Modeling non-stationarity of kernel weights for k-space reconstruction in partially parallel imaging

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Purpose: In partially parallel imaging, most k-space-based reconstruction algorithms such as GRAPPA adopt a single finite-size kernel to approximate the true relationship between sampled and nonsampled signals. However, the estimation of this kernel based on k-space signals is imperfect, and the authors are investigating methods dealing with local variation of k-space signals.

Methods: To model nonstationarity of kernel weights, similar to performing a spatially adaptive regularization, the authors fit a set of linear functions using concepts from geographically weighted regression, a methodology used in geophysical analysis. Instead of a reconstruction with a single set of kernel weights, the authors use multiple sets. A missing signal is reconstructed with its kernel weights set determined by k-space clustering. Simulated and acquired MR data with several different image content and acquisition schemes, including MR tagging, were tested. A perceptual difference model (Case-PDM) was used to quantitatively evaluate the quality of over 1000 test images, and to optimize the parameters of our algorithm.

Results: A MOdeling Non-stationarity of Kernel wEightS (“MONKEES”) reconstruction with two sets of kernel weights gave reconstructions with significantly better image quality than the original GRAPPA in all test images. Using more sets produced improved image quality but with diminishing returns. As a rule of thumb, at least two sets of kernel weights, one from low- and the other from high frequency k-space, should be used.

Conclusions: The authors conclude that the MONKEES can significantly and robustly improve the image quality in parallel MR imaging, particularly, cardiac imaging. © 2011 American Association of Physicists in Medicine. [DOI: 10.1118/1.3611075]

Key words: image quality, perceptual difference model, parallel MR imaging, spatial analysis theory, GRAPPA

I. INTRODUCTION

High image quality with short acquisition time is desirable for any fast MR imaging application. Parallel MRI is an important technology to achieve these goals. By deploying multiple receiver coils, parallel MR imaging can achieve several-fold reductions in scan-time. To reconstruct high quality full-FOV images from down-sampled data, a good reconstruction algorithm is needed. Several different reconstruction algorithms have been proposed working either in the spatial domain (image-space) or in the frequency domain (k-space). Among them, some most well-known methods are SMASH (Ref. 1) (k-space), SENSE (Ref. 2) (image-space), and GRAPPA (Ref. 3) (k-space). All these techniques directly or indirectly require the coil sensitivity information, which can be derived

from a one-time prescan, from a few additionally acquired k-space lines for every subsequent parallel MRI experiment (autocalibration), or from a combination of the two.⁴

There have been many proposals to improve estimation process (or so called “autocalibration”) in parallel imaging k-space reconstruction, which is often performed with global linear regression (GLR). This requires the assumption of stationarity in which data characteristics are not taken into account. The reconstruction can usually be formulated as linear equations that need to be inverted.^{5,6} SMASH and GRAPPA need to invert equations formed with k-space data. Very often the inverse problem is overdetermined.⁶ An inadequate solution to the problem may significantly worsen image quality, thus choosing an appropriate technique to

solve the inverse problem is important. One can use the Moore–Penrose pseudoinverse technique to get a partial solution, but small noise perturbations in sampled data can lead to large variations in the solution.^{5,6} There are many regularization techniques to solve the overdetermined problem numerically, and two are frequently used. One is truncated singular value decomposition (T-SVD),⁷ which eliminates some singular values and keeps major information. The other is Tikhonov regularization,⁸ which introduces additional information, such as an assumption on the smoothness or a bound on the norm.⁸ Both techniques have been applied to the parallel imaging reconstruction. Qu *et al.*⁹ applied both T-SVD and Tikhonov regularization techniques to improve GRAPPA reconstruction based on prior information of noise level in the autocalibration signals (ACS). However, in T-SVD, it is difficult to define a criterion for truncation,^{9,10} and the trade-off between SNR and aliasing artifacts is unavoidable in Tikhonov regularization.⁹

Other improvements to GRAPPA have emerged that have focused on the k-space data characteristics instead of complex algorithms to solve the overdetermined problem. Huo *et al.*¹¹ developed an algorithm to remove the regression outliers, which usually correspond to high amplitude variation of signals, in calibration for better estimation of complex kernel weights (we call it kernel weights hereafter). Park *et al.*¹² noticed that GRAPPA coil calibration is performed on signals that exhibit large amplitude variation, while the reconstruction is performed using signals with small amplitude variation. They suspected such huge differences in signal variations may cause high reconstruction residuals. As such, they excluded center ACS lines that very often exhibit large amplitude variation, and found better kernel weights estimation. These two implementations adopt the selective-sample GLR strategy to approximate the stationarity of kernel weights. With an idea similar to selective-sample strategy, Yeh *et al.* used the k-space locality principle to develop a new algorithm PARS (Ref. 13) for efficient implementation of parallel MRI reconstruction. The k-space locality principle assumes that only a few nearby points within a small k-space radius contribute to the determination of the synthesized samples.^{13,14} However, the method uses the same assumption as GRAPPA and a simple k-space radius constraint may not be sufficient for modeling the stationarity of kernel weights. Continued along the same research line, Huang *et al.*¹⁵ processed the ACS data with a high-pass filter (point-wise multiplication with the filter in k-space) at k-space center prior to GLR process. Miao *et al.*¹⁶ proposed a different idea of applying high-pass filter at center k-space. Instead of directly weighting ACS data, regression equations are weighted by a bivariate Gaussian function to solve for better kernel weights. Although the weighted regression strategy is considered more general than the selective-sample GLR strategy, this method is limited by off-center or multiple significant component(s) in k-space. It is noteworthy that the above algorithms^{11,12,15,16} require ACS integration for final reconstruction. In this work, we develop a new algorithm that requires no ACS integration and takes local k-space data characteristics into account making the kernel weights vary accordingly for better reconstruction. The distinction between GLR

and localized linear regression is their local dependency of the independent variables. The latter method assumes an important hypothesis of nonstationarity in the underlying relationship between the independent variables. Resting on the premise that such nonstationarity can be quantified as localized parameters, a general mathematical framework that built on the foundation of spatial analysis,¹⁷ Geographically weighted regression (GWR) (Ref. 18) is introduced for quality reconstruction.

The rest of paper is organized as follows. We begin with the description of theoretical background. Then we describe experiments to optimize the new algorithm and to compare the results with GRAPPA and an existing GRAPPA implementation. We use Case-PDM, a perceptual difference model, which has been validated by psychophysical experiments,¹⁹ as an objective metric to quantify the image quality. A hypothesis test and a multifactorial experiment were conducted to show the nonstationarity of generalized kernel weights and to determine dependent factors of an algorithmic parameter, respectively. Finally, the algorithm's performance is evaluated, and the directions of future research are discussed.

II. THEORY

II.A. GRAPPA algorithm and GLR

In parallel MRI, sinusoidal “spatial harmonics,” of order m can be approximated by linear combinations of measured component coil sensitivities with kernel weights. These linear combinations can be applied to component coil signals to generate signals missing because of omitted gradient steps. This idea was first put proposed by Sodickson *et al.*, for SMASH reconstruction.^{1,20}

The GRAPPA algorithm³ further developed this idea of linearly combining signals from multiple coils but with greater generality. In GRAPPA, additional autocalibration signal (ACS) lines are sampled at Nyquist rate. The ACS lines are then used for kernel weight calibration (and may be included in the final reconstruction). The calibration is a least-square fitting of complex-coefficients weighted ACS signals [this is depicted graphically in Fig. 1(a)]. Mathematically, the fitting is defined as follows:

$$\mathbf{S}_j^{\text{ACS}}(k_x, k_y + m\Delta k_y) = \sum_{a=1}^X \sum_{b=1}^Y \sum_{l=1}^L n_{a,b,l}^{j,m} \mathbf{S}_l^{\text{ACS}} \times (k_x + (a - \lfloor X/2 \rfloor \Delta k_x), k_y + (b - Y/2) \Delta k_y), \quad (1)$$

where, x and y are space variables, k_x and k_y are a k-space variables, Δk_x or $\Delta k_y = 2\pi/\text{FOV}$, m is an integer that may be positive or negative depending on the desired direction of k-space shift. $\mathbf{S}_j^{\text{ACS}}$ is ACS lines from the j th coil ($j \in [1, L]$, L is the number of coils) and $n_{a,b,l}^{j,m}$ is the kernel weight at location (a, b, l) of the coil weight kernel $\mathbf{N}^{j,m} = (n_{a,b,l}^{j,m})_{X \times Y \times L}$ for the j th coil and m th missing line ($X = 2k - 1$, $Y = 2k$, and $k \in \mathbb{Z}^+$ are dimension of the kernel), as illustrated in Fig. 1(a). $m \in [1, A - 1]$, A is the accelerating factor (AF) defining the number of every other acquired k-space lines, Δk_x is a unit step in FE direction, and Δk_y is a unit step in phase encoding (PE) direction. Once the kernel weights are determined, one can calculate missing k-space signals with

FIG. 1. (a) is a diagram for the GRAPPA coil weights kernel with dimension of $X \times Y \times L$. This kernel will move along both PE and FE direction to create procedures of coil weights calibration in ACS region. Small circles represent ACS signals. Triangle denotes a target spot where a signal is fitted as the weighted sum of signals covered by the kernel (circles inside squares). (b) demonstrates the visualization for GRAPPA formulation in matrix format with symbols depicted in (a).

Eq. (1) by replacing the left-hand-side (LHS) ACS signals with the missing one.

The system of linear equations in Eq. (1) can be rewritten in matrix format

$$\hat{s}_j^{ACS} = S_m \hat{n}_j^m, \quad (2)$$

where $\hat{s}_j^{ACS}$ is a $H \times 1$ column vector (H is the number of equations in the system), whose elements enumerating the ACS signals on the LHS of Eq. (1). $\hat{n}_j^m$ is a column vector having XYL elements with the $(a + bX + lXY)$ th element given by the kernel weight $n_{a,b,l}^m$. S_m is a $H \times (XYL)$ matrix that tabulates ACS data on the right-hand-side (RHS) of the system of equations accordingly. To determine the kernel weights from Eq. (2), one has to invert the matrix S_m . However, this matrix does not have a determinant and therefore is not invertible²¹ making it an overdetermined problem. There is no exact solution for $\hat{n}_j^m$. To solve this overdetermined problem, GRAPPA adopts the Moore–Penrose pseudoinverse to find a partial solution:^{3,5}

$$\hat{n}_j^m \approx (S_m^T S_m)^{-1} S_m^T \hat{s}_j^{ACS} \quad (3)$$

It is noteworthy that this procedure is equivalent to GLR on the ACS signals. The original GRAPPA reconstruction assumes a single set of kernel weights. Our new method is based on a different assumption described in the Sec. II B.

II.B. Generalized K-space reconstruction and nonstationarity of Kernel weights

For a generalized k-space reconstruction, the task is to synthesize the missing k-space data from sampled values to obtain a full FOV image. Hence, knowing the relationship between sampled and nonsampled k-space data, which is estimated as the kernel weights, is essential for a successful k-space reconstruction. From the theory of data formation, we know there is only one set of ideal global kernel weights needed for a perfect k-space reconstruction.^{22,23} Such a set of ideal global kernel weights can be approximated through solving Eq. (2). However, this equation system is overdetermined. Thus, it is difficult to find a close solution and very often regularization techniques are helpful. It is commonly known that the SNR of MR signal varies across different k-space locations, because noise is usually constant throughout

k-space. For example, SNR near the DC component is much higher than SNR at periphery of k-space. To better approximate this one set of ideal kernel weights, the regularization should be made spatially adaptive according to the SNR distribution.^{24,25} Thus, we introduce nonstationarity of k-space location, which models the spatially adaptive weights used in regularization, into the approximation of kernel weights. In our proposed method, instead of using regularization, we use a spatially weighted linear regression (e.g., GWR) with its weight adapted to signal variation in k-space. We believe our method is similar to the method based on spatially adaptive regularization with our method being simpler and having no regularization free parameters. Several studies^{11,12,15,16} have shown that better estimation of kernel weights can be obtained by treating low frequency and high frequency signals differently. From these studies, we found that the kernel weights are correlated to k-space location. This implies that kernel weights should not be constant over k-space. As such, we argue that a single set of kernel weights from GLR is insufficient for quality reconstruction. We suggest that the kernel weights should be localized—varied with the acquired k-space data—according to spatial analysis theory.¹⁷ This leads to the development of the novel MOdeling Non-stationarity of KErnel wEightS (MONKEES) k-space reconstruction algorithm.

II.C. k-space reconstruction by MONKEES

GWR method has been proven its ability to resolve much of the spatially autocorrelated error in the GLR model^{18,26} and produces a more accurate estimation.²⁷ In the GWR framework, kernel weights $\hat{n}_j^m$ are continuous functions in a space Ω . In other words, a neighborhood in Ω is expected to have similar kernel weights. By introducing an index i to $\hat{n}_j^m$, we have spatially (in Ω) varied kernel weights $\hat{n}_j^m(i)$, which can be obtained as follows on the realm of GWR:

$$\begin{aligned}\hat{n}_j^m(i) &\approx (\mathbf{S}_m^T \mathbf{W}_m(i) \mathbf{S}_m)^{-1} \mathbf{S}_m^T \mathbf{W}_m(i) \hat{s}_j^{\text{ACS}}, \\ \mathbf{W}_m(i) &= \text{diag}(w_{1,m}(i), w_{2,m}(i), \dots, w_{h,m}(i), \dots, w_{H,m}(i)),\end{aligned}\quad (4)$$

where $\mathbf{W}_m(i)$ is an $H \times H$ diagonal matrix containing locality weights that help model the underlying nonstationarity. Locality weight $w_{h,m}(i)$ that approaches 1 denotes data stationarity between indices h and i . In this work, diagonal elements of $\mathbf{W}_m(i)$ should capture the similarity in the acquired k-space data, which follows the aforementioned analytical finding. To simplify the calculation of similarity, we exploit average k-space data magnitude μ as the metric. Therefore, $w_{h,m}(i)$ is an inverse distance between the μ at h and i .

Regarding the reconstruction of missing signal at (k_x, k_y, l, m) , we calculate μ at (k_x, k_y, l, m) and those for all the acquired ACS signals, then we compute the diagonal matrix $\mathbf{W}_m$ at (k_x, k_y, l, m) and obtain the kernel weights with Eq. (4). As a final step, reconstruct the missing data in a way identical to original GRAPPA.

Compared with the GRAPPA, MONKEES requires extra coil calibrations. At each point in the ACS region, an inde-

pendent calibration is needed. Similar extra computation applies to the reconstruction. In Sec. II D, we give implementation details on speeding the computation with an approximation.

II.D. Implementation of MONKEES

II.D.1. Partition by clustering

Running the MONKEES algorithm on a point-wise basis is computationally expensive. We suggest clustering the Ω space into homogenous areas, such that we can approximate the point-wise operation by a cluster-wise one, which significantly reduces the computation effort. This simplified algorithm is depicted in Fig. 2. Clustering is based on the average k-space data magnitude μ at different sampling locations. We employ the commonly used clustering algorithm in image processing, k -means partitioning.²⁸ Though there are other better clustering algorithms, we found k -means gave satisfactory result in our data sets. This clustering method takes a predefined number of clusters and finds partitions by iteratively minimizing the within-cluster sum of squares error (SSE) to the cluster centroid. In order to avoid under-estimated error due to the deficiency of regression target data, we set limit for the size of partition so that each cluster has at least XYL regression target data.

II.D.2. The Ω space

By the spatial analysis theory, spatial trends in data can be identified and described by first-order statistics (i.e., mean value).¹⁷ As such, we exploit the average signal magnitude covered by the weight kernel as the metric to capture nonstationarity in kernel weights. The Ω space is defined by a $1 \times L$ vector $\vec{\mu}_{i,m}$, whose l th element is the average signal magnitude within the kernel acquired by the l th coil.

II.D.3. Cluster-wise operation

Instead of calculating kernel weights at each ACS point in coil calibration, we compute P sets, where P is the number of clusters. For each cluster, we obtain the average of all of the μ s, $\vec{\nu}_{p,m}$ and define an l^2 -norm distance $d_{h,m,p} = \|\vec{\mu}_{h,m} - \vec{\nu}_{p,m}\|$ on the Ω space, where h denotes regression target index. The diagonal matrix in GWR is obtained with the Shepard inverse distance-weighted function²⁹

$$v_{h,m}(p) = 1 / (d_{h,m,p})^\tau, \quad (6)$$

where $\tau > 1$ as the following:

$$w_{h,m}(p) = v_{h,m}(p) / \sum_{n=1}^P v_{h,m}(n). \quad (7)$$

The denominator is for normalization.

Reconstruction of missing signal at (k_x, k_y, l, m) requires only calculation of the l^2 -norm distance $\|\vec{\mu}(k_x, k_y, l, m) - \vec{\nu}_{p,m}\|$ on Ω space and interpolation of the corresponding kernel weights from the P sets using interpolating weights in Eq. (7). The algorithm is graphically demonstrated in Figs. 2(a)–2(c). Figures 2(d)–2(g) show the partitioned Ω space images for a 4-channel brain data set.

FIG. 2. A diagram demonstrating simplified MONKEES algorithm. (a) depicts two vectors, $\vec{\mu}_{i,m}$ and $\vec{\mu}_{h,m}$, used to partition ACS and subsampled k-space data, respectively. (b) is a flowchart for kernel weights calibration procedure. (c) is a flowchart for missing signal reconstruction procedure. (d)–(e) are log-magnitude images for ACS and subsampled k-space signals from one coil of the 4-channel brain data set. These k-space data characteristics can be depicted by k-space clustering with three clusters in (f)–(g), which are the partitioned Ω spaces corresponding to signals of ACS and subsampled k-space, respectively, with different gray value representing different cluster.

II.D.4. The kernel shape and size

The shape and size of the kernel used in the MONKEES can affect the accuracy of detection of k-space spatial pattern that will be mapped into clusters in the Ω space. From the spatial analysis theory,¹⁷ we should use an isotropic shape kernel (e.g., a square, a circle, or a hexagon) to detect an isotropic spatial pattern, and anisotropic shaped kernels to detect anisotropic spatial patterns. The k-space anisotropy is correlated to both known and unknown factors (e.g., B_1 field inhomogeneity, orientation of imaged object, etc.). And especially in k-space from non-Cartesian sampling scheme (e.g., spiral and radial), much of the information is localized at the center than

periphery, so the kernel should adapt its shape as it traverses the k-space. If the spatial pattern is unknown in advance, a small size isotropic shaped kernel is recommended.¹⁷ In this paper, we used a rectangular-shape kernel of size 4×5 ($Y \times X$ or rows by columns). Investigating the relationship between k-space spatial pattern and kernel shape is our future work.

III. METHODS

There are two important free parameters associated with our algorithm, one is the value of Shepard constant τ [in Eq. (6)] and the other is the number of clusters P in k-space partitioning. We optimized both parameters with the perceptual

difference model (Case-PDM). Our algorithm was tested with both phantom and *in vivo* MR data of different image contents and different acquisition schemes (including MR tagging data). Importantly, we tested the kernel weights non-stationarity with randomization and cross-validation experiments. We also investigated the important factors that affect the optimal number of clusters P_{best} based upon Case-PDM.

III.A. Case-PDM and parameter optimization

The perceptual difference model (Case-PDM), developed in our laboratory, is used to mimic human vision system in evaluating image quality. The model was inspired by the visual difference predictor (VDP) model reported by Daly,³⁰ and we had made multiple modifications to improve its performance over the years. It has been validated for evaluations for fast MRI applications and described in details in publications.^{19,31,32} A detailed description is in Ref. 31. Case-PDM has been shown in a variety of MR experiments (including parallel MR imaging) to correlate well with human observers (details in Refs. 19, 31, and 32). It has been used for comparing competing MR reconstruction methods and for optimizing algorithmic free parameters.^{11,31,32} Inputs to the model are a reference image reconstructed from full k-space data, and one of the test images reconstructed from under-sample k-space data. The output of PDM is a spatial map representing the magnitude of differences that a human observer would perceive between the input images. This map can be summed over a region of interest (ROI) with relevant anatomy to give a scalar PDM score. Zero score indicates perceptual identity to the chosen comparison reference. The two free parameters, the Shepard constant τ and the number of clusters P , are optimized by finding the minimum PDM score with an exhaustive search strategy. Minimum, maximum, and increment numbers of clusters, 1, 15, and 1, respectively, were evaluated.

III.B. Phantom and *in vivo* experiments

An implemented GRAPPA method (WGRAPPA (Ref. 16), in which regression equations are weighted by a high-pass filter applied at k-space center, was included as a compared metric in this study. This filter is constructed by a bivariate Gaussian function with optimized parameters published in Ref. 16, 6 MR data sets having various significant component locations in k-space and acquired with different schemes and numbers of channels, were used for the experiments. They are: Dataset 1, 4-channel fully sampled MR data of a human brain with DC component in the central k-space (matrix size = 256×256); Dataset 2, 12-channel down-sampled MR data of a cylindrical phantom with off-centered and multiple significant components (acceleration factor = 3 and matrix size = 92×256); Dataset 3, same as Dataset 2 but with spin tagging; Dataset 4, 6-channel down-sampled MR data of a human liver (acceleration factor = 3 and matrix size = 77×256) with ACS obtained from a prescan; To simulate different load for the calibration scan and actual scan, two artificial data sets were created. They are: Dataset 5, 8-channel full simulated MR data created from Shepp–Logan phantom, see Fig. 3(e) (matrix size = 256×256); Dataset 6,

Fig. 3. Images of raw data used for synthesizing artificial MR data sets. (a)–(d) were acquired from the same receiver coil and they are used for calibration experiments. (e)–(f) are two different Shepp–Logan numerical phantom images used for creating artificial non-VD acquisition scheme MR data in algorithm demonstration experiments.

same as Dataset 5 but with the phantom rotated 90° and flipped down [Fig. 3(f)]. An array of eight circular receiver coils, surrounding the imaging plane, was assumed in datasets 5 and 6. The coil complex sensitivities were calculated using Biot–Savart’s law.³³ White noise with equal variance in all channels was added to the artificial signal. A brief description of all the data sets is summarized in Table I.

III.C. Testing Kernel weights nonstationarity

Brundson *et al.*³⁴ proposed a randomization significance test to evaluate the spatial nonstationarity. We follow their approach to test the kernel weights for potential nonstationarity using a simplified Monte Carlo test. Two tests were conducted, one is at the cluster level and the other is at the k-space location level. In the cluster level test, we obtained P sets of kernel weights by calibration within each cluster, and assigned these parameter sets to different clusters for GRAPPA reconstruction. The clustering is on the average data magnitude of the k-space domain (the Ω space in Sec. II D). All possible assignments were tested by exhaustively enumerating the combinations. By comparing these reconstructions, we can investigate if the kernel weights calibrated from different clusters are significantly different and hence non-

TABLE I. Summary of experimental data sets.

Dataset	Data matrix size (rows $\times$ columns $\times$ channels)	Image size	Anatomy	Data description
1	$256 \times 256 \times 4$	256×256	Brain	FLAIR; Obtained from healthy subject 1
2	$92 \times 256 \times 12$	256×256	Water phantom	Significant component off-centered
3	$92 \times 256 \times 12$	256×256	Water phantom	Spin tagging
4	$77 \times 256 \times 6$	256×256	Liver	T ₂ weighted; ACS prescanned
5	$256 \times 256 \times 8$	256×256	Numerical phantom	Shepp Logan phantom
6	$256 \times 256 \times 8$	256×256	Numerical phantom	Image rotated and flipped from dataset 5
7	$198 \times 256 \times 4$	256×256	Brain	T ₂ weighted; Obtained from healthy subject 2
8	$256 \times 256 \times 8$	256×256	Numerical phantom	Different coil setting than dataset 5

stationary. In the second test, we shuffled the clustering results/labels on the k-space location level and performed GRAPPA reconstruction with calibrated kernel weights per cluster. We then compared the reconstruction with those from one-cluster (i.e., original GRAPPA) and P -cluster without the label shuffling. Two *in vivo* MR data sets were used for the experiment. They are: Dataset 1; and Dataset 7, 4-channel fully sampled MR data of a different healthy brain (matrix size = 198×256).

Furthermore, to confirm our theoretical assumption for k-space clustering (i.e., coil sensitivity and image details are dominant in low and high frequency regions, respectively), we designed a third test. Two-cluster MONKEES, at low and high frequencies, was performed to reconstruct the missing k-space samples. The kernel weights estimated from these two clusters in two different MR datasets were interchanged. We tested two scenarios: (a) two different imaged objects with identical coil settings and (b) identical imaged object with two different coil settings. The goal was to check the role of coil sensitivity and object on reconstructed image quality. Three synthetic MR datasets are used. They are Datasets 5, 6, and 8 (same as Dataset 5 but with a different 8-channel coil setting).

III.D. Dependence on imaging parameters

In practice, parameters (e.g., kernel size) of the GRAPPA algorithm are predefined for the reconstruction of various data sets with different number of channels and coil arrangement. Our free parameters can also be predefined in the same purpose. To justify this, we employed a mixed-level factorial design³⁵ to investigate the possible parameter-dependent factors. Simulated MR data created from high-resolution cylindrical phantoms and brain images (all image matrix size = 198×256) by FFT and resampling along the respective k-space pattern were used in the study.

For each imaged object, two images taken from different orientations or slices were studied, as shown in Fig. 3. Four arrays of circular receiver coils (6 or 8 channels with different coil arrangement) surrounding the image object without overlapping were assumed. The coil complex sensitivities were calculated using Biot–Savart’s law.³³ Two different medium levels of white noise with equal variance in all channels were added to the simulated signal. This is to mimic different scanning conditions. We also tested different

sampling patterns: Two acceleration factors (2 and 3) and two different ACS sizes (15% and 20% of full data). These different imaging parameters are summarized in Table II. In total, $2 \times 2 \times 4 \times 2 \times 2 \times 2 = 128$ simulated MR data sets were created. We recorded PDM scores of MONKEES reconstruction from “subsampled” k-space data with six different numbers of clusters (1–6). Scores were computed with reference to the full k-space data. As such, there are $128 \times 6 = 768$ PDM scores in total. For each data set, we recorded also the optimal number of clusters P_{best} , P that gives minimum PDM score. A mixed-level factorial design³⁵ was performed to determine the dependent factors (imaged object, coil sensitivity, noise level, and sampling pattern) of P_{best} .

IV. RESULTS

IV.A. Parameter optimization

We tested the algorithm on all the six data sets described in Sec. III B with different Shepard constant τ and number of clusters P . PDM scores were calculated with the full-sampled k-space data as reference. We observed that at a fixed P , as τ increases, the PDM score decays and saturates at a minimum value when $\tau \geq 6$. A Shepard constant of six gives a very sharp-edge, this opens opportunity to speed up the reconstruction by simplifying the interpolating weight computations, Eq. (7), to nearest neighbor interpolation,

$$w_{h,m}(p) = \begin{cases} 1 & \forall n, d_{h,m,p} \leq d_{h,m,n} \\ 0 & \text{otherwise} \end{cases} \quad (8)$$

This is analogous to partitioning the missing k-space into subregions and reconstructing the unsampled data with calibrated kernel weights of the closest (in Ω space) cluster. Hereafter, results presented are based on this simplification.

Regarding the number of clusters P , we found that the PDM score becomes saturated at small P ($P = 2$ –5, detailed experimental results are given in Sec. IV B).

TABLE II. Summary of imaging parameters.

	Image slice	Coil array size	Coil arrangement	Noise level	Acceleration factor	ACS size
Num of settings	2	2	4	2	2	2

FIG. 4. Algorithm demonstration for a 4-channel MR brain data set (full-sampled data size = $256 \times 256 \times 4$). For the VD undersampled data ($AF=3$ and $ACS=30$), plot (a) shows more clusters used can improve image quality of MONKEES reconstruction until the image quality saturates at $P=5$. Letters in the plot index some images showed in the following. (b) is a reference image created from full k-space data with a PDM score of zero. For the two undersampled data sets ($AF=[2,3]$ and ACS size = 30), (c) and (d) are original GRAPPA reconstructions, their PDM scores = [5.42 and 9.86] with corresponding PDM maps shown in (k) and (l); (e) and (f) are WGRAPPA reconstructions, their PDM scores = [3.44 and 5.04] with corresponding PDM maps in (m) and (n); (g) and (h) are 5-cluster MONKEES reconstructions, their PDM scores = [2.39, 4.17] with corresponding PDM maps in (o) and (p). (i) and (j) are reconstructed from the data used in plot (a) by MONKEES with two and ten clusters, respectively. And their corresponding PDM scores = [5.03 and 4.20] and PDM maps are in (q) and (r). Our algorithm significantly reduced the noise and aliasing artifacts as compared to both the original GRAPPA and WGRAPPA.

FIG. 5. Algorithm demonstration for a 12-channel subsampled MR cylindrical phantom data set ($AF=3$, subsampled data size $=92 \times 256 \times 12$, and ACS size $=24 \times 256 \times 12$) with no spin tagging applied. (a) and (b) are log-magnitude images for ACS and subsampled k-space signals from one of the 12 channels. Significant component is shifted off-center in the k-space data. (c) is a full-FOV image by original GRAPPA reconstruction. (d) is a full-FOV image by WGRAPPA. (e) is a full-FOV image by 2-cluster MONKEES reconstruction. Noise is significantly reduced in (e) by MONKEES.

IV.B. Phantom and *in vivo* experiments

To demonstrate the robustness of our algorithm, all MR images were reconstructed without any ACS integrated into final reconstructions, even in some cases, where combinable ACS were available.

IV.B.1. ACS acquired simultaneously

For Dataset 1, both GRAPPA and MONKEES reconstruction were applied to undersampled MR data created by using $AF=[2,3]$ and ACS size $=30$. In all cases, reconstructed image quality (evaluated by PDM score) is improving as P is increasing. The improving quality is saturated for $P \geq 5$, as given in Fig. 4(a), which shows the result of one of the undersampled data sets ($AF=3$ and ACS $=30$). Noise was significantly reduced in images reconstructed by 5-cluster MONKEES [Figs. 4(g)–4(h)] giving PDM scores $= [2.39, 4.17]$ with corresponding perceptual difference maps in Figs. 4(o)–4(p); on the contrary, original GRAPPA [Figs. 4(c)–4(d)] gives PDM scores $= [5.42, 9.86]$ with corresponding perceptual difference maps in Figs. 4(k)–4(l), and WGRAPPA [Figs. 4(e)–4(f)] gives PDM scores $= [3.44, 5.04]$ with corresponding perceptual difference maps in Figs. 4(m)–4(n). For Datasets 2 and 3, noise is also significantly reduced with using 2 and 3 clusters, respectively. No extra artifact is introduced as observed in Figs. 5(e), 6(i) and 6(j).

FIG. 6. Algorithm demonstration for a 12-channel subsampled MR cylindrical phantom data set ($AF=3$, subsampled data size $=92 \times 256 \times 12$, ACS size $=24 \times 256 \times 12$) with spin tagging applied. (a) and (b) are log-magnitude images for ACS and subsampled k-space signals from one of the 12 channels. There are multiple significant components in the k-space data, and none of them is at center. These k-space data characteristics can be truly reflected by k-space clustering with three clusters in (c) and (d), which are corresponding to signals of ACS and subsampled k-space, respectively, and where different gray value represents different cluster. (e) is a full-FOV image by original GRAPPA reconstruction with zoomed-in image of (f). (g) is a full-FOV image by WGRAPPA reconstruction with zoomed-in image of (h). (i) is a full-FOV image by 3-cluster MONKEES reconstruction with zoomed-in image of (j). Both noise and artifacts are significantly reduced by our algorithm.

k-space partitioning with three clusters [Figs. 6(c) and 6(d), clusters are colored by black, gray and white] reflects the underlying k-space data characteristics of the MR tagging data. Therefore, these three methods are ranked as: *MONKEES* $>$ *WGRAPPA* $>$ *Original GRAPPA*.

IV.B.2. ACS acquired differently

For Dataset 4, ACS was obtained from a prescanned low image resolution data. Noise was obviously reduced by a 2-

FIG. 7. Algorithm demonstration for a 6-channel subsampled MR liver data set (AF=2, subsampled data size = $77 \times 256 \times 6$, and ACS size = $24 \times 256 \times 6$) with ACS acquired differently than subsampled signals from the same subject. (a) and (b) are log-magnitude images for ACS and subsampled k-space signals from one of the six channels. ACS signals are so different than subsampled signals that copying ACS is not feasible. (c) is a full-FOV image by original GRAPPA reconstruction. (e) is a full-FOV image by 2-cluster MONKEES reconstruction. Noise is significantly reduced by our algorithm. The noise reduction is more obvious when comparing (f) to (d) which are zoomed-in images of (e) and (c), respectively.

cluster MONKEES reconstruction (Fig. 7). No extra artifact was introduced [Figs. 7(e) and 7(f)]. A noise-free under-sampled MR data set was created from Dataset 5 and 6 using AF=2 and ACS of size 30, respectively. Results of those two data sets show that the original GRAPPA produced images with severe residual artifact [Fig. 8(b)] giving PDM score = 5.90, whereas our 5-cluster MONKEES algorithm gave an almost perfect reconstructed image [Fig. 8(c)] with PDM score = 0.43.

IV.B.3. Residual analysis

We compared reconstruction residuals of the original GRAPPA and the proposed method on Dataset 1 under-sampled data (AF=2 and ACS=30). The reconstructed images are given in Figs. 4(b) and 4(h), respectively. Residuals were computed as the modulus differences between the reconstructed k-space data and the reference full k-space data. Compared with the original GRAPPA, ours gives low residuals in the vast majority (>88%). The minority relatively high residuals are from high frequency low power region, which only affect the image quality insignificantly.

IV.C. Nonstationarity test experiment

A cluster number $P=2$ was used in the experiment. For descriptive simplicity, here we use capital letters {A, B} to

FIG. 8. Algorithm demonstration for an 8-channel artificial MR data set (full data size = $256 \times 256 \times 8$). We used AF=2 to create subsampled k-space data, and we created ACS of size $30 \times 256 \times 8$ from the second Shepp-Logan numerical phantom [Fig. 3(f)] to represent differently acquired ACS. (a)–(c) are from noise-free data, with (a) is from full k-space data, (b) is by original GRAPPA reconstruction and (c) is by 5-cluster MONKEES reconstruction. Artifacts are cleaned by our algorithm to produce a perceptibly equivalent image to the reference (a).

represent the high and low spatial frequency clusters, respectively, and letters {a, b} to represent the corresponding sets of kernel weights. In the cluster-wise hypothesis test, we assigned these two sets of kernel weights to different clusters. There are four resulting MONKEES reconstructions: {AaBb, AaBa, AbBa, AbBb}, where AaBb is the proposed method. These reconstructions were then evaluated by Case-PDM. A scalar PDM score was used to indicate their image quality. In the location-wise test, we shuffled the cluster labels (pixels labeled with “A” or “B”) inside and outside the ACS independently. This is to avoid under-estimation in kernel weights calibration. For Datasets 1 and 7, which were acquired from different subjects and sequences, the two methods (GRAPPA and MONKEES) were applied to under-sampled MR data created by AF=2, ACS=30 and AF=4, ACS=50, respectively. The PDM scores (smaller score implies better image quality) are tabulated in Table III. The images reconstructed from Dataset 7 are displayed in the first column of Fig. 9, with the second column being the corresponding PDM maps. From the results, the large variation in PDM scores of 2-cluster MONKEES reconstructions indicates the kernel weights per cluster are significantly different. Shuffled clusters created image with worse quality and the proposed method gave the best image quality.

In the third test, to evaluate the sensitivity of weights, we swapped weight sets. That is, kernel weights estimated from the low and high frequency clusters in Datasets 5, 6 and 8 (denoted as “phantom 1 + coil setting 1,” “phantom 2 + coil setting 1,” and “phantom 1 + coil setting 2,” respectively) were interchanged, and the effect on image quality was evaluated. For each pair of datasets, we swapped low frequency

TABLE III. Nonstationarity test.

	1-Cluster	2-Cluster				
		AaBb	AaBa	AbBa	AbBb	Shuffled AaBb
Dataset 1	5.42	3.23	19.18	20.97	4.79	4.81
Dataset 7	10.29	6.05	24.09	38.65	42.42	40.32

Note: PDM scores for GRAPPA (1-cluster) and MONKEES (2-cluster) reconstructions with different settings (smaller score implies better image quality).

kernel weights, high frequency kernel weights, or both, and performed the reconstruction. In each case, the image quality improvement for the 2-cluster MONKEES reconstruction with the swapped kernel weights was compared with that when weights were not swapped. Results are summarized in Table IV. Low frequency region kernel weights are indeed highly influenced by coil sensitivity and insensitive to the imaged object.

IV.D. Dependent factor of cluster numbers

We ran a factorial experiment with mixed-level factorial design³⁵ to investigate the dependent factors of P_{best} . Four

FIG. 9. GRAPPA and MONKEES reconstructions for a 4-channel MR brain data set (full data size = $198 \times 256 \times 4$). We used $AF=4$ and $ACS=50$ to create undersampled VD data. (a) is reference image. (b) was reconstructed by 1-cluster MONKEES (i.e., original GRAPPA), (d) was reconstructed by 2-cluster MONKEES, and (f) was reconstructed by 2-cluster MONKEES with cluster labels shuffled. The images on the second column are the corresponding PDM maps for the images on the first column. PDM maps were displayed at the same window level. (d) has the least noise and aliasing artifacts, while (f) demonstrates the most noise and aliasing artifacts.

TABLE IV. Coil weights swapping experiment.

	Swap low frequency kernel	Swap high frequency kernel	Swap both high and low frequency kernels
Phantom 1 + Coil setting 1	0.00%	-17.76%	-18.15%
Phantom 2 + Coil setting 1	0.00%	3.17%	3.17%
Phantom 1 + Coil Setting 1	-415.42%	-585.47%	-415.42%
Phantom 1 + Coil Setting 2	N/A	N/A	N/A

Note: Image quality improvement for 2-cluster MONKEES reconstruction after swapping complex kernel weights (minus sign indicates image quality decrement). We used $AF=2$ and $ACS=20$ to create undersampled VD data.

factors were studied: *A*, four different sets of complex coil sensitivities; *B*, four different images—two phantom and two brain images; *C*, two different noise levels; *D*, two accelerating factors; and *E*, two ACS sizes. We found that only factors *A*, *B* and *E* are significant ($p < 0.05$). We further ran several individual factorial experiments with two-level factorial design³⁵ to determine if the coil sensitivity and slices of imaged object matter. Factor *A* was decomposed into *A'*—containing two sets of coil sensitivities with the same number of channels: four and eight; and factor *B* was divided into *B'*—denoting two different slices with the same imaged object: phantom and brain. Totally, 16 individual factorial experiments were conducted to study if factors *A'*, *B'*, and *C* are dependent factor of P_{best} (factors *D* and *E* were fixed at one of the two levels). Findings show that in all the statistical tests none of the three factors is significant ($p > 0.5$). This suggests only the number of channels (factor *A*), type of imaged object (factor *B*) and ACS size (factor *E*) would affect the choice of P_{best} .

V. DISCUSSION

V.A. Regression in generalized k-space reconstruction

GRAPPA adopts a truncated kernel, which is approximated using ACS data rather than perfect coil sensitivity, to represent the theoretical convolution kernel; hence an idealized k-space reconstruction cannot be achieved in practice. Determining the weights of such a truncated kernel with GLR may not give satisfactory performance, leaving room for improvement. There are at least two options for the improvement: one is to regularize the inverse problem by given prior information such as ACS noise level,⁹ and another is to preprocess local samples used in the regression with prior knowledge of k-space data such as amplitude variation.^{11,12,15,16} The former comes at the cost of aliasing artifacts. The latter approach filters samples that exhibit different characteristics in the ACS, which may be problematic, if ACS is acquired differently and cannot be integrated to get a full-FOV image. Motivated by several studies,^{11,12,15,16} we found that the kernel weights should vary in k-space. The randomization tests revealed nonstationarity of the kernel weights. As such, we introduced GWR, a framework to localize the regression procedure, to the original GRAPPA

reconstruction, and proposed our new algorithm MONKEES. Localization is defined upon a k-space regional signal statistic. Kernel weights are no longer globally constant in our implementation. In fact, they are continuous functions on the signal statistical space. Our novel algorithm is capable of lowering the majority of reconstruction residuals and reducing noise significantly without adding artifacts to the reconstructed full-FOV image. Most importantly, it does not require copying of any ACS data.

It is worth mentioning that GWR can be applied to other GLR-based reconstruction algorithms. Although we only demonstrated the GWR framework with GRAPPA, it could be extended to other parallel MR k-space reconstruction algorithms such as SMASH and PARS. There might be room for additional improvements. For example, the accuracy of GWR could be boosted by filtering local outliers¹⁸ or by applying other regularization methods developed for GLR.³⁶ Moreover, as GWR is robust and flexible in modeling non-linearity,³⁷ it can be applied to non-linear algorithms as well.

V.B. k-space clustering

Park *et al.*¹² and Huo *et al.*¹¹ suggested that ACS data with high amplitude variation should be excluded in the GRAPPA regression so as to give better reconstructions outside the ACS where signals are very often exhibit low amplitude variation. Huang *et al.*¹⁵ tried to filter high spatial frequency ACS samples prior to the GLR process by applying a high-pass Gaussian filter at k-space center; and Miao *et al.*¹⁶ tried to weight regression equations with a high-pass Gaussian filter applied at the k-space center. However, copying of the ACS is necessary in their methods. Our method can be regarded as a generalization of all the above algorithms. We cluster the average data magnitude of the k-space domain (the Ω space in Sec. II D). GLR is then performed on each cluster in a manner identical to the GLR-based GRAPPA implementation. In the reconstruction phase, we synthesize the missing data with kernel weights obtained from regression of data with similar local amplitude variation.

Experimental results showed that the MONKEES gave significantly better reconstruction (in terms of image quality) than the original algorithm, if the number of clusters $P \geq 2$. Regarding the number of clusters P , we found that the PDM score becomes saturated at small P ($P = 2-5$, detailed experimental results are given in Sec. IV B). This suggests that a few clusters are sufficient for our algorithm to reconstruct good quality images. Nonetheless, a universal value of P for high quality reconstruction may not exist; custom parameter optimization may be required. The simulation experiment about dependent factor of optimal cluster numbers P_{best} (detailed description is given in Sec. IV D) suggests only the number of channels, type of imaged object and ACS size would affect the choice of P_{best} . Those factors are often invariant in scanning protocols for clinical imaging. Therefore, we argue that, in a clinical environment, one can perform parameter optimization once (per anatomy, coil array, sampling trajectory, etc.) and use the P_{best} as the predefined value with the MONKEES algorithm. In the situation in

which P_{best} is made unavailable, we suggest the use of $P = 2$, as a rule of thumb.

This result reflects the insufficiency of GLR in GRAPPA reconstruction and affirms our claim that the nonstationarity assumption in our algorithm is valid. The assumption is also confirmed by our nonstationarity test experiment (its description and result are detailed in Secs. III C and IV C, respectively) which indicate the kernel weights per cluster are significantly different. Since our approach uses every ACS signal in the regression phase, it can reconstruct central missing data along the phase encoding direction without copying the ACS into final reconstruction. This is a vital feature in situation which ACS is acquired with a different sequence making ACS copying not possible (Figs. 7 and 8). Since we do not hard-code the data partitioning as in Ref. 12, our method is robust; it can reconstruct less noisy images even from k-space data with shifted or multiple significant components (Figs. 5 and 6). What is more, as usually there is cluster(s) spanning ACS region, the corresponding reconstruction(s) quality can be further improved by incorporating information from subsampled regions. Iterative GRAPPA (Ref. 38) could be improved by our method, too.

However, inappropriate and/or imprecise k-space clustering would lead to different reconstruction artifacts. Our experiment results in Sec. IV C shows that shuffled clusters created image with worse quality and the proposed method gave the best image quality by both visual inspection and PDM evaluation; therefore a proper clustering matters. An incorrect partitioning for low and high frequency k-space data could lead to aliasing and blurring artifacts, respectively. As such, noise reduction in Fig. 7 and aliasing reduction in Fig. 8 were due to the correct partitioning for high and low frequency k-space data, respectively. K -means partitioning,²⁸ a supervised clustering algorithm in image processing, was used. But this method is sensitive to the predefined cluster number and has limited precision for clustering k-space. Therefore, a better clustering method is expected for a better performance of MONKEES in terms of artifact reduction.

V.C. Computational cost

Rather than use a more computationally intensive interpolation scheme such as proposed by Shepard,²⁹ we used nearest neighbor, greatly simplifying calculations. That is, instead of doing multiple GLR's at each datum and several reconstructions for each missing datum per cluster, we only perform regression and reconstruction once for each cluster (so one kernel is calculated for each cluster). With this simplification, computational complexity should be comparable to the original GRAPPA reconstruction. The only extra computational load is the k -means clustering. This partitioning process took less than a minute on average, which is one-third of the regression and reconstruction processing time in our unoptimized MATLAB code. Recently, GPGPU accelerated the clustering a few hundred times faster than in a single core CPU.³⁹ Thus, under a proper code optimization and implementation, we expect this extra load would not hinder the application of the proposed method in the clinical environment.

V.D. Algorithm applicability

Our algorithm works for all parallel MR data acquired with different sampling schemes, including partial k-space data (result not shown here). Even for ideal noise-free data on which the original GRAPPA does not perform well, our algorithm gives an almost perfect reconstruction (Fig. 8). The approach can be extended to non-Cartesian GRAPPA reconstruction. We have shown experimentally that MONKEES does well with undersampled MR data with ACS acquired from a prescan (Figs. 7 and 8) and high acceleration factor (Fig. 4). We predict that it will work well for dynamic MR imaging (e.g., cardiac and functional MRI), where one uses the ACS from a prescan and high acceleration factors to speed acquisition. In particular, MONKEES well suits cardiac MR imaging with MR spin tagging (Fig. 6). TGRAPPA,⁴⁰ a dynamic parallel MR imaging method, which uses integrated full k-space from consecutive interleaved undersampled frames to calibrate kernel weights, can be improved by MONKEES as well. Moreover, our algorithm has two obvious advantages in both 3D imaging and dynamic imaging. First, one only needs to calibrate the low frequency region kernel weights once and then apply those to all other slices or time-frames because they share the same coil setting (because our simulation experiment in Sec. IV C shows that low frequency region kernel weights are highly influenced by coil sensitivity and insensitive to imaged object). Therefore, the computational cost can be significantly reduced. MONKEES can be further speeded up by parallel implementation to make real-time imaging possible. Second, one can use a pre-defined number of clusters for the best reconstruction because imaged object type and imaging condition are usually not changed.

VI. CONCLUSIONS

The proposed MONKEES reconstruction algorithm using GWR is a generalization of GLR-based GRAPPA. With a single cluster, the new algorithm reduces to the original implementation. We found that as few as two clusters, in low and high frequency k-space, are sufficient to greatly improve reconstruction image quality. We also found that the kernel weights from the low frequency region are only influenced by coil sensitivity and are relatively insensitive to the imaged object in our simulated MR datasets. Further, the novel algorithm is capable of synthesizing missing data along central phase encoding direction without cloning the ACS. This allows high quality reconstruction of k-space data even when the ACS is acquired from a different prescan sequence, a situation very common in dynamic MR imaging. From the factorial design experiments, we know that there are three factors that affect the optimal number of clusters in the algorithm; they are: the tissue being imaged, the number of channels, and the ACS size. Although there may not be a universal optimal number of clusters, we believe that this can be set for a given scanning protocol. Alternatively, at least two clusters should be used for a good quality yet possibly nonoptimal reconstruction. Case-PDM, an objective, quantitative image quality measure, was invaluable in this work. We used it to optimize MR reconstruction parameters

and determine the dependent factors of the optimal cluster number. We expect that the proposed novel reconstruction framework can be extended to other parallel image reconstruction algorithms. Also, we believe that MONKEES will be well suited for dynamic MR imaging, especially cardiac MR imaging with spin tagging.

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