GRAPPA accelerated CSI and its impacts for metabolites quantifications

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Target Audience: MRI scientists and clinicians who are interesting in applying CSI for various brain diseases

Purpose: Multi-receiving arrays and parallel imaging (GRAPPA and SENSE) has been a vital part for various MRI imaging methods. However, there are only a few studies that applied the GRAPPA to accelerate CSI data acquisitions [1]. There are also a few publications of using parallel imaging for fast CSI imaging (e.g. echo planar or spiral) [2, 3]. In this abstract we investigated the possibility of applying GRAPPA method and its effects of CSI quantifications.

Methods: Fully sampled CSI data was acquired on four volunteers was acquired on a 3-T whole-body MRI scanner (TimTrio, Siemens) with a 12 channel head coil. The method described in reference [4] was implemented and CSI data were acquired with the following parameters, TR = 2s, TE = 50ms, FOV = 200 mm, matrix size 24×24, and slice thickness = 10mm. The lipid suppression was achieved by a non-slice selective inversion pulse (inversion time, 220ms). To investigate the potentials of using GRAPPA to accelerated CSI data acquisition, we simulated the 2×2 accelerations by undersampling the outer k-space data (as in Fig.1) while keeping the k-space center (8×8 or 12x12 blocks) fully sampled. These two simulated cases correspond to an effective acceleration factor of 3.0 and 2.3, respectively. The study was approved by the institutional review board (IRB), and written informed consent was obtained prior to the examination. The GRAPPA kernel is 3×3. Each missing data point in Fig.1 was filled with its own GRAPPA weights using the acquired data. The weights were derived from the fully sampled k-space center data. The filling process for the missing data is then slides through all the k-space and a weighted average (weights are inversely proportional of the standard deviation of training data versus the predicted data) was used for a given k-space location that needs to be filled. In this way, the edges of k-space were properly handled.

Results and Discussion: Fig.2 shows the typical NAA, Cr, and Cho metabolites maps obtained for the four subjects when the fully sampled k-space center block is 12×12 (with effective acceleration factor = 2.3). The third column shows the absolute difference between fully sampled data and accelerated data acquisition, which are scaled by a factor of 10. Fig.3 shows all the NAA maps for the rest subjects. The metabolite maps shown that the accelerated metabolites map matches well with the fully sampled data. Fig.4 shown the correlations between the NAA concentration (arbitrary units) determined from the accelerated data acquisition versus these obtained from the fully sampled data for all four sujects. When the effective acceleration is 2.3, the data correlation for NAA is excellent with R^2 = 0.96. For the Cr and Cho, the R^2s are 0.92 and 0.93, respectively. On the other hand, the R^2 for NAA decreased significantly to 0.64 when the effective acceleration increased to 3.0. Thus, our data indicates that, at 3T with current implementations and a 12 channel Rx coil, a modest acceleration of 2.3 is achievable without really impact the metabolite quantifications. On the other hand, the data acquired on another 5 subjects on our 7T scanner (data not shown here) have much better SNR and an acceleration of 3.0 seems to be still adequate.

Conclusion: We demonstrated that GRAPPA can be potentially applied to CSI data acquisition to shorten the total scan times. Further data process and investigations are needed.

Fig. 1 GRAPPA kernel

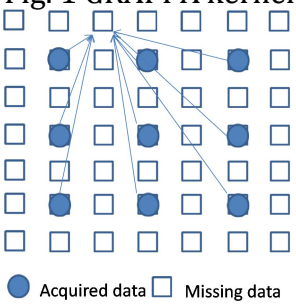


Fig. 2 NAA, Cr, Cho maps for one of subjects

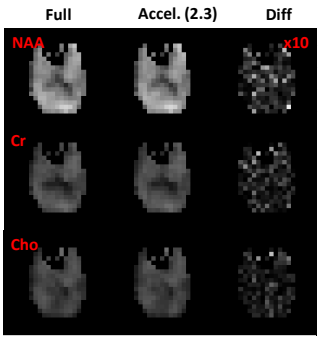


Fig. 3 NAA maps for the rest of subjects

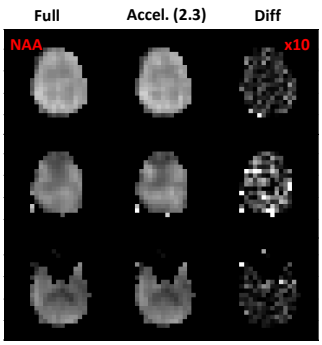
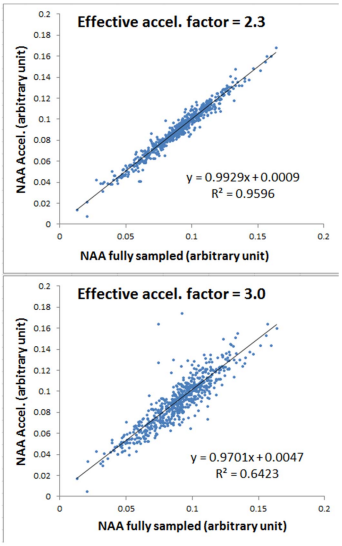


Fig. 4 Correlations between fully sampled data and accelerated data



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