Multi-Fascicle Model Reconstruction from Acquisitions of DWI at a Single B-Value with a Population-Informed Prior

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Purpose. Diffusion tensor images (DTI) have been widely used to characterize the white matter microstructure. The incapacity of DTI to represent crossing pathways has motivated the development of novel diffusion models, such as the multi-tensor model. However, to estimate a multi-tensor model, one needs to acquire the diffusion-weighted images (DWI) at multiple b-values[1], unlike the common single-shell HARDI acquisition that has been used for years. This incompatibility comes with a high financial burden since studies based on single-shell HARDI acquisitions should be renewed and completed with novel acquisitions. In this study, we propose a method to retrospectively reconstruct a multi-tensor model from single-shell HARDI data, based on a multi-tensor atlas.

Methods. Let a two-tensor model be parameterized by its fraction and two tensors, $(f, \mathbf{D_1}, \mathbf{D_2})$. Its DWI signal for a gradient $\mathbf{g}$ is:

$$S = S_0 \left(f e^{-b\mathbf{g}^T \mathbf{D_1} \mathbf{g}} + (1-f) e^{-b\mathbf{g}^T \mathbf{D_2} \mathbf{g}} \right).$$

For a given b-value, an infinite number of models would result in the exact same DWI response[1]. These models all have identical diffusion directions (eigenvectors) but have eigenvalues and fraction that vary according to a free parameter α:

$$\left(\alpha f, \mathbf{D_1} + \frac{1}{b} \log \alpha \mathbf{I_3}, \mathbf{D_2} + \frac{1}{b} \log \left(\frac{1-\alpha f}{1-f} \right) \mathbf{I_3} \right), \text{ for any } e^{-b\lambda_1^{\min}} < \alpha < \frac{1}{f} \left(1 - (1-f) e^{-b\lambda_2^{\min}} \right). \quad [1]$$

As an illustration, all the multi-fascicle models of Fig. 1(a) cannot be distinguished based on a single b-value. To circumvent this problem, other researchers have proposed simplified multi-fascicle models in which tensors are replaced by sticks[2], preventing their use to investigate the microstructure (FA, MD, AD, RD) of the white matter. By contrast, we hypothesize that the fraction f can be learned from an external population of subjects for which DWI were acquired at mutiple b-values. We used a recent method to build a two-tensor atlas[3] and then proceed in four steps:

1) **Initialization** - Construct a two-stick model from the DWI data and a poorly determined two-tensor model
2) **Registration** - Spatially align the multi-tensor atlas to the two-stick model using a multi-tensor registration framework[3]
3) **Estimation** - Estimate the maximum a posteriori fraction f, hence α, at each location, with the population fractions as a prior
4) **α-correction** - Reconstruct the multi-tensor model by applying the transform [1] to the multi-tensor model from *Step 1*

Results and Discussion. To validate our approach, we acquired DWI data from 19 subjects with b-values between 1000 and 3000 s/mm^2. For each subject, we first built, as a ground truth, a two-tensor model using all DWI. We then estimated a multi-tensor model using the subsets of DWI with b=1000 s/mm^2, based on the proposed method and we compared its accuracy with results obtained without α-correction. To assess the accuracy of these models, we computed the mean squared error (MSE) of the full tensors, the FA and the trace of the tensors. α-Correction introduces an average 55% decrease in MSE of the full tensor and a 45% decrease in MSE of tensor traces (for both: one-tailed paired t-test: $p<10^{-6}$) (Fig. 1(b-c)). This brings the accuracy close to the absolute minimum obtained when α is specifically fixed to optimize performance (lowest '+' in the grey bars of Fig. 1(b)). No decrease in the average MSE of the FA was observed, potentially due to the absence of representation of the free water component that contaminates the two-tensor model. The proposed method can be readily adapted to integrate the free water component and this integration is part of our future work. The maximum observed MSE of the FA was, however, decreased by more than 25% (uppermost '+' in the boxplot).

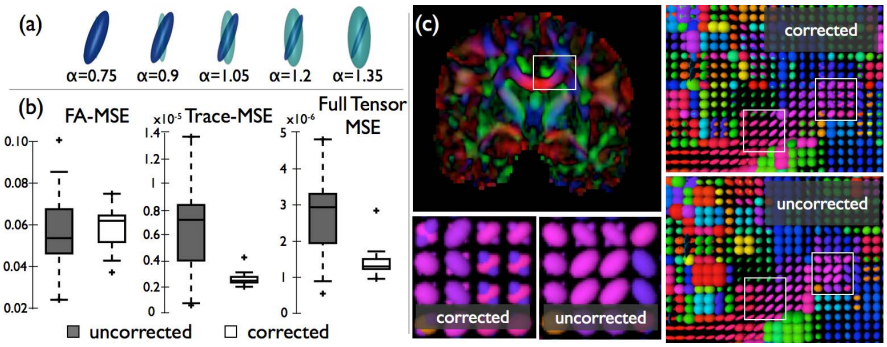

Fig. 1 (a) Different multi-fascicle models would generate the same DWI signals at a single b-value. Examples are given for different values of α. (b) Mean squared errors of the tensor trace and full tensor show a significant advantage of the corrected multi-tensor models over the uncorrected ones. (c) Due to the uncertainty in the parameter α, some multi-tensor models will have one component with inflated eigenvalues and one component with much lower eigenvalues (see eq. [1]) potentially occluded by the first one. Areas that are well represented by a single-fascicle (such as the corpus callosum) are not affected.

Conclusion. This study showed that multi-tensor models can be reconstructed retrospectively with available DWI acquired at a single b-value. Results on 19 brain volumes show that reconstruction accuracy is close to the best achievable accuracy at b=1000 s/mm^2. This allows improved accuracy of estimation of FA, MD, AD and RD at voxels where two fascicles cross. Future work will focus on applying the methods in practical cases, as well as releasing the source code and atlas for others to use.

References [1] B Scherrer and S K Warfield, "Why multiple b-values are required for multi-tensor models: evaluation with a constrained log-Euclidean model," in ISBI 2010: from nano to Macro, Rotterdam, Netherlands, 2010, pp. 1389–1392, IEEE Press. [2] Behrens, T. E. J., et al. "Probabilistic diffusion tractography with multiple fibre orientations: What can we gain?" Neuroimage 34.1 (2007): 144-155. [3] M Taquet *et al*, "Registration and Analysis of White Matter Group Differences with a Multi-Fiber Model", in proceedings of Medical Image Processing and Computer Assisted Interventions, 2012, LNCS 7512, p. 313 ff.