IMPROVING THE FIT OF THE DIFFUSION KURTOSIS TENSOR BY EMPHASIZING THE DIRECTIONS OF RESTRICTED WATER MOTION

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Introduction

In conventional diffusion tensor imaging (DTI), a Gaussian propagator function of the diffusing spins is postulated. In biological tissue however, substantial deviations from this Gaussian diffusion are observed [1], containing additional information on the tissue microstructure. For the quantification of these deviations, the kurtosis of the propagator function has been proposed [2]. The directional dependence of the kurtosis can be modelled using the diffusion kurtosis tensor (DKT) [3]. Usually, the DKT is calculated from the kurtosis values measured in different directions using a pseudoinverse matrix. The aim of this work was to evaluate the currently proposed kurtosis tensor model, especially considering the fit quality of the DKT and to improve the calculation if needed. This is investigated under well-defined conditions using recently developed diffusion phantoms.

Theory

The kurtosis can be approximately determined from the diffusion weighted signal $S(b)$ using equation (1), where D_{app} is the apparent diffusion coefficient and K_{app} is the apparent kurtosis. To account for the directional dependence of the kurtosis, the DKT W_{ijkl} is introduced (Eq. 2) which can be obtained from measurements with at least 15 gradient directions [2,3].

$$\ln[S(b)/S(0)] = -b\,D_{app} + b^2 D_{app}^2\,K_{app} \quad (1)\,; \qquad L := K_{app}\,D_{app}^2 / M_D^2 = \sum_{i,j,k,l=1}^{3} n_i\,n_j\,n_k\,n_l\,W_{ijkl} \quad (2)\,, \text{ where } M_D = \sum_{i=1}^{3} D_{ii}/3$$

Methods

The phantom datasets were acquired on a 1.5 T MR scanner (Avanto, Siemens) using a standard spin echo EPI diffusion sequence (TR=2000 ms, TE=165 ms, voxel size 2.5×2.5×5 mm³, FOV 320×190 mm², 16 *b* values ranging from 0 to 10000 s/mm², 30/7 and 256/3 directions/averages. The DTI phantoms consisted of parallel polyester fibres and were constructed as described in [4]. A healthy volunteer was examined on a 3 T MR scanner (Trio, Siemens) using the same EPI sequence (TR=2000 ms, TE=108 ms, voxel size 2.5×2.5×5 mm³, FOV 320×320 mm², GRAPPA, 13 slices, 2 averages, 11 *b* values ranging from 0 to 2500 s/mm², 30 directions). To account for the noise, equation (1) was extended by a noise parameter which was determined in the image background. For each direction, D_{app} and K_{app} were obtained using the Levenberg-Marquardt fitting algorithm.
The calculation of the DKT from the K_{app} values was performed using two methods:

1. Solving the linear system of equations (2) by means of the standard method of the pseudoinverse matrix.
2. Direct fit of W to K_{app}: Minimizing the sum of squared deviations between the measured K_{app}-values and the kurtosis values obtained from the DKT by varying the elements of W using the Levenberg-Marquardt algorithm.

Results

Fig. 1 shows the measured kurtosis values for a ROI in the phantom as blue cones and the kurtosis values calculated from the fitted DKT as pink-coloured surfaces. Calculating the DKT using the pseudoinverse matrix completely fails (Fig. 1a): The surface does not represent the measured values. The reason for the failure of method 1 is that the DKT W is not fitted to K_{app} directly but to L (eq. 2), as the pseudoinverse matrix minimizes the squared errors in L. Parallel to the fibres, the L values are larger than orthogonal to them because K_{app} is relatively small, but D_{app} is larger than M_D as a result of the anisotropy and appears quadratically in L (Fig. 2a). Therefore the calculation of the DKT is dominated by the large L values parallel to the fibres, corresponding to small K_{app} values with large errors due to the influence of noise. For a correct calculation however, large kurtosis values are to be weighted dominantly, emphasizing the restricted diffusion orthogonal to the fibres. Using the pseudoinverse matrix, the fit fails especially for large kurtosis values (Fig. 2). The calculation of the DKT using method 2 minimizing the error of K_{app} is successful as a result of the correct weighting of the large K_{app} values (Fig. 1b, 2b).
When comparing measured Kapp values (blue cones) with the resulting DKT-fit (pink) in Fig. 1b, an unexpected shape of the DKT is observed. To verify the plausibility of this fit, datasets using 256 directions were acquired (Fig. 1c), showing a good agreement with the tensor calculated using 30 directions (Fig. 1b) confirming the high quality of the tensor model when combined with the calculation of the tensor elements introduced here.
Fig. 3 depicts a comparison of the two methods for a ROI in the splenium of the corpus callosum. Contrary to the phantom measurements, the calculation of the DKT with method 1 does not fail completely, but applying the method 2 improves the result considerably.

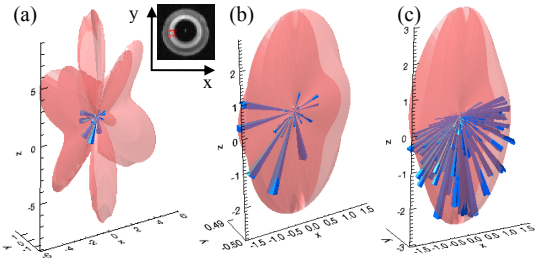

Fig. 1: Blue cones: Measured kurtosis values shown for a ROI (red) in the phantom; rose-coloured surfaces: K_{app} values obtained from the fitted tensors. While fitting the tensor fails using method 1 (pseudoinverse matrix) (a), method 2 is successful (directly fitting W to K_{app}) (b,c). Comparing the tensor calculated using 30 directions (b) with the measurement in 256 directions shows the quality of the tensor model.

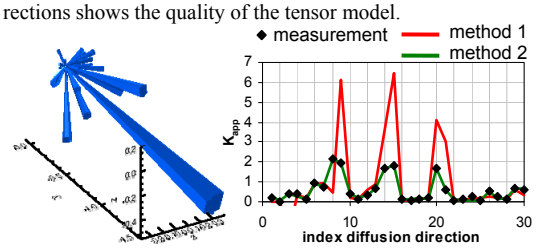

Fig. 2: (a) L values for 30 directions (large in fibre direction); (b) Comparison of the measured K_{app} values and the kurtosis values obtained from the tensor for the two calculation methods. Method 1 fails for the large, important kurtosis values.

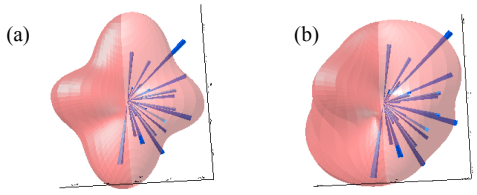

Fig. 3: Surface representation of the kurtosis values for a ROI in the splenium of the corpus callosum of a healthy volunteer using the DKT calculated using (a) method 1 and (b) method 2.

Discussion

While the solution of eq. 2 using the pseudoinverse matrix is unsuitable for the phantom data, method 2 allows a reliable fit of the DKT. Using method 2 is also desirable in vivo as it puts more weight on the physiologically important directions orthogonal to the fibres with large kurtosis values reflecting the restrictions. The comparison between 30 and 256 directions demonstrates that the kurtosis tensor model is remarkably successful, especially it is superior to a simple interpolation of the measured values. This is noteworthy, because the measurement of K_{app} depends on various parameters such as the maximal *b* value, the number of *b* values and the order of the fitting function.

References

[1] Clark, Le Bihan, MRM 2000; [2] Jensen et al. MRM 2005; [3] Lu et al. NMR in Biomed. 2006; [4] Laun et al. MRI 2009