A Bayesian random effects model for enhancing resolution in diffusion MRI

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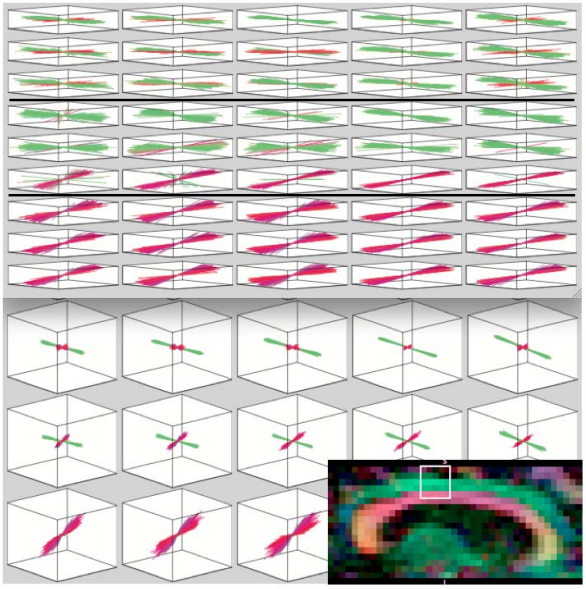
Introduction

One of the major limitations of diffusion MRI (dMRI) is poor resolution relative to the structure under investigation. Typical dMRI maps do not provide spatial information with the same detail seen in high resolution structural MRI and this can limit their clinical value. A number of methods have been developed for dealing with voxels that contain multiple fibers [1], but none of these provide a spatial resolution of the components. The present work outlines a Bayesian latent variables random effects modelling approach to achieving a subvoxel spatial separation of the underlying structures.

Methods

Diffusion-weighted data were acquired from 3 healthy volunteers on a 1.5 T Siemens Avanto system. A twice-refocused eddy-current-nulled EPI sequence was used with diffusion-weighting gradients applied along 20 noncollinear directions with a b-value of 1000 $s mm^{-2}$. 50 contiguous slices were imaged by averaging two acquisitions. The imaging parameters were: echo time, 89ms; repetition time, 7s; slice thickness, 2.5mm; FOV, 240 by 240mm; matrix size, 96 by 96. Data processing was restricted to regions-of-interest, each of which consisted of a 5-by-5 array of voxels centred at the junction between the cingulum and corpus callosum. Details of the Bayesian statistical model are given in a previous publication [2]. The likelihood was based on the diffusion model proposed by Behrens et al. [3]. The main feature of the statistical model is a Markov random field treatment in which spatial prior distributions were assigned to the spherical coordinates and B_0 signal intensity. Intrinsic Gaussian conditional autoregressive (CAR) distributions [4] were adopted. These take the form $U_i|U_j, i \neq j, \sim N(\overline{u}_i, w_u^2/m_i)$, that is, a normal distribution with mean ($\overline{u}_i$) given by the average of the neighbouring voxel values, and variance w_u^2/m_i, where *i* and *j* are voxel labels, w_u^2 is a scaling parameter and m_i is the number of voxels adjacent to the *i*th voxel. A gamma distribution was assigned to the inverse of the normal variance. The set of neighbours included all those voxels with one or more corners in common with the *i*th voxel. The remaining parameters were assigned exchangeable prior distributions. Posterior distributions were sampled using Markov chain Monte Carlo (MCMC) implemented in WinBUGS/GeoBUGS [5] together with the WinBUGS development interface [6].



Results

The figure shows the results obtained for one of the three subjects in the region of the junction between the cingulum and corpus callosum. Similar results were obtained in the other subjects. The lower half of the figure shows an array of vector cluster plots, as obtained when the signal intensity data were modelled at the resolution provided by the native dMRI data. The upper half of the figure shows the corresponding results generated by modelling the signal intensity data in each voxel as a mixture of signals from 3 vertically resolved sub-voxels. The analysis was performed on a native 5-by-5 ROI, a 3-by-5 portion of which is shown in the figure. At the native resolution the boundary between the cingulum and corpus callosum gives rise to a row of crossing fibres. A largely successful separation of the two structures has been achieved by using the latent variables random effects model. In particular, the row of voxels at the junction between the two structures is partitioned into a single row of subvoxels assigned to the corpus callosum and two rows assigned to the cingulum. The resulting pattern of subvoxel fibre orientations is entirely consistent with the underlying white matter structure at the junction between the cingulum and corpus callosum.

Discussion

Spatial resolution is a limiting factor in diffusion tractography and other dMRI applications. The concept that an increase in resolution can be achieved through post-acquisition data processing has been investigated previously [7-9], motivated by the need for methods that can deal with bending, fanning and partial volume problems that occur due to poor spatial resolution. The results presented here show that the Bayesian random effects model provides a plausible separation of components at the subvoxel level, despite the relatively low information content of the 20-directions dMRI data and moderate b-value (1000 s mm^{-2}) used in this study. In particular, the model has the potential to offer a solution to the crossing fibre problem that arises due to partial volume effects.

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