Simplified Iterative GRAPPA for fast and robust parallel MRI with arbitrary trajectories

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Introduction: General formulations for parallel MRI using arbitrary k-space trajectories are mainly based on iterative algorithms, such as CG-SENSE [1]. In addition, an iterative GRAPPA approach for arbitrary k-space sampling has been presented [2]. However, the reconstruction process includes several steps, including gridding, GRAPPA convolution and re-sampling operations during each iteration. Here, we present a simplified iterative GRAPPA algorithm that does not require gridding and resampling during each iteration allowing a computationally efficient reconstruction.

Theory and Methods: The proposed algorithm is illustrated in Fig. 1. In a first step, the measured data are gridded onto a Cartesian coordinate system using GRAPPA-operator gridding (GROG) [3,4]. The gridded data points are then filled into the reconstruction matrix and a Cartesian GRAPPA convolution kernel is applied to the reconstruction matrix. To check convergence, the measured data after GROG are compared with the corresponding GRAPPA reconstructed data. If there is no convergence, the reconstruction matrix is updated with the measured data after GROG and the Cartesian GRAPPA convolution kernel is applied for a second time. This process is repeated until the iteration process is converged. The iteration loop is entirely accomplished in

Figure 1: Reconstruction Scheme.

Cartesian space and does not require any gridding or re-sampling. The Cartesian GRAPPA convolution kernel used here is equivalent to the kernel described in Ref. [2]. Computer simulations using random sampling (acceleration factor R=3) and in-vivo dynamic cardiac MRI experiments using a FLASH sequence with radial projections [5] (64 projections, 192 read-out points) were performed. Additionally, accelerated (R=3) abdominal PROPELLER experiments were performed. All in-vivo data were acquired on healthy volunteers on a 1,5 T clinical scanner using 16 channels of a 32-channel coil array.

Results: Results are shown in Fig 2 (computer simulation) and Fig 3 (in-vivo experiments) demonstrating the significant reduction of blurring and aliasing artifacts after a few numbers of iterations. Please note that the initial image after GROG is blurred as compared with standard convolution gridding. This can be explained by the GROG gridding procedure, in which data points are directly shifted to the nearest Cartesian locations instead of being convolved with a dedicated kernel; the signal at all other Cartesian locations are set to zero.

Discussion: The key element of the proposed algorithm is the GROG step prior to the iteration loop which removes the need for gridding and re-sampling during each iteration. Only GRAPPA convolution, convergence check and matrix update are performed during each iteration. In addition, no density compensation function (DCF) has to be computed and therefore, this approach is feasible for reconstruction of a wide range of trajectories, including radial, spiral, rosette, PROPELLER and random. In principle, the algorithm could also be applied to Cartesian parallel MRI which would be similar to the method described in Ref. [6]. In summary, the simplified iterative GRAPPA algorithm represents a robust and computationally efficient solution for parallel MRI with arbitrary trajectories.
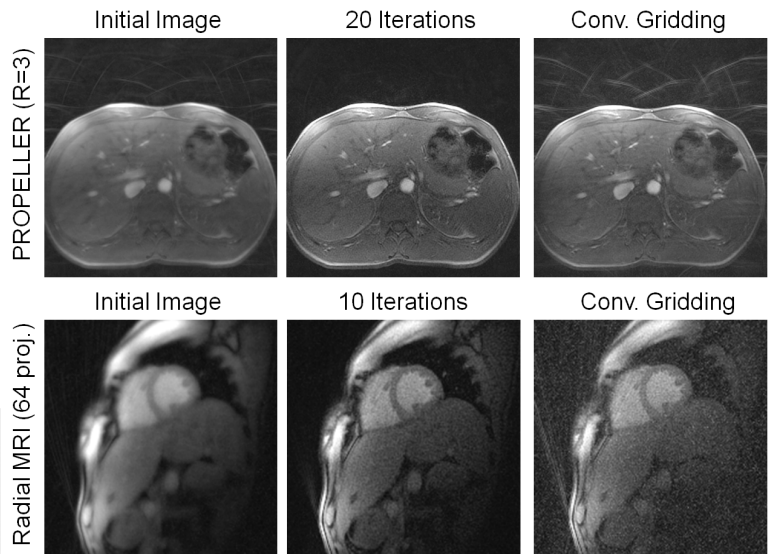
References: [1] Pruessmann KP, et al. *MRM* 2001;46(4):638. [2] Lustig M, Pauly JM. *Proc ISMRM 2007* (Berlin). [3] Seiberlich N, et al. *MRM* 2007;58(6):1257. [4] Seiberlich N, et al. *MRM* 2008;59(4):930. [5] Winkelmann S, et al. *IEEE Trans Med Imaging* 2007;26(1):68. [6] Thao T, Hu X. *MRM* 2008;59(4):903.
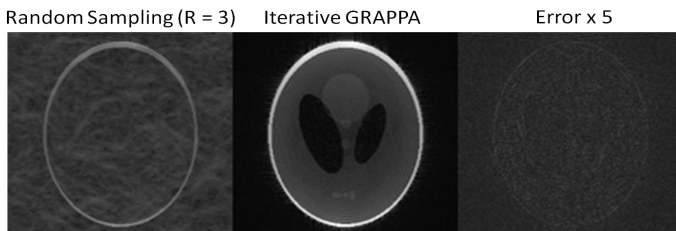
Figure 2: Simulation results using random undersampling (acceleration factor R = 3, matrix 128 x 128, 12 channels)
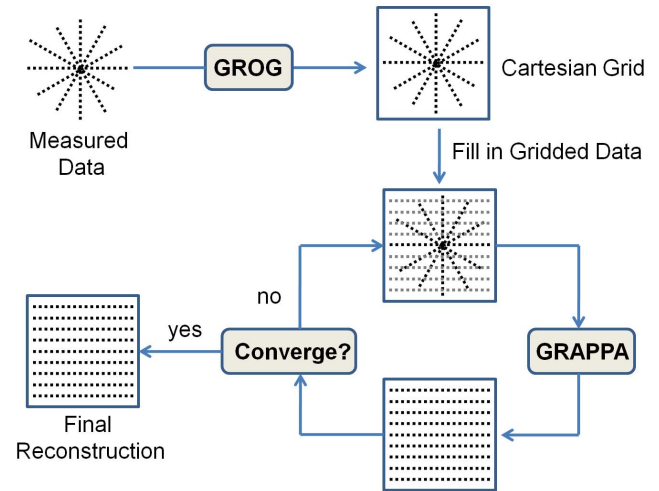
Figure 3: In-vivo results from accelerated PROPELLER and radial MRI experiments. Illustrated are the initial images after GROG (left column) and images after several GRAPPA iterations. For comparison, images from the corresponding undersampled data sets after convolution-gridding are shown (right column).