Comparison of Acceleration Techniques Applied to Multi-shot 3D EPI for fMRI Studies

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Introduction:

Multi-shot 3DEPI[1] sequence is a recently introduced alternative to the standard 2DEPI sequence for fMRI studies. An important advantage of 3DEPI is the ability to accelerate effectively in the 3D slice encoding direction, which directly reduces the scan time. In this work we evaluated the temporal performance of three acceleration techniques applied to multi-shot 3D EPI for fMRI. In particular we implemented a multi-shot sequence accelerated by GRAPPA[2], UNFOLD[3], and a combination of UNFOLD and GRAPPA, all along the slice encoding direction. We show results from a phantom experiment and an in-vivo fMRI study that compares the accelerated sequences to full 3DEPI acquisition in terms of temporal SNR, temporal artifacts, and functional sensitivity.

Methods:

Experiments were performed with an 8-channel InVivo head coil on a 3T GE SIGNA scanner with gradient constraints Gmax=40mT/m, slew rate S=140T/ms. For all experiments the FOV was 192x192x150mm^3 with 64x64x50 matrix, 3mm isotropic resolution. A spatial-spectral 2D RF pulse with a 15^o angle was used to excite the whole FOV at each TR, and readout bandwidth was 100kHz. For all the datasets the kx-ky plane (64x64) was fully sampled with an echo train length of 64 with an echo time of 30ms, resulting in a 60ms TR. Sagittal orientation was chosen to accommodate GRAPPA for the 8-channel coil configuration. Four different acquisitions were performed with the following parameters (for matrix size and scan time see Table 1):

a) Full k-space coverage, ***b)*** GRAPPA applied along the slice encoding direction with an acceleration factor of 2 and 6 reference slices, ***c)*** UNFOLD applied along the 3D encoding direction with an acceleration factor of 2, ***d)*** Both UNFOLD and GRAPPA applied along the z direction, with a combined acceleration factor of 4 with 6 reference slices. fMRI Paradigm: A visuospatial-motor task was tested where subjects (N=3) were exposed to visual quadrants with high-contrast random noise patterns with a finger tapping response in the left and in the right hand when the stimulus appeared in the upper left and lower right quadrant respectively. Block length of stimulus quadrants was between 5s and 15s. Total scan time was 3 minutes for all experiments; accelerated experiments had improved temporal resolution. Data Processing: All images were reconstructed off-line using published UNFOLD and GRAPPA implementations [4]. A low-pass filter with a cut-off at 92% of the full frequency band was used for UNFOLD. Drifts in signal magnitude were corrected and images were realigned before tSNR measurements, calculated for each voxel, as the voxel mean over time divided by the standard deviation. For fMRI studies all images were realigned and smoothed with a 6 mm wide kernel. All analysis was performed with SPM8. For the visuospatial-motor task, T-scores were kept at $p<0.001$ uncorrected.

Results and Discussion:

Table 1 compares four sequences in terms of median tSNR values in phantom and fMRI studies, maximum t-values observed for motor and visual cortex, and number of active voxels for each experiment. tSNR values in phantom experiments were consistent with the expected SNR loss due to the under-sampling in k-space.

$$(\text{SNR} \propto \sqrt{Acc.factor/BW})$$

Table 1	Full Acq.	2x GR	2x UNF	2x UNF+ 2xGR
Acquired matrix size	64x64x50	64x64x28	64x64x25	64x64x17
Scan time for each volume	3 sec	1.68sec	1.5 sec	1.02 sec
Median tSNR for phantom experiments	111.85	78.72	76.41	68.13
Median tSNR for fMRI studies	57.28	44.89	45.21	40.58
Maximum t-value (Motor Cortex)	8.51	13.18	13.79	15.33
Maximum t-value (Visual Cortex)	9.13	11.31	10.49	12.76
Number of active voxels	158	166	163	174

For in-vivo studies, the tSNR loss for accelerated sequences was less than theoretical predictions due to physiological noise. For all experiments, similar regions and approximately equal numbers of voxels were found to be activated. The accelerated sequences traded lower tSNR, compared to the full acquisitions, for improved temporal resolution yielding higher t-scores. To identify temporal artifacts for each sequence, tSNR maps were calculated for the whole brain. A sample slice from a tSNR map is shown in Figure 1. GRAPPA based methods appear to suffer from tSNR losses near the center of the images, consistent with g-factor SNR losses, whereas UNFOLD based methods performed worse in regions with flow and motion.

Conclusions: The accelerated sequences sustained an expected tSNR loss in phantom experiments compared to the full 3DEPI acquisition but outperformed the full version in in-vivo experiment through a statistical gain due to an increased temporal resolution and more volumes acquired per time unit. Compared to 2xUNFOLD acceleration, combination of UNFOLD and GRAPPA acceleration produced a more uniform tSNR map.

References: 1. Goerke et.al. NMR in Biom. 2005,18:534-542 **2.**Madore et al. MRM 1999;42:813-828 **3.** Griswold et al. MRM. 2002;47:1202–1210. **4.** NCIGT Fast Imaging Library (http://www.ncigt.org/pages/Research_Projects/ImagingCoreToolbox)

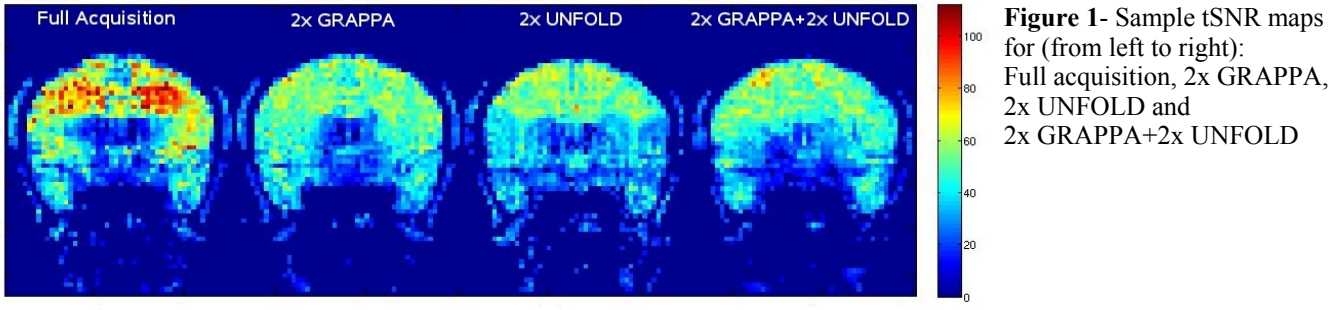

Figure 1- Sample tSNR maps for (from left to right): Full acquisition, 2x GRAPPA, 2x UNFOLD and 2x GRAPPA+2x UNFOLD