Multi-Shot, Diffusion-Weighted Imaging at 3T using Readout-Segmented EPI and GRAPPA

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Introduction

Diffusion-weighted, single-shot EPI suffers from considerable susceptibility-based distortion artefact at 3T. Although the effects can be mitigated by using a partially parallel imaging (PPA) technique to reduce the effective echo-spacing [1], there are significant residual artefacts and real resolution is limited by the requirement to keep the echo-train short due to T_2^* decay. A number of multi-shot imaging techniques [2-5] have been introduced for performing motion-insensitive, diffusion-weighted imaging, which could potentially provide a significant improvement in image quality at 3T. One of these techniques is the readout-segmented EPI method [5], which achieves a substantial reduction in susceptibility artefacts by using a much shorter echo-spacing than single-shot EPI. The technique has the potential advantage over TSE based methods of reduced SAR and insensitivity to the failure of the CPMG condition caused by motion-induced phase errors. CPMG errors may present a particular challenge at 3T due to the higher B_1 field inhomogeneity than at lower fields. However, whilst TSE methods can effectively remove susceptibility artefacts, readout-segmented EPI shows residual susceptibility artefacts at 3T, consistent with a typical EPI echo-spacing of around 300µs. In addition, as the echo-train length is determined by the number of phase-encoding lines, a relatively long echo-train is required at high imaging resolutions, leading to loss of detail due to T_2^* decay. This study addresses these limitations by combining readout-segmented EPI with GRAPPA [6] to reduce both the effective echo-spacing and the EPI echo-train length.

Methods

Sequence Design: The sequence uses two spin echoes to sample imaging and navigator data respectively using an EPI echo-train with a short echo-spacing. Each echo samples a subset of contiguous k_x points and the full extent of k_y. For the imaging echo the sampled k_x segment has a different offset from the centre of k-space at each shot and for the navigator echo the central k_x segment is sampled each time. Due to the acquisition of contiguous data points, the Nyquist sampling condition is fulfilled for each shot, making it possible to perform a 2D non-linear phase correction in image space without the influence of aliased signal contributions.

Data Acquisition: The sequence was implemented on a Siemens 3T MAGNETOM Trio system, equipped with a 12-channel head matrix coil. Images were acquired from healthy subjects using: FOV 210mm; matrix 224 x 224; pixel size 0.9mm x 0.9mm; slice thickness 5mm; slices 19; shots per image 11; echo-spacing 320µs; TR 3380ms; TE 68ms; one scan at b=0 and three at b=1000s/mm^2 in orthogonal directions; no cardiac triggering; measurement time 3min 6secs, including phase correction scans and an additional time for the automatic re-acquisition of unusable data with extreme motion artefact (technique described elsewhere). An acceleration factor of 2 was used with under-sampling of the data in the k_y direction to give an EPI echo-train with 112 echoes and an effective echo-spacing of 160µs. Auto calibration signals (ACS) for the GRAPPA reconstruction were acquired in a separate single-shot measurement of the fully sampled central k_x segment. Diffusion-weighted, single-shot EPI images were acquired for comparison using a standard protocol with FOV 230mm, matrix size 192 x 192 and GRAPPA with an acceleration factor of 2.

Image Reconstruction: Images were reconstructed off-line using MATLAB (The Mathworks, Inc.). After Nyquist ghost phase correction and data regridding (due to a sinusoidal readout gradient waveform), a GRAPPA reconstruction was applied to both imaging and navigator data from each shot to reconstruct the missing lines, having previously derived the coil weights from the ACS using a Moore-Penrose pseudo-inverse to solve the linear system of equations. After reconstruction of the complete k-space data for each shot, the navigator data were used to apply a 2D non-linear phase correction in the image domain for each receive channel independently. The data from all k_x segments were then combined to provide a separate image for each receive channel. The image data from the 12 receive channels were then combined in the standard way using the square root of the sum of squares. No spatial normalization was applied to the images.

Results

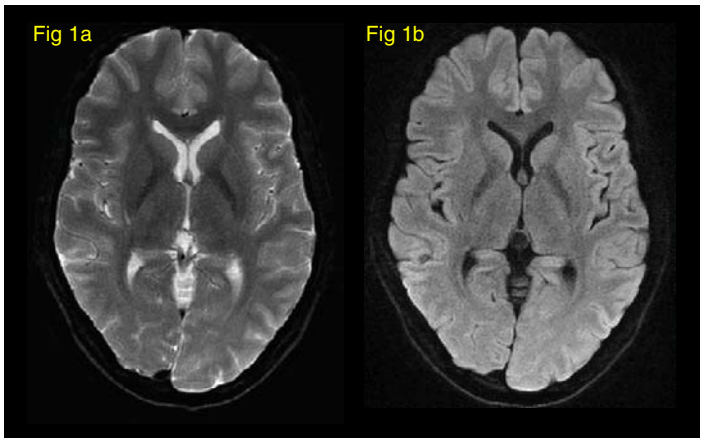

Figure 1: 3T multi-shot images using readout-segmented EPI and GRAPPA. TE 68ms, total scan time ~3min. **(a)** T_2-weighted image. **(b)** Trace-weighted image.

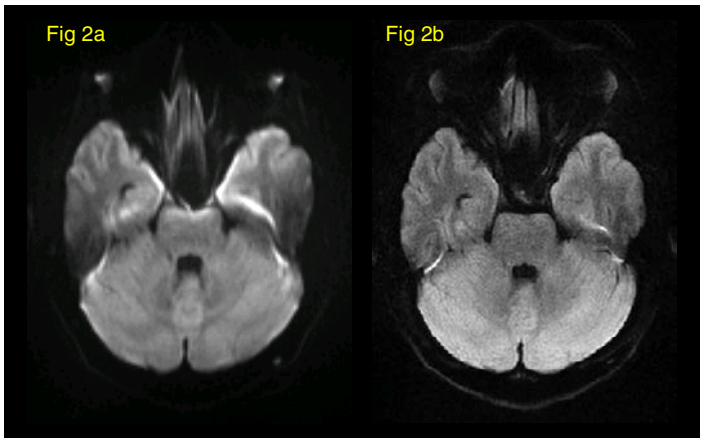

Figure 2: Comparison between single-shot EPI **(a)** and readout-segmented EPI **(b)**. Both images are trace-weighted with b=1000s/mm^2.

Discussion

As shown in figure 1, readout-segmented EPI produced both T_2- and diffusion-weighted images with a high level of detail that was consistent with the nominal resolution, This reflects a minimal degradation of the point-spread function due to T_2^* decay during the echo-train and the successful removal of motion-induced phase errors in the diffusion-weighted scans. The GRAPPA algorithm allowed a robust reconstruction of the under-sampled data, providing images without detectable aliasing artefact. As seen in figure 2, the readout-segmented EPI method provides a substantial reduction in susceptibility artefact compared to standard single-shot EPI protocols, as well as an increased level of detail. In addition, the short echo-time accessible with the technique minimizes signal losses due to T_2 decay, which is an increased problem at 3T due to the reduced T_2 in brain tissue [7]. The short echo-time provides sufficient SNR at 3T to perform high-resolution diffusion-weighted studies in reasonably short examination times, which should be of substantial benefit in routine clinical imaging.

References

[1] Griswold MA et al. ISMRM, p423, 1998. **[2]** Pipe et al. MRM 47, p621, 2002. **[3]** Miller et al. MRM 50, p243, 2003. **[4]** Liu et al. MRM 52, p1388, 2004. **[5]** Porter et al. Proc. ISMRM, p442, 2004. **[6]** Griswold et al. MRM 2002; 47:1202-1210. **[7]** Lu et al. JMRI 22, p13, 2005.