

Non-linear phase correction in model-based reconstruction of the diffusion tensor

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Target audience: Researchers and clinicians interested in multi-shot diffusion imaging and nonlinear image reconstruction.

Purpose and background: To investigate the value of a non-linear phase correction algorithm for model-based reconstruction of diffusion tensor images measured with non-Cartesian multi-shot diffusion-weighted sequences.

Background: EPI is the method of choice for most diffusion measurements. However, EPI fails to provide adequate image quality for those applications that require high-resolution (e.g. articular cartilage) and in anatomic areas of high B0 inhomogeneity (e.g. spine, orbitae, spinal cord...). Multiple shot sequences can solve these issues at the cost of having a much longer acquisition times than EPI. Thus, there is need to accelerate image acquisition of multi-shot sequences while keeping the quality of the parameter maps. Model-based reconstruction for DTI is a compressed-sensing approach to reconstruct the diffusion tensor components directly from the raw data, without having to reconstruct the intermediate diffusion-weighted images.^{1,2} The model-based reconstruction explicitly incorporates the signal model into the reconstruction algorithm. Model-based reconstructions can better discriminate between the noisy diffusion-weighted signal and the background Rician noise, thus outperforming standard compressed sensing reconstruction of the diffusion-weighted images. Accurate model-based reconstruction of the data needs to include phase errors induced by macroscopic motion that are measured with 2D phase navigators.

Methods: A radial spin-echo diffusion tensor imaging (RAISED) sequence was used, which provides high signal-to-noise (SNR) efficiency, excellent image quality and robustness against motion. The RAISED sequence included a 2D echo planar imaging navigator after each readout (spoke). The model-based approach reconstructs directly the diffusion tensor components by including the DTI signal model:

$$x_n = I_0 e^{-A_n D},$$

where I_0 is the signal intensity with no diffusion-weighting, A_n contains the b-matrix of each of the N diffusion-weighted images and D includes all six components of the diffusion tensor. In the model-based reconstruction the diffusion tensor is iteratively reconstructed for each slice by minimizing the functional

$$S(D) = \sum_{n=1}^N \|E_n(D) - y_n\| + \alpha \sum_i |\Psi(D)|, \quad \text{with} \quad E_n(D) = \sum_{coil=1}^{n_{coil}} \sum_{spoke=1}^{n_{spoke}} FT_{n,spoke} (c_{n,coil} e^{i\Phi_{n,coil,spoke}} I_0 e^{-A_n D}).$$

The indices i and n indicate the corresponding elements of the diffusion tensor D and the number of diffusion-weighted images (N). The total variation seminorm was used as the sparsifying transform Ψ , applied individually to each tensor element. E_n is the extended forward operator that transforms the Diffusion tensor components to the k-space. The diffusion tensor components are first transformed in diffusion-weighted images. Then for each diffusion-weighted image, coil, and spoke we multiply the diffusion-weighted image by the measured phase map of the navigator (

$e^{i\Phi_{n,coil,spoke}}$) and also multiply by the corresponding coil sensitivity ($c_{n,coil}$). This image is then Fourier transformed and inverse-gridded ($FT_{n,spoke}$) to the non-Cartesian k-space.

We acquired RAISED sequence data of the brain in two subjects using the 16 head channels of a 20-channel head/neck coil and of the right knee of three healthy volunteers using a 15 channel transmit receive knee coil. All experiments were performed on a 3 T whole body scanner (Magnetom Skyra, Siemens Healthcare, Erlangen, Germany). The brain protocol was TE/TR=60/1500 ms, 6 directions, in-plane resolution=1x1 mm², 75 radial spokes, b-values=1, 1000 s/mm², undersampling factor of 4.1 compared to a fully radial acquisition and a total acquisition time (t_{acq}) of 16 min. The knee protocol has higher resolution in plane (TE/TR=40/1500 ms, 6 directions, in-plane resolution=0.7x0.7 mm², 70 radial spokes, b-values=1, 150, 300 s/mm², undersampling factor of 4.2, t_{acq} =19:50 min). Model-based image reconstruction was performed with and without phase correction for comparison. In the brain datasets we defined regions of interest (ROIs) on the splenium and the gray matter. In the knee acquisitions we defined ROIs in the articular cartilage and in muscle.

Results: Figure 1 shows examples of the MD and FA maps in the brain and the knee. Table 1 summarizes the mean MD and FA on each of the regions averaged over the subjects. Without phase correction there were systematic overestimations of the MD and FA. The reconstruction times scaled with the number of spokes. Reconstruction times per spoke were 0.3s/spoke for gridding, 0.45s/spoke for the model-based without phase correction and 17s/spoke with the non-linear phase correction.

Discussion: Phase correction is a critical step in the reconstruction of multishot diffusion-weighted images. Non-linear phase correction performed in the model-based reconstruction is time consuming due to the necessity of adding the phase to each spoke individually. This also impose conditions in the memory side, due to the large size of the navigator data. Navigators are necessary even in the case that the diffusion weighted images do not show trace of motion as evident in the case of the cartilage. Since with increased diffusion-weighting we are more sensitive to smaller motions, image degradation is more evident in the brain. Data obtained with the model based motion correction is in the same range as data reported in the literature.³

Conclusion: Non linear phase correction is mandatory for model-based reconstruction.

References: [1] Welsh et al. MRM 2013;70:429, [2] Knoll et al. ISMRM 2014;p4466, [3] Raya JG, et al. Radiology. 2012;262:550.

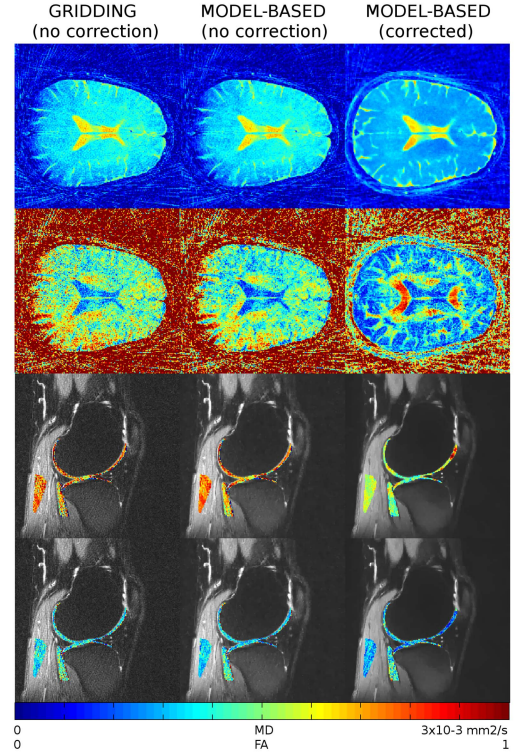


Figure 1: Example of MD (1st and 3rd row) and FA maps (2nd and 4th row) in the brain and the knee without and with phase correction.

Method		Muscle	Cartilage	Corpus callosum	Gray matter
Gridding (no corr)	MD	2.17 (0.57)	2.22 (0.82)	1.10 (0.11)	0.94 (0.27)
	FA	0.42 (0.17)	0.44 (0.23)	0.43 (0.10)	0.45 (0.19)
Model-bas. (no corr)	MD	2.15 (0.43)	2.12 (0.66)	1.10 (0.08)	0.94 (0.27)
	FA	0.39 (0.15)	0.41 (0.22)	0.40 (0.09)	0.45 (0.17)
Model-bas. (corr)	MD	1.61 (0.22)	1.54 (0.46)	0.76 (0.07)	1.02 (0.25)
	FA	0.35 (0.12)	0.35 (0.16)	0.67 (0.07)	0.18 (0.07)

¹ MD in units of $\mu\text{m}^2/\text{ms}$. Values are mean and standard deviation in brackets.