Iterative IIR GRAPPA: A Novel Improved Method for Parallel MRI

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INTRODUCTION GRAPPA [1] is one of the most popular image reconstruction methods for Parallel MRI. This method interpolates downsampled k-space data with moving average (MA) kernel estimated using a set of fully acquired Auto-Calibrating Signal (ACS) lines in k-space; consequently, its reconstruction quality depends greatly on the estimation and generality of the kernel. Improving kernel estimation and generality in GRAPPA has therefore attracted much research attention recently. An iterative approach called iGARPPA has been proposed in [2] to refine MA kernel estimation and an IIR kernel approach called IIR GARPPA has been introduced in [3] to enhance kernel generality. As we pointed out in [3], while these novel approaches both reuse interpolated data to improve conventional GRAPPA, the IIR kernel approach only reuses these data in auto-regression and has the potential for further improvement if the IIR kernel is refined with the iterative approach. Based on this observation, we propose an Iterative IIR GRAPPA (IIR iGRAPPA) method that uses the iterative approach to refine IIR kernel estimation and hence achieves an image quality superior to that of GRAPPA, iGRAPPA and IIR GRAPPA.

METHOD As shown in Fig. 1 and Equation (1), IIR iGRAPPA uses a 2D auto-regressive (AR) moving average model for iterative kernel estimation and data reconstruction, equivalent to an IIR filtering of downsampled k-space data. The AR part uses neighbouring reconstructed

$$s_i(Mk_y - m, k_x) = -\sum_{l=1}^{L}\sum_{q=-Q_b}^{Q_a}\sum_{r=-R_b}^{R_a} a(l,m,i,q,r)s_l(Mk_y - m - q, k_x - r) + \sum_{l=1}^{L}\sum_{b=-N_b}^{N_a}\sum_{h=-H_b}^{H_a} b(l,m,i,b,h)s_l(M(k_y - b), k_x - h) \quad (1)$$

data points in the phase-encoding and readout directions, while the MA part uses acquired exact data points. The method iteratively performs two stages — model estimation and data reconstruction. In the first stage, an IIR kernel of a fixed order is estimated, and in the second stage, the estimated kernel is used as in [3] to reconstruct the missing data points.

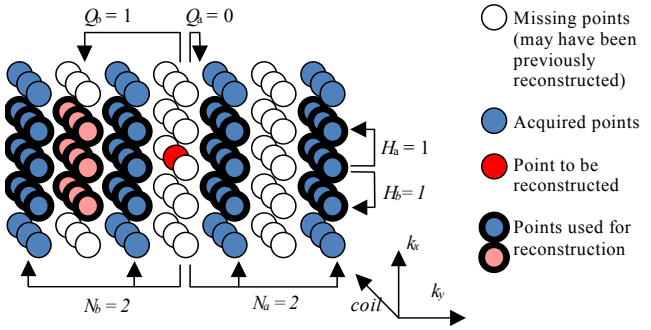
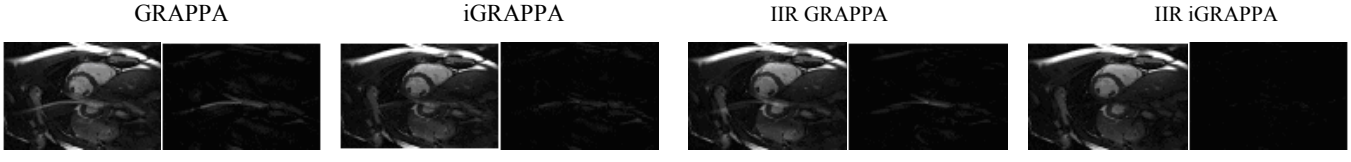


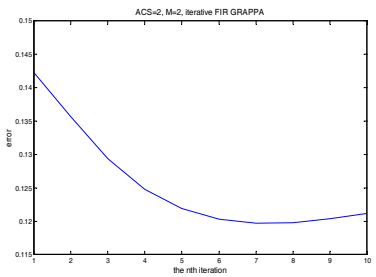
Fig. 1: 2D IIR iGRAPPA interpolation kernel used in results section

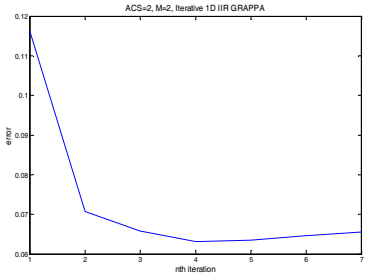
During the first iteration, only actual ACS points are used for kernel estimation. Subsequent iterations expand the ACS dataset to include all the acquired data points and the data points reconstructed at the second stage of previous iteration, and then produce the IIR kernel by fitting to the acquired data points (only) in the expanded ACS dataset. The IIR kernel thus produced is used to recalculate all missing data points and update their previously reconstructed values. In the first iteration, reconstructed data may be unavailable when required by the IIR kernel, and arbitrary initial values such as zeros are used instead. In subsequent iterations, actual reconstructed values are used. Iterations terminate when the intensities of reconstructed images converge. For comparability, IIR iGRAPPA with IIR kernel (N_b, N_a, Q_b, Q_a; R_b, R_a, H_b, H_a) = (2,2,2,0;0,0,0,0) are tested and compared with iGRAPPA and GRAPPA with MA kernel (N_b, N_a, Q_b, Q_a; R_b, R_a, H_b, H_a) = (2,2,0,0;0,0,0,0) in this work.

The cardiac dataset used in tests is acquired of a healthy male volunteer using a Siemens 1.5T Avanto scanner with an eight-element surface array (Nova Medical, Wilmington, MA). A segmented prospective ECG triggered true-FISP sequence was used to capture 35 cardiac phases with readout flip angle = 50°, FOV = 380mm × 285mm, slice thickness = 6mm, image matrix size = 384 × 108 (readout × phase-encoding), spatial resolution = 2mm × 2.6mm, echo time (TE) = 1.34ms, repetition time (TR) = 2.69ms. To test pMRI reconstruction methods, the fully-sampled dataset is downsampled to a factor of 2 in the phase-encoding direction with extra 2 ACS lines in the center and then used to reconstruct GRAPPA, iGRAPPA, IIR GRAPPA and IIR iGRAPPA images. These images are subtracted from reference image reconstructed from fully-sampled dataset to form the difference images. The (percentage) 2-norm ratio between the difference and reference images is used to evaluate the reconstruction error of these images.

RESULTS Given below are GRAPPA, iGRAPPA, IIR GRAPPA and IIR iGRAPPA images (left), corresponding difference images (right) and reconstruction errors. The two curves below compare the reconstruction errors of iGRAPPA (left) and IIR iGRAPPA (right) in relation to the number of iterations. These results clearly demonstrate the performance of each method and show that IIR iGRAPPA attains the minimum reconstruction error which is about 10% lower than that of conventional GRAPPA. Moreover, IIR iGRAPPA consistently outperforms iGRAPPA at every iteration, with the minimum reconstruction error about half of that of iGRAPPA.







CONCLUSION Incorporating iteratively refined kernel estimation of [2] into IIR GRAPPA of [3], a novel IIR iGRAPPA method has been developed for parallel MRI. Preliminary test results have demonstrated that this method outperforms the GRAPPA [1], iGRAPPA [2] and IIR GRAPPA [3] methods and significantly improves the quality of reconstructed image.

References [1] M. A. Griswold et al, *Mag. Res. Med.* 2002, 47:1201-1210. [2] T. Zhao and X. Hu, *Mag. Res. Med.* 2008, 59:903-907. [3] Zhaolin Chen et al, "IIR GRAPPA for parallel MR image reconstruction", *Mag. Res. Med.*, Published Online: Oct 26 2009