Effects of b-Matrix Correction on Fiber Tractography in High Resolution DTI with Short-Axis Propeller EPI

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INTRODUCTION –Short-Axis Propeller EPI (SAP-EPI) has been shown to be very effective in obtaining high- resolution, artifact-free DTI data [2]. One challenge with SAP-EPI is that in the presence of head rotation each blade of SAP-EPI data is potentially encoded with a different diffusion-encoding direction (i.e. b-matrix) (Fig. 1). Since the diffusion-encoding is 'imprinted' on the magnetization, a simple counter-rotating of blades does not suffice. It has been shown recently that this necessitates non-linear methods to reconstruct diffusion tensors accurately [1]. In this study, we investigated the effects of our correction scheme on SAP-EPI and its consequences on tractography.

MATERIALS and METHODS – (a) Acquisition: The following parameters were used for the SAP-EPI sequence: 5 blades with a blade width of 64, a target in-plane resolution of 192 x 192, a GRAPPA-acceleration factor R = 3, NEX = 3, partial Fourier encoding with 18 overscans (i.e. partial Fourier factor = 56%), a slice thickness of 3 mm, 38 slices, TR = 4 s, FOV = 24 cm. Twenty-four isotropically distributed diffusion-encoding directions with b = 1,000 sec/mm^2 and 3 b=0 images were acquired. The total scan time was 27 minutes. Two separate scans were carried out: (1) the volunteer was asked to stay still; (2) the volunteer was asked to perform an in-plane head rotation once every 3 minutes. Due to the lack of a true gold standard for tractography, the first dataset served as the gold standard surrogate for further analyses. The second dataset was reconstructed using 3 methods as explained next. **(b) Post-processing:** For both datasets, SAP-EPI data was post-processed using GRAPPA reconstruction, ghost correction, phase correction and motion correction, as described in [2]. After the initial post-processing, the motion corrupted data was reconstructed using 3 methods: **A)** No correction **B)** Motion Correction only **C)** Motion and b-matrix correction, as described in [1]. **(c) Fiber Tracking and Comparison**: Fiber Tracking was performed using the visualization and fiber tracking software SmartTrack [3] using the same seed region for all datasets. For each seed, fibers obtained from the different reconstructions of the motion corrupted dataset were compared to our gold standard in pairs using two metrics:

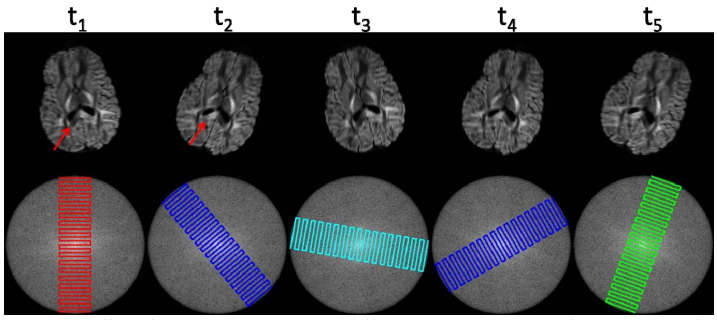

Figure 1 - *Effect of rotational motion on the diffusion-encoding direction for SAP-EPI.* In the presence of diffusion-encoding gradients, rotational head motion causes the effective diffusion encoding to be different for each blade. The change in contrast is mostly visible in the splenium of corpus callosum (red arrows). The reconstruction of diffusion tensors in this case requires non-linear methods.

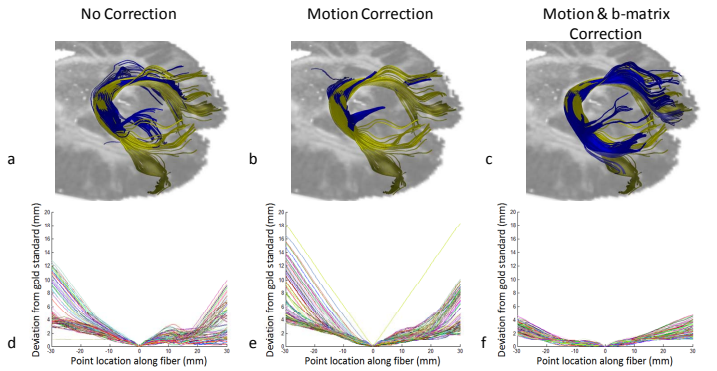

Figure 2 - *Fiber Tracking Results*. Seeds were planted in the middle of the splenium of corpus callosum. The top row shows the fiber tracts corresponding to the three different reconstruction methods obtained from the motion corrupted dataset (blue) and the gold standard fibers (gold). The bottom shows the deviation of fibers shown in the first row along the fiber. It can be seen that the fibers reconstructed with motion & b-matrix correction show the best agreement with the fibers obtained from the gold standard.

1) The distance between the fibers from the reconstructed and gold standard datasets:

$$m_1(i,j) = \inf_k \left\| \mathbf{r}_{REF}(i,j) - \mathbf{r}_{A,B,C}(i,k) \right\|$$

2) The Hausdorff distance between the gold standard and reconstructed dataset:

$$m_2(i) = \max\left\{ \sup_j \inf_k \left\| \mathbf{r}_{REF}(i,j) - \mathbf{r}_{A,B,C}(i,k) \right\|, \sup_k \inf_j \left\| \mathbf{r}_{REF}(i,j) - \mathbf{r}_{A,B,C}(i,k) \right\| \right\}$$

Here, i is the seed or fiber index, j and k are the point indices on the corresponding fibers, $\mathbf{r}_{REF}$ is the 3D point coordinate on the reference fiber and $\mathbf{r}_{A,B,C}$ is the 3D point coordinate on the fiber from the dataset that was constructed either with method *A, B,* or *C*.

RESULTS – Results are shown in Figure 2. The first row shows the reconstructed fibers using an ROI placed in the splenium of corpus callosum. The second row shows the deviation of fibers from the reference dataset as a function of the position along the fiber for the fibers that are displayed in the first row. It can be seen that the fiber tracts reconstructed from the dataset with motion & b-matrix correction agree the most with the fibers from the gold standard dataset, and the least deviation was also observed for this dataset. The mean Hausdorff distances over all fibers between the fibers reconstructed from the reference data and the motion corrupted dataset were found to be 11.2±4.5, 15.0±4.5 and 5.3±1.4 mm for methods A, B, and C, respectively.

DISCUSSION – Influence of b-matrix correction on fiber tracking has been shown previously for single shot sequences [4]**.** In this study, we looked at the effects of b-matrix correction on fiber tracking for high resolution, multi-shot DTI scans. Our results showed that in order to obtain high-fidelity tracking information in the brain, it is essential to correct for b-matrix alterations that arise as a result of patient motion. Our data demonstrate that for DTI sequences which require multiple-shots to gather all the k-space data to form an image, more elaborate schemes are necessary to perform such corrections [1].

References [1] Aksoy et al, MRM, 59:1138–1150 (2008) [2] Skare et al, MRM, 55:1298–1307 (2006) [3] Aksoy et al, ISMRM Workshop on Diffusion MRI, 2005 [4] Leemans et al, MRM, 61:1336-1349 (2009) **Acknowledgements** This work was supported in part by the NIH (1R01EB008706, 5R01EB002711, 1R01EB006526, 1R21EB006860), the Center of Advanced MR Technology at Stanford (P41RR09784), Lucas Foundation, Oak Foundation and GE Healthcare.