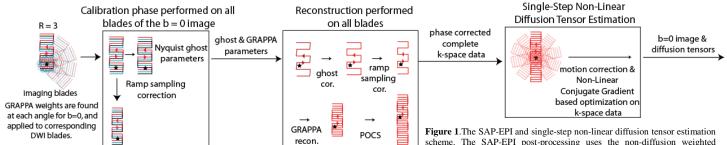# b-Matrix Correction Applied to High Resolution DTI

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INTRODUCTION – High resolution Diffusion Tensor Imaging (DTI) has been challenging for several reasons. Perhaps the major obstacle is due to the random phase effects that change between successive shots and pixel-by-pixel misregistration caused by patient motion. In addition, DTI images acquired with EPI are typically hampered by geometric distortion, blurring, and – in the case of multi-shot EPI – suffer from aliasing artifacts in the presence of motion. Short Axis readout PROPELLER-EPI (SAP-EPI) has been very effective in reducing distortion and motion artifacts in high resolution DTI while keeping the scan time within reasonable limits [1]. One shortcoming of SAP-EPI is that it cannot correct for the alterations in the diffusion encoding direction (i.e., the b-matrix) due to gross subject motion. In this study, we combined SAP-EPI [1] with the single-step non-linear diffusion tensor estimation [2] to perform b-matrix correction for SAP-EPI and achieve high-resolution motion corrected DTI datasets.

Figure 1. The SAP-EPI and single-step non-linear diffusion tensor estimation scheme. The SAP-EPI post-processing uses the non-diffusion weighted (b=0s/mm²) image to get the ghost correction parameters and GRAPPA weights for each blade separately. These calibration parameters are then used to reconstruct all blades for all b=0 and diffusion weighted images [1]. Then, the motion & phase corrected k-space data are fed into the non-linear conjugate gradient based single-step tensor estimation scheme to estimate diffusion tensors and the b=0 image directly from the k-space data [2].

MATERIALS and METHODS – **(a) Acquisition**: Experiments were conducted on a healthy volunteer with a 1.5T whole-body MRI unit and an eight-channel head coil. Two b=0 and 15 diffusion directions were acquired with b = 1000 s/mm². The following parameters were used for the SAP-EPI sequence: 9 blades with a blade width of 64, a target in-plane resolution of 288 x 288, a GRAPPA-acceleration factor R = 3, NEX = 3, partial Fourier encoding with 18 overscans, a slice thickness of 5 mm, TR = 3 s, a FOV = 26 cm, and a scan time of 23 mins. A second DTI dataset was acquired with the same parameter settings as above, except the volunteer was asked to rotate their head in-plane by ~10º. The data from the two DTI datasets were mixed such that every second blade came from the rotated dataset.
(b) SAP-EPI post processing: Post-processing is shown in figure 1. In the calibration stage, the non-diffusion weighted image was used to get the GRAPPA weights and ghost parameters for each blade. In the reconstruction stage, the calculated GRAPPA weights and ghost parameters were used to reconstruct each blade of all b=0 and diffusion weighted volumes. The data were then phase and motion corrected using a low resolution replica of blade images [1]. **(c) Single-step non-linear estimation of diffusion tensors:** Due to gross patient motion, each blade is potentially encoded with a different diffusion direction, which makes it incorrect to combine all blades to form one diffusion weighted image. Instead of this, the k-space data corresponding to all blades and diffusion encoding directions are used at once to estimate the diffusion tensors directly from the k-space data. This was done by minimizing the discrepancy between the acquired and estimated k-space data over all blades and diffusion encoding directions using non-linear conjugate gradient [2]:

$$\left(\mathbf{D}, m\right) = \underset{\mathbf{D}', m'}{\arg\min} \left\| d\left(\mathbf{k}\right) - \sum_{\mathbf{r}} m'\left(\mathbf{r}\right) e^{-\sum \mathbf{b} * \mathbf{D}'\left(\mathbf{r}\right)} e^{-j\mathbf{k}\cdot\mathbf{r}} \right\|_2^2$$

RESULTS – The top row of Figure 2 shows the FA maps reconstructed using three different methods. The bottom row shows the angular deviation of eigenvectors corresponding to the maximum eigenvalues from their reference orientations in the splenium of corpus collosum. The quality of the FA maps increased significantly with the application of motion correction. There was no significant improvement in FA map quality after b-matrix correction was applied. However, the angular deviation maps show that the eigenvectors reconstructed with b-matrix correction were significantly closer to the true orientations compared to the other methods. In the ROI selected, the mean FA values were 0.42, 0.57 and 0.59, and the mean error in angular deviation was 13.8, 12.0 and 5.5 degrees for the non-corrected, motion corrected, and motion & b-matrix corrected cases respectively. The slight increase in the mean FA maps after b-matrix correction is also consistent with previous studies [3].

DISCUSSION – Due to the high bandwidth in the phase-encode direction and self-navigated phase and motion correction capabilities, SAP-EPI is a promising candidate for high-resolution DTI. However, simply correcting for motion using the blades can result in eigenvector maps that deviate from their true orientation. This would be especially problematic, for example, in the case of fiber-tracking
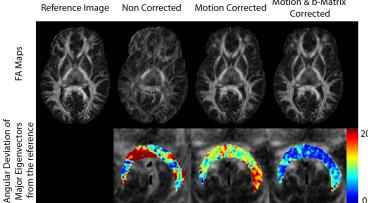

Figure 2. Top Row : FA maps reconstructed using 3 different methods. Bottom row: Angular deviations of major eigenvectors from the reference orientations for the 3 methods. The reference dataset was obtained from the non-motion corrupted k-space data. It can be observed that the major eigenvector orientations obtained with motion & b-matrix correction are closest to the reference orientations

[4]. The non-linear conjugate gradient based single-step tensor estimation scheme circumvented the issue of changing diffusion encoding direction between successive interleaves due to motion, and increased the accuracy of the data even further. While geometric distortions are significantly reduced in SAP-EPI, future work would be to further eliminate the geometric distortions for SAP-EPI using an extended gradient polarity method [5], and combine this method with the b-matrix correction scheme.

References [1] Skare et al, MRM, 55:1298–1307 (2006) [2] Aksoy et al, MRM, 59:1138–1150 (2008) [3] Maniega et al, ISMRM-ESMRMB, 2007 p 312 [4] Leemans et al, ISMRM, 2008, p 25 [5] Skare et al, ISMRM, 2008, p 81