Comparison of diffusion kurtosis modeling algorithms: accuracy and application

Daniel Olson[1], Volkan Arpinar[2], and L Tugan Muftuler[2]
[1]*Biophysics, Medical College of Wisconsin, Milwaukee, Wisconsin, United States,* [2]*Neurosurgery, Medical College of Wisconsin, Wisconsin, United States*

Target Audience: Researchers interested in advanced Diffusion MRI techniques.

Purpose: Diffusion Kurtosis Imaging (DKI) is becoming increasingly popular in diffusion weighted imaging due to its higher sensitivity to tissue microstructure compared to conventional DTI, while remaining within a clinically acceptable scan time. However, the kurtosis tensor model is not as robust to noise, resulting in implausible convergence of the fitting algorithm that may be mistaken as pathology. Several approaches have been proposed including outlier removal[1], directional weighting and regularization[2], and a sparsity constraint[3]. Our goal is to evaluate the effectiveness of the methods and explore the most robust DKI estimation technique.

Methods: For simulation, DKI data were modeled by extracting average kurtosis tensor (KT) values from the corpus callosum of in vivo dMRI data from the Human Connectome Project (HCP)[4]. Single voxel diffusion data were calculated (18 b0 images and 180 diffusion-weighted images with b=1000s/mm^2 and 2000s/mm^2, 90 directions each shell). Two levels of Gaussian noise were added (SNR 20, SNR 60) to characterize robustness of DKI estimation methods. Data were first processed through software developed in-house based on the KT model by Jensen et al[5]. The KT is fitted via unconstrained singular value distribution (SVD). REKINDLE[1] and the directional weighting and regularization[2] (DWAR) methods followed their published algorithms. The percent differences were calculated for metrics, which were mean diffusivity (MD), fractional anisotropy (FA), mean kurtosis (MK), axial kurtosis (Kax), and radial kurtosis (Krad). The methods were then applied to whole brain in vivo dMRI from HCP. REKINDLE was chosen as the "gold standard" based on the simulation results and was used as the reference for the difference (error) maps.

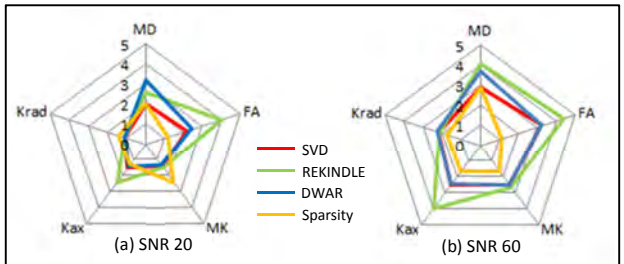

Fig.1. Algorithm accuracy from simulation

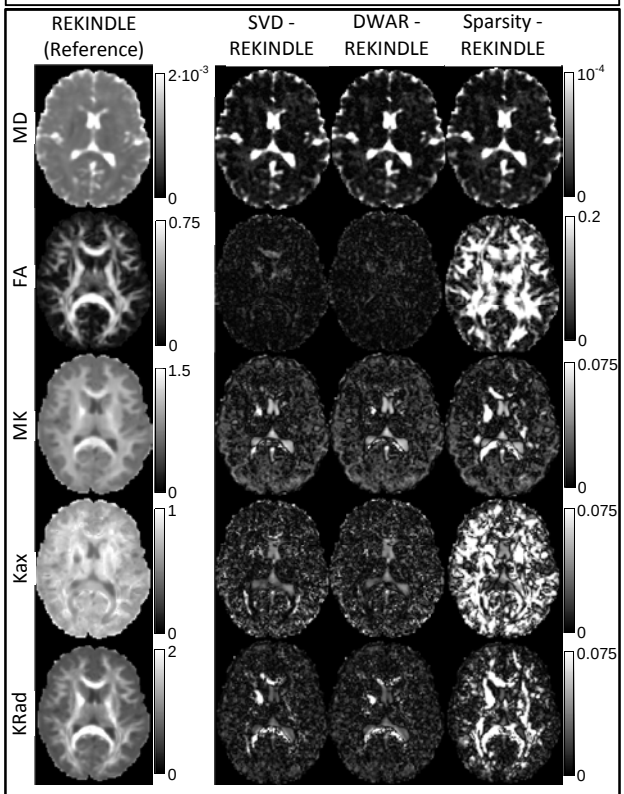

Fig.2. In vivo reference and difference images

Results: Fig. 1 shows results from the simulations. Accuracy of each method is calculated as -log(%difference). Therefore, a plot value of 2 translates to 1% difference, and a value of 5 is 0.001%. Low (a) and high (b) SNR cases are presented. Algorithms noted as: SVD (red), REKINDLE (green), DWAR (blue), and Sparsity (yellow). Fig. 2 presents MD, FA, MK, Kax, and Krad difference images with REKINDLE as the reference. Scaling is consistent between difference images of the same metric.

Discussion: From the simulation, REKINDLE performed best in the majority of the metrics. It detects outliers by determining the residual between the measurements and the model fit in the linear domain. With low SNR, data from the higher shells are more likely to be considered outliers reducing the accuracy of the kurtosis metrics as seen in Fig. 1. DWAR constrains the KT and was found to slightly underestimate the kurtosis metrics in white matter. Overall, DWAR performed similarly to SVD. The sparsity constraint was originally intended for gray matter. It fits the signal to the main 6 KT elements, instead of 15 in the full KT. The other 9 elements are set to zero. We found those elements are more susceptible to noise (Fig. 1(a)), but they are necessary with higher SNR (Fig. 1(b)) for accuracy. It had the largest errors for the in vivo data. An important consideration is processing time. The processing times relative to SVD for REKINDLE, DWAR, and Sparsity were about 25x, 2x, and 0.75x, respectively. While effective, the high processing demand of REKINDLE for minor accuracy gains might limit its feasibility for routine images with limited motion artifact.

References: 1. Tax et al. MRM. 2014 Mar 31: 1-15 [Epub ahead of print]; 2. Kuder et al. MRM 67:1401-1411; 3. Tabesh et al. ISMRM 19 (2011) Abstract; 4. Van Essen et al. NeuroImage 80: 62-79; 5. Jensen et al. MRM 53:1432-1440.