths after affine transformation; (e) Further coregistered Mean Paths and the calculated Mean Path of these coregistered Mean Paths; (f) Group analysis result of 12 left handed volunteers along arcuate fasciculus (mean value & standard error of the mean).

Discussion

MPA is a robust way to project 3D information onto 1D coordinate. Since the information of the brain size and orientation is lost after projection, the estimation of these two factors should be done in the structural image domain. Using MPA approach, the length of mean path could be inhomogeneously normalized with respect to the 1D coordinate and the group analysis of regional change can be accomplished in a robust and efficient way.

Reference

[1] Alexander et al., IEEE 2001 [2] Jones et al., NeuroImage 2002 [3] Xu et al., NeuroImage 2002 [4] Lange et al., IEEE 2004 [5] Chiang et al., ISMAR 2007 [6] Wedeen et al., MRM, 2005 [7] Tuch, MRM, 2004.