On Optimality of Parallel MRI in k-Space

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Introduction: *k*-Space-based parallel MRI (pMRI) methods such as GRAPPA [1] and PARS [2] provide a number of advantages including fast reconstruction, convenient self-calibration, tolerance to calibration data errors [3], and efficient non-Cartesian data processing [4]. Surprisingly, most benefits come from their assumption that only a few samples from a local *k*-space subset contribute to the synthesis of a given datum. The reconstruction accuracy of such techniques strongly depends on the *k*-space subset selection. Increasing the size of the subset from a single sample (SMASH, [5]) to a few samples distributed in the phase encoding direction [1], and further enlarging it to a 2D configurations [2,6,7] led to gradual improvement of image quality for a wide variety of phased array coils. At the same time, enlarging the *k*-space subset impedes the described benefits of GRAPPA/PARS.

In general, there is a poor understanding how to automatically control the error in the methods without resorting to larger *k*-space subsets. Obviously, the optimal *k*-space subset depends on coil sensitivities, the placement of coils, and on the object itself for self-calibration. We present theoretical analysis of the problem and fast and efficient method for designing optimal *k*-space based parallel MRI reconstruction.

Theory: Multicoil acquisition may be seen as multichannel convolution in *k*-space: $\mathbf{Cf}=\mathbf{s}$, $[\mathbf{C}]_{(m,\gamma),n}=c_\gamma(\mathbf{k}_m-\mathbf{k}_n)$. Here, $c_\gamma(\mathbf{k})$ is γ^{th} coil sensitivity of n_c, $\mathbf{f}$ is vector of target *k*-space values indexed by *n*, $\mathbf{s}$ is the all coil data vector, each acquired *k*-space sample is indexed by *m*. To find $\mathbf{f}$, the pseudoinverse of $\mathbf{C}$, $\mathbf{P}$, is calculated and applied to $\mathbf{s}$. It may be shown that *k*-space pMRI methods approximate $\mathbf{P}$ with a sparse matrix. For more accurate approximation, the sparse pseudoinverse $\mathbf{P}_\gamma$ may be calculated for each coil γ [8]. The approximation error is given by Frobenius matrix norm $\rho_\gamma=\left\|\mathbf{C}_\gamma-\mathbf{P}_\gamma\mathbf{C}\right\|_F$, where $\mathbf{C}_\gamma$ is the γ^{th} coil convolution matrix. It may be shown that ρ_γ is related to power of residual aliasing in image space. Hence, the optimal $\mathbf{P}_\gamma$ should minimize ρ_γ. Minimization of ρ_γ may be done via separate minimization of $\rho_\gamma^{(n)}=\left\|\mathbf{c}_\gamma^{(n)}-\mathbf{p}_\gamma^{(n)}\mathbf{C}\right\|_2$. Here, $\mathbf{p}_\gamma^{(n)},\mathbf{c}_\gamma^{(n)}$ are the n^{th} rows of $\mathbf{P}_\gamma$ and $\mathbf{C}_\gamma$.

We propose to find the optimal distributions of non-zero elements in the rows of $\mathbf{p}_\gamma^{(n)}$ or, equivalently, the *k*-space subsets for reconstruction of the n^{th} sample, as the ones that minimize $\rho_\gamma^{(n)}$. Finding the exact sparse solution is of exponential complexity, and is intractable even for small problems. Instead, we propose a method inspired by earlier work on efficient construction of sparse approximate matrix preconditioners [9]. The idea is that on each step of the algorithm a set of nonzero entries in $\mathbf{p}_\gamma^{(n)}$ (or, equally, the *k*-space subset) is enhanced with a point that ensures the largest decrease in $\rho_\gamma^{(n)}$. The samples are chosen from a *k*-space area of limited size using an efficient recursive algorithm. The details of the algorithm are not presented due to space limitations.

Methods: The BrainWeb digital phantom (http://www.bic.mni.mcgill.ca/brainweb/) was multiplied by coil sensitivities ($n_c=4$) calculated using a B1 simulator (http://www.nmr.mgh.harvard.edu/~fhlin/tool_b1.htm). Phantom data were collected on GE XMR 1.5 T system (GE Healthcare, Milwaukee, WI) using 3 elements of a spine array (image size 192x256). In either case, thirty two (32) central lines were used for calibration. Images were reconstructed from data uniformly undersampled with reduction factor *R*=2. Truncated SVD (threshold=1e-4 of the maximum singular value) was used for matrix inversion. 2D GRAPPA reconstruction of actual data employed samples from within a *k*-space radius of 2.5 samples. The optimized subset of the same size was calculated in ~25 s (MATLAB, standard PC).

Results: Plots in Fig. 1a show that approximation error ρ_γ and measured image space RMS error correlate well supporting our idea that ρ_γ is a valid metric for optimization. The new method provides much less error compared to 2D GRAPPA. Both adaptive and 2D GRAPPA *k*-space subsets are shown in Fig. 1b (reconstruction of 1st coil data). The coil channels contribute unevenly to the optimal reconstruction, or even don't contribute at all (coil 3). The effect of optimal reconstruction on image quality may be appreciated in Fig. 2. Residual aliasing and noise are much more visible in 2D GRAPPA than in the image from the proposed algorithm.

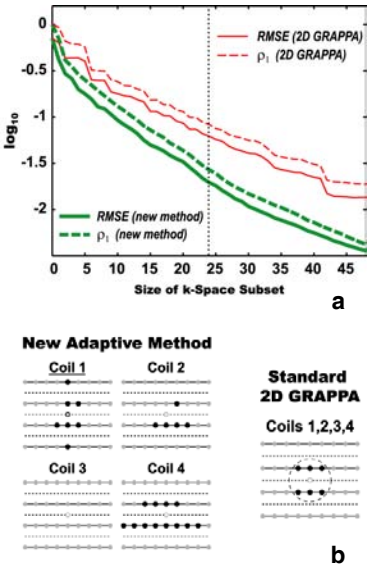

Figure 1. Comparison of new and 2D GRAPPA methods in simulated studies. **a:** Approximation error (ρ_1) and image RMS error (RMSE) vs. *k*-space subset size; **b:** *k*-Space subsets of 24 samples (a dotted line on ***a***). Coils contribute unevenly to the optimal reconstruction.

Discussion: Our studies demonstrated that errors due to the approximate nature of *k*-space pMRI may be reduced by adjusting the *k*-space subset automatically with the proposed method. Besides minimized aliasing, the new method consistently provided less noise gain than non-adaptive method. The improved conditioning may be due to the fact that the method chooses the *k*-space samples giving the most independent information from sensitivity encoding. The method proposed in [6] also seeks to compute adaptive subsets, but minimizes the condition number instead. We found that the approach may result in residual aliasing, which is minimized in our method.

We found that the method gives the most improvement for non-symmetric arrays such as spine array. The results may imply that *k*-space pMRI techniques such as GRAPPA and PARS must be tuned as proposed here for each type of phased array coil. GRAPPA/PARS with small optimized *k*-space subsets may be of particular benefit for faster pMRI required in interventional/real time imaging and non-Cartesian and 3D applications.

The theory and methods developed here are directly applicable for optimization of other *k*-space MRI data reconstruction techniques such as regridding method BURS [10] and dynamic imaging technique ktGRAPPA [7,11].

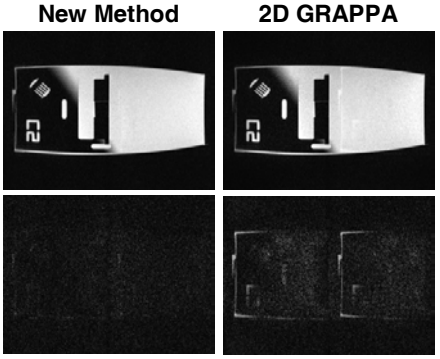

Figure 2. Reconstruction of actual phantom data. Images and errors (5x) are shown in top and bottom rows, respectively. New method reduced residual aliasing and noise gain.

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