

Reduced Encoding Persistent Angular Structure

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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} , as the convolution of the fibre orientation distribution (FOD) with a response function R over the unit sphere:

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

where f is the FOD represented as a non-linear combination of basis functions aligned with the uniformly distributed directions $\{\mathbf{v}_1, \dots, \mathbf{v}_L\}$. Essentially, the method works by searching for the parameters $\{\lambda_0, \dots, \lambda_L\}$ that provide the best fit to the measured data. As in [1] we use $R(\mathbf{q}, \mathbf{x}) = \cos(r \mathbf{q}^T \mathbf{x})$ 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 limits 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

For testing, we simulate data from test functions defined by mixtures of Gaussians, similar to those in [1], which contain one, two or three components and where each component loosely corresponds to a fibre. The orientations of the components within a single voxel are randomly generated, but are constrained so that the crossing angles between them are at least $\pi/4$ radians. For each test function, we generate 256 voxels of synthetic data with $N = 54$ and $b = 1150 \text{ s/mm}^2$ (3 s.f.) 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 $b = 1200 \text{ s/mm}^2$, and only consider 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 PD is within $\cos^{-1}(0.95)$ of the closest ground truth PD. 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 three different cases: C_1 only compares the most significant PD of the ground truth with that of the reconstructed FOD; C_2 compares, at most, the two most significant PDs of each; and C_3 compares, at most, the three most significant PDs of each. All data are reconstructed for L in $[4, \dots, N]$ using a laptop computer ($2 \times 2.5 \text{ GHz}$ and 4 GB RAM).

Results

Figure 1 plots C against the number of encoding parameters and demonstrates that performance of a reduced encoding generally matches, and occasionally exceeds, that of the full encoding ($L = N = 54$) once $L \geq 16$ for all test functions. Note that performance is generally poor in the presence of three components. Figure 2 shows that C_1 of the reduced encoding reconstruction on brain data is perfect for all values of L . Additionally considering the possible secondary PD causes C_2 to drop to a smaller value of 0.936 (3 s.f.) for $L = 16$. Differences in the tertiary PDs cause a more significant drop in C_3 to 0.782 (3 s.f.) for $L = 16$, after which performance temporarily drops further, 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

A reduced encoding PAS MRI reconstruction ($L = 16$) only exhibits significant deviations from the full encoding when more than two PDs are compared and reduces reconstruction time by a factor of around 4 for typical HARDI acquisition schemes. Experiments on synthetic data show that the reduced encoding at least matches the absolute performance of the full encoding, 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 in performance always exists, except when the fractional anisotropy of a single Gaussian component is particularly low. Reconstruction for the reduced encoding ($L = 16$) 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.

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References

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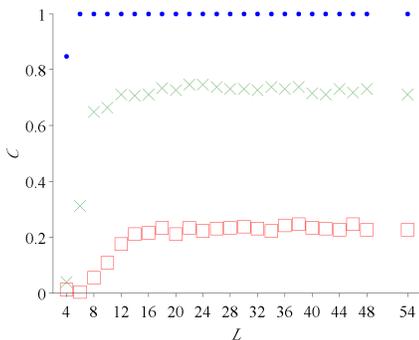


Figure 1. Consistency fraction (C) of PAS MRI reconstruction on synthetic data with one (\bullet), two (\times) and three (\square) crossing fibres using reduced numbers of encoding parameters (L) and the full encoding ($L = N = 54$).

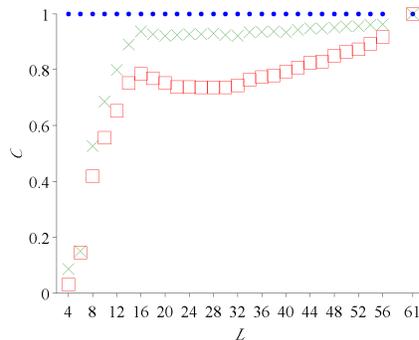


Figure 2. Consistency fraction (C) of PAS MRI reconstruction on real brain data for C_1 (\bullet), C_2 (\times) and C_3 (\square) using reduced numbers of encoding parameters (L) and the full encoding ($L = N = 61$).

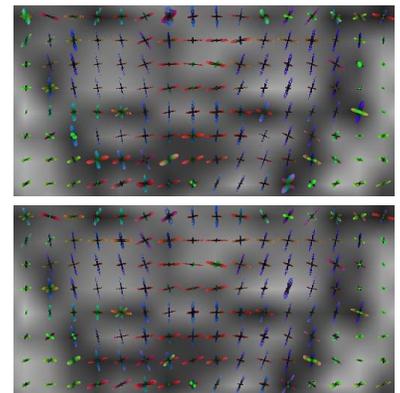


Figure 3. PAS MRI reconstruction plots for $L = 16$ (top) and $L = N = 61$ (bottom) at the fibre crossing of the pons in a coronal slice of real brain data. The background map is of the diffusion tensor fractional anisotropy.