

Investigations on Motion Corruption for Diffusion Weighted Imaging from Population Analysis

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INTRODUCTION:

Pulsatile brain motion can induce DTI data corruption and affect DTI metrics, such as fractional anisotropy (FA) [1]. Data rejection techniques have been proposed, which can be categorized into rejecting corrupted data in k-space [2-4] and rejecting corrupted pixels or images in image domain during tensor fitting [5]. Previous study using pixel outlier rejection showed potential effects of corrupted data on DTI analysis [1]. Even though, not enough attention is paid to this by the community during the protocol setup and data analysis. In this study, we use large cohort data to investigate the severity of motion induced data corruption. We also propose a strategy on how to adjust the data acquisition scheme based on our statistical results.

METHODS:

Data Acquisition: 77 volunteers were included in this study. All data were collected on a GE 3T scanner (GE Healthcare, Waukesha, WI), using an 8-channel head coil. Imaging parameters were: 4-shot interleaved EPI DTI, FOV=240mm, acquisition matrix size=256×256, 34 axial slices covering the whole brain, slice thickness=4mm, b=800 s/mm² using six diffusion encoding directions with NEX=2.

Image Reconstruction: The multi-shot DTI reconstruction was performed using Self-Feeding MUSE [4]. Corrupted data was detected by calculating the k-space signal intensity dispersion (SID) using $SID = \sum \sum |S_k(k_x, k_y)| |r|^4$ within a 64×64 region from signal peak for each shot. $S_k(k_x, k_y)$ was the signal intensity at coordinate (k_x, k_y) and r was the distance from signal peak. Among all shots for each slice, data with SID exceeding a defined threshold, which was 1.13 times the minimum of all SID values was rejected from the reconstruction. Data rejection rate for each slice was defined as the sum of number of rejected shots from 6 directions divided by the total number of shots within this slice.

Data Postprocessing: Postprocessing (Fig. 1) was performed using in-house developed scripts in Matlab (MathWorks Inc., Natick MA) and FSL: 1) For each subject, based on the b=0 image, generate a rejection rate image, SR, for each slice with each voxel equal to the corresponding rate; 2) Normalize the b=0 image of each subject to the MNI152 2mm brain template, then generate a 12-degree-of-freedom affine transform operator, F; 3) Register the SR image to the template using F, yielding a normalized rejection rate image, NR; 4) Calculate the mean and standard deviation of NR images from all subjects and generate a generalized data rejection rate map GR mean and GR S.D.

RESULTS: Fig. 2 shows the generalized data rejection rate (GR) map calculated from all subjects. The horizontal strip-like patterns (arrows in a) indicate that some transverse slices have higher data rejection rate. For example, the slices around the brainstem and the cerebellum have about an 8% data rejection rate on average, around the ventricles about 6%, while the slices near the parietal lobe have a lower rejection rate 2%~3%. Regions with higher mean rejection rate also have higher standard deviation (b in Fig.2).

DISCUSSION: **a)** High rejection rate indicates high possibility of motion induced data corruption. Areas with higher mean rejection rate also have higher standard deviation, reflecting spatial consistency of motion affection, but the extent varies across individuals, which is consistent with previous studies using single-shot EPI diffusion imaging [1,6]. **b)** Cardiac gating can reduce motion artifacts [6-8]. However, the scan efficiency is sacrificed by about 50% using standard gating method or 20% using optimized gating method [8]. Sampling more diffusion encoding directions or repetitions can be a more efficient solution. Based on our statistical analysis, DTI metrics can maintain accuracy by acquiring about 15% (the maximum of mean rejection rate plus one S.D.) more directions or repetitions. To specify, multi-shot diffusion acquisition can utilize this 15% of data to compensate for the potential SNR loss caused by shot rejection, while single-shot acquisition can use these data to compensate for the image outliers for consistent quality of DTI metrics. In addition, noting the spatial diversity of rejection rate, we may also optimize the data acquisition or online reacquisition [2,3] scheme by applying variable oversample factors for different slices according to the GR map. **c)** The limitation of this study is the slice-wise evaluation of data rejection rate instead of voxel-wise, since the data is rejected in the k-space by shots during reconstruction. Due to the axially acquired images with slightly different tilting angles, we see variations along the horizontal direction on the GR mean map. However, from the main horizontal trend, we can still see the extent to which a transverse region suffers from data corruption.

CONCLUSION: In summary, our results suggest that, data corruption in diffusion imaging can't be ignored in image reconstruction and tensor fitting especially in some regions near the cerebellum, the brainstem and the ventricles. About 15% more data may be required for reliable DTI metrics with data rejection.

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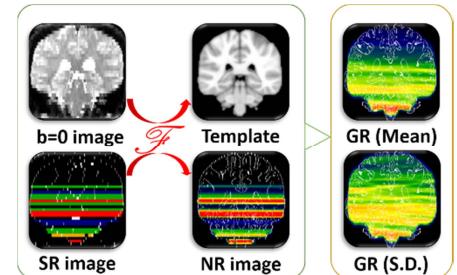


Fig.1 Flow chart of data postprocessing.

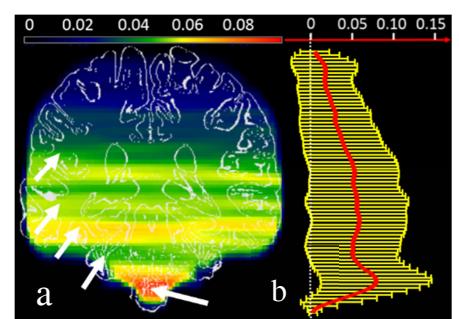


Fig.2 (a) Generalized rejection rate map (GR) in one coronal view. (b) Mean and standard deviation of rejection rate along the horizontal direction.