(2+1)D-CAIPIRINHA Accelerated FID Based MRSI of the Brain at 7T

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Target Audience: Scientists interested in brain MRSI, parallel imaging (PI) and clinical applications of MRSI.

Purpose:

Proton MRSI in the brain is an important tool for investigating several neurological diseases. However, the clinical usage of high-resolution MRSI is restricted due to low Signal to Noise Ratios (SNR) and long scan times. The problem with low SNR can be addressed by using ultra-high magnetic field strengths, array coils with an optimized signal combination[1], and FID based sequences with ultra-short acquisition delays[2]. The long measurement times, especially when measuring several slices, can be shortened with the aid of PI. Both, PI acceleration in slice direction (multi-slice Caipirinha) and in-plane acceleration in phase encoding direction (2D-Caipirinha or GRAPPA) have been shown to be versatile tools for accelerating MR acquisitions[3,4]. The purpose of this study is to combine multi-slice Caipirinha with 2D-Caipirinha to fully exploit the sensitivity variations of the array coil and accelerate MRSI acquisition in all three spatial dimensions to provide clinically acceptable scan times.

Methods

To evaluate the feasibility of 3D (2D+1D) accelerated CSI in the brain at 7T, pulse cascaded Hadamard encoded MRSI[5] data with two slices were fully sampled in two volunteers with a 32-channel coil at 7T. The sequence parameters were: Matrix size 64x64x2, acquired with elliptical weighting and in a pseudo-spiral pattern, voxel size 3.4x3.4x8 mm³, slice gap 8 mm, acquisition delay 2.3 (slice 1) and 1.3 ms (slice 2), scan time 60 minutes. A fast 128x128x2 gradient echo image was acquired with similar sequence parameters to serve as auto-calibration signal for the (2+1)D-Caipirinha reconstruction and as coil combination weights. Based on these fully sampled data, a (2+1)D-Caipirinha acquisition was simulated by modifying the k-space data and the performance of different reconstruction patterns was evaluated. The two slices were shifted against each other in the range of (0.3 - 0.5) x Field of View (FoV) in both phase encoding directions independently to maximize the difference in the sensitivity profiles of the coils. The slices were then aliased in post-processing as if they were acquired at the same time. Different 2D-Caipirinha patterns were simulated by omitting parts of the k-space, The data was unaliased by first performing a GRAPPA-based in-plane, and then a GRAPPA-based slice reconstruction. The best combination of the FoV shifts and the 2D-Caipirinha pattern was estimated by minimizing the artifact power for one volunteer within the brain. Both volunteer data sets were undersampled/aliased with the best (2+1)D-Caipirinha combination, noise decorrelated, (2+1)D-Caipirinha reconstructed, and Hamming filtered. The resulting spectra were fitted with LCModel and the SNR was computed using the pseudo-replica method[6]. The same processing was performed with a standard in-plane 3x3 GRAPPA pattern with a similar acceleration factor, and also with the fully sampled data set as a reference. The resulting g-Factor values were compared between (2+1)D-Caipirinha and the GRAPPA accelerated data. Spectra and metabolic maps were compared qualitatively.

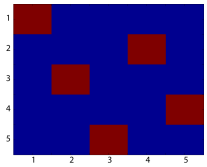

Figure 1: Undersampling pattern with the lowest artifact power of 7.7. The red points show sampled k-points, the blue ones omitted. This pattern is replicated to the actual data size.

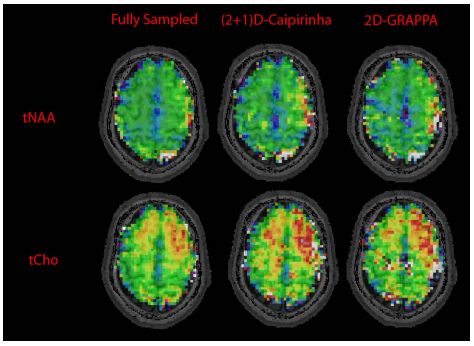

Figure 2: Metabolic maps of tNAA (upper row) and tCho (lower row) for the fully sampled (left), (2+1)D-Caipirinha (middle) and 2D-GRAPPA (right) undersampled MRSI data. The 2D-GRAPPA reconstructed show stronger artifacts than the (2+1)D-Caipirinha data.

Results

The lowest artifact power of 7.7 was achieved with an FoV-Shift of [FoVx, FoVy] = [0.5, 0.5] between the two slices and for a 2D-Caipirinha pattern shown in figure 1, resulting in R = 8.7. The reference 2D-GRAPPA pattern was chosen as 3x3 with R = 8.8, and an artifact power of 9.3. This acceleration would result in 7 min scan time if implemented in the sequence. The median and the inter quartile range of the g-Factors of the (2+1)D-Caipirinha undersampled data was 1.39 ± 0.97, while that of the 2D-GRAPPA was 1.47 ± 0.95. The SNR of the fully sampled data was in average 24 ± 11. In figure 2, metabolic maps of the fully sampled data, the (2+1)D-Caipirinha and of the 2D-GRAPPA undersampled data are shown for tCho and tNAA. Spectra of the same data sets can be seen in figure 3.

Discussion and Conclusions

(2+1)D-Caipirinha was shown to be superior over standard PI methods such as 2D-GRAPPA if phase encoding is performed in two dimensions and multi-slice acquisition in the third. High acceleration factors could be achieved with a 32-channel head coil, restricted mainly by the base SNR of MRSI, since the g-Factors were small. This would lead to a clinically desirable measurement time of 7 min for two slices, or 14 min for four slices. The proposed method can be easily extended to acquiring more than two slices.

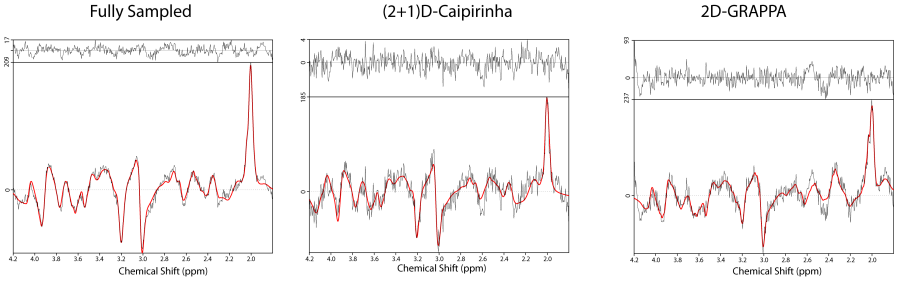

Figure 3: Comparison of the spectra resulting from fully sampled (left), (2+1)D-Caipirinha (middle), and 2D-GRAPPA (right) undersampled MRSI data. The latter shows a changed tCho peak in comparison to the reference (left). The spectra have a first order phase due to the acquisition delay.

References:

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