

Comparison between kurtosis and biexponential models for diffusion-weighted brain imaging with high resolution and high b-factor

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Introduction: Use of high diffusion weighting in brain MRI has taken on great importance recently, particularly in relation to the Connectome Project. However, attaining high b-factors seriously limits achievable signal to noise ratio (SNR). Not only does the application of large diffusion gradients attenuate most of the MRI signal, but the extra-long echo time additionally required to achieve large b-factors produces further attenuation due to transverse relaxation. For these reasons, there are very few high b-factor studies of human brain *in vivo*, and these use very large voxel sizes [1,2,3] or very long scan times [4]. For DWI tractography, the question arises of how best to fit the dependence of signal on b-factor. In ideal conditions, a bi-exponential fit has been highly successful [5], but doubts have been raised whether this approach is useful when there are major partial volume effects due to large voxel size and low SNR at high b-factors [7,8]. Instead, it has been proposed to map kurtosis [9], which is less dependent on a specific model of attenuation of signal by diffusion. In this study we have used diffusion weighted STEAM-EPI [6] at 7 Tesla to achieve high b-factors with good image SNR at the relatively high resolution of 2 mm isotropic. Because brain tissue has a high T1 at 7T, STEAM-EPI can use a long diffusion time (Δ) to achieve high b-factors without losing much signal to T2 decay. We compared the goodness-of-fit of the bi-exponential model with the kurtosis model at b-factors up to 8000 s.mm⁻². The results show that a bi-exponential fit performs much better than a kurtosis fit at these high b-factors in human brain.

Methods: 7 healthy consenting volunteers were scanned, after ethics approval, at a 7T Siemens system equipped with a whole body gradient set (max. strength 70 mT/m) and a 24 channel receive coil (Nova). 12 axial slices were acquired with a 2D single shot DW-STEAM-EPI (TR/TE/ Δ / δ = 3000/59/121/16 ms) sequence giving 2 mm isotropic resolution and 4 mm spacing between slices. The acquisition covered from the dorsal surface of the corpus callosum to the top of the brain in most subjects. 16 diffusion weightings were applied in 3 orthogonal (X,Y,Z) directions. Gradients were incremented linearly with b-factors increasing quadratically from 30, 137, 290...to ...7070, 8000 s.mm⁻². The measurement was repeated 16 times, taking a total of 38 minutes. Data obtained from 16 averages were used to find the maximum likelihood estimate (MLE) under the Rician distribution. Only data points larger than 2.5 standard deviations of noise distribution under MLE were used for further analysis. This gives 90% confidence that the estimated value lies within 20% of its true value. The curves obtained for each voxel in each of the three directions were fitted using a bi-exponential fit (Eq 1) and with a kurtosis fit, which is the Taylor expansion of the logarithm of signal decay (Eq 2). Fit parameters for bi-exponential and kurtosis were obtained by minimizing the expressions in Eq 3 and Eq 4. Since the bi-exponential fit has one more parameter to fit, it is natural that it gives smaller chi-squared values. To compare the goodness-of-fit between the two fits, F-values were computed for gray and white matter with chi from Kurtosis as numerator.

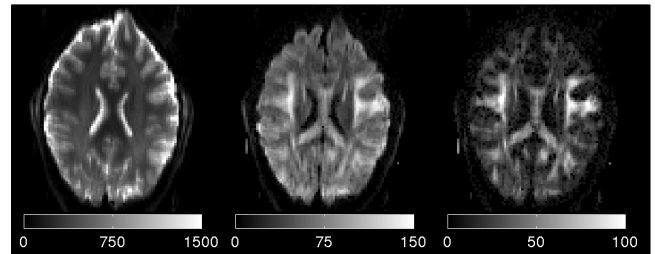


Figure 1. MLE of diffusion weighted signal in Z-axis. B-factors are 130 (left), 3800 (mid) and 8000 (right) s.mm⁻².

$S_{bi} = w_1 e^{-bD_1} + w_2 e^{-bD_2}$ - [1] $\ln(S_{cum}) = \ln(S_0) - bD_{app} + \frac{1}{6} K_{app} (bD_{app})^2$ - [2]

$\sum_n [S_{bi}(b_n) - S_o(b_n)]^2$ - [3] $\sum_n S(b_n)^2 [\ln(S_{cum}(b_n)) - \ln(S(b_n))]^2$ - [4]

Results: Figure 1 shows MLE values for 3 diffusion weightings in z-direction at low (130 s.mm⁻²), medium (3800 smm⁻²) and high (8000 s.mm⁻²) b-factors. Corpus callosum (CC) signal remains high at high b-factor, while cerebrospinal tract (CST) and gray matter have less but still usable signal. Figure 2 (top left) shows a maximum intensity projection of the kurtosis value obtained from three orthogonal gradient directions. Figure 2 (top right) shows the apparent diffusion map, the sum of D_{app} from all three directions. This map lacks any GM/WM contrast, similar to the conventional ADC map from a diffusion tensor analysis. Figure 2 (bottom) shows the trace of the fast and slow diffusion components (D_{fast} & D_{slow}) resulting from bi-exponential fitting. While D_{fast} is low in contrast, D_{slow} shows striking contrast between gray and white matter. Figure 3 shows log (F) histograms obtained by comparing chi-squared values from the two analyses. The histograms should be symmetric around 0 if the two models could equally explain the data. The histograms show that with the F-test the bi-exponential fit explains the data better in more than 80% of the voxels.

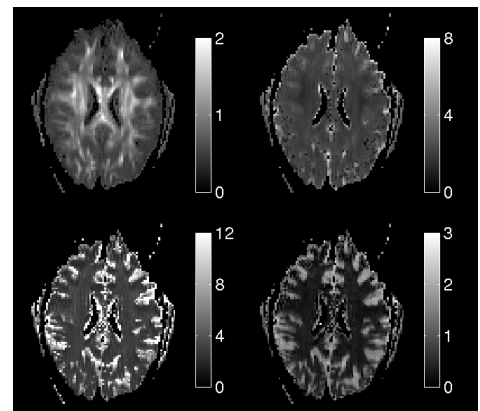


Figure 2. Top: Maximum intensity projection of K_{app} in 3 directions (left) and trace of D_{app} (right). Bottom: Traces of D_{fast} (left) and D_{slow} (right) obtained from a bi-exponential fit.

Discussion: Use of Maximum Likelihood Estimation for a Rician distribution at each b-factor shows that the non-Gaussian diffusion curves obtained were not noise floor effects. Comparing different models at high resolution and good SNR reduces partial volume effects, allowing improved localization and sensitivity for the study of bi-exponential diffusion in brain tissue, especially gray matter.

References: [1] Clark & Le Bihan, 44 MRM (2000) 852. [2] Mulkern et al, MRI 19 (2001) 659. [3] Maier et al, MRM 51 (2004) 321. [4] Maier and Mulkern, MRI 26 (2008) 897 [5] Mulkern et al, JMIR 27 (2009) 1151 [6] Dhital & Turner, Proc. ISMRM (2010) [7] Kiselev & Il'yasov MRM, 57 (2007) 464. [8] Bennett et al, MRM 50 (2003) 727. [9] Jensen et al, MRM 53 (2005) 1432.

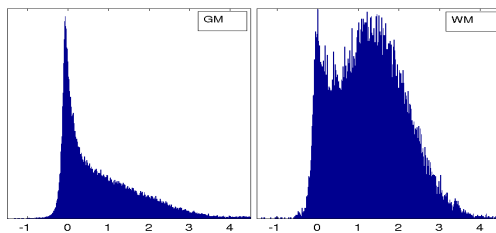


Figure 3. Histograms of logarithms of F-value comparing kurtosis fit vs. bi-exponential fit in gray matter (left) and white matter (right). If both the models were equally good the histogram would be symmetric around 0.