On the Problem of Gradient Calibration in DWI

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1. Introduction: Imperfections in the diffusion-weighted (DW) gradients may cause errors in the estimation of the scalar and vector characteristics of the diffusion tensor such as fractional anisotropy (FA), eigenvalues and eigenvectors. The sources of gradients errors are various and may arise from long-term eddy currents, background gradients, imaging gradients, and spatial nonlinearity and nonuniformity of the gradients. The conventional gradient calibration procedure does not exclude significant bias in the diffusion-weighted signal during MR experiments. The error varies among the different diffusion gradient directions and exhibits different extent of the offsets. Herein, we propose a strategy which consists of finding the correction curve. The purpose of this curve is to rescale the magnitude of the diffusion-weighted images and minimise the systematic error. The developed calibration protocol and gradient error estimation framework can be used to monitor gradient performance on a regular basis and compare measurements between scanners.

2. Methods: For validation of the calibration method, two different groups of experiments were carried out. One group of experiments was performed in a distilled water phantom to calculate the calibration curve, and another group experiments was performed *in vivo* to acquire datasets requiring correction. An isotropic liquid phantom was stored in the scanner room with air conditioning to maintain a constant temperature of 25ºC. Before every experiment the phantom was placed in scanner for about 20 min to reduce effects of random fluxes. For 60 DW images the b-value was 800 s/mm2 and the other 4 images were non-diffusion weighted. Non-diffusion weighted images were randomly distributed between diffusion-encoded images and used as a references for the motion correction procedure [1]. Diffusion gradients were distributed according to the icosahedral scheme. This allows us to minimise the condition number for the calculation of the pseudo inverse matrix which is important for the extraction of the major characteristics of the diffusion tensor [2]. DWI was used for the implementation of the correction procedure described here. All experiments were performed on a 3T whole-body scanner (Tim-Trio, Siemens) equipped with an 8-channel PA coil. The parameters of the single-shot, spin echo, twice-refocused diffusion encoding EPI sequence were: TR/TE = 10000/92ms, isotropic resolution = 1.8 mm, field of view = 230 mm. For the estimation of the extent of the influence of the correction strategy on the diffusivity associated with brain anatomical structures, we used MP-RAGE sequence with the following parameters: TR/TE = 2040/4.37ms, isotropic resolution = 1.0 mm, flip angle = 8º *in vivo*.

3. Results: In each phantom experiment a 10x10 voxel region of interest (ROI) was taken from the 5 slices in the phantom isocentre (Fig.1). The calculated apparent diffusion coefficient (ADC) is presented in Fig.2a for all 60 directions. The white curve in the middle is a mean curve, and upper and lower curves depict standard deviation. It is clear that for properly calibrated gradients the mean curve should not have a distinct modulation. We calculated a double mean curve (flat line in Fig.2a) and the differences between mean and double mean curves. The ordinate of double-mean curve was chosen as a prescribed value of diffusion in distilled water and agrees well with known value from the literature [3]. The difference curve we call the correction curve and we used it for the calibrating procedure. We repeated measurements in phantom several times to increase the number of degrees of freedom for the statistical analysis and calculated an averaged correction curve. The correction curve was stable and did not depend on the number of the experiment significantly. The diffusion weighted signal acquired in the phantom was rescaled using the correction curve (Fig.2b) and for the selected ROI FA maps and their distributions before and after correction protocol were calculated. We subtracted corrected and uncorrected FA maps from each other and plotted a histogram of difference (Fig. 3). The histogram shows corrections of up to 1.5%. An example of the impact of the correction procedure in one selected voxel is presented in Fig.4. The ADC profile possesses a distinct peak before correction (Fig.4a) which is cancelled out after correction (Fig.4b). In Fig.5a and Fig.5b FA maps are presented before and after correction. The difference in FA maps in Fig.5c shows the regions most affected by the calibration procedure regions. The histogram of the difference of FA maps in Fig.6 demonstrates the weight for various values of correction. It is shown that the FA map changes values up to 10%. Using SPM5 [4] and a set of images acquired with the MP-RAGE sequence, we segmented brain into white matter (WM), grey matter (GM) and cerebral fluid (CSF). We transformed diffusion weighted images onto anatomical images and used masks of WM, GM and CSF for extraction of FA maps for selected brain areas. The results are presented in Table 1 for mean and standard deviation values of FA map before and after correction for a single slice.

4. Discussion: ADC values exhibit a non-uniform structure with high variability, in percent, due to the systematic error. We propose the correction procedure to mitigate the effect of modulation of the diffusion-weighted signal and justified it in *in vivo* measurement. This calibration can improve the results of studies that rely on the diffusion-weighted signal such as fibre tracking [5]. The protocol and retrospective correction are shown to be effective. The method can be used for prospective correction if an actual diffusion gradient correction curve is available. The proposed calibration protocol may be performed regularly to monitor the systematic drifts in diffusion gradient and pulse sequence performances.

References: [1] Smith S., et al, Neuroimage 2004 (23): 208-219. [2] Batchelor P., et al, MRM 2003 (49): 1143-1151. [3] Phys. Rev., V.III (5), 1958. [4] http://www.fil.ion.ucl.ac.uk/spm/software/spm5/. [5] Parker G. et al, JMRI 2003 (18): 242-254.

Fig.1. T2 weighted image of a water filled spherical phantom with a selected rectangular ROI in the isocentre. **Fig.2.** Distribution of the ADC in the ROI in the phantom as a function of direction (**a**) before correction, and (**b**) after correction. The correction curve is the difference between flat and middle curled lines. **Fig.3.** Distribution of the difference of the FA maps obtained before and after correction. **Fig.4.** Example of results of the correction procedure in one selected voxel (**a**) before, and (**b**) after correction. **Fig.5.** FA map (**a**) before correction, (**b**) after correction, and (**c**) difference of the FA maps. **Fig.6.** Histogram of the difference of the corrected and uncorrected FA maps. **Table 1.** Changes in global FA: mean and standard deviation values for white matter (WM), grey matter (GM) and cerebral fluid (CSF) in a selected slice.

Fig.1

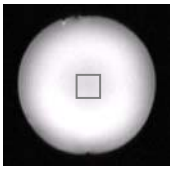

Fig.2a

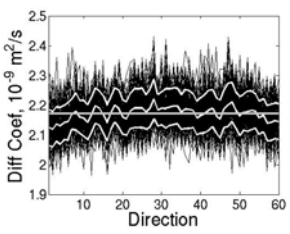

Fig.2b

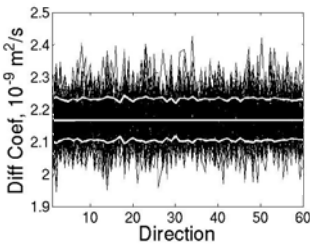

Fig.3

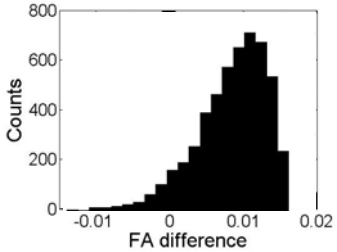

Fig.4a

Fig.4b

Fig.5a

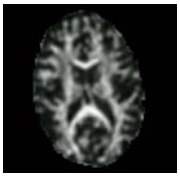

Fig.5b

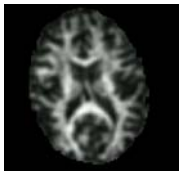

Fig.5c

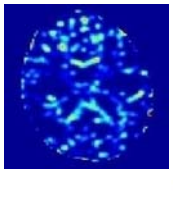

Fig.6

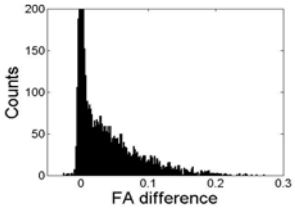

Table 1.

	FA before correction	FA after correction
WM	**0.44±0.19**	**0.40±0.17**
GM	**0.22±0.12**	**0.19±0.10**
CSF	**0.29±0.18**	**0.23±0.14**