Straightforward Method to Improve Sensitivity in Diffusion Imaging Studies of Subjects Who Move

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Introduction: Diffusion-weighted (DW) imaging techniques have been established as valuable clinical and research tools. However, we have observed that in studies of pediatric populations, many slices are corrupted by severe motion artifacts, despite the use of single-shot EPI, which is generally insensitive to bulk motion. This likely occurs due to head rotations during diffusion weighting that shift the center of k-space outside the data acquisition window [1], and results in an image of mostly noise. See Fig. 1A. Such an artifact

cannot be corrected retrospectively, and is more likely to occur for partial Fourier acquisitions as well as for uncooperative subjects, e.g. children. If such corrupted data is included in diffusion tensor (DT) calculations, it will significantly bias the results. Corrupted data can be removed in post-processing for oversampled datasets [2]. However, this will lead to an increased variance in the group analysis as the DT-derived quantities have been shown to be biased by the number of DW volumes used in the calculation [3] and the number of DW volumes removed for each subject will vary. Accordingly, the goal of this work is to develop a method that can rapidly detect images corrupted by severe motion and reacquire that DW volume, in near real-time.

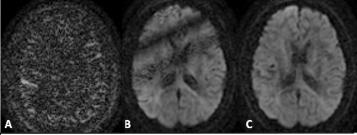


Fig. 1: DW image corrupted by severe motion before, A, and after registration in preprocessing, B. Reacquired DW image, C.

Methods: A straightforward QA procedure for DW data was assembled using standard AFNI functions: 1) all DW data volumes are aligned to the first b=0 s/mm² volume using a rigid body registration, 2) a mask of all brain voxels is created from this same volume and the total number of brain voxels (N_b) is extracted, 3) the trend and median absolute deviation (MAD) in each voxel, within the mask, for volumes with b=1100 s/mm² is calculated and voxels with values more than 3*MAD from the trend were considered outliers and tallied (N_{out}) for each volume, 4) the percentage of outliers per DW volume is calculated as N_{out}/N_b , 5) if $N_{out}/N_b > 1.5\%$ then the DW volume is tagged for rescan. For real-time usage, the detection method was implemented in a software framework that automatically transfers image data to an ancillary computer [4], executes the diffusion QA script, and creates a rescan DW gradient table that is automatically pushed back to the scanner for reacquisition. The 1.5% of N_b threshold was determined empirically through simulations, and was met when at least 1 central slice out of 62 were noise. A retrospective study was performed on a data set of 9 typically developing and 9 children with attention deficit hyperactivity disorder (ADHD) aged between 7 and 10 years. Data was collected on a 3T scanner using an 8-channel phased-array coil. 6 b=0 s/mm² and 42 b=1100 s/mm² volumes were acquired with the following scan parameters: TE/TR=89/21,000 ms, 96x96, FOV=24 cm, slice thickness=2.5 mm, gap=0 mm, 62 slices, acceleration factor=2. The real-time method was tested on 2 healthy subjects with the same scan parameters as above. Each subject was asked to perform several quick head rotations (roll) during acquisition and the corrupted DW volumes detected were reacquired. Data was processed using TORTOISE [5] in three subsets: including all original data, removing corrupted DW volumes, and reacquired corrupted DW volumes.

Results: In the retrospective pediatric study, motion corrupted DW volumes were detected, and verified by visual inspection, in more than half of the scans; 5 of 9 subjects in both the typically developing and ADHD groups had corrupted DW volumes with an average of 4.8 (11%) and 6.4 (15%) volumes, respectively. In data acquired using the real-time diffusion QA and reacquisition, corrupted DW volumes were detected in 9 (21%) and 8 (19%) volumes. The effect of computing DT quantities with corrupted DW data is illustrated in the difference image shown in Fig. 2B. There are both increases and decreases in FA, depending on the tissue type. The effect of computing DT quantities with less DW volumes, due to removal of corrupted data, is visually subtle (Fig. 2C). Further analysis of the data reveals the expected trends for number of DW volumes [3]; tissue with underlying low FA is biased

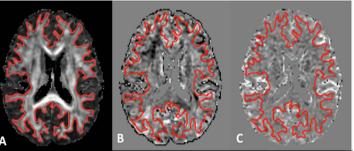


Fig. 2: A, FA map from reacquired data with white matter outlined in red. Difference images of original-reacquired and removed-reacquired in B and C, respectively.

higher and tissue with high FA is biased lower for the removed data set, with the low FA values more affected. The average FA in gray matter over the whole brain was 0.17 and 0.15 for removed and reacquired data, respectively. ROIs in white matter regions showed a trend of decreased standard deviation and increased FA: internal capsule FA=0.67±0.078 and 0.65±0.075, splenium FA=0.82±0.069 and 0.821±0.069, and cerebral peduncle FA=0.741±0.088 and 0.742±0.087 for the removed and reacquired data, respectively.

<u>Discussion/Conclusions</u>: We have presented a straightforward method for detection and reacquisition of DW volumes that are severely corrupted by motion. In addition, we have shown a bias in FA when corrupt data is removed compared to reacquired. The pediatric data analyzed in our retrospective study showed widespread corrupt DW volumes with a greater number in the patient population. Utilizing the real-time diffusion QA and reacquisition method will provide consistent data sets in participants who find it difficult to lie still, and improve sensitivity to changes in DT-derived quantities between groups. Other published methods that reacquire motion corrupted DW data work on k-space data and require phase unwrapping, which can fail with large rotations. The presented method works directly with reconstructed DICOM images from any manufacturer, and can detect a variety of head motion artifacts.

References: [1] Wedeen *et. al.*, MRM, 32:116-120, 1994. [2] Chang *et. al.*, MRM, 53:1088-1095, 2005. [3] Tannazi *et. al.*, 19th ISMRM #1939, 2011. [4] Bodurka and Bandettini, 14th HBM meeting, 2008. [5] Pierpaoli *et. al.*, 18th ISMRM #1597, 2010.