

Combination of a radial sequence for in vivo DTI of articular cartilage with an iterative model-based reconstruction

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Purpose: Diffusion tensor imaging (DTI) of the articular cartilage has demonstrated high accuracy (90%) for the early diagnosis of osteoarthritis (OA) at ultra-high field scanners (7 T).¹ However, the applicability of DTI in clinical scanners (3 T) is still challenging from the acquisition point of view due to the low T2 values in articular cartilage (~30 ms) and the high resolution needed (<1 mm). To overcome these problems we have implemented a radial spin-echo diffusion tensor imaging (RAISED) sequence which provides high signal-to-noise (SNR) efficiency, excellent image quality, and robustness against motion^{2,3}. Recently, we implemented a model-based iterative reconstruction for non-Cartesian acquisition with regularization on the diffusion tensor to improve diffusion parameter calculation. The model-based iterative reconstruction directly reconstructs the diffusion tensor without having to reconstruct the intermediate diffusion-weighted images. This provides more flexibility in the data acquisition because it allows undersampling of k-space, which can be invested in further imaging acceleration, acquisition of more b-values or diffusion directions and improvement of the imaging resolution. Purpose of this work is to investigate the optimal acquisition strategy for the RAISED sequence combined with an iterative model-based reconstruction.

Methods: We acquired four different protocols (Table 1) in an anisotropic diffusion phantom consisting of polyethylene fibers and the right knee of two subjects using the RAISED sequence. All four protocols had the same following parameters TE/TR of 40/1500 ms, slice thickness of 3 mm, a field of view of 154 mm², and six diffusion directions per b-value ($\Delta = 21$ ms, $\delta = 16$ ms). Protocol A represents the optimal protocol using gridding (SNR ≥ 15 in the diffusion-weighted image). Protocol B improves resolution (0.6 mm instead of 0.74 mm, i.e. 34% higher resolution). Protocol C increases the diffusion-weightings, and protocol D accelerates the acquisition (~1/2). All images were reconstructed with gridding and with our model-based approach. Model-based estimations are obtained by minimizing the non-linear problem:

$$S(D) = \sum_{n=1}^N \|E_n(D) - y_n\| + \alpha \sum_i^N \|\Psi(D)\|, \text{ with } E_n(D) = FT_n(I_0 e^{-b_n g_n^T D g_n^T} c_n e^{i\Phi_n}),$$

where D is the diffusion tensor, y_n is the acquired raw data with the diffusion-weighting b_n and in the direction g_n , with the index n running for the number of diffusion-weighted images (N). $E_n(D)$ is the forward operator that maps between k-space data and the diffusion tensor. I_0 is the signal intensity with no diffusion-weighting, c_n are the coil sensitivities and Φ_n is the phase error induced by macroscopic motion (measured with a 2D echoplanar navigator). FT_n is the non-uniform Fourier transform. As the sparsifying transform Ψ we used a total variation seminorm, applied individually over each component of the diffusion tensor (index i running along the components of the diffusion tensor, N_D). α is the regularization parameter, which was optimized for the protocol A and kept constant for all images ($\alpha = 2.5 \cdot 10^{-3}$). From each reconstruction the mean diffusivity (MD) and the fractional anisotropy (FA) were obtained.

To evaluate the different protocols in the phantom in two regions of interest (ROIs), one in water (no anisotropy) and the other in the fibers (FA~0.3). We also segmented the cartilage in the knee dataset and defined a ROI in the muscle. Averaged MD and FA in cartilage and muscle were calculated. To assess differences in average MD and FA between the gridding and the model-based reconstruction we used a t-test after testing for normal distribution with the Kolmogorov-Smirnov test. We used the F-test to test for differences in the standard deviation.

Results: Phantom validation: Results of phantom measurements are summarized in Table 2. In water both reconstructions showed consistent values of MD ($P > 0.93$). The model-based reconstruction resulted in significant ($P < 10^{-14}$) reduction of FA values (~30%) towards zero, the true FA value in water. There were no significant differences in the region of the anisotropic fibers between the gridding and the model-based reconstruction either in MD ($P > 0.84$) or in FA ($P > 0.14$). Model-based reconstruction always resulted in lower standard deviation in MD and FA values in water (MD: -41%, $P < 10^{-7}$; FA: -17%, $P < 0.04$) and the fibers (MD: -35%, $P < 0.03$; FA: -6%, $P > 0.21$).

Clinical validation: Figure 1 shows examples of the MD and FA parameter maps. The MD and the FA values calculated from the model-based reconstructions were significantly lower than the values calculated with gridding in cartilage ($P < 0.04$), but not in muscle ($P > 0.18$). FA was significantly lower in muscle and cartilage ($P < 10^{-10}$).

Discussion: The model-based iterative reconstruction method is an extension of the Compressed-Sensing principle, which incorporates the signal-decay model directly into the reconstruction algorithm and, thus, inherently exploits correlation (or “compressibility”) of the diffusion-weighted images. Estimations of the diffusion tensor with the model-based approach resulted in improvement of the measured diffusion parameters in phantoms, where reference MD and FA are known. The same trend is observed in vivo, although there is lack of a standard of reference. FA showed larger variability through the protocols, since it is more sensitive to noise. Protocol B resulted in unacceptable large bias in FA both in phantom and in vivo. Protocol D resulted in a slight bias in FA. The optimal acquisition will include an intermediate number of spokes of protocols A and D (~85, TA~14 min).

Conclusion: The RAISED sequence with a model-based reconstruction results in improvement of the diffusion parameters.

References: [1] Raya et al. Radiology 2012;262:550, [2] Trouard TP et al. Magn Reson Med 1999;42:11, [3] Dietrich O et al. MAGMA 2001;12:23, [4] Fieremans E, et al. Phys Med. 2008;53:5405.

Table 1: RAISED Protocols¹

| | Spokes | b-values | Resolution | TA |
|---|--------|-------------|--------------------|-------|
| A | 114 | 1, 300 | 0.74 \times 0.74 | 19:50 |
| B | 80 | 1, 300 | 0.60 \times 0.60 | 14:00 |
| C | 61 | 1, 150, 300 | 0.74 \times 0.74 | 19:50 |
| D | 61 | 1, 300 | 0.74 \times 0.74 | 10:40 |

¹ b-values in mm²/s; Resolution in plane (mm²); TA= acquisition time in min.

Table 2: MD/FA for each subject in all cartilage plates¹

| | Water ROI | Fiber ROI | Cartilage ROI | Muscle ROI | | | | |
|---|-----------|-----------|---------------|------------|----------|----------|----------|----------|
| | Gridding | Model | Gridding | Model | | | | |
| A | 2.3/0.08 | 2.3/0.06 | 1.8/0.33 | 1.8/0.32 | 1.7/0.45 | 1.6/0.37 | 1.7/0.32 | 1.7/0.24 |
| B | 2.1/0.15 | 2.1/0.11 | 1.6/0.44 | 1.6/0.40 | 1.7/0.64 | 1.5/0.50 | 1.5/0.51 | 1.5/0.27 |
| C | 2.3/0.10 | 2.3/0.06 | 1.8/0.31 | 1.8/0.30 | 1.7/0.50 | 1.6/0.37 | 1.6/0.50 | 1.6/0.42 |
| D | 2.3/0.12 | 2.3/0.09 | 1.7/0.34 | 1.7/0.32 | 1.6/0.56 | 1.5/0.43 | 1.6/0.56 | 1.6/0.47 |

¹ Mean MD ($\times 10^{-3}$ mm²/s)/mean FA over the ROI.

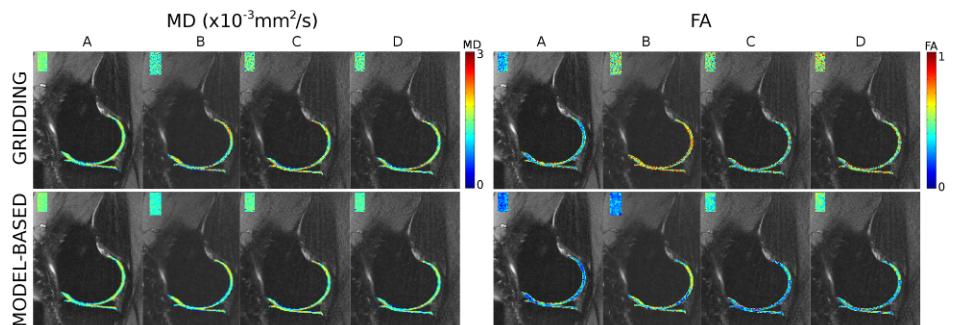


Figure 1: Example of MD (left panel) and FA (right panel) maps of a healthy volunteer calculated from all protocols (A to D, Table 1) using gridding (Top) and the model-based reconstruction (bottom).