3D Cartesian and Elliptical GRAPPA Based Spectroscopic Imaging of Gliomas at 3 Tesla

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Introduction: 3D MR spectroscopic imaging (3D MRSI) is a powerful tool for diagnosis of brain tumors but long acquisition times in the order of 20-30 minutes causes patient discomfort and motion artifacts. In recent years, several pulse sequence developments proposing different trajectories in *k*-space such as elliptical sampling (sampling the central elliptical portion of *k*-space) or echo-planar imaging have been proposed in the literature to reduce the scan time. Alternatively, sensitivity encoding (SENSE) method of partially parallel imaging (PPI) has been employed to accelerate the acquisition in MRSI [1,2]. The generalized autocalibrating partially parallel acquisition (GRAPPA) method of PPI was recently applied to 3D MRSI for imaging brain phantoms and healthy volunteers at 1.5 Tesla (T) and 3 T [3,4]. In this work, we have implemented a GRAPPA based technique for cartesian as well as elliptically sampled 3D MRSI spectral data, and have applied it to imaging glioma patients at 3 T.

Methods: Variable density sampling was incorporated in the traditional PRESS sequence for acquiring autocalibrating (AC) lines. MR exams were conducted on a 3 T clinical MR scanner (GE Healthcare, Milwaukee, WI) equipped with an eight channel RF coil (MRI Devices Inc, Gainesville, FL). The imaging protocol included axial T1 weighted SPGR, axial T2 weighted FLAIR, and proton-density weighted coil sensitivity images. Tumor regions, defined as hyperintense regions on FLAIR images were segmented by an in house region growing algorithm. Spectroscopic imaging was conducted with PRESS volume localization in conjunction with CHESS water and VSS outer volume suppression (TR/TE=1.1s/144 ms). 3D cartesian GRAPPA spectroscopic data with two fold acceleration and 2 AC lines in each of the first two phase-encoding (PE) direction of a 12x12x8 spectral array (time:10:06 min) was acquired from 2 volunteers and 3 patients. Full 12x12x8 spectral datasets (time:21:12 min) were acquired from volunteers and elliptical 12x12x8 spectral datasets (time:9:28 min) were acquired from patients because of time constraints, for comparison with GRAPPA datasets. 3D elliptical GRAPPA spectroscopic data was acquired from 3 volunteers and 6 glioma patients with 2x2 acceleration and 2 AC lines of a 16x16x8 spectral array (time:9:25 min). For comparison, original elliptical 16x16x8 spectral array (time: 17:32 min) was acquired from the volunteers and elliptical 12x12x8 spectral array (time:9:28 min) was acquired from patients. The sampling pattern for the cartesian and elliptical GRAPPA acquisitions is shown in Fig. 1. The unaccelerated spectral data from individual coil elements were processed and combined by coil sensitivity weighting on a Linux cluster using software developed in our laboratory [5]. The undersampled datasets were reconstructed by two successive 1 D reconstructions using a multi-column GRAPPA based algorithm implemented in our lab in MATLAB 7.0. In case of the elliptical undersampled datasets, the data was first extrapolating the data to an undersampled 16x16 cartesian grid followed by GRAPPA reconstruction and multiplication with a 3D elliptical sampling mask. GRAPPA reconstructed datasets were subsequently processed identical to the full datasets on the Linux cluster. Spectral parameters were quantified using in house software [5]. The signal to noise ratio (SNR) of Cho, Cr, NAA, were estimated by normalizing their heights with the standard deviation of the spectral noise calculated from the left end of the spectrum. Spearman rank correlation coefficients (r) were computed to assess the similarity in trend of Cho/NAA ratio between the full and GRAPPA spectra for normal and tumor regions. A Mann-Whitney rank sum test was utilized to assess if the tumor regions had significantly different Cho/NAA values than normal regions for full or GRAPPA spectra for the patients.

Table 1 . Median Cho/NAA values for full and GRAPPA methods with their correlation coefficient (r) and p–value (p), and the number of lipid contaminated voxels for the whole PRESS box. (C: Cartesian **CG:** Cartesian GRAPPA **E:** Elliptical **EG:** Elliptical GRAPPA Volt: Volunteer Pat: patient)

	Volt1	Volt2	Pat1	Pat2			Volt1	Volt2	Volt3	Pat1	Pat2	Pat3	Pat4	Pat5	Pat6
C med(Cho/NAA)	0.46	0.49	0.51	0.64		**E**	0.46	0.53	0.45	0.87	0.55	0.79	0.8	0.68	0.68
CG med(Cho/NAA)	0.49	0.52	0.52	0.63		**EG**	0.47	0.55	0.45	0.88	0.54	0.81	0.78	0.68	0.68
r	***0.69***	***0.78***	***0.69***	***0.43***		***r***	***0.78***	***0.77***	***0.71***	***0.64***	***0.34***	***0.58***	***0.27***	***0.43***	***0.58***
C/CG # Lipid voxels (Lipid>NAA)	0/0	0/5	2/4	0/36		**E/EG**	0/0	0/0	0/0	1/11	1/5	13/1	24/38	1/1	26/42

Figure 1: k-space sampling pattern for the cartesian and elliptical GRAPPA

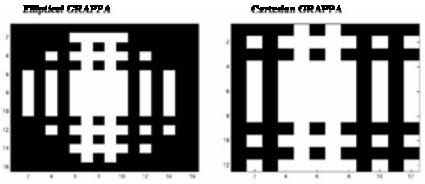
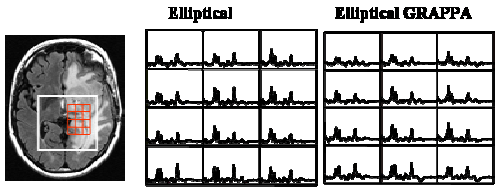


Figure 2: Elliptical and Elliptical GRAPPA spectra comparison from the red grid for a patient



Results: Although a total undersampling factor of 4 (Rx=2, Ry=2) was employed, scan time reduction was 2.12 folds with cartesian GRAPPA compared to full cartesian acquisition, and 1.87 folds with elliptical GRAPPA compared to full elliptical acquisition due to the acquisition of AC lines. Median signal-to-noise ratio (SNR) decrease in GRAPPA datasets was 1.91±0.9 for the cartesian case and 1.27±0.9 in the elliptical case. The SNR efficiency was calculated by normalizing SNR by square root of the scan time. The SNR efficiency decrease was 1.3 folds for cartesian and 0.93 folds for elliptical sampling between full and GRAPPA datasets- so, there was actually a slight increase in SNR efficiency for the elliptical case. Metabolic parameters had good agreement between full and GRAPPA datasets. Median Cho/NAA ratios of full and GRAPPA spectra and their correlation coefficients and the number of lipid contaminated voxels in each case for all the subjects are shown in Table 1. Cho/NAA ratios were significantly ($p<0.001$) correlated for all the subjects between parallel and unaccelerated method for both sampling cases. There was an increase in lipid contamination in the GRAPPA method compared to the conventional method. The Cho/NAA ratio was not significantly different ($p>0.05$) between the tumor and normal regions for both methods in the first patient while only the full method was able to detect a significantly ($p<0.05$) higher Cho/NAA ratio in the tumor region for the second patient in the cartesian sampling case. For the elliptical case, tumor region was distinguished from the normal region by both methods in 2 patients ($p<0.05$) and undetected by both methods in 1 patient ($p>0.05$). Figure2 shows a representative glioblastoma multiforme case, where the abnormal characteristics can be observed in the tumor region from both elliptical and elliptical GRAPPA spectra.

Discussion: In this work, we developed a GRAPPA based autocalibrating technique for 3D MRSI that can be used with cartesian as well as elliptical sampling of kspace. Elliptical GRAPPA based MRSI allowed for larger spatial coverage compared to regular elliptical 12x12x8 acquisition within the same time. The GRAPPA datasets correlated well with their unaccelerated counterparts and had the ability to detect tumor regions in patients. However, GRAPPA datasets had increased lipid contamination and less defined cavity regions.

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