2D distribution analysis of DTI in two phenotypes of dystonia patients

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Introduction

Hereditary dystonia is a neurological movement disorder where the subjects have abnormal motions due to muscle contractions [1]. Only a subset of the patients who carry the gene show the overt symptoms [2]. Although the pathology is not completely understood, purkinje cells, basal ganglia and part of the motor circuit are all implicated in this disorder [3, 4]. According to the diffusional characteristics, diffusion tensor imaging can be used to characterize normal and pathological tissues [5, 6]. We propose to use a 2D distribution analysis with a physical brain model, which can automatically determine the different tissue types according the inherent diffusional characteristics [7]. Development of this type of analysis may be used to help to diagnose non-focal disease state.

Subjects and Methods

Three groups of subjects were studied: (1) Seven dystonia patients with DYT1 genotype (4M/3F, age 39.8±19.4); (2) four non-manifesting DYT1 mutation carriers (2M/2F, age 46.9±15.4); and (3) eight normal subjects (5M/3F, age 50.1±10.6) [4]. Images were acquired in a clinical 3T scanner. A single-shot spin-echo EPI sequence was used with 55 isotropically distributed diffusion gradient directions and one b0 image. The b-value in the DWIs was 1000 s/mm^2. The DTI protocol included 72 slices with 1.8mm thickness, FOV 23cm, TE 68.3 ms and TR 7s. Images were zero filled to a matrix size of 256 × 256, yielding an image resolution of 0.9 × 0.9× 1.8 mm^3. After data acquisition, Dav (=Trace/3), FA maps are calculated. Using a physical diffusion brain model of four compartments, 2-D distribution map was fitted using four 2-D Gaussian functions as:

$$f(D_{av},FA)=\sum_{i=1}^{4}C_i(2\pi)^{-1}\det\left(\overline{\overline{V}}_i\right)^{-\frac{1}{2}}\exp\left\{-\frac{1}{2}\left[D_{av}-D_i,FA-FA_i\right]\begin{bmatrix}V_{i11} & V_{i12}\\ V_{i21} & V_{i22}\end{bmatrix}^{-1}\begin{bmatrix}D_{av}-D_i\\ FA-FA_i\end{bmatrix}\right\}.$$

The covariance matrix can be re-written as:

$$\overline{\overline{V}}=\begin{bmatrix}\cos\theta & -\sin\theta\\ \sin\theta & \cos\theta\end{bmatrix}\begin{bmatrix}a^2 & 0\\ 0 & b^2\end{bmatrix}\begin{bmatrix}\cos\theta & \sin\theta\\ -\sin\theta & \cos\theta\end{bmatrix}.$$

Parameters { C_i, D_i, FA_i, θ_i, a_i, b_i} of 2-D distribution are fitted using EM algorithm [8]. Four 2-D Gaussian functions represent white matter, gray matter, CSF and mixing compartments. For each compartment, C_i represents the proportion of volume, D_i and FA_i are the means of and D_{av} and FA. a_i and b_i are the standard deviations of D_{av} in the θ direction and of FA in the direction orthogonal to the θ direction. We computed the mean and standard deviation of parameters in each group. The t-test was used to make between group comparisons. The significance level was set at P< 0.05. We also segmented the brains, using the four compartments of the 2-D distribution as shown in Fig. 3. A voxel is classified as belonging to compartment i, if the gaussion function i has the maximum intensity at that voxel.

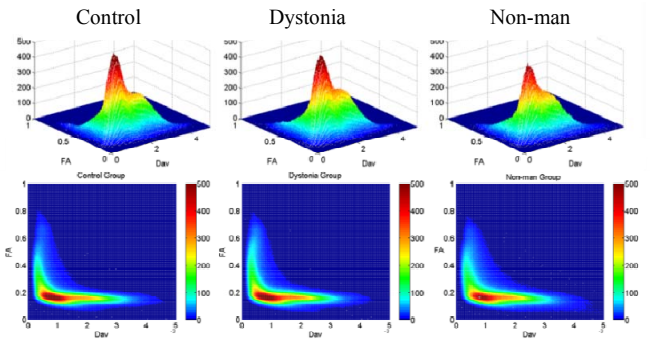

Figure 1: 2-D distribution maps

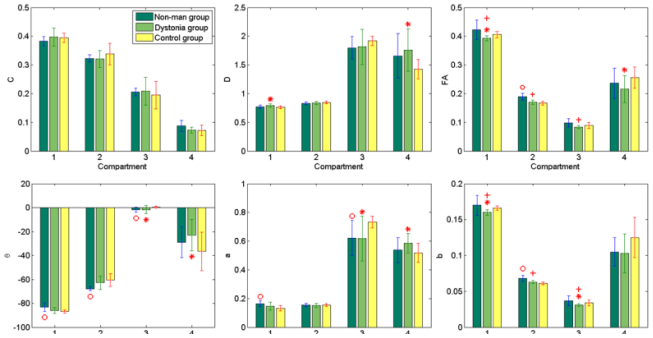

Figure 2: The measured parameters of 2-D distribution in the control, dystonia and non-man groups

Results

We processed the control, dystonia DYT1, non-man DYT1 subjects with the 2-D distribution analysis. Figure 1 shows the 2-D distribution maps fitted with four 2-D Gaussian functions for each group. Fig. 2 shows a comparison of parameters of 2-D distribution in the control, dystonia and non-man groups. (*P < 0.05 control group vs. dystonia group, **o** P < 0.05 control group vs. non-man group and +P < 0.05 non-man group vs. dystonia group). Four compartments are visualized by segmenting the brain images. Fig. 3 shows segmentation results of dystonia subject using 2-D distribution of diffusion tensor imaging data. The white matter compartment is shown in green, the gray matter in yellow, the CSF in blue and the mixing in red. Arrow points a red region (mixing/ pathological compartment) in putamen which was previously hypothesized to be involved in the disease process [9].

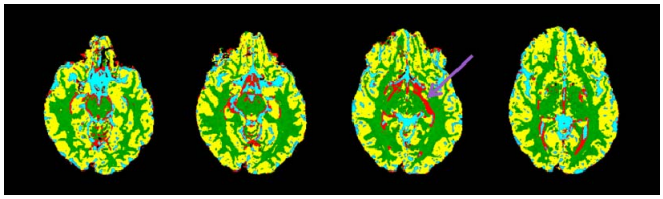
Figure 3: Segmentation results of a dystonia subject using 2-D distribution

Discussion/Conclusions

The results show that the brain tissue can be characterized by diffusion parameters using distribution analysis in 2-D. There are considerable differences among three groups studied in terms of the parameters measured. Considering that the disease of dystonia has not known to affect brain globally, this finding is significant. We also found changes in the putamen region shown in red (Fig. 3) in brain segmentation results of a DYT1 subject that could be a signal of DYT1 disease process. The metabolic dissociation as indicating an over-activity of direct inhibitory projections from the putamen to GPi was suggested in [9]. In this study, excellent tissue characterization is achieved automatically using 2-D distribution analysis that uses a physical brain model. This completely automated analysis can help in understanding the pathophysiology of dystonia.

References:

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