Introduction

Persistent angular structure (PAS) MRI [1] is one of many approaches that recover complex white-matter fibre configurations within single voxels of high angular resolution diffusion MRI (HARDI) data. It continues to exhibit impressive performance compared to other state of the art methods [2], but at the expense of unreasonably long reconstruction times. Here, we propose and test a simple adaptation to the algorithm that makes computation time manageable without significantly affecting performance.

Method

PAS MRI may be thought of as a spherical deconvolution algorithm [3, 4], which models the measurement A, at wavevector $\mathbf{q}$, to be the convolution of the fibre orientation distribution (FOD) with a response function R:

$$A(\mathbf{q}) = \int_{\mathbb{S}^2} f(\hat{\mathbf{x}}) R(\mathbf{q}, \hat{\mathbf{x}}) \mathrm{d}\hat{\mathbf{x}} \,, \quad f(\hat{\mathbf{x}}) = \exp\left(\lambda_0 + \textstyle\sum_{i=1}^{L} \lambda_i R(\mathbf{v}, \hat{\mathbf{x}})\right)$$

where f is the FOD represented as a non-linear combination of basis functions aligned with the uniformly distributed directions $\{\mathbf{v}_1, ..., \mathbf{v}_L\}$. The method works by searching for the parameters $\{\lambda_0, ..., \lambda_L\}$ that provide the best fit to the measured data. As in [1] we use $R(\mathbf{q}, \mathbf{x}) = \cos(r\,\mathbf{q} \cdot \mathbf{x})$ with $r = 1.4$. In the original method the number of encoding directions, L, is the same as the number of wavevectors, N, in the HARDI acquisition. Here, we *reduce* the encoding so that $L < N$. This decreases the number of λ parameters and reduces computation time, but also reduces the representational flexibility of f. We further reduce computation time by avoiding expensive fidelity checks on numerical integration in the original implementation, as suggested in [5].

Experiments

We consider three configurations of simulated FODs that contain one, two and three crossing fibres and follow the model in [1] where the diffusion scatter pattern of each fibre is represented by a diffusion tensor. The orientations of the fibres within a single FOD are randomly generated so that the crossing angles between them are at least $\pi/4$ radians. For each type of FOD, we generate 256 voxels of synthetic data with $N = 54$ and $b = 1600$ s/mm^2 and add Rician noise at a $b = 0$ SNR of 16. We also examine a coronal slice of real brain data acquired with $N = 61$ and $b = 1200$ s/mm^2, only considering the 2150 voxels where the diffusion tensor fractional anisotropy is greater than 0.2. To evaluate reconstruction performance we compute the consistency fraction [1], denoted by C, which is the fraction of reconstructed FODs that have the same number of significant peak directions (PDs) as the ground truth, where each peak is within $\cos^{-1}(0.95)$ of the closest ground truth peak. In the case of the real data, we use the full encoding reconstruction as a substitute for the non-existent ground truth and compute C for all reconstructions by limiting the maximum number of PDs compared between the FODs to one, two and three separately. All data are reconstructed for L in $[4, N]$ using a modern laptop computer (2 × 2.5 GHz and 4 GB RAM).

Results

Figure 1 plots C against the number of encoding parameters and demonstrates that the performance of a reduced encoding generally matches, and occasionally exceeds, that of the full encoding once $L \geq 14$ for all types of FOD. Note that performance is generally poor for reconstruction of three crossing fibres. Figure 2 shows that the primary PD of the reduced encoding reconstruction on brain data is consistent with that of the full encoding for all values of L. Additionally considering the possible secondary PD causes C to drop by a small amount to 0.94 (2 d.p.) at the initial performance of peak for $L = 16$. Differences in the tertiary PDs cause a more significant drop in C to 0.78 (2 d.p.) for $L = 16$, but many of these small tertiary peaks are likely to be spurious. A visual comparison between a reduced encoding ($L = 16$) and the full encoding at the fibre crossing in the pons (Figure 3) illustrates the similarity of the reduced encoding, where noticeable differences only appear in areas of low fractional anisotropy.

Conclusions

For typical HARDI acquisition schemes, a reduced encoding PAS MRI reconstruction ($L = 16$) approximately reduces reconstruction time by a factor of 4 compared to the original method and only exhibits significant deviations from the original reconstruction when more than two PDs are compared. Experiments on synthetic data show that the reduced encoding at least matches the performance of the original method, suggesting that differences on real data do not necessarily represent a decrease in performance. Other exhaustive tests on synthetic data, not detailed here, demonstrate that this similarity of performance always exists except when the fractional anisotropy of a single fibre's diffusion scatter pattern is particularly low. Reconstruction for $L = 16$ only takes around 0.25s per voxel of brain data on a modern laptop computer, thereby making the algorithm a practical, yet still powerful, alternative for multiple fibre reconstruction. Thanks go to Geoff Parker and Karl Embleton (Division of Imaging Sciences, University of Manchester) for providing the real brain data used in this study.

References

[1] K. M. Jansons and D. C. Alexander. *Inverse Problems* 19: 1031-1046, 2003. [2] A. Ramirez-Manzanares et al. *Proc. MICCAI 2008*, 305-312. [3] J.-D. Tournier et al. *NeuroImage* 23: 1176-1185, 2004. [4] D.C. Alexander. *Proc. IPMI 2005*, 76-87. [5] K. Sakaie. *Workshop on CDMRI, MICCAI 2008*, 138-147.

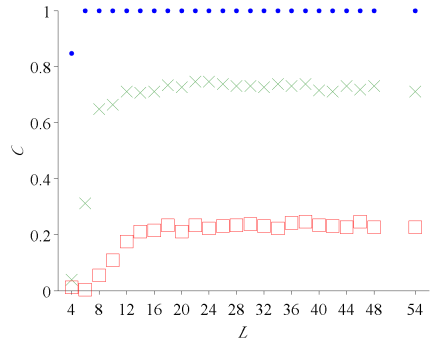

Figure 1. Consistency fraction (C) of PAS MRI reconstruction on synthetic data with one (●), two (×) and three (□) crossing fibres using reduced numbers of encoding parameters (L).

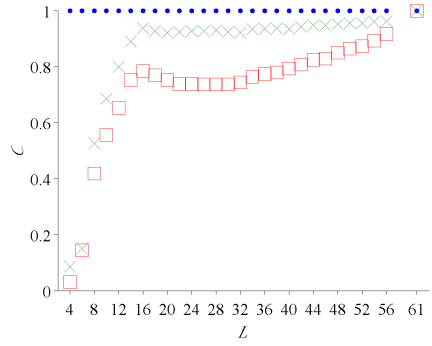

Figure 2. Consistency fraction (C) of PAS MRI reconstruction on real brain data with respect to the major (●), major two (×) and major three (□) peak directions of the full encoding using reduced numbers of encoding parameters (L).

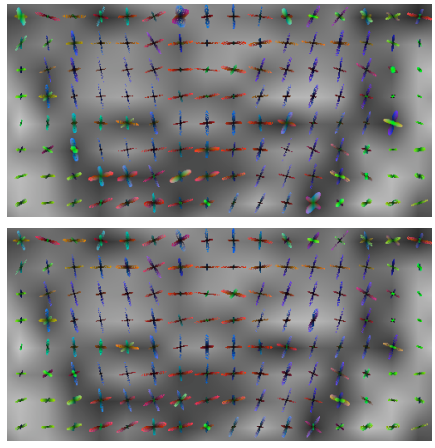

Figure 3. PAS MRI reconstruction plots (projected onto the xz plane) for $L = 16$ (top) and $L = N$ (bottom) at the fibre crossing of the pons in a coronal slice of real brain data. Background map is of diffusion tensor fractional anisotropy.