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Fast magnetic resonance spectroscopic imaging at 3 Tesla using autocalibrating parallel technique

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Abstract—**Magnetic resonance spectroscopic imaging (MRSI) is a powerful tool for diagnosis of many pathologic conditions. However conventional MRSI involves long scan times, in the order of 20 minutes. This work simulated an autocalibrating parallel technique based on GRAPPA algorithm for accelerating MRSI and applied it to 3 dimensional (3D) MRSI of the brain at 3 Tesla. Employing two fold undersampling in two phase-encoding directions, a four fold reduction in scantime was simulated. Metabolic parameters showed close agreement between the full and GRAPPA reconstructed spectral data.**

Keywords: **Magnetic resonance spectroscopic imaging, parallel imaging, GRAPPA**

I. Introduction

Magnetic resonance is based on the interaction of atoms and molecules with the external magnetic field. In clinical settings, the combination of magnetic resonance imaging (MRI) and magnetic resonance spectroscopy (MRS) is a powerful tool for diagnosing disease conditions from observed variations in morphology and chemical composition of tissues. Resonance frequency is specific to the molecular environment of an atom. So, MRS, a study of specific resonance frequencies absorbed by a tissue, is a probe of molecular structure. Brain tumors and other neurological diseases, stroke, prostatic tumors are some of the many clinical application areas beneficially impacted by MRS. Magnetic resonance spectroscopic imaging (MRSI) combines the features of both imaging and spectroscopy, by collecting spectral data from multiple voxels that have been spatially localized by phase-encoding gradients. The obvious advantages of MRSI over single voxel spectroscopy are finer spatial resolution and the provision of overlaying spectral maps on anatomical images. However, MRSI involves long acquisition times, in the order of 20-40 minutes which can cause patient discomfort and motion induced artifacts. Several pulse sequences were developed to accelerate MRSI by collecting more data points per excitation [1]. Partially parallel imaging (PPI) takes a different fast scanning approach based on the coil sensitivity modulation of the received MR signal [2]. In PPI, the MR signal is received by an array of coils and the measurement time is reduced by undersampling the signal space, which is in the Fourier domain, in the phase-encoding direction. Undersampling by a factor of R accelerates acquisition time by R folds, although penalty is paid in terms of signal-to-noise ratio (SNR). Reduction in the sampling density in the Fourier domain by a factor of R is equivalent to reduction of the image field-of-view (FOV) by R times. The missing data points are synthesized post-acquisition, by incorporation of the spatial information in the array elements. The "unaliasing" or "parallel reconstruction" can be performed either in the Fourier or the spatial domain, by direct inversion or indirect reconstruction techniques. Direct techniques like Sensitivity Encoding [3] estimate the localized sensitivity of each coil element from a low resolution coil calibration scan to compute the sensitivity encoding/ reconstruction matrix and solve the reconstruction problem by direct inversion of this matrix. Indirect techniques such as Generalized Autocalibrating Partially Parallel Acquisitions (GRAPPA) [4] acquire a small set of additional phase-encoding (PE) lines at the Nyquist sampling frequency that serve as training lines for estimating the interpolation weights that are then used to synthesize the skipped PE lines from the acquired lines. Since the coil calibration is built into the actual acquisition in these methods, they are also known as autocalibrating techniques. Using the SENSE algorithm, Dydak et al presented a sensitivity encoded 2D spectroscopic imaging technique, with undersampling in 2 phase-encoding directions resulting in net four folds reduction of scan time [5]. However, SENSE reconstruction has certain limitations when there is slight aliasing in the FOV even in the fully encoded acquisition. Furthermore, its accuracy largely depends on the accuracy of the coil sensitivity estimation. In this paper we present a fast MRSI method using a GRAPPA based autocalibrating parallel technique and apply it to 3D MRSI data at 3 Tesla (T) with an acceleration of two in two phase-encoding directions, k_x and k_y.

II. Methodology

A. GRAPPA based reconstruction of MRSI

GRAPPA is a robust parallel reconstruction technique operating in the Fourier domain that reconstructs the full FOV data from each individual coil allowing subsequent array combination. The sampling scheme for the Cartesian autocalibrating acquisition is shown in Figure 1. GRAPPA employs a block-wise reconstruction in which 1 block consists of 1 acquired line and R-1 skipped lines for an acceleration factor of R. The interpolation weights for an individual coil j are obtained by least square fitting of the acquired lines from all the coils to the AC lines of the j^{th} coil:

$$S_j(k_y - m\Delta k_y) = \sum_{l=1}^{L}\sum_{b=0}^{N_b-1} n(j,b,l,m) S_l(k_y - bR\Delta k_y) \qquad (1)$$

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where $S_j(ky-m\Delta ky)$ is the signal in the j^{th} coil at $m\Delta ky$ offset from the k_y^{th} PE position in kspace, b is the number of blocks used for the reconstruction, L is the number of coil elements and n(j,b,l,m) is the weighting of $S_l(ky-bR\Delta ky)$ for synthesis of S_j (ky-mΔky). Several variations of the data fitting described above have been presented in the literature, such as performing the fitting piecewise for segments along the unaccelerated direction.

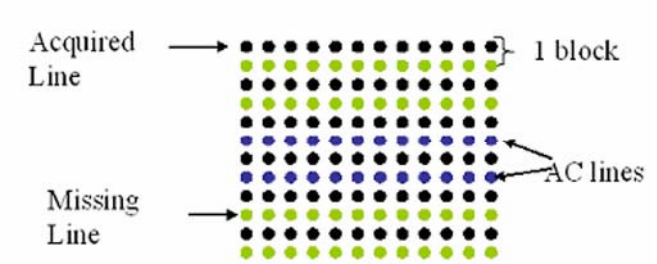

Figure 1 shows Cartesian variable density sampling for autocalibrating parallel acquisition with an acceleration factor, R=2 and 2 AC lines. Black, green and blue dotted lines indicate acquired PE lines, skipped PE lines and AC lines respectively.

Wang et al proposed a floating node fitting (FNF) which allows additional data fits compared to conventional GRAPPA during the calibration. The authors also proposed a multi-column multi line interpolation (MCMLI) that uses the nearest neighboring points in the unaccelerated direction as well for synthesis of missing lines [6].

The data from 3D MRSI acquisition has 3 spatial frequency dimensions – kx, ky, kz and a time dimension for the free induction decay. After an inverse Fourier Transform in the z direction the spectral data can be processed by two-dimensional GRAPPA reconstruction slice by slice. Griswold et al showed that multi-dimensional GRAPPA reconstruction can be broken up into several separate one-dimensional GRAPPA reconstructions [7]. In our case, we broke up the 2D GRAPPA reconstruction into two 1D GRAPPA reconstructions along kx and ky.

$$G_{kykx} = G_{ky}.G_{kx} \qquad (2)$$

The matrix formulation of Eq. (1) is:

$$\mathbf{S}_j(\mathrm{ky}-\mathrm{m}\,\Delta\mathrm{ky},\mathbf{k}) = \mathbf{n}^T\mathbf{S} \qquad (3a)$$

$$\mathbf{n}^T = \left[\mathbf{n}_1^{(m)T} \ldots\ldots \mathbf{n}_L^{(m)T}\right],$$

$$\mathbf{S} = \begin{bmatrix} \mathbf{S}_1(\mathrm{ky}-\mathbf{b}\,\mathrm{R}\,\Delta\mathrm{ky},\mathbf{k}) \\ \cdot \\ \cdot \\ \mathbf{S}_L(\mathrm{ky}-\mathbf{b}\,\mathrm{R}\,\Delta\mathrm{ky},\mathbf{k}) \end{bmatrix} \qquad (3b)$$

For G_{ky}, the vector **k** of length (N_{kx} x $N_{spectra}$) specifies the two-dimensional position in (kx, t) space, $\mathbf{n}_i^{(m)}$ is the vector of interpolation weights of length N_b for coil i and the matrix **S** has a size of LN_b x (N_{kx} x $N_{spectra}$), where N_{kx} and $N_{spectra}$ are the sizes of the kx and the spectral dimensions respectively. Si(ky-**b**RΔky,**k**) represents the signals in the i^{th} coil at offsets of **b**RΔky from the ky^{th} PE position and at position **k** in (kx, t) space. It has a matrix size of N_b x (N_{kx} x $N_{spectra}$). We programmed four GRAPPA based reconstruction schemes in MATLAB (MathWorks, USA). The schemes were: a) MC interpolation using neighboring spectral points and FNF, b) MC interpolation using neighboring spatial frequency points and FNF, c) MC interpolation using neighboring spectral points without FNF and d) GRAPPA reconstruction in which the unaccelerated spatial frequency axis is segmented. The matrix structure of S for the first reconstruction strategy described above is shown in Figure 2. We used two AC lines, blocksize N_b=4 and floating node fitting for the parallel reconstruction.

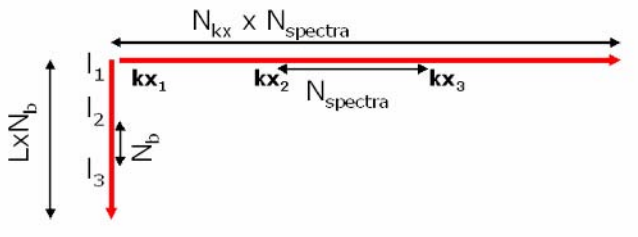

Figure 2 shows the arrangement of spectral and spatial dimensions in the S matrix described in Eq. (3) for the first reconstruction scheme described above.

B. MR Data Acquisition

Brain spectroscopic imaging experiments were performed on five healthy volunteers on a 3 T GE Signa EXCITE scanner (GE Healthcare, Milwaukee, WI) using uniform excitation by a body coil and reception by an eight channel phased array head coil (MRI Devices Inc, Gainesville, FL). Informed consent was obtained from the volunteers prior to scanning. The imaging protocol included the acquisition of T1-weighted 3D spoiled gradient recalled (SPGR) pulse sequence (repetition time (TR) =26 milliseconds (ms), echo time (TE)=3 ms, 3 mm slice thickness, 256x256 matrix, FOV=240x240 mm, flip angle = 40°) and proton-density weighted fast gradient echo coil sensitivity images (TR=150 ms, TE=2.1 ms, 3 mm slice thickness, 64x64 matrix, FOV=300x300 mm, flip angle=20°). Proton 3D MRSI data was acquired using point resolved spectroscopy (PRESS) volume localization. A chemical shift selective saturation (CHESS) sequence was used for water suppression and the signal outside the prescribed region was later suppressed using high bandwidth very selective suppression (VSS) pulses. The spatial array dimensions were 12x12x8 and spectral dimension was 1024 with 1 cc nominal spatial resolution. The spectra was acquired with TR=1.1seconds (s), TE=144 ms and total data acquisition time of 21:12 min.

C. Data Processing

The spectral data was moved to a Sun (Solaris, U.S.A.) workstation and decimated in kx and ky to simulate acceleration of 2 in each of the two directions, while retaining 2 AC lines. The acquisition time corresponding to this decimated dataset was 9:25 minutes. All the four reconstruction schemes described in the previous section were performed on a single dataset. APj, the mean artifact power between the GRAPPA-reconstructed data and the fully encoded data for each individual coil j was calculated for each of the reconstruction schemes as:

$$AP_j = \sqrt{\sum_{p=1}^{N} \frac{(S_j^{GRAPPA}(p) - S_j^{FULL}(p))^2}{(S_j^{FULL}(p))^2}}$$

Here p denotes the position in (kx, ky, kz,t) space and N is the total number of data points. The net artifact power for a reconstruction scheme was calculated as the median of the mean artifact power in all the coils. The optimal reconstruction technique was chosen on the basis of minimum net artifact power. This chosen optimal reconstruction technique was then applied to the other four decimated datasets The GRAPPA reconstructed data of each individual coil element was processed identically as the full dataset, on a Linux cluster, and data from all the coil elements were combined using coil sensitivity weighting by a software developed in our lab [8]. The spectral processing included inverse Fourier transformation in the spatial frequency directions kx and ky, apodization and Fourier transformation in the FID direction, frequency and phase correction and water baseline removal [8].

D. Data Analysis

In spectra acquired from the brain, primarily the signals coming from Choline (Cho), Creatine (Cr) and N-acetyl aspartate (NAA) are studied since they provide information about cellularity of tumor, cell membrane breakdown, cellular energetics and neuronal activity. Additionally, the relative levels of Choline and NAA have been found to be the most critical metabolic parameter in distinguishing tumor from normal tissue [8]. So, the peak heights of Cho, Cr and NAA, normalized by the standard deviation of spectral noise, were estimated from each spectral dataset. To evaluate the performance of the GRAPPA reconstruction, the relative level of Cho and NAA, the normalized peak height of Cho and the normalized peak height of NAA were compared between the GRAPPA-reconstructed spectral data and the corresponding full spectral data and were also tested for statistically significant difference by Wilcoxon signed rank test . Additionally, the agreement of the Cho/NAA value between the GRAPPA-reconstructed and full spectral data was examined by Bland Altman plot.

Figure 3
Fig 3a

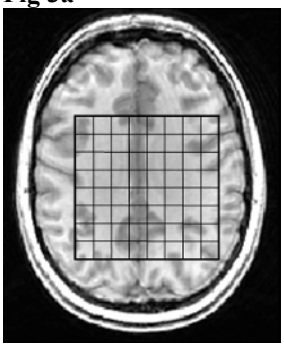

Figure 3: Fig. 3a shows the position of the PRESS box on an anatomical brain image. Figure 3b and 3c show the full spectra and GRAPPA–reconstructed spectra obtained from the PRESS-excited brain tissue volume respectively.

Fig 3b. Spectra from full dataset

Fig 3c. Spectra from GRAPPA-reconstructed dataset

A common problem in MRSI is the folding in of subcutaneous lipid that was excited by PRESS due to chemical shift, into the spectral FOV, giving rise to high

lipid peaks in the spectra of some voxels. To test the effect of parallel imaging on lipid contamination, the number of voxels having higher lipid peak height than NAA and number of voxels having higher lipid peak height than Cho were compared between the GRAPPA-reconstructed and full spectral data.

III. RESULTS

The spectral reconstruction employing FNF and MC interpolation using neighboring spectral points was found to have the minimum net artifact power for the test dataset and was chosen as the optimal reconstruction technique to be applied to the other four datasets. Representative full spectral data and GRAPPA-reconstructed spectral data from a single slice of a volunteer dataset are shown in Figure 3. The location of the PRESS box is also shown on an anatomical brain image in the figure (Figure 3a). As expected, the GRAPPA spectra (Figure 3c) has lower peak heights compared to full spectra (Figure 3b) due to lower SNR. However, it can also be seen that the full spectra and GRAPPA spectra have very similar spectral pattern. In some cases, the GRAPPA-reconstructed spectra showed additional intensity variation across the voxels, the reason for which will have to be further investigated. Metabolic parameters showed good agreement between the full and GRAPPA-reconstructed data. Wilcoxon signed rank test did not detect a statistically significant difference for values of relative level of Cho and NAA and the normalized peak height of Cho between the full and parallel reconstructed spectra for any of the volunteer datasets but showed a statistically significant difference for values of the normalized peak height of NAA for one dataset . Bland Altman plot of Cho/NAA values between parallel and full datasets showed very few outliers datapoints in the former. However, the number of lipid contaminated voxels was higher in the GRAPPA-reconstructed data compared to the full data. This is probably due to residual aliasing artifacts. A comparison of the metabolic parameter median (Cho/NAA) and the count of lipid contaminated voxels between full and GRAPPA-reconstructed spectra for the four datasets is shown in Table 1 and Table 2 respectively

Table 1 Comparison of median (Cho/NAA) between full and GRAPPA spectral data

	Full	GRAPPA
Volunteer 1	0.51	0.54
Volunteer 2	0.43	0.43
Volunteer 3	0.45	0.45
Volunteer 4	0.54	0.54

Table 2a Comparison of lipid contaminated voxels (Lipid > NAA) between full and spectral data

	Full	GRAPPA
Volunteer 1	1	8
Volunteer 2	0	0
Volunteer 3	0	0
Volunteer 4	1	6

Table 2b Comparison of lipid contaminated voxels (Lipid > Cho) between full and spectral data

	Full	GRAPPA
Volunteer 1	1	20
Volunteer 2	1	13
Volunteer 3	0	0
Volunteer 4	3	8

IV. DISCUSSION AND CONCLUSION

In this work we showed the feasibility of accelerating MRSI acquisitions nearly four folds by a GRAPPA based technique. Such techniques might have an advantage over direct methods like SENSE when there is considerable lipid aliasing into the spectral FOV, as suggested by the results shown in Table 2a or when coil sensitivity cannot be estimated accurately. Future work will include implementing the GRAPPA based reconstruction without using AC lines by applying the shift properties of the GRAPPA operator [7].

V. REFERENCES

[1] Posse, S., Tedeschi, G., Risinger, R., Ogg, R., Le Bihan, D., "High speed 1H spectroscopic imaging in human brain by echo planar spatial-spectral encoding", *Magn Reson Med* vol. 33, pp. 34-40, Jan 1995

[2] Sodickson, D. K., McKenzie, C. A., Ohliger, M. A., Yeh, E. N., Price, M. D., "Recent advances in image reconstruction, coil sensitivity calibration, and coil array design for SMASH and generalized parallel MRI", *Magma* vol. 13, pp. 158-63, Jan 2002

[3] Pruessmann, K. P., Weiger, M., Scheidegger, M. B., Boesiger, P., "SENSE: sensitivity encoding for fast MRI", *Magn Reson Med* vol. 42, pp. 952-62, Nov 1999

[4] Griswold, M. A., Jakob, P. M., Heidemann, R. M., Nittka, M., Jellus, V., Wang, J., Kiefer, B., Haase, A., "Generalized autocalibrating partially parallel acquisitions (GRAPPA)", *Magn Reson Med* vol. 47, pp. 1202-10, Jun 2002

[5] Dydak, U., Weiger, M., Pruessmann, K. P., Meier, D., Boesiger, P., "Sensitivity-encoded spectroscopic imaging", *Magn Reson Med* vol. 46, pp. 713-22, Oct 2001

[6] Wang, Z., Wang, J., Detre, J. A, "Improved data reconstruction method for GRAPPA", *Magn Reson Med* vol. 54, pp. 738-42, Sep 2005

[7] Griswold, M. A., Blaimer, M., Breuer, F., Heidemann, R. M., Mueller, M., Jakob, P. M., "Parallel magnetic resonance imaging using the GRAPPA operator formalism", *Magn Reson Med* vol. 54, pp. 1553-6, Dec 2005

[8] Nelson, S. J., "Analysis of volume MRI and MR spectroscopic imaging data for the evaluation of patients with brain tumors", Magn Reson Med vol. 46, pp. 228-39, Aug 2001