A Sliding-Window Re-Acquisition Scheme for Multi-Shot, Diffusion-Weighted Imaging with 2D Navigator Correction

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Introduction: A number of multi-shot, diffusion-weighted imaging sequences apply a phase correction using signals from a low-resolution 2D navigator to remove non-linear, shot-to-shot phase variations caused by CSF pulsation in the brain [1]. The extent of the 2D navigator in *k*-space is usually limited along at least one *k*-space axis so that high-spatial-frequency phase errors cannot be corrected, resulting in residual artifacts in the final image. Typically, these extreme phase errors are infrequent and can be avoided by using a re-acquisition scheme [2], in which unusable scans are identified from the 2D navigator signals during the measurement and replaced by re-acquired data. In previous work with readout-segmented EPI (rs-EPI) [3], a re-acquisition scheme was used in which all re-acquisitions were performed at the end of the measurement. This has the advantage that all scans can be compared, so that the re-acquisition can focus on the most corrupt scans. However, there is the disadvantage that all raw data have to be saved until the end of the measurement, which is not practical when very large data sets are acquired. A further disadvantage is that long scan times can result in an excessively long time interval between readout segments when the data for some segments are replaced by re-acquired data at the end of the scan. This paper describes the use of rs-EPI with a modified re-acquisition scheme that avoids this problem, making it possible to perform high-resolution diffusion tensor imaging (DTI) in combination with a large number of diffusion directions and a 32-channel head coil.

Methods: ***Sliding-Window Re-Acquisition Scheme:*** An automated procedure was used by the sequence at the start of the scan to split the measurement up into separate blocks, each of which corresponded to the acquisition of a complete volume (all slices and readout segments) for a given number of diffusion scans. The number of diffusion scans was determined by considering the amount of memory available to store raw data. The sequence started by acquiring all raw data for the first measurement block, followed by the corresponding re-acquisition. As described previously [4], the width of the raw navigator signal distribution (w_x) along the k_x direction was used as a measure of the level of high-spatial-frequency phase error. A normalized parameter $W_x=(w_x-m)/m$ was calculated, where m is the minimum value of w_x for all readout segments relating to a single image. All scans with a W_x value greater than a threshold of 0.05 were re-acquired, subject to a limit of a 20% increase in the overall scan time. Once the re-acquisition was complete, the images were reconstructed in parallel with the same data acquisition procedure for the subsequent measurement blocks.
Scanning Protocol: Data were acquired from healthy volunteers using a 3T MAGNETOM Verio system (Siemens Healthcare) with a standard 32-channel head coil and the following parameters: 25 slices; FOV 220mm; Matrix 258x252; slice thickness 4mm; GRAPPA acceleration factor 3; 9 readout segments (shots); TE 75ms; TR 4100ms; EPI echo-spacing 360µs; 5 scans with b=0; 30 diffusion-gradient directions with b=1000 s/mm^2 [5]. The sliding-window re-acquisition scheme automatically split the scan into 6 measurement blocks and performed between 7 and 11 re-acquisitions for each block. The overall scan time including reference scans was 20min 59s, of which a total of 3min 50s was used to re-acquire data.

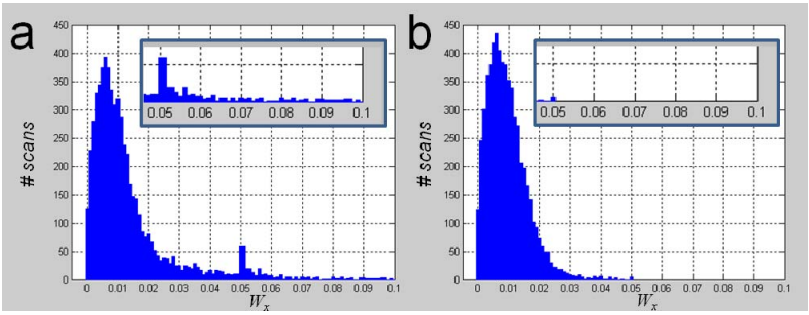

Fig. 1: Histograms showing the spread of navigator distribution widths (W_x) for all scans in an rs-EPI DTI acquisition. (a) Original acquisition. (b) After replacing data with re-acquired scans.

Results and Discussion: The histograms in Fig. 1 show the spread of the parameter W_x for data from all measurement blocks in a single subject. As seen in Fig. 1a, before data re-acquisition there is a small number of scans with high W_x values, which correspond to data with high-spatial-frequency phase errors. Note that the small peak around W_x=0.05 is a consequence of weighting the scans over threshold according to the readout segment number (to ensure that segments near to the centre of *k*-space are re-acquired first) [4]. As shown in Fig. 1b, when these corrupt scans are replaced by the re-acquired data, the anomalous high values have disappeared and overall there is a narrower spread of W_x values, demonstrating the effectiveness of the sliding-window re-acquisition scheme. Because only a small proportion of scans are affected in the original acquisition, it is possible with a relatively modest increase in scan time to have a significant effect on the quality of the data and substantially reduce the risk of artifact in the reconstructed images. Fig. 2 shows typical trace-weighted and FA maps from the study, demonstrating the absence of motion-induced phase artifacts and a low level of residual susceptibility artifact.

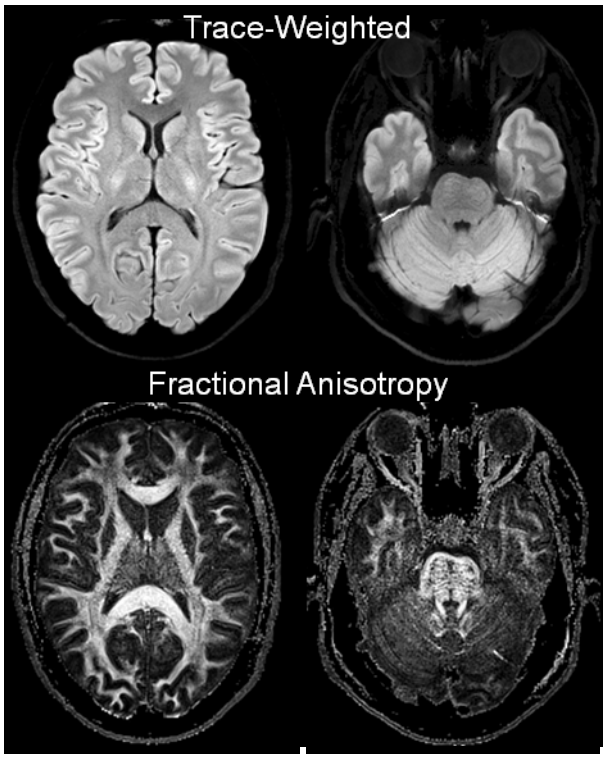

Fig. 2: DTI parameter maps from an rs-EPI acquisition with 30 diffusion-gradient directions and a voxel size of 0.85 x 0.87 x 4.0 mm^3.

References: [1] Miller, et al. MRM 2003;50:343-53. [2] Nguyen, et al. ISMRM 1998, #134. [3] Porter. ISMRM 2006; #1047 . [4] Porter, et al. MRM 2009;62:468-75. [5] Jones, et al. Human Brain Mapping 2002;15:216-30.