

GRAPPA Reconstruction of Sensitivity Encoded 2D and 3D Proton Echo Planar Spectroscopic Imaging (PEPSI) with SNR Adaptive Recalibrating

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INTRODUCTION: We recently introduced the accelerated Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) with SENSE and GRAPPA parallel imaging [1,2]. In this study we demonstrate that 4T PEPSI data with an 8-channel coil array can be reconstructed with up to 4-fold acceleration using GRAPPA algorithm [4]. We show the feasibility of 2D encoding in 16 seconds and 3D spatial encoding in about 2 minutes without significant loss in spectral quality. In addition, we showed that it is crucial to match the SNR level of the reference data used for calibrating GRAPPA to the SNR level of the PEPSI data for optimal GRAPPA reconstruction.

METHODS: PEPSI data were acquired on healthy volunteers using a 4T Bruker MedSpec scanner equipped with an 8-channel surface coil array. Both 2D data and 3D data were acquired from axial slices using a trapezoidal readout gradient train along the left-right direction (TR: 2 sec, TE: 15 msec, FOV 260 mm, slice thickness: 1-2 cm, reconstructed spectral width after even-odd echo sorting: 1.1 kHz, 512 complex spectral points). Complete 8-slice outer volume suppression was applied along the perimeter of the brain. Data acquisition included water suppressed (WS) and non water suppressed (NWS) scans. Fully sampled data were acquired with a 32x32 spatial matrix for 2D (64 sec acquisition time) and 32x32x8 matrix for 3D (8.5 min acquisition time). Acceleration was simulated by decimating the PEPSI data along the PE-direction (anterior-posterior). Due to the employment of high bandwidth in readout, temporal information is thus uncoupled from spatial information in the PEPSI acquisitions. Thus we reconstructed each time point independently. The spatial matrix of the first time point was used as reference for the following 4 GRAPPA calibration methods: a) using only the first time point of the (fully sampled) NWS data set as reference for reconstructing both the (decimated) NWS data and WS data. b) calibrating GRAPPA separately for the NWS data and the WS data by using the first time point of the (fully sampled) NWS data and the WS data respectively. c) additionally recalibrating the GRAPPA kernel from b) for time points >150 with noise added references to account for the decreasing SNR in later time points. This is done by adding Gaussian noise to the reference (which is as in b) the 1 time point of both WS data and NWS data) and recalculate the GRAPPA weights based on this modified reference. The magnitude of the added noise (real part and imaginary part) was chosen as the averaged voxel signal in the spatial slice of the first time point. d) separate the time domain into 6 consecutive sections and recalibrate GRAPPA for each section separately. The noise level used in c) was then additionally multiplied by the ratio of the avg. intensity between first time point and target time point. The GRAPPA reconstruction was done coil-by-coil with a kernel of 5x4 source points per coil as described in [4]. The k-space edges were extended by zero padding instead of applying a circular assumption. The metabolite maps and spectra were obtained by spectral fitting of 15 metabolites using LCMoDel [8].

THEORY: As discussed in SMASH [5], high SNR in references used for calibrating GRAPPA results in a severely increased noise amplification for the following mathematical reason. We denote the kernel weights as vector \mathbf{n} , the auto calibrating points as vector \mathbf{a} , and the matrix with the corresponding GRAPPA source points as $\mathbf{S} = \mathbf{S}^0 + \mathbf{w}$ with noise \mathbf{w} , where \mathbf{w} is uncorrelated zero-mean noise, the solution of the kernel weights [7] can be approximated as $\mathbf{n} = \mathbf{a} \mathbf{S}^{-1} (\mathbf{S}^0 \mathbf{S}^{0H} + \mathbf{w} \mathbf{w}^H)^{-1}$, which implies for the individual kernel weights, that $\ln |\mathbf{n}_{noise}| < \ln |\mathbf{n}_{noise-free}|$ [6]. Smaller kernel weights transfer less noise from the source points to the estimated data points, resulting in increased SNR, which turns out to be much more severe than increasing aliasing artifacts due to smaller weights.

RESULTS: The GRAPPA reconstruction results in Figs. 1 and 2, for which both NWS- and WS references were used, show little degradation up to 4-fold acceleration, which corresponds to a PEPSI scan duration of approximately 2 min. for 3D and 16 sec. for 2D spatial encoding. Table 1 shows the averaged Cramer-Rao

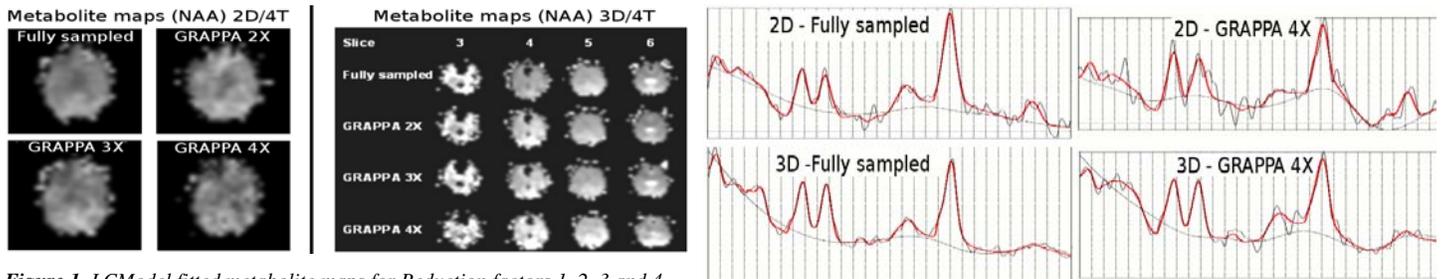


Figure 1. LCMoDel fitted metabolite maps for Reduction factors 1, 2, 3 and 4

Figure 1. LCMoDel fitted spectra from an example voxel of both 2D and 3D

Lower Bounds [8] (CRLB) of choline, creatin and NAA across the PEPSI slice, using 4 GRAPPA calibration methods described above. Using only a NWS reference (method a) resulted in the highest CRLB values. Using both a NWS reference and a WS reference (method b) resulted in lower CRLB values. Method c resulted in a further decrease of the CRLB values. This is also true using method (d), where GRAPPA recalibrating was done after every ninetieth data points. Overall, recalibration of the GRAPPA kernel to improve SNR matching between reference and unfolded data improved reconstruction performance and thus lowered CRLBs in the spectra.

| Used Reference | NAA+NAAG | GPC+PCh | Cr |
|-----------------------|----------|---------|------|
| a) NWS | 8.37 | 13.6 | 13.2 |
| b) NWS; WS | 6.99 | 12.1 | 11.4 |
| c) NWS; WS; 1x Recal. | 6.39 | 11.3 | 11.0 |
| d) NWS; WS; 6x Recal. | 6.07 | 10.8 | 10.6 |

Table 1. Comparing the CRLB for different GRAPPA calibration methods using different references

DISCUSSION: Up to 4-fold accelerated PEPSI data can be reliable reconstructed with GRAPPA. The quality of the reconstruction depends on GRAPPA calibrating. Since the SNR is decaying exponentially in the time domain, re-calculated GRAPPA with adjusted noise level can improve the reconstruction.

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