Multi-Fascicle Model Reconstruction from Acquisitions at a Single b-value with a Population-Informed Prior

Maxime Taquet[1,2], Benoit Scherrer[1], Benoit Macq[2], and Simon K Warfield[1]
[1]*Computational Radiology Laboratory, Harvard Medical School, Boston, Massachusetts, United States,* [2]*ICTEAM Institute, Université catholique de Louvain, Louvain-la-Neuve, BW, Belgium*

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 developement of novel diffusion models, such as the multi-tensor models. 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 acqusition 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 response is:

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

An infinite number of models would result in the exact same DWI response[1]. These models are related by 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 multi-fascicle models of Fig. 1(a) cannot be distinguised 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 properties of the white matter. By contrast, we hypothesize that the fraction f can be learnt 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 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 mutli-tensor model of *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 square error (MSE) of the full tensors, the FA and the trace. 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 specically fixed to optimize performance (lowest '+' in the uncorrected bars). No decrease in MSE of the FA was observed, potentially due the large dependence of FA on the b-value, hence the difficulty to compare the FA at different b-values.

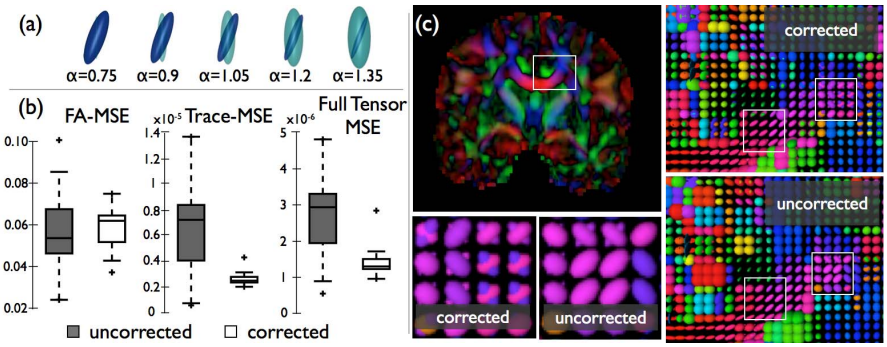

Fig. 1 (a) Different multi-fascicle models would generate the same DWI signals at a single b-value. Examples are given for different values of α. (b) Mean square errors of the tensor trace and full tensor show a significant advantage of the corrected multi-tensor models over the uncorrected ones. (c) 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 potentially hidden 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. Future work will focus on applying the methods in practical cases, as well as releasing the 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.,