

Accelerating Diffusion Kurtosis Acquisition using SIR and Model-Based Reconstruction

Christopher Lee Welsh¹, Edward W Hsu¹, and Edward VR DiBella²

¹Department of Bioengineering, University of Utah, Salt Lake City, UT, United States, ²Radiology, UCAIR, University of Utah, Salt Lake City, UT, United States

Introduction: Diffusion kurtosis imaging (DKI) [1] can more accurately characterize non-monoexponential decay with increasing diffusion weighting (b-value), as opposed to diffusion tensor imaging (DTI). DKI is also able to differentiate crossing fibers since it fits a fourth-order kurtosis tensor in addition to the traditional second-order diffusion tensor. Because the kurtosis tensor is a fully-symmetric fourth-order tensor, there are 15 parameters to fit in addition to the 6 from the diffusion tensor for a total of 21. The higher number of parameters that need to be fit, in addition to multiple diffusion weightings acquired per direction, result in long scan times that limit the usability of DKI. In order to accelerate acquisition time, fewer measurements could be taken and a model-based reconstruction could be applied to the acquired data. A model-based algorithm, in which diffusion tensor (DTI) parameters are reconstructed directly from the acquired k-space using a compressed sensing construct, has been presented previously [2]. Here, the previous DTI model-based approach is extended to undersampled DKI data by reconstructing all 21 unknown variables of the kurtosis and diffusion tensors directly from the undersampled k-space data. Its performance is compared against using fully-sampled k-space, reconstructed traditionally.

Methods: Model-based reconstruction of undersampled data is performed by fitting the diffusion tensor, \mathbf{D} , and the kurtosis tensor, \mathbf{W} , directly to the acquired data via minimizing the cost function in Eq. (1), where E_n is the undersampled Fourier operator (Fourier transform followed by undersampling of k-space), d_n is the undersampled DTI k-space data, $\varphi(\cdot)$ is a sparsifying transform (spatial total variation) with a regularization weight, α , and N is the total number of diffusion weighted images. The signal model, S_n , is defined in Eq. (2), where S_0 is the non-diffusion weighted reference image, b is the diffusion weighting factor, \mathbf{g}_n is the diffusion encoding directional vector, \bar{D} is the mean diffusivity and ϕ_n is the image phase. Minimization is accomplished via gradient descent, requiring the derivative of Eq. (1) with respect to each element of \mathbf{D} and \mathbf{W} . The process is repeated until all parameters have converged (within 300 iterations).

$$C(\mathbf{D}, \mathbf{W}) = \sum_{n=1}^N \|E_n S_n - d_n\|_2^2 + \alpha \varphi(S_n) \quad (1)$$

$$S_n(b; \mathbf{D}, \mathbf{W}) = S_0 \exp \left(-b \sum_{i,j=1}^3 g_{in} g_{jn} D_{ij} + \frac{1}{6} b^2 \bar{D}^2 \sum_{i,j,k,l=1}^3 g_{in} g_{jn} g_{kn} g_{ln} W_{ijkl} \right) \exp(i\phi_n) \quad (2)$$

To test the performance of the proposed approach, fully-sampled Cartesian k-space DTI data (64 encoding directions, $b = [500, 1000, 2000, 4000] \text{ s/mm}^2$, coils = 12) were acquired with a healthy patient on a Siemens Trio 3T scanner with an EPI readout and TR=8700ms, TE=151ms, voxel size = $2.5 \times 2.5 \times 2.5 \text{ mm}^3$. The acquired k-space was retrospectively undersampled to simulate a read out acceleration factor, R , of 3. If used in conjunction with SIR [3,4], an overall scan time saving of 3 can be achieved while maintaining the same TE if three slices are excited for a single diffusion preparation. The performance of the proposed model-based approach was compared to fitting \mathbf{D} and \mathbf{W} using a constrained linear least squares [5] approach from the fully-sampled k-space data.

Results and Discussion: Figure 1 compares the results of the fully-sampled case and the proposed model-based approach. Fig. 1(a) shows a region of interest in the resulting FA, Fig. 1(b) shows the primary eigenvectors projected on the x-y plane, for reference. Figs. 1(c) – (f) show the spheroid representations of the apparent diffusion and kurtosis tensors in areas with FA greater than 0.2, which are colored according to their prominent direction and scaled to fit within each voxel. The correlation between the fully-sampled and model-based apparent diffusion spheroids was 0.98 and the root mean square error of the model-based kurtosis spheroids was 0.49. The model-based approach preserves the main direction of diffusion and the crossing fibers visualized through the kurtosis tensors.

References: [1] Jensen JH et al, Magn Reson Med. 2005; 53:1432-1440. [2] Welsh CL et al, Magn Reson Med. 2013; 70:429-440. [3] Adluru G et al, ISMRM. 2012; 20:2248. [4] Feinberg DA et al, Magn Reson Med. 2002; 48:1-5. [5] Tabesh A et al, Magn Reson Med. 2011; 65:823-836.

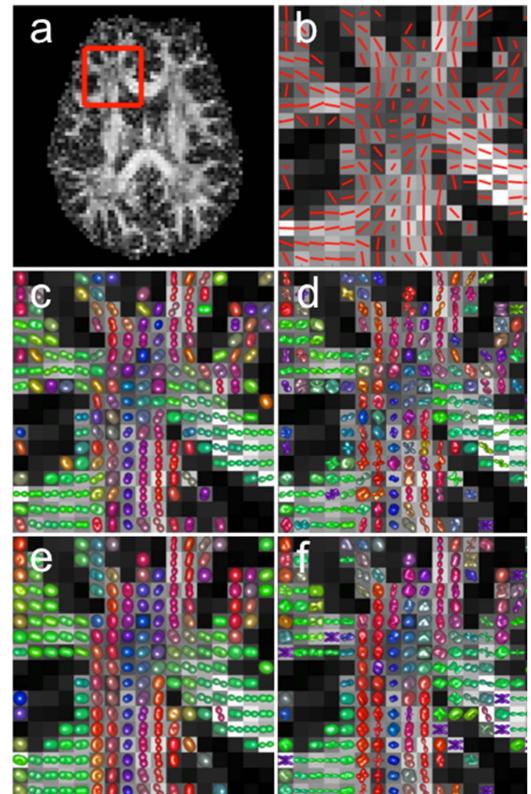


Figure 1: Results from reconstruction of diffusion kurtosis data. (a) Fractional anisotropy map with highlighted region of interest, (b) projected primary eigenvectors in ROI, (c) apparent diffusion and (d) kurtosis tensor spheroids from fully sampled case, (e) apparent diffusion and (f) kurtosis tensor spheroids from model-based reconstruction using $R = 3$ undersampled data.