Does Kurtosis or Stretched-Exponential Model Fit Experimental Diffusion-weighted Data Better?

E. S. Hui[1,2], A. Y. Ding[1,2], and E. X. Wu[1,2]

[1]Laboratory of Biomedical Imaging and Signal Processing, The University of Hong Kong, Hong Kong SAR, China, People's Republic of, [2]Department of Electrical and Electronic Engineering, The University of Hong Kong, Hong Kong SAR, China, People's Republic of

Introduction

Diffusion-weighted (DW) signal dependence on b-value in neural tissues deviates from monoexponential decay. As a result, numerous models have been proposed to characterize such non-monoexponential decay. Diffusion kurtosis imaging (DKI) is a 4th order diffusion analysis that characterizes the restricted non-Gaussian diffusion (1). Stretched-exponential model describes the diffusion process with a continuous distribution of apparent diffusion coefficients (ADC) (2). In these two models, two free fitting parameters are used, which is one less than in the biexponential model (3). In addition, both models make no assumption on the number of compartments. Thus, compared to monoexponential and bioexponential models, kurtosis and stretched-exponential models may provide potentially more robust and meaningful fitting of DW signals observed in neural tissue that has inherently complex cellular microstructures. This study aimed to evaluate the performance of these two models in describing the experimental DW signals obtained from rodent brains in vivo.

Methods

In vivo experiments were performed on 3 normal adult SD rats using a 7T Bruker scanner. DW images were acquired with a respiration-gated SE 4-shot EPI with encoding scheme of 30 gradient directions and 5 b_0 using: TE/TR=32.3/3000ms, δ/Δ=7/17ms, image resolution=313x313x1000μm^3, 5 b-values of 500, 1000, 1500, 2000 and 2500s/mm^2, and NEX=4. DWI data was fitted to

$$S(b) = S(0)\cdot\exp\left(-bD + (1/6)b^2D^2K\right) \text{ (1,4)} \qquad [1]$$

and

$$S(b) = S(0)\cdot\exp\left(-(b\cdot DDC)^{\alpha}\right) \text{ (2)} \qquad [2]$$

along each diffusion encoding direction, where D, K, DDC, α represent ADC, kurtosis, distributed diffusion coefficient and stretching parameter respectively. Curve-fitting quality along each direction was assessed by using goodness-of-fit which was calculated on the pixel basis by $GOF = \sqrt{(1/P)\cdot\sum_{i=P}(y_i - y_i')^2}$, where P represents the number of data (or b-value) points. The corresponding mean error (ME) was computed as $ME = (1/N)\cdot\sum_{j=N} GOF_j$, where N represents the number of diffusion encoding directions.

Results and Discussions

Normalized DWI signals averaged along all diffusion encoding directions from the cortex and corpus callosum of a typical rat together with the fitted data using the two models are plotted in log-scale in Fig. 1. It can be clearly seen that kurtosis model provides better fitting quality than stretched-exponential model especially in the high b-value regime. Note that red line (raw data) and green line (kurtosis model fitting) overlap almost perfectly. To further compare the two models, the fitting ME maps are illustrated in Fig. 2. The corresponding mean diffusivity (MD), fractional anisotropy (FA) and mean kurtosis (MK) as computed from kurtosis model, and mean alpha (MA) maps as computed from stretch-exponential model in the same animal are also shown. Kurtosis model is seen to fit better in all tissue structures except in CSF and voxels that surround the CSF ventricles. Similar findings are also observed in fitting the DWI data obtained from other animals studied. These results suggest that kurtosis model generally provides better and excellent fitting in voxels located in either white or gray matter structure. Interestingly, stretched-exponential model yields better fitting in voxels that partly contain CSF, which may likely be ascribed to the fact that these voxels can be better described with a distribution of ADCs. In conclusion, our analysis of the experimental in vivo DWI data demonstrates that the quadratic diffusion kurtosis model (as described in Eq. [2] above) provides better fitting, suggesting that DKI is a more accurate and robust diffusion model for characterizing the complex diffusion processes in vivo in neural tissue.

References

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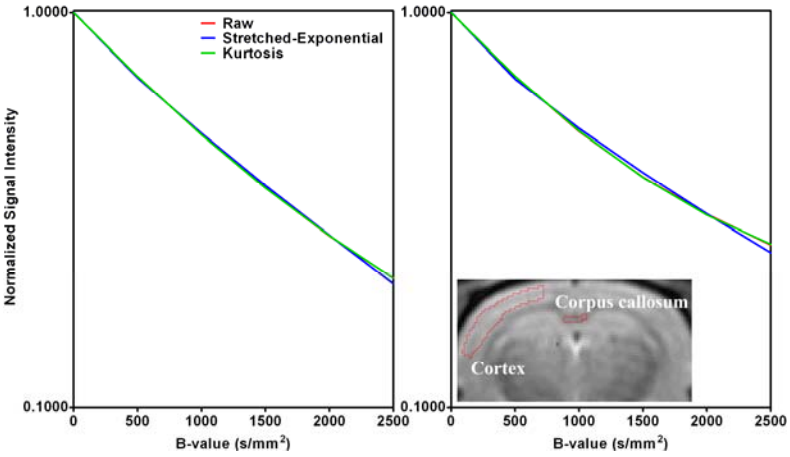

Figure 1. Normalized signal intensity in log-scale vs. b-value averaged along all diffusion encoding directions of raw and fitted data from stretched-exponential and kurtosis model in a ROI in a typical rat cortex (left) and corpus callosum (right) as shown in the upper right corner. Note that RED line (raw data) and GREEN line (kurtosis model fitting) overlap almost perfectly.

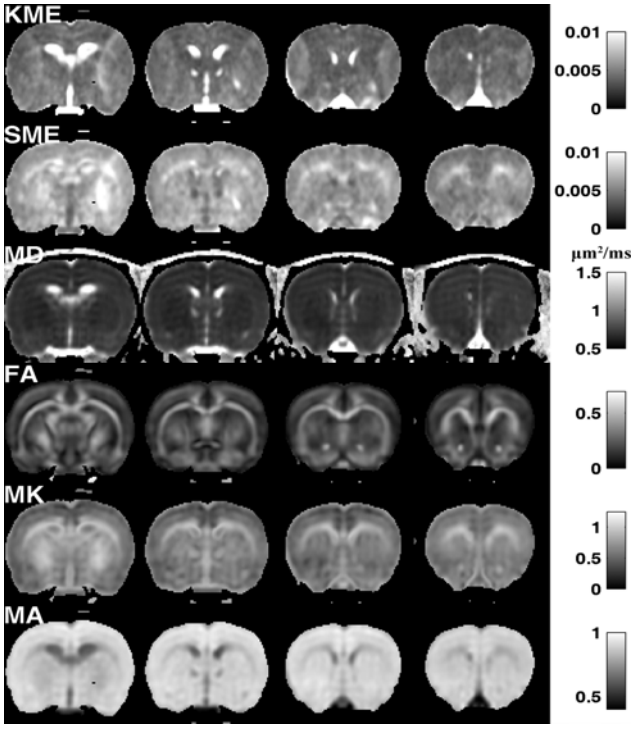

Figure 2. Kurtosis (KME), stretched mean error (SME), mean diffusivity (MD), fractional anisotropy (FA), mean kurtosis (MK) and mean alpha (MA) maps.