

A Novel Robust Algorithm to Correct for Eddy Current Distortions in High b-value Diffusion MRI

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Introduction

Eddy currents (EC) are known to distort diffusion-weighted (DW) images. The image distortions increase in magnitude with increased diffusion sensitisation (b -value) while the signal to noise (SNR) decreases simultaneously. This is challenging for post processing correction methods that compare DW image volumes with a non-DW image volume. Such methods have been confirmed to work well for b -values up to about 1000 s/mm² [1]. In this study, a novel algorithm is described which corrects distortions in image sets with high b -values (up to 3000 s/mm²) and low SNR . The algorithm compares entire image sets with several b -values to maximize local correlation between images, and produces protocol specific parameters that can be applied for fast correction of following image sets.

Theory

Diffusion-weighted images are sheared, scaled and translated in the phase direction due to eddy currents arising from the applied diffusion encoding gradients. The eddy currents and distortions are proportional to the amplitude of the diffusion gradients [2]. Furthermore, potential B_0 -drift of the magnet field causes a translation in the phase direction, here approximated as linearly increasing with scan time [3]. We model the distortions using six parameters, which give the shearing (α), scaling (β) and translation (γ) according to

$$\begin{bmatrix} \alpha \\ \beta - 1 \\ \gamma \\ 1 \end{bmatrix} = \begin{bmatrix} p_1 & p_2 & 0 & 0 \\ p_3 & p_4 & 0 & 0 \\ 0 & 0 & p_5 & p_6 t \\ 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} g_x^d \\ g_y^d \\ g_z^d \\ 1 \end{bmatrix} \quad (1)$$

where g_i^d is the amplitude of the diffusion gradient in direction i , and t is the time since the start of the imaging sequence. If the slices are rotated, a rotation matrix must be applied to α and β (the effect of changes in z is a translation in the phase direction regardless of slice rotation).

Method

Diffusion-weighted images were obtained on a Philips 3T Achieva system, using 25 volumes consisting of 35 slices. The volumes were: one $b = 0$ s/mm² volume and 24 DW volumes obtained with $b = 1000, 1500, 2000$ and 3000 s/mm² in six diffusion encoding directions. The total scan time was approximately two minutes. This protocol was repeated in nine scans on one healthy volunteer. Two different correction algorithms were applied to the image sets: our method and the eddy current algorithm from the post processing toolbox FLIRT, using twelve degrees of freedom [4]. Note that FLIRT is designed to handle DW images obtained with b -values up to 1000 s/mm².

Our method estimates the model parameters in eq. (1) by maximizing the average local correlation in the complete image set using a particle swarm algorithm [5, 6]. In every evaluation, each transformed image was compared to an image in the same diffusion encoding direction, but with a lower b -value, as well as to an image with a different direction, but the same b -value. Note that the image set requires several volumes with different b -values for our method to function correctly.

The EC corrected data sets were used to calculate apparent diffusion kurtosis (ADK) maps, by fitting the equation $S(b) = A \cdot \exp(-b \cdot ADC + 1/6 \cdot b^2 \cdot ADC^2 \cdot ADK)$ to the signal-versus- b curves geometrically averaged over the measured directions [7]. ADK maps were also generated from the uncorrected data set.

Results

Figure 1 shows α , β and γ generated by the employed correction algorithms. The two methods share the same tendency for translation and scaling, where the latter is varying with the direction of the diffusion gradients. Figure 2 shows three different ADK maps from data with and without applied correction algorithms. The model parameters found from our method were: $p_1 = 2.7 \pm 2.7 \cdot 10^{-3}$, $p_2 = 5.5 \pm 1.6 \cdot 10^{-3}$, $p_3 = -1.3 \pm 0.23 \cdot 10^{-2}$, $p_4 = 3.1 \pm 0.20 \cdot 10^{-2}$, $p_5 = 3.3 \pm 0.12 \cdot 10^{-1}$ (all in mT⁻¹) and $p_6 = 6.1 \pm 0.10 \cdot 10^{-3}$ s⁻¹ (mean \pm 1 standard deviation). The time related parameter has the greatest influence on the final transformation.

Discussion and conclusion

The method proposed in this study gives a better correction of DW images obtained with high b -values than the FLIRT algorithm does. The ADK maps based on non-corrected data and data corrected by FLIRT show regions of black stripes, indicating alignment problems (Fig. 2a and 2b, arrows), while the maps from images corrected using our method do not suffer from these (Fig. 2c). The parameters p_1 and p_2 are very close to zero, rendering minimal image shearing (Fig. 1). Importantly, our method shows low standard deviations in α , β and γ , compared to the mean values, between the nine data sets. Hence, it is likely that the obtained parameters are system and protocol specific. This allows transformation parameters estimated in a calibration calculation to be applied in subsequent image sets acquired with the same scanning parameters, which enables EC correction within seconds.

Our method maximizes the local correlation of the whole image set. This makes the transformations of the 25 acquired volumes dependent, as opposed to the independent corrections made when comparing each volume to the non-distorted volume only, as FLIRT does. FLIRT corrects for patient movement in addition to EC distortions, which our method does not. However, our method is intended for application prior to a rigid body motion correction algorithm.

In conclusion, we have presented a new algorithm that gives the possibility to correct for eddy current distortions in high b -value DWI, and also allows for immediate correction of images from the same protocol after an initial calibration calculation is completed.

References

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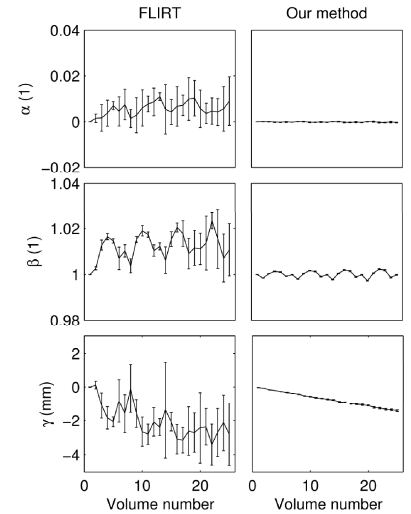


Fig 1. Mean values and standard deviations for shearing (α), scaling (β) and translation in image phase direction (γ) for FLIRT and for our method. The x axis shows the 25 different imaging volumes in the image set. The b -value increases with the number, each b -value except zero being represented by six subsequent data points for the different gradient directions.

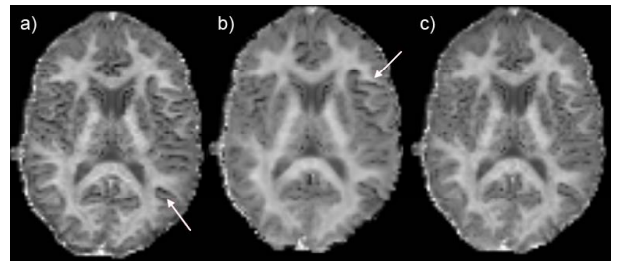


Fig 2. a) ADK map obtained from un-corrected data b) corrected with FLIRT, and c) corrected with our algorithm. The ADK maps are calculated from the geometric mean of six diffusion encoding directions using all the acquired b -values. The arrows show regions of black stripes indicating misalignment artefacts.