2D-GRAPPA accelerated FID based MRSI of the brain at 7T

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Target Audience: Scientists interested in brain MRSI or parallel imaging

Purpose:

Proton Magnetic Resonance Spectroscopic Imaging (MRSI) in the brain is an important tool for investigating several neurological diseases such as brain tumors, multiple sclerosis or Alzheimer disease. However, conventional MRSI is slow and offers low signal to noise ratio per unit time (SNR/t). For clinical applications, the long scan times of high resolution MRSI have to be reduced. At higher magnetic field strength the SNR/t is significantly increased. In addition, FID based sequences with ultra-short acquisition delay [1,2] and optimized signal combination of array coils (AC) [3] further improve the available SNR/t. This significant gain in SNR/t can then be traded for the required acceleration in data acquisition. One way to increase measurement speed is the use of parallel imaging techniques. In this work, the 2D-generalized autocalibrating partially parallel acquisitions (GRAPPA) -Operator method [4] is used to efficiently decrease the scan times of high resolution MRSI to clinically feasible durations.

Methods

Fully sampled 2D-MRSI data of the brains of five volunteers were acquired with a 32-channel coil and a volume coil (VC) at 7T. The sequence parameters were: Matrix size 64x64, acquired with elliptical weighting and in a pseudo-spiral pattern, voxel size 3.4x3.4x12 mm³, acquisition delay 1.3 ms, scan time 32 minutes. Two gradient echo images with a size of 128x128, one with reversed gradients to correct for gradient delays, were acquired within 1.2 s with similar sequence parameters to serve as auto-calibration signal for the 2D-GRAPPA-Operator method and as coil combination weights. The highest possible acceleration factor and the best undersampling pattern that still lead to acceptable reconstructions were estimated for one data set by computing the artifact power, a measure of remaining aliasing artifacts and noise enhancement. For that, undersampled MRSI data were simulated by omitting different parts of the fully sampled k-space, which was then reconstructed using 2D-GRAPPA-Operators. All fully sampled data sets were then undersampled in post-processing with the best undersampling pattern and reconstructed with the 2D-GRAPPA-Operator method. Coil combination using an image based combination [3] and additional noise decorrelation to optimize the gain in SNR/t were performed. Data were Hamming filtered, fitted with LCModel, and the SNR of each spectrum was computed with a MATLAB script. As a reference, the same processing was performed with the VC data and the fully sampled data sets, i.e. the data without artificial undersampling. The spectra, metabolic maps and Cramer-Rao Lower Bonds (CRLB), were compared between those data sets. The g-factors were compared between a variable density undersampling and a uniform undersampling pattern.

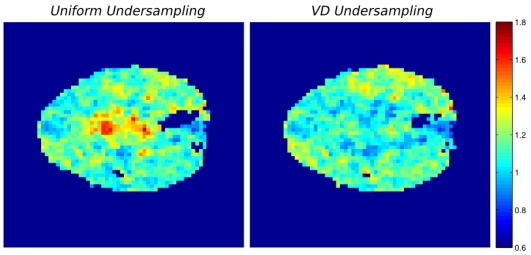

Figure 1: g-factor maps for uniform undersampling with $ORF_x \approx 3$, $ORF_y \approx 3$, $R \approx 8.8$ (left) and variable density undersampling with $ORF_x \approx 3$, $ORF_y \approx 3$, $R \approx 8.2$ (right).

Results

The evaluation of the artifact power showed that undersampling patterns with equal reduction factors in both directions ($R_x = R_y$) perform much better than patterns with unequal reduction factors for the used coil. It also showed that for fixed overall reduction factors R, uniform k-space sampling causes smaller artifact powers than variable density sampling with higher outer reduction factors (ORF). However, when comparing g-factor maps, a small number of additional k-space points in the k-space center can eliminate hot spots of the g-factors (Fig 1). Thus, an undersampling pattern with $ORF_x \approx 3$, $ORF_y \approx 3$ and a full sampling radius of 3 voxels was chosen, which results in $R \approx 8.2$ and about 4 minutes scan time. A comparison between the spectra resulting from the VC, the fully sampled AC data, and the reconstructed data is shown in Fig. 2. Fig. 3 shows metabolic ratio maps of tCho/tNAA for the same three sets. The average CRLB-values of the most important metabolites for the fully sampled data were $CRLB_{Fully}^{tNAA} = 3.8 \pm 4.3$, $CRLB_{Fully}^{tCho} = 5.7 \pm 5.5$, $CRLB_{Fully}^{tCr} = 5.7 \pm 6.3$ and increase for the reconstructed data in average by 1.65 ± 0.73, 1.65 ± 0.71 and 1.83 ± 0.79, for tNAA, tCho, and tCr, respectively.

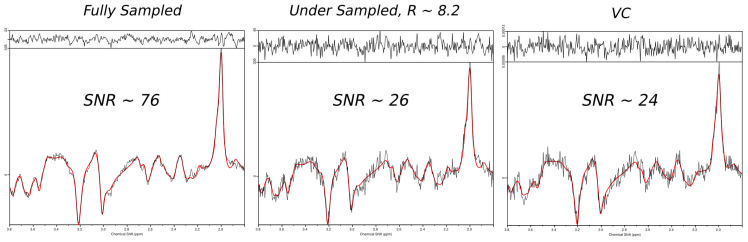

Figure 2: Comparison of the spectra resulting from fully sampled (left), undersampled (middle), and VC MRSI data (right).

Discussion and Conclusions

This work shows that FID based high-resolution MRSI at 7T with ultra-short acquisition delays and optimized coil combination can be efficiently accelerated by 2D-GRAPPA based parallel imaging to under 4 minutes while still providing high spectral quality. The quality of the accelerated data is comparable to those obtained in an 8 times longer measurement using a VC.

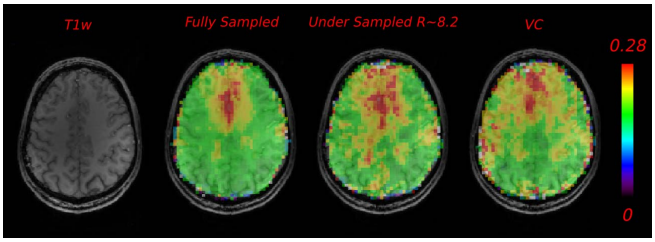

Figure 3: Ratio maps of tCho/tNAA comparing the fully sampled, undersampled and VC data.

References:

1. Bogner et al., NMR Biomed. 2012; 25(6):873-82.
2. Henning et al., NMR Biomed 2009;22(7):683-696.
3. Strasser et al., Proceedings ISMRM 20 (2012):1746
4. Blaimer et al., Magn Reson Med. 2006, 56(6):1359-64