Model-Based Reconstruction of Undersampled DTI Data

C. L. Welsh[1,2], E. W. Hsu[1,2], and E. V. DiBella[1,2]

[1]Bioengineering, University of Utah, Salt Lake City, Utah, United States, [2]UCAIR, University of Utah, Salt Lake City, Utah, United States

Introduction: Diffusion Tensor Imaging (DTI) [1] is useful for characterizing tissue microstructure, allowing determination of, for example, fiber orientations of the myocardium or brain white matter that are not evident in conventional MRI. DTI requires a minimum of seven scans of the same image to fully solve the diffusion tensor. The low temporal resolution and the associated low spatial resolution and SNR present a significant challenge for the practical utility of the technique. To accelerate the acquisition time, strategies for undersampling and iterative reconstruction of DTI data have been proposed [2]. Rather than first reconstructing the diffusion weighted images then fitting the tensors, in the current study diffusion tensor fields are directly estimated from k-space data via model-based reconstruction. The rationale is that better performance might be achieved by direct estimation and estimating fewer unknowns in the reconstruction. Model-based reconstruction algorithms have been proposed for DTI [3-4], but not for undersampled data.

Methods: Model-based reconstruction of undersampled data is performed by fitting the diffusion tensor $\mathbf{D}$ directly to the acquired data via minimizing the L2-norm cost function in Eq. (1), where W is the undersampling matrix, F is the Fourier operator, I_0 is the non-diffusion weighted reference image, b is the diffusion weighting factor, $\mathbf{g}_n$ is the diffusion encoding directional vector, φ_n is the image phase and d_n is the measured k-space for the nth diffusion direction. Minimization is done by first computing the derivative $\delta C(\mathbf{D})/\delta Dij$ of Eq. (1) with respect to the ij^{th} element of the tensor, then updating it using a step size λ according to the gradient descent algorithm in Eq. (2). The process is repeated until all parameters have converged, in which Eq. (1) has reached a minimum.

$$C(\mathbf{D}) = \sum_{n=1}^{N} \left\| WFI_0 e^{-b\mathbf{g}_n^T \cdot \mathbf{D} \cdot \mathbf{g}_n} e^{i\phi_n} - d_n \right\|_2^2 \quad (1) \qquad D_{ij}^{n+1} = D_{ij}^n - \lambda \frac{\delta C(\mathbf{D})}{\delta D_{ij}} \quad (2)$$

To test the performance of the proposed approach, fully-sampled Cartesian k-space DTI (95 encoding directions) was acquired on a fixed, excised macaque brain hemisphere using a Bruker 7T scanner. A subset of images encoded in 12 directions was chosen, phase-corrected, and based to simulate undersampling using an accelerating factor R of 2 but different patterns, including variable density (MBVD), center only (MBC) and center offset (MBCO). Performances of sampling schemes and reconstruction were assessed by comparing the mean white matter fiber orientation deviation ($\Delta\alpha$), root mean squared (RMS) error of the fractional anisotropy (FA) and mean diffusivity (MD) over the whole hemisphere to those obtained from 12- and 6-image fully-sampled datasets, against the entire 95-image "gold standard".

Results and Discussion: Figure 1 demonstrates the FA maps and Table 1 lists the quantified performance metrics for the cases discussed. All reconstruction schemes converge within 1000 iterations, taking approximately 5 minutes on a machine with a Quad-Core processor and 4GB RAM. Overall, performances of the model-based reconstruction for estimating the white matter orientation and FA are generally comparable to the 12-image fully sampled case and are better than the 6-image case, which serves as the control based on equivalent acquisition time. The performances for estimating the MD is less impressive, possibly because unlike the case of fiber orientation or the FA, estimation biases in the diffusivities do not self normalize. For all DTI parameters, minor differences in the performance are observed among the model-based schemes. Specifically, the MBCO case performs the best in terms of $\Delta\alpha$ and RMS FA, whereas MBVD has the best RMS MD. These observations suggest that DTI scan time is better spent acquiring partial k-space of more directions than full resolution of fewer directions, and that different regions of k-space may contribute differently toward the accuracy in estimating different DTI parameters.

Conclusion: The model-based algorithm is a promising reconstruction method for undersampled DTI data, capable of achieving comparable accuracy for estimating the DTI fiber orientation and FA but requiring only half of the acquisition time, in the case of phase-corrected data. Phase correction doesn't affect the results of MBC, but future work will be in estimating image phase for the other sampling schemes. Different regions of k-space appear to contribute to DTI accuracy unequally, which warrants further investigation.
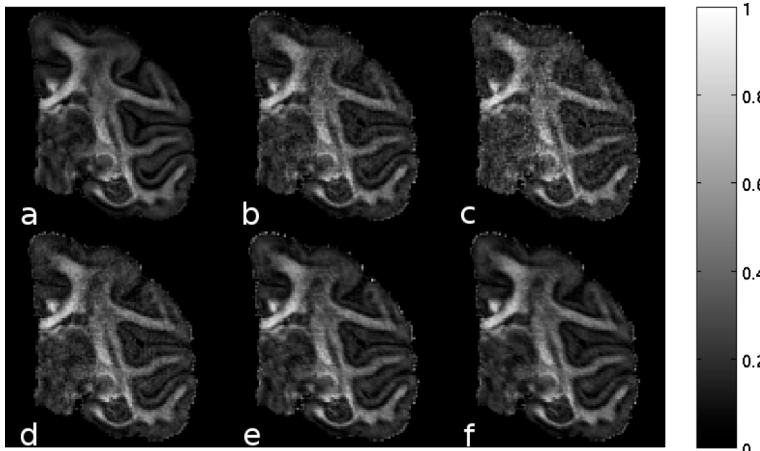

Figure 1. FA maps for (a) 95 directions "gold standard", (b) 12-direction full images, (c) 6-direction full images as control (d) model-based variable density (MBVD), (e) model-based centric sampling (MBC), and (f) model-based center with offset (MBCO).

Table 1. Metrics of performance in terms of estimation error for DTI parameters compared against the 95-image "gold standard" dataset. Angular deviation $\Delta\alpha$ and RMS MD are reported in degrees and 10^{-5} cm^2/s, respectively. RMS FA is dimensionless.

Scheme	$\Delta\alpha$	RMS FA	RMS MD
MBVD	8.66	0.0479	0.0057
MBC	7.28	0.0403	0.0077
MBCO	6.94	0.0361	0.0086
6 full img	14.05	0.0790	0.0074
12 full img	8.70	0.0445	0.0046

References: [1] Basser PJ et al, Biophys J, 66:259-267, 1994. [2] Adluru G et al, LNCS, 4466:91-99, 2007. [3] Yendiki A, Proc. ISBI, 924-927, 2007. [4] Cheryauka AB et al, Magn Reson Imaging, 22:139-148, 2004.