

# RLS-GRAPPA: RECONSTRUCTING PARALLEL MRI DATA WITH ADAPTIVE FILTERS

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## ABSTRACT

GRAPPA is one of the predominant methods used to reconstruct accelerated parallel MRI data. It has been shown previously that spatially varying the GRAPPA reconstruction coefficients can be advantageous. A significant problem with these approaches, however, is an increase in computation time due to an increase in the number of linear system solves needed. Here, we leverage the fact that these systems vary slowly over the coordinate space and employ recursive adaptive filters in place of explicit system solves. This approach produces high quality spatially variant GRAPPA reconstructions with a computation time comparable to standard GRAPPA.

**Index Terms**—Magnetic resonance imaging, Parallel MRI, GRAPPA, RLS

## 1. INTRODUCTION

Parallel MR imaging (pMRI) employs multiple receiver coils to acquire data. These coils contribute an inherent spatial domain encoding that complements traditional Fourier encoding. This enables one to subsample during image acquisition, allowing one to reduce image acquisition time, improve spatial and/or temporal resolution, or some combination of both. A good review of pMRI can be found in [1].

GRAPPA [2] is one of the most widely used parallel MR reconstruction algorithms in clinical use today. The technique is based on finding correlations in the acquired data, which originate from the multi-coil view of the imaged plane. GRAPPA is often referred to as an auto-calibrated k-space technique, as the reconstruction parameters can be derived directly from the acquired data in certain scenarios, and the processing typically takes place completely in the Fourier domain—in contrast to SENSE [3] and similar methods, which require explicit estimates of the acquisition coil sensitivities. Because explicit coil sensitivity estimates are not required in GRAPPA, the technique remains robust in many situations where SENSE can fail, e.g. [4].

To improve the performance of GRAPPA, many extensions have been proposed including processing in the image- and/or hybrid- (both k- and x- space) domains to reduce computation time [5] and the use of coordinate dependent reconstruction parameters to improve image quality [6, 7, 8]. It was shown in [9] that an alternative to using a 2D k-space ( $k_x, k_y$ ) reconstruction kernel is to use instead a 1D kernel in hybrid-space, ( $x, k_y$ ). It was further shown in [5] that employing the reconstruction parameters in the hybrid-space is more efficient computationally.

Similarly, it was shown in [6] and [7] that varying the reconstruction parameters across the coordinate space produces higher quality reconstructions. For example, in KIPA [6] one employs a set of reference data fully sampled at the Nyquist rate to calculate reconstruction coefficients for a number of different locations in k-space. These coefficients are then used in subsequent accelerated acquisitions. The authors claim high acceleration rates, although the method is currently limited to scenarios where the reference data closely matches the accelerated data.

Varying the reconstruction parameters substantially increases the computational load, however, as the number of system solves needed to identify those parameters necessarily increases. Previous approaches to mitigate this included computing the reconstruction coefficients at only a few locations and then interpolating between them, as in SV-GRAPPA [7]. However, the linear system associated with finding these coefficients changes in a structured way, from point-to-point along data coordinate space. Specifically, points at the trailing edge of the contribution window are removed, while points at the leading edge are added. All points in between remain.

This scenario mirrors the data flow that drove development of adaptive filtering algorithms. We demonstrate below that through the use of adaptive filters, one can dramatically reduce the computational load in SV-GRAPPA, while simultaneously capitalizing on efficiencies provided by hybrid-domain calculations. Furthermore, the approach may provide a mechanism to achieve a self-referenced version of KIPA.

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## 2. THEORY

The acquired data in each coil  $W_l$  of an accelerated pMRI acquisition can be modeled as  $s_l(\mathbf{k}) = \int W_l(\mathbf{r})\rho(\mathbf{r}) \exp\{j\pi(\mathbf{k} \cdot \mathbf{r})\}d\mathbf{r}$  where  $\rho(\mathbf{r})$  is the spatial distribution of excited spins as seen by coil  $W_l(\mathbf{r})$ , the product of which is Fourier encoded and then sampled. Here, we consider the case of sampling  $s(\mathbf{k})$  on a rectilinear grid, sampling at the Nyquist rate along the frequency encode direction,  $k_x$ , while sampling below the Nyquist rate—i.e. *subsampling*—along the phase encode direction,  $k_y$ .

### 2.1. GRAPPA and related variations

In GRAPPA, one seeks to reconstruct missing data points in  $s_l(k_x, k_y)$  through a linear combination of measured neighboring data points. Specifically, the reconstruction is performed as

$$s_l(k_x, k_y + m\Delta k_y) = \sum_{j=1}^L \sum_{b,c} g_l(j, m, b, c) s_j(k_x + c, k_y + bf) \quad (1)$$

where  $g_l$  refers to the reconstruction coefficients for coil  $l$ , which combine data from all coils,  $j \in [1, L]$ , using multiple points along  $k_y$ ,  $b \in [0, M]$ , and  $k_x$ ,  $c \in [0, N]$ . The size of the reconstruction kernel,  $M$ -by- $N$ , is set by the number of points used. That is, a 2x3 kernel employs two  $k_y$  points and three  $k_x$  points from data in *each* coil,  $s_j$ , to reconstruct one data point in  $s_l$ .  $f$  refers to the distance along  $k_y$  between acquired data points, and  $m$  refers to the offset between the kernel and the reconstructed point. For example, to use a 2x3 kernel to reconstruct 3x accelerated data,  $m$  would be limited to  $m \in \{1, 2\}$ , one value for each missing line within the reconstruction kernel span.

The reconstruction coefficients are identified by constructing a linear system relating known source measurements to known targets. In self-referenced reconstructions, these are obtained from a set of auto-calibration signals (ACS) sampled at the Nyquist rate. For each target point in the ACS region, one row of the linear system is written as

$$s_l^{ACS}(k_x, k_y + m\Delta k_y) = \sum_{j=1}^L \sum_{b,c} s_j(k_x + c, k_y + bf) g_l(j, m, b, c). \quad (2)$$

Given a sufficient number of rows, one can solve the linear system and identify GRAPPA parameters to perform a reconstruction of the data.

One can reformulate this reconstruction approach into either the spatial-domain,  $(x, y)$ , or the hybrid-domain,  $(x, k_y)$ , through appropriate use of the Fourier transform. This converts the 2D k-space convolution kernel into a point-wise multiplication or a 1D convolution kernel, respectively. A mentioned previously, there are computational incentives for these conversions, [5].

### 2.2. Adaptive Filtering

Given the view of GRAPPA as a convolution, we consider here using adaptive algorithms to perform the reconstruction. Many adaptive filtering algorithms exist [10, 11], and we choose to study here the use of a Recursive Least Squares (RLS) filter for its simplicity. RLS aims to minimize the cost function  $J(n) = \sum_{j=0}^n \lambda^{n-j} |y(j) - w(j)^* u(j)|^2$  where  $y(j)$  is the desired filter output,  $u(j)$  is the filter input,  $w(j)$  are the filter coefficients, and  $\lambda$  is a *forgetting factor* used to control the filter adaptation response time, i.e. lower values of  $\lambda$  yield faster adaptation times at the cost of higher filter coefficient variability.

The RLS algorithm is given in Table 1, with  $\mathbf{u}$  a vector of *input data*,  $\mathbf{w}$  a vector of the *filter weights*, and  $\boldsymbol{\kappa}$  is the *filter gain vector* used to vary the filter weights at each step of the algorithm.  $\mathbf{P}$  is an estimate of the inverse of the input auto-correlation matrix,  $\Phi = E\{\mathbf{u}\mathbf{u}^H\}$ . An important feature of the RLS algorithm is that this inversion,  $\mathbf{P}(n) \approx \Phi(n)^{-1}$ , is replaced at each algorithm step by a scalar division [10] (lines 2 and 5), leading to greatly reduced computation costs.

### 2.3. RLS-GRAPPA along $x$

We describe here a simple RLS implementation for Spatially Variant GRAPPA, [7], which operates in the hybrid-domain,  $(x, k_y)$ . Although any kernel size and number of ACS lines can be accommodated, to visualize the implementation of RLS-SV-GRAPPA it is easiest to first consider a 1x1 GRAPPA kernel with 1 ACS line. In this case, the input vector,  $\mathbf{u}$ , contains data from the non-ACS line used in coefficient calibration, and the desired signal,  $d(n)$ , is a point on the ACS line. As the filter proceeds along the frequency encoding dimension,  $x$ , at each step new data points are introduced into the filter and the filter weights are updated. For multiple ACS lines, this process is repeated until all ACS points associated with a given  $x$  location have entered the recursion. Larger kernels operate in a similar fashion, but with multiple rows of data replaced at each  $x$  step. After all of the ACS points at a given point  $x$  have been processed, the missing data along the phase-encode dimension,  $k_y$ , are reconstructed.

### 2.4. RLS-GRAPPA along $k_y$

With adaptive filters, one can also consider RLS processing along the subsampled phase encode dimension. One goal here is to enable KIPA [6] reconstructions from self-referenced data. The approach in [6] employs an unaccelerated frame

#### RLS Algorithm (with forgetting factor $\lambda$ ):

- 1)  $\mathbf{a}(n) = \lambda^{-1} \mathbf{P}(n-1) \mathbf{u}(n)$
- 2)  $\boldsymbol{\kappa}(n) = \mathbf{a}(n) / (1 + \mathbf{u}^H(n) \mathbf{a}(n))$
- 3)  $\eta(n) = d(n) - \mathbf{w}^H(n-1) \mathbf{u}(n)$
- 4)  $\mathbf{w}(n) = \mathbf{w}(n-1) + \boldsymbol{\kappa}(n) \eta^*(n)$
- 5)  $\mathbf{P}(n) = \lambda^{-1} \mathbf{P}(n-1) - \boldsymbol{\kappa}(n) \mathbf{a}^H(n)$

**Table 1.** The RLS algorithm

of k-space to determine the varied reconstruction coefficients, typically provided by a pre-scan image before the accelerated acquisition. This is because accelerated acquisitions employing additional self-referenced ACS data necessarily reduces the achievable acceleration rate. Adaptive filtering offers an attractive mechanism to adapt the reconstruction weights over the k-space data grid where little additional ACS are available.

We have investigated three approaches to meet this goal. In all cases the adaptive filtering proceeds in a manner similar to RLS-SV-GRAPPA described above. The only change is that new data is introduced into the recursion as one moves along  $k_y$  instead of  $x$ . The differences between the methods relate to how often the filters are updated and the filter input sources.

In Method 1, we sought to reconstruct-and-adapt on the data as the reconstruction kernel advanced through k-space. That is, the reconstruction parameters calculated from a previous  $k_y$  location were used to reconstruct missing data in the present location. This reconstructed data was then used to update the recursive filter to produce updated reconstruction parameters.

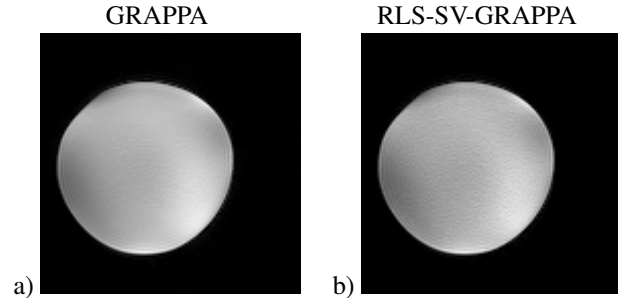
In Method 2, we employed measured phase-encode lines as *both* target and source data. That is, we employed a modified GRAPPA reconstruction kernel to use data in all but one coil. Then, a measured line in the remaining coil was used as the ACS data. It was shown in [12] that GRAPPA kernels are closely related, and one can interpolate between them. So, in the case of a 2x1 SV-GRAPPA kernel, one could potentially use each of the measured lines seen by the kernel to track changes in the signal space, then interpolate between them to identify the reconstruction parameters needed for the missing k-space data. Adaptation is performed only on measured lines.

In Method 3, our approach is to combine the previous two. Specifically, the adaptation is performed on both measured and estimated lines, but the reconstruction kernel employs only data from coils other than the coil being reconstructed. Preliminary results indicate that this approach is able to track signal changes in the underlying data in a manner similar to KIPA, resulting in similar parameter variations across k-space. These parameter variations, however, do not appear to achieve the performance reported in the original KIPA paper.

### 3. RESULTS

#### 3.1. RLS-SV-GRAPPA: adapting along $x$

Fig 1 shows two reconstructions of accelerated partial-Fourier EPI data (3.34x acceleration (38/128 phase-encodes), TR/TE:4sec/94.4msec, thickness:4.5mm) acquired using a standard 8-channel head coil on a 3T Signa/Excite GE Scanner. The non-uniform sampling pattern applied local acceleration factors of 2x, 1x, 2x, 3x, and 4x, in 5 equally sized regions starting at  $-16 \Delta k$  steps below DC and ending at  $63 \Delta k$  at the edge of k-space. This provided 8 or 9 ACS



**Fig. 1.** Reconstructions of variable density subsampled data using (a) GRAPPA and (b) RLS-SV-GRAPPA.

lines for each of the six GRAPPA kernel patterns employed. The GRAPPA image in Fig 1(a) was constructed using a 2x5 kernel, whereas the RLS-SV-GRAPPA image in (b) was constructed using a 2x1 kernel and a forgetting factor  $\lambda = 0.96$ . After pMRI processing was complete, each set of coil data was homodyne filtered to compensate for the partial-Fourier distribution of the data, then a root-sum-of-squares was performed across the coil set to produce the final image.

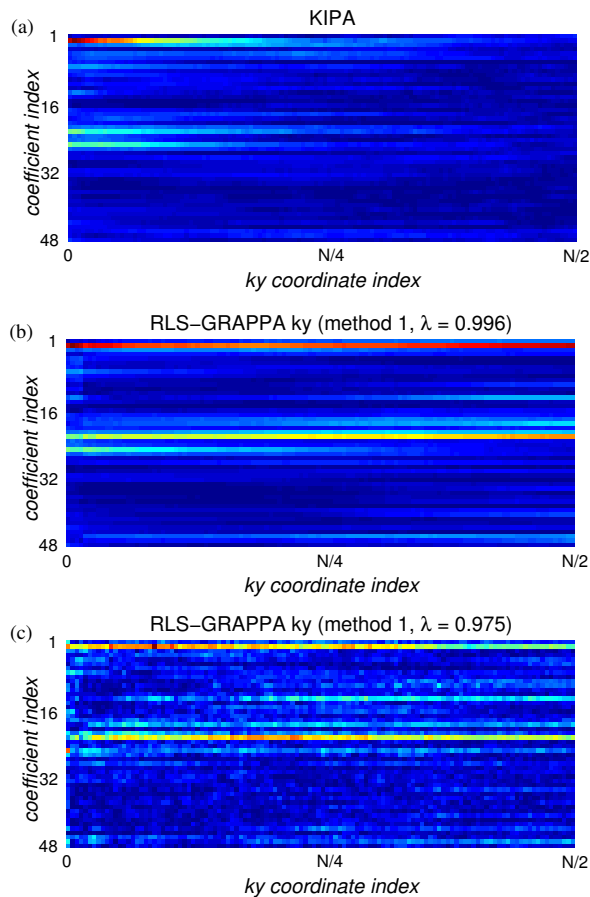
Both images show minimal artifact or noise. The significant difference between the two approaches was that it took 2.66 sec to identify the reconstruction parameters for the 4 local acceleration factors using GRAPPA, but only 1.45 sec in RLS-SV-GRAPPA using Matlab on a modest laptop.

#### 3.2. RLS-GRAPPA along $k_y$

Our investigation into RLS-GRAPPA along  $k_y$  employed unaccelerated data from the ACR phantom acquired on a 1.5T GE Scanner using an FSE sequence (TR/TE:500ms/20ms, thickness:5mm, FOV:25cm, matrix size:256x256). A 3x accelerated acquisition was simulated by sampling every third line of the data, with an additional 16 lines near DC for auto-calibration. This gave 24 lines at the Nyquist rate  $[-11\Delta k..12\Delta k]$  for auto calibration and a net acceleration of 2.53x (101 lines of 256).

Fig 2 shows the parameters determined by KIPA and RLS-GRAPPA Method 1 along the  $k_y$  direction at  $k_x = 0$ . The KIPA derived parameters, Fig 2(a), show a smooth variation as the kernel moves across k-space. In contrast, the RLS-GRAPPA derived parameters *do not* show this same variation, remaining nearly constant. Reducing the forgetting factor, Fig 2(c), provides no benefit, as the reconstruction parameter estimation appears to go unstable and exhibits significant noise. Method 2, which uses tracking on measured lines, exhibits similar results but is not shown here for brevity.

Method 3, which employs tracking and uses estimated data, is the most promising, as shown in Fig 3. Here, the variation in the RLS-GRAPPA estimation of the reconstruction parameters *from the accelerated data* closely mirrors the KIPA parameters calculated *from unaccelerated data*. Somewhat surprisingly, reconstructed images (not shown for brevity) exhibit only marginal improvement over standard GRAPPA.



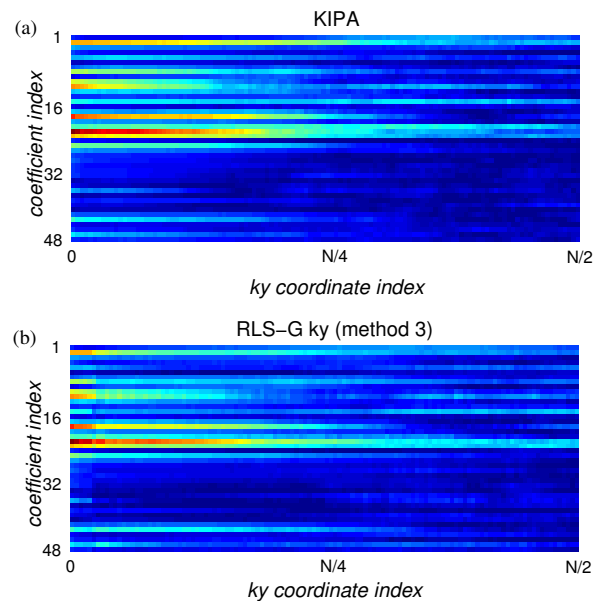
**Fig. 2.** Comparison between KIPA and RLS-GRAPPA along  $k_y$  coefficients for method 1.

#### 4. SUMMARY

This work demonstrates that the use of adaptive filters in GRAPPA reconstructions can provide significant benefit. We demonstrated that the use of RLS with SV-GRAPPA provides a fast method to identify and reconstruct accelerated pMRI data. Secondary benefits include elimination of the need for varied kernel size along  $x$  when computed in a hybrid domain as done in RLS-SV-GRAPPA. RLS along  $k_y$  also shows promise. One could certainly employ RLS on the reference frame in KIPA, to identify the reconstruction parameters for every  $k$ -space location in a reasonable computation time. The ability to leverage adaptive filters for self-referenced KIPA requires further investigation.

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