Impact of Accurate b-Matrix Calculation on DTI Accuracy

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Introduction

Quantitative Diffusion Tensor Imaging (DTI) is a novel method of Magnetic Resonance Imaging providing information on the brain's microstructure *in vivo*. DTI can be effectively measured with modern clinical MR-scanners. However, imaging sequence details required for accurate b-matrix calculation and for subsequent DTI quantification are normally invaluable for the user. In this work, we investigated the accuracy of b-value approximation when the b-matrix is calculated without taking into account the effect of imaging gradients.

Methods

DTI-measurements were performed on a 1.5T Sonata Siemens MRI scanner (Siemens Medical Systems, Erlangen, Germany) with a commercially available twice-refocused spin echo DWI EPI sequence. The imaging parameters were as follows: echo time TE 91 ms, repetition time TR 8 s, image size SI 128x120 and 2x2 mm^2 in-plane resolution, diffusion encoding along 12 different DE directions, b-factor 1000 s/mm^2, 6 averages. The whole brain was covered with 51 contiguous 3 mm axial slices.

The Siemens pulse sequence simulation tool was applied in order to generate the exact gradient shape. Exact b-matrix calculations were done numerically.

In vivo data comparison: Whole brain DTI data were compared on a pixel-by-pixel basis. Due to susceptibility induced image distortions intrinsic to EPI, classical brain segmentation was not possible. Instead, we masked all pixels that (1) had on b0 images intensities below threshold (the threshold was chosen to cut off regions with no signal and the most signal from soft tissues) and (2) D' below $0.35x10^{-3}$ mm^2/s and above $3.3x10^{-3}$ mm^2/s. Thus almost all non-brain signal was eliminated.

Results

The correlations between mean diffusivity D' and the FA-index data, which were calculated on the base of the exact b-matrix and on b-value approximation, showed systematic errors in D' and FA (Fig.1). Ignoring cross terms resulted in underestimation of the b-matrix and hence D' was on average overestimated by 4.3%. Additionally, D' and FA were dependent on diffusion tensor orientation (Fig.1b). D' and FA tended to be low when the principal eigenvector was along magnet axis (z-direction), and for orthogonal DT orientation the FA index tended to be overestimated.

In anatomical structures such as the Splenum of Corpus Collosium and Thalamus, errors between D' calculated with b-value approximation and exact calculations were –4.7% and -5.4%, respectively (data averaged over 12 normal volunteers). For FA, corresponding errors were –0.4% and 0.5%. The pixels where FA was over- or underestimated grouped in well-defined clusters which correlated with brain structures (Fig.2). For corticospinal tracts spreading in the superior-inferior direction (z-direction), FA was systematically underestimated. In contrast, in the case of fiber tracks with other orientation, systematic overestimation of FA was observed.

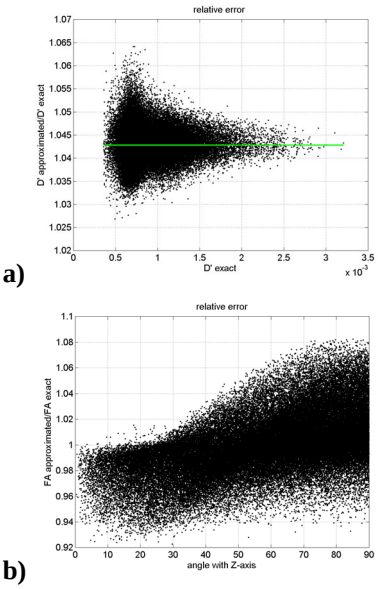

Fig.1. Scatter plots for *in vivo* data measured on a healthy volunteer. *a* - error in D' estimated with b-factor approximation relative to exact calculated D'; *b* - angular dependence of relative error in FA, for clarity only data with FA in the range 0.15 – 0.95 is presented.

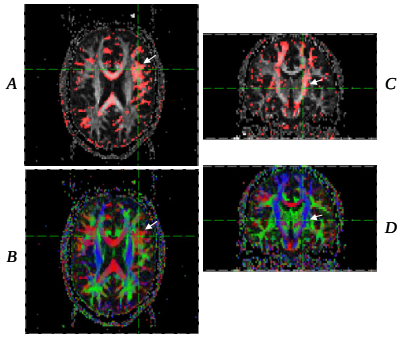

Fig.2. Systematic errors in FA-maps: *a* - FA maps overlapped with a mask indicating pixels with FA overestimation over 0.5%; *b* – corresponding color-coded direction map. Red color for the region marked with the arrow indicates fibers in left-right direction; *c* - coronal FA maps overlapped with a mask indicating pixels where FA was underestimated by more than 0.5%; *d* - corresponding color-coded direction map. Blue color for the region marked with the arrow indicates cortical-spinal fibers in superior-inferior direction. Asymmetry in FA maps and in marked ROIs is due to the slight oblique position of the patient in the scanner.

Discussion

The effect on D' was on average 4.3%, what exceeds the errors caused by noise [1,2] and will make comparison of quantitative DTI data measured on different MR scanners problematic. For a particular imaging protocol such systematic errors can be estimated and compensated by gradient calibration. However, for another imaging parameter set, a new calibration will be required.

For the particular imaging protocol, absolute errors in FA were close to the noise level for pixel-by-pixel DTI quantification. On the other hand, such systematic errors for large enough regions of interest would exceed the noise level. Since the errors depend on fiber direction the total variation could be even higher and could make diagnosis of brain diseases impossible, such as, for example, multiple sclerosis or ongoing demyelination by adrenoleukodystrophy [3,4].

In conclusion, accurate b-matrix calculations are important for adequate comparison of data acquired on different MR-scanners and for data measured with different imaging protocols. Since quantitative DTI is becoming more and more important for *in vivo* brain investigation, information like the exact b-matrix or at least details of the gradients shape is crucial in evaluation and quantification for the routine MRI user.

References

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