Brain tissue segmentation for diffusion tensor imaging (DTI) data using multi-tensor estimation

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Introduction

To study the apparent diffusion coefficient (ADC) and fractional anisotropy (FA) of the cerebral cortex in neurological and neurodegenerative diseases, brain tissue segmentation methods for diffusion tensor imaging (DTI) data have been proposed, which utilize three eigenvalues, ADC and FA maps [1-3]. However, in these methods, white matter (WM) voxels in fiber crossing regions might be misclassified into gray matter (GM) region because of denoting low FA values due to the partial volume (PV) effect of the diffusion tensors. Our purpose was to develop a new brain tissue segmentation method for DTI data in which effect of the PV averaging is taken into account by using multi-tensor estimation for WM crossing regions.

Materials and Methods

Our segmentation method: Our method consisted of three steps. First, initial segmentation was performed by use of a fuzzy c-means clustering based on the ADC and FA values [3]. In this step, the fiber crossing voxels might be misclassified into GM region due to low FA values. Second, for the GM voxels adjacent to WM region, we estimated the tensors based on the multi-tensor model [4]. Assuming the two-component model in fiber crossing region, the MRI signal for the diffusion gradient direction g_i was estimated by $\hat{S}_i = fS_{10}\exp\left(-bg_i^T D_1 g_i\right) + (1-f)S_{20}\exp\left(-bg_i^T D_2 g_i\right)$, where b is the b-value, f is the volume fraction, S_0 and D are the signal intensity with b=0 s/mm^2, and the diffusion tensor at each component, respectively. To estimate the f, S_0, and D, the objective function was defined by $E(f, D_1, D_2) = \sum_{i=1}^{d}\left(\hat{S}_i - S_i/S_i\right)^2 + \alpha(1 - e_{1,com}\cdot e_{1,WM})$, where S_i is the measured MRI signal, e_{1com} and e_{1WM} are the major eigenvectors of the component and the neighboring WM voxel, respectively. Based on the objective function, we divided the tensor of the GM voxels adjacent to WM region into two tensors. If FA values of both two tensors are high, the tensor of the interesting voxel was replaced by estimated tensor denoting higher FA value. Finally, based on the following five images derived from DTI, i.e., images of the three eigenvalues, ADC and FA, our method estimates the PV fractions of WM, GM, and cerebrospinal fluid (CSF) in each voxel using a *maximum a posteriori* (MAP) probability principle. The segmentation was performed by assigning each voxel to a tissue class based on the largest PV fraction among all of the tissue types.

Digital DTI phantom data: The digital phantom used in this study was shown in Fig. 1a. The DTI phantom data consisted of 6 diffusion-weighted image volumes (b = 800 s/mm^2) and an unweighted image volume (b = 0 s/mm^2) with a 128×128 in-plane resolution and 40 slices (FOV: 230×230 mm^2, 3 mm thick). The voxel size was 1.8×1.8×3 mm^3, which is the same as the voxels used in our clinical data. We evaluated the performance of the accuracy by use of an overlap measure given by $J(V_{seg}, V_{true}) = |V_{seg} \cap V_{true}|/|V_{seg} \cup V_{true}|$, where V_{seg} is a segmented volume and V_{true} is the ground truth (Fig. 1b), respectively.

Human DTI data: The DTI data of five healthy volunteers were acquired using a 1.5-tesla clinical scanner (Magnetom Symphony, Siemens) with an 8-channel phased-array coil. The data covering the whole brain were obtained using a single-shot echo-planar-imaging pulse sequence with TR = 8600 ms and TE = 119 ms. The DTI data acquired using a six-directional diffusion encoding scheme at a b-value of 800 s/mm^2 , and the voxel size was the same as that of the DTI phantom data.

Results and discussion

Table 1 shows the volume overlap measure between the segmentation results and the ground truth data of the digital DTI phantom. In all three tissue types, the values of volume overlap with proposed method were greater than those with the previous method [3]. Whereas the ground truth data (Fig. 1b) and the result by proposed method (Fig. 1e) were qualitatively in good agreement, in the previous method, the fiber crossing voxels, which denote low FA as shown in Fig. 1c, were misclassified into GM region (Fig. 1d). In human DTI data as shown in Fig. 2, WM/GM/CSF regions estimated by proposed method (Fig. 2d) were more similar to the corresponding regions depicted in the structural image (Fig. 2b) than those estimated by the previous method (Fig. 2c). For example, the parietal deep WM, which denote low FA as shown in Fig. 2a, were clearly depicted by proposed method, while these structures could not be identified in the results by the previous method (yellow arrows).

Conclusions

We have presented a partial volume estimation and segmentation method for brain tissue based on DT-MRI data. The results of the digital phantom experiment and human DT-MRI data demonstrate that our method was able to perform a reasonable estimation and segmentation for brain tissue on DT-MRI data compared with the previous segmentation method. Our method may be useful in evaluating the cortical and subcortical diffusivity in neurological diseases.

References

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Table 1: Volume overlaps between segmentation results and ground truth of DTI phantom in each tissue type.

	WM	GM	CSF
Proposed method	0.838	0.921	0.942
Previous method	0.608	0.878	0.941

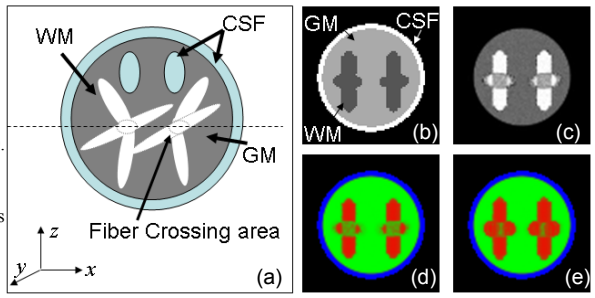

Fig.1. Digital DTI phantom images. (a) Schematic diagram of the phantom object, (b) ground truth, (c) FA map, (d) result by previous method, and (e) result by proposed method.

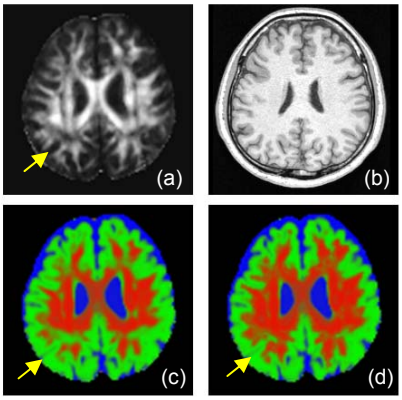

Fig.2 (a) FA map, (b) The structural image (T_1-weighted image), (c) result by previous method, and (d) result by proposed method.