Comparison of DTI Data in 5-year old children acquired using Standard and Navigated DTI Sequences

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Target Audience: This study is relevant to researchers and clinicians who perform DTI in young children and restless subjects.

Purpose: Head motion and motion correction may introduce positive or negative bias in DTI[1,2] data. This bias may be undetectable and affect findings of group analyses. The aims of this study were: (1) to evaluate patterns of head motion in children aged 5-6 years using the navigated diffusion sequence to measure motion, (2) to explore differences in whole brain FA due to prospective and retrospective motion correction, and (3) to investigate the effect of rotating the diffusion table following retrospective motion correction.

Methods: A twice-refocused two-dimensional diffusion pulse sequence[3] that minimizes the effects of eddy current was previously modified to perform prospective motion correction with reacquisition of a specified number of corrupted diffusion volumes[1]. Eighteen children (5.1±0.5 years) were scanned on a Siemens Allegra 3 T. All procedures were approved by the Faculty of Health Sciences Human Research Ethics Committee of the University of Cape Town; parents/guardians provided written informed consent and children provided oral assent. DTI data were acquired using both the standard (basic) and navigated (vNav_all) diffusion sequences at the end of a lengthy scanning protocol. Parameters were TR 9500 ms or 10026 ms for the basic and navigated sequences, respectively; TE 86 ms, 72 slices, resolution 2 x 2 x 2 mm^3, FOV 224 mm, single channel birdcage coil, 30 diffusion directions with b = 1000; four b=0 acquisitions; five reacquisitions. The diffusion data from all subjects were quantified using Diffusion Toolkit (http://trackvis.org/), which generates all the diffusion maps. The whole brain histogram (WBH) of FA was calculated and normalized for the total number of tracks. DTI maps were registered to each subject's T1-weighted structural image. Since there was no way to monitor head pose inside the scanner when using the standard diffusion sequence in this study, DICOM volume images were inspected visually for the presence of motion. The navigated acquisitions were inspected for the presence of motion by analyzing the log files of the motion estimates that are generated by the navigated sequence. Retrospective motion correction (retro) using 'mcflirt' with a mutual information cost function and 6 degrees of freedom was implemented with and without rotating the diffusion table only for data acquired using the standard sequence (basic).

Results:

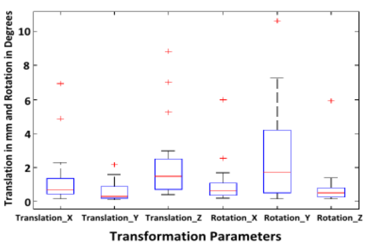

Figure 1: Ranges of motion in different directions in image space. In the scanner coordinate system, these parameters correspond to: X = **AP**, Y = **LR** and Z = **SI**

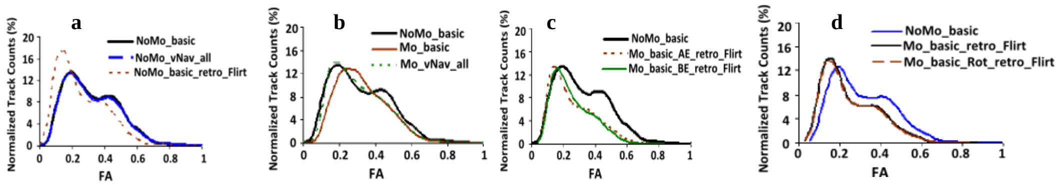

Figure 2: (a) Normalized WBHs of FA for one child who did not move (NoMo) in both the basic and the navigated sequences and effect of retrospective motion correction on the basic scan. (b) Normalized WBHs of FA for a child who did not move compared with those of a child who moved (Mo) during both the basic and the navigated sequences. (c) Changes to WBH FA due to retrospective motion correction before (BE) and after (AE) elimination of corrupted diffusion volumes. (d) The effect of retrospective motion correction without and with rotation (Rot) of the diffusion table.

Figure 1 compares the ranges of motion in different directions averaged for all 18 children as determined from the motion estimates of the navigated sequence. Figure 2a shows the WBHs for a child who did not move (NoMo) during either the basic or navigated acquisitions as well as the effect of retrospective motion correction on the basic data. Motion increases gray matter (GM) FA and reduces white matter (WM) FA (Fig. 2b). Although the navigated sequence was affected by a lot of motion and signal dropouts, it was successful in recovering the DTI data. Retrospective motion correction failed to recover the FA histogram properties, even after elimination (AE) of the motion corrupted diffusion volumes (Fig. 2c). Figures 2d and 3 illustrate the effect of rotating the diffusion table after retrospective motion correction on the WBHs of FA and FA maps, respectively. Motion increases the FA in gray matter (blue in Fig. 3a), while retrospective motion correction causes an overall decrease in FA (yellow in Fig. 3b). The results are similar for the other pediatric scans not illustrated here.

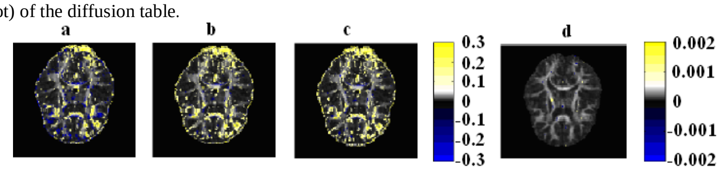

Figure 3: Maps showing differences in FA for a single slice between a child's *at rest* navigated acquisition and (a) the child's basic acquisition during which motion occurred (Mo_basic), (b) Mo_basic with retrospective motion correction, and (c) same as b) but with rotation of the diffusion table following retrospective motion correction. Shown in (d) is the difference map between Mo_basic_retro with and without rotating the diffusion table. Difference maps were overlayed on the FA map of the NoMo_vNav_all acquisition. All FA maps were co-registered in T1 space.

Discussion: Children in this age range predominantly displayed translation along the superior-inferior axis and rotation around the left-right axis which corresponds to nodding motion. Retrospective motion correction not only failed to recover DTI data in the presence of motion, but corrupted DTI data in scans with no motion. Rotation of the diffusion table following retrospective motion correction affected data negligibly (Fig. 2d; Fig. 3c), as resulting changes were of the order of ±0.002 (Fig. 2d). These changes are consistent with those reported previously[4].

Conclusion: The results of this work demonstrate the risk of misinterpreting DTI findings in pediatric studies in the presence of motion and retrospective motion correction. This study also highlights that motion and corrupted diffusion volumes should be prospectively dealt with to ensure valid DTI results.

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