Parsimonious Model Selection for DTI Tissue Segmentation and Classification Applied to Clinical Data

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ABSTRACT

We used a statistical method for parsimonious model selection to choose the most appropriate water diffusion model (isotropic, oblate, prolate, or general anisotropic) for *in vivo* DTI of the human brain. We found that the prolate model reliably identifies structures with orientationally coherent fibers (e.g., the mid sections of the corpus callosum). However, most white matter regions are identified by the general anisotropic model, suggesting that their underlying fiber architecture is consistent with multiple fiber population within a voxel. The information provided by this method may be useful for optimal experimental design of diffusion MRI experiments and for selecting approaches to data analysis.

INTRODUCTION

Diffusion Tensor Magnetic Resonance Imaging (DT-MRI or DTI) is extensively used for noninvasive quantitative measurements of the apparent diffusion tensor of water molecules in tissue. For instance, in brain white matter, DTI provides information about fiber orientation and organization. Based on its extensive use, it is increasingly important to develop new tools for efficient and accurate tissue analysis and segmentation of DT-MRI data, since better characterization of organization of different tissue types may enhance our understanding of structure/function relationships in organs. In addition, quantitative tissue segmentation may advance intrasubject comparisons between tissue compartments. In this work, we test the appropriateness and relative efficiency of the parsimonious model selection algorithm[1], which currently includes four predefined diffusion models, for segmenting *in vivo* DTI data of the human brain. The four models are: isotropic ($\lambda_1 = \lambda_2 = \lambda_3$), general anisotropic ($\lambda_1 > \lambda_2 > \lambda_3$), and cylindrically symmetric, i.e., prolate ($\lambda_1 = \lambda_2 > \lambda_3$) and oblate ($\lambda_1 > \lambda_2 = \lambda_3$).

The parsimonious model selection maps were compared with the results obtained with the Diffusion Orientation Transform (DOT)[2] technique. The DOT method calculates the orientation maps without fitting a particular model to the data. It is based on analytically evaluating radial part of the Fourier integral at a fixed distance away from the origin. The tubular structures in the DOT images correspond to well-organized fiber bundles with coherent spatial orientations. However, the "bumpy" surfaces of probability profiles identify voxels with multiple fiber population and different spatial orientations. The spherical surfaces correspond to the isotropic regions.

THEORY

The parsimonious model selection method[1] is based on the Schwarz Criterion (*SC*)[3]. The *SC* imposes penalties for models with a larger number of free parameters and a larger mean squared residual error between the model and the data. The general anisotropic model is represented by 7 independent parameters (6 elements of the symmetric diffusion tensor, **D**, and the log of the signal, log[*S*(0)] (a signal in the absence of the diffusion weighting). For cylindrically symmetric (oblate and prolate) models the number of estimated free parameters is reduced from 7 to 5. For the isotropic model the number of unknown parameters is 2.

METHODS

The data was obtained using a 1.5-T GE (General Electric, Milwaukee, WI) MRI scanner using diffusion-weighted EPI pulse sequence. Each diffusion-weighted scan was collected at a b-value of 1100 s/mm^2, applied along 50 different directions with 10 image acquired at b=0 s/mm^2. The isotropic resolution was set to $2.5\times2.5\times2.5$ mm^2. The diffusion tensors and the surfaces of probability profiles were estimated with DTI and DOT, respectively

RESULTS

The T2-weighted amplitude image, fractional anisotropy (FA), and Model Selection maps of a representative axial slice of the brain of a healthy volunteer are shown in Figure 1. Figure 2 shows the orientation profiles map (blue represents surfaces of probability profiles), obtained with DOT, overlaid on a color-coded parsimonious model selection map. The inset in Figure 2 is selected to show enlarged probability profiles. As it can be seen from Figure 2, the prolate model corresponds to the tubular structures (in- and through the image plane) in the DOT image and is consistently selected in the mid section of the genu and splenium of the corpus collosum, as well as peripheral portion of the u-fibers. The general anisotropic model identifies voxels with "bumpy" surfaces of the diffusion displacement profiles in the DOT image in most white matter regions, including the internal capsule and most association pathways. At the given resolution, commonly used in the clinical studies, the isotropic model is found to be appropriate for gray matter regions (spherical shapes), whereas the oblate model predominantly identifies boundaries between structures with different architectures ("pancake" shapes).

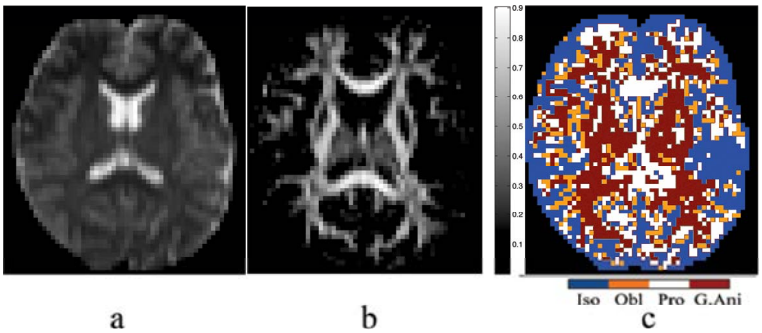

Fig 1. a) T2-weighted image; b) FA and c) Model Selection maps

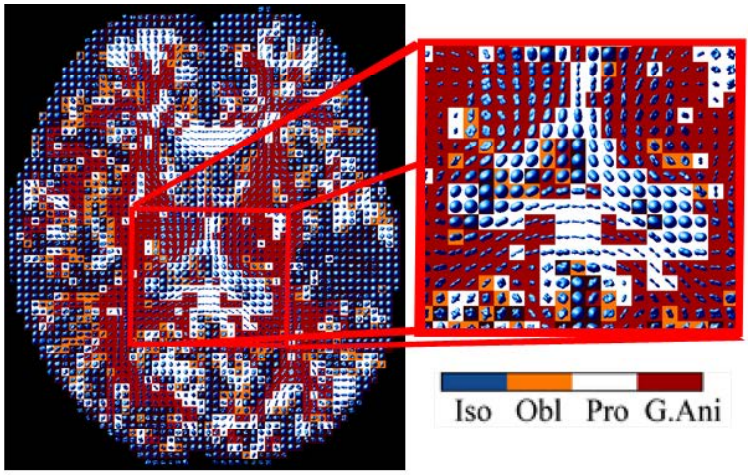

Fig 2. The orientation profiles map (blue represents surfaces of probability profiles), obtained with Diffusion Orientation Transform (DOT), is overlaid on the color-coded parsimonious model selection map.

DISCUSSION and CONCLUSION

The proposed parsimonious model selection method provides a meaningful unsupervised classification of brain DTI data that appears to reflect features of the underlying tissue structure and architecture reliably. This approach can be useful for planning parsimonious experimental designs of diffusion MRI experiments and to select the most appropriate approach for data analysis. For example, in regions identified as "prolate" fiber tractography based on the assumption of a single fiber population should be appropriate while regions that are identified by the general anisotropic and oblate models, may require more complex tractography approaches because of their more complex underlying fiber architecture. Furthermore, the isotropic regions can be represented by further simplified model, i.e. the scalar diffusion coefficient.

BIBLIOGRAPHY: [1] Freidlin RZ et al. *IEEE-TMI* 2007;26(11):1576-1584. [2] Ozarslan E et al. *NeuroImage* 2006;31: 1086–1103. [3] Schwarz G. 1978;6:461–468.