## Probabilistic Determination and Model Based Regularization of Intra-Voxel Multiple Fibre Architecture in High Angular Resolution Diffusion Imaging Data Sets

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Introduction

Methods to reconstruct nerve fibre tracks in brain and spinal cord using diffusion weighted MRI are now widespread. Such methods allow connectivity to be assessed in subjects in a non-invasive way. This has particular utility in human imaging where invasive studies are not possible. Current techniques make assumptions regarding fibre heterogeneity within the voxel being imaged which are overly simplistic in some areas of the brain. A diffusion tensor model of the diffusion profile within a voxel, which only allows for a single nerve fibre orientation, is frequently used. This will produce results inconsistent with the underlying anatomy in regions where fibres cross[2]. An algorithm is applied to the problem of tractography which is capable of inferring Probability density functions (PDFs) of the orientations of one or two intra-voxel fibre bundles based on each model's relative probability of describing the data.

## Algorithm

A Monte Carlo Markov chain Bayesian inference method was used to analyse multi-directional diffusion weighted MRI images[1,3]. Such techniques allow us to draw samples from the probability distribution P(Model paramater|Data,Model). Hence if we have a model which attempts to describe a data-set we can calculate the probability distribution of the model paramaters given the measured data if we make the assumption that the model is correct. We constructed a model for the signal due to diffusion within the imaged voxels population of nerve fibres for a constant b-value. The equation for N distinct fibres and an isotropically diffusing component can be calculated using equation (1), where each fibre has a partial volume fraction  $f_i$ , and  $v_i$  is the i<sup>th</sup> fibre's orientation, and the i<sup>th</sup> fibre's diffusion tensor has two degenerate eigenvalues  $D_{perp,i}$  and a major eigenvalue  $D_{para,i}$ . Equation (1) can be rewritten as equation (2), where  $S_i$  and  $S_{iso}$  are given by equations (3) and (4) respectively. For a constant b-value so by fixing the b-value we clearly reduce the number of paramaters we need to fit for.

A Markov Chain Monte Carlo Method was implemented in C++ to calculate PDFs for the parameters  $S_{i}S_{iso}, \Delta\lambda_i$  and  $v_i$  from the diffusion weighted data set. The data was fitted using both one and two fibre models. Once the PDFs have been fitted for we can evaluate which model is the more appropriate for the voxel being analyzed. To assess the quality of a model its parameters were sampled from P(**X**|Data,Model) using the Markov chain where **X** is the vector of model parameters. The parameter  $\Psi_{model}$  (representing the average probability of the data

$$(1) S = S_0 \left( f_{iso} e^{-bD_{uo}} + \sum_{i=0}^N f_i e^{-bD_{pep,i} - b(D_{per,i} - D_{pep})(n_i \cdot v)^2} \right)$$

$$(2) S = S_{iso} + \sum_{i=0}^N S_i e^{-b\Delta\lambda_i (n \cdot v_i)^2}$$

$$(3) S_i = S_0 f_i e^{-bD_{pep,i}}$$

$$(4) S_{iso} = f_{iso} e^{-bD_{uo}}$$

$$(5) \Psi_{model} = \frac{1}{M} \sum_{j=1}^M P\left( Data | \mathbf{X}_j, Model \right)$$

$$(6) \Psi_{model} \approx \int d^N X P\left( Data | \mathbf{X}, Model \right) P\left(\mathbf{X} | Data, Model \right)$$

$$(7) \Phi = \ln\left(\Psi_{2 \ fibres}\right) - \ln\left(\Psi_{1 \ fibre}\right)$$

given the model and its inferred parameters) was calculated according to equation (5) (where  $X_j$  is the j<sup>th</sup> sample of X sampled from the Markov chain and M is the number of Markov chain samples) using the well known Rician distribution for noise in MRI images[4]. For a large enough number of samples  $\Psi_{model}$  can be represented by equation (6). The parameter  $\Phi$  given by equation (7) was then calculated to assess which model was most appropriate. With Bayesian inference problems we can incorporate the prior probabilities of our model parameters into the fitting. We used this capability to incorporate neighbourhood information to regularize our distribution of fibre orientations by making low deviations between the orientations of neighbouring voxels more likely subject to a curvature constraint.



Data Diffusion datasets were acquired on a Bruker Medspec S300 3T system. 63 diffusion directions were acquired with b=1000 mm<sup>2</sup>/s. A diffusion weighted gradient duration, of  $\delta=27.5$  ms and evolution delay of  $\Delta$ =40ms was used. The images were coregistered to remove motion and eddy artifacts. It current should be noted that in the analysis of the data that no b=0 mm<sup>2</sup>/sec

images were used, as this is not necessary for characterising the direction of diffusional anisotropy. The images were reconstructed to a matrix size of 128x128 from an EPI matrix size of 100x100 for 63 slices. This gave a voxel dimension of 1.56 mm x 1.56 mm x 2mm.

## Results

Figure 1 comprises three monochrome intensity images combined on the red, green and blue colour channels. The green channel corresponds to the value of  $S_{iso}$  from a two fibre model and the blue channel corresponds to the value of  $S_o$  from fitting the one fibre mode, and the red channel denotes regions of high  $\Phi$  which correspond to a high likelihood of having a double fibre architecture. Figure 2 shows the directions sampled from the PDF of the one or two fibre model depending upon which the algorithm has determined to be the most plausible by thresholding the value of  $\Phi$  to correspond to a two fibre model if greater than 13 (such voxels are represented using green vectors). Figure 3 shows the same voxels but sampled whilst incorporating neighbourhood information to regularize the directions. It can be seen that this results in tighter PDFs.

## References

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