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Introduction

Diffusion MRI provides a useful tool to study the structure and organization of human brain white matter. Due to anatomical differences between individual brains, spatial normalization of the data is usually needed to make comparisons between subjects. However, simple normalization of the diffusion weighted images is not sufficient to retain the orientation information of the underlying structure. The PPD algorithm has been proposed to rotate the diffusion tensor so that the principal direction of the tensor is preserved [1]. Compared with DTI [2], High Angular Resolution Diffusion Imaging [3] is able to provide more accurate estimates of the fiber orientation. However, effective spatial normalization of the HARDI data has not yet been demonstrated. In this study we propose an algorithm to transform the Fiber Orientation Distribution (FOD) function based on HARDI data, taking into account not only translation, but also rotation, scaling, and shearing effects. The algorithm is tested by both numerical phantom and *in vivo* human data.

Methods

The FOD derived from spherical deconvolution methods [4,5] is a function over a unit sphere. When sampled in a number of directions evenly distributed over a sphere, the FOD function can be approximated by the set of sampling vectors whose lengths represent the fiber volume fraction along the corresponding directions. The transformation of a FOD is performed in 5 steps. First, the FOD is calculated based on the transformed DW images. Second, the Jacobian matrix J for each voxel is derived from the deformation field of the spatial transformation applied to the DW images. Third, J is applied to each of the sampling vectors to obtain the transformed orientation. Fourth, the length of each of these vectors is corrected according to the following rule. Assume that the volume fraction of a fiber going through a small patch on the spherical surface should remain the same after the patch is transformed: $P(\theta, \phi) \sin \theta d\theta d\phi = P'(\theta', \phi') \sin \theta' d\theta' d\phi'$, where $P(\theta, \phi)$ and $P'(\theta', \phi')$ are the FOD magnitudes along the original direction (θ, ϕ) and the transformed direction (θ', ϕ') , respectively. Therefore, the length of the transformed vector should be $P'(\theta', \phi') = P(\theta, \phi) (\sin \theta d\theta d\phi) / (\sin \theta' d\theta' d\phi')$. The transformed FOD is approximated by the set of transformed sampling vectors. Note that due to noise and truncation artifact the FOD may have negative values along some orientations. These negative vectors are transformed in the same way as the positive ones.

This algorithm was tested using a numeric phantom containing various fiber structures, including a single fiber, 2 fibers crossing or kissing at various angles, and 3 crossing fibers, as well. FODs were calculated using the FORECAST model [5] through 6th order. Then arbitrary affine transformations combining translation, rotation, scaling, and shearing were applied to the FODs.

We also tested the technique with human data. HARD images of a group of subjects were acquired on a 3T Philips scanner, using the following imaging parameters: $b=1000\text{s/mm}^2$, 92 diffusion-sensitizing directions, 2.5mm isotropic voxel size. High resolution T1-weighted images were also obtained for registration purposes. Transformations were calculated by first creating a study-specific average template from a series of intra- and inter-subject registration steps using linear [6] and nonlinear methods [7] and then registering (nonlinear) the DW images of individual subjects to that template. FODs were calculated using the FORECAST model through 6th order, with negative peak regularization [8]. The FODs before and after applying the transformation were compared.

Results

The phantom before and after transformation is shown in figure 1. It's obvious that the fiber structure is retained. Figure 2 shows an example of the human data where the left cingulum is re-oriented by the image registration. It is clear that the FODs derived from the transformed DW images without transformation still take the orientation of the fiber before registration, not along the transformed fiber. After transformation, the FODs are more consistent with the transformed cingulum track.

Conclusion and discussion

We developed an algorithm to perform spatial normalization of the FOD function derived from HARDI data, which makes it possible to compare the intra-voxel fiber distribution between subjects. This is an important step forward from spatial normalization of scalar images and diffusion tensors, since the FOD function derived from HARDI provides more detailed information about the intravoxel fiber structure than scalar measures such as FA, and the diffusion tensor. This technique will be helpful in various clinical studies of white matter diseases.

Acknowledgements This work was supported by grants from the NIH/NIBIB (R01-EB02777)

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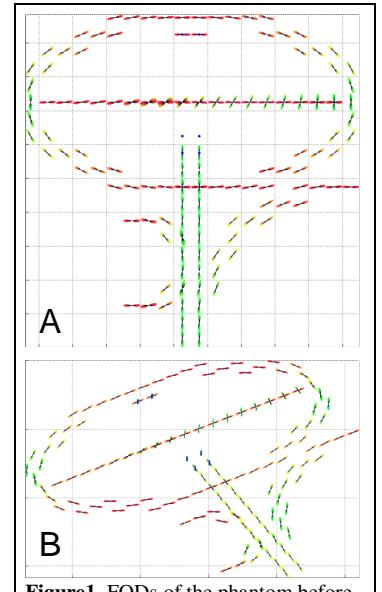


Figure 1. FODs of the phantom before (A) and after (B) transformation.

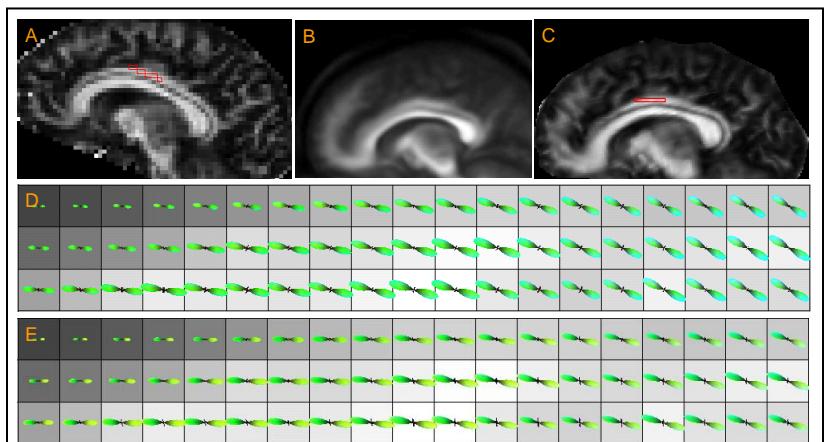


Figure 2. Results of human data. (A) and (B): a sagittal slice of the source and target FA map, respectively. (C): the transformed FA map. (D) and (E): FOD surfaces before and after transformation, respectively, in an ROI in the left cingulum plotted on top of the transformed FA map. The FODs are color-encoded according to the orientation: red-RL, blue-IS, green-AP. The ROI is highlighted in a red box in (C), and the corresponding position before transformation is highlighted in (A).