Published in final edited form as:

NMR Biomed. 2011 August ; 24(7): 844–854. doi:10.1002/nbm.1630.

A Radial Self-Calibrated (RASCAL) GRAPPA method using Weight Interpolation

Noel C. F. Codella, M.Eng.¹, Pascal Spincemaille, Ph.D.², Martin Prince, M.D., Ph.D.², and Yi Wang, Ph.D.^{1,2}

¹Department of Physiology, Biophysics, and Systems Biology, Weill Medical College of Cornell University, New York, NY

²Department of Radiology, Weill Medical College of Cornell University, New York, NY

Abstract

A generalized autocalibrating partially parallel acquisition (GRAPPA) method for radial k-space sampling is presented that calculates GRAPPA weights without synthesized or acquired calibration data. Instead, GRAPPA weights are fit to the undersampled data as if it were the calibration data itself. Because the relative k-space shifts associated with these GRAPPA weights are varying for a radial trajectory, new GRAPPA weights can be resampled for arbitrary shifts through interpolation, which is then used to generate missing projections between the acquired projections. The method is demonstrated in phantoms and in abdominal and brain imaging. Image quality is similar to radial GRAPPA using fully sampled calibration data, and improved compared to a previously described self-calibrated radial GRAPPA technique.

Keywords

GRAPPA; self-calibrating; radial; projection; MRI; parallel imaging; interpolation; weight

INTRODUCTION

The reduction of scan time has long been an important interest for research in magnetic resonance imaging (MRI). One of the most successful methods to shorten scan time has been parallel imaging, which utilizes data from multiple receiver coils with varying spatial sensitivities to reduce aliasing artifact when sampling below the Nyquist limit (1–4). Parallel imaging has had a profound impact on all MRI techniques, including cardiac functional imaging (5,6), angiography (7,8), diffusion weighted liver imaging (9), and spectroscopy (10).

Efficient non-Cartesian k-space sampling has also been used to reduce scan time. In particular, radial sampling has been applied to rapid single breath hold cardiac imaging (11) and free-breathing cardiac imaging (12,13). Radial k-space trajectories have been known for their advantages over Cartesian trajectories, including reduced motion artifacts and dense sampling of the k-space center region. The latter property is useful for respiratory and cardiac self-gating (12,13). In addition, radial sampling has had advantages over other non-Cartesian sampling trajectories, such as spiral, as its main artifacts from gradient delays can be readily corrected for in the pulse sequence (12,14).

Combining radial k-space sampling trajectories with parallel imaging has been performed to further reduce scan time and improve image quality. Cartesian-like GRAPPA was applied to the radial trajectory partitioned into regions for which unique sets of GRAPPA weights are fit (15). However, this GRAPPA method required fully sampled calibration data due to the variable density nature of radial sampling. Acquiring fully sampled calibration data has several drawbacks, including the necessity of additional scan time and data corruption due to motion.

In practice, it is highly desirable to eliminate the need for calibration data. Several studies have achieved this by elegantly synthesizing fully sampled calibration datasets. Image data are multiplied with a mask that is calculated either through image processing or using coil sensitivity maps from the fully sampled low-resolution data. The multiplication of the mask in image space amounts to convolution in the k-space domain. The convolved k-space data are then resampled with additional radial projections to use as synthetic fully sampled calibration data (16,17). Extra computation is required to calculate sensitivity profiles (16), perform image processing (17), image multiplication, and gridding in both forward and inverse directions, which may increase reconstruction time and cause error propagation into the sets of GRAPPA weights. Another approach reported has been to first regrid to Cartesian coordinates with GROG (18). Various GRAPPA kernel configurations depending on acceleration factor and k-space location are fit to the Cartesian calibration data in the k-space center and used to reconstruct the periphery. The authors reported good image quality, but at the cost of increased processing time compared to radial GRAPPA using fully sampled calibration data.

This work proposes an alternative self-calibrating GRAPPA reconstruction of radial k-space data, called RASCAL (Radial Self-CALibrated) GRAPPA, which eliminates the need to generate synthetic calibration data or grid to Cartesian coordinates before the derivation of the sets of GRAPPA weights. All computation takes place on the original k-space data in polar coordinates, directly generating additional projections. Sets of GRAPPA weights are calculated from fitting the acquired data back onto itself, as if it were the fully sampled calibration data. Due to the inherent variation in the radial k-space sampling density, the set of relative k-space shifts corresponding to each measured set of GRAPPA weights is unique, providing a diverse sampling of weights over a range of relative k-space shifts. These measured sets of GRAPPA weights are then used to interpolate new sets of GRAPPA weights for relative shifts that are appropriate for positions between acquired projections. Finally, new radial projections at those positions are generated to increase the sampling density towards the Nyquist limit. The presented technique is compared with radial GRAPPA calibrated using fully sampled calibration data, as well as a previously reported self-calibrated technique (16).

EXPERIMENTAL

Review of GRAPPA

In the following, we will use the word “target point” for those k-space positions $\mathbf{t}$ whose signal $m(\mathbf{t})$ we wish to write as a linear combination of the signal of an ordered set of “source points” $S = \{s_0, s_1, \dots, s_{N-1}\}$, consisting of N_n k-space “neighbors” across N_c coils, such that $N = N_n \times N_c$. The “relative k-space shifts” or “relative shifts” of S are defined as the ordered set $\delta = \{\Delta s_0, \Delta s_1, \dots, \Delta s_{N-1}\}$, where $\Delta s_j = (\mathbf{t} - s_j)$, which is the difference in k-space position between the target point and its source point. An ordered set of “GRAPPA weights” $W = \{w_0, w_1, \dots, w_{N-1}\}$ is associated with the source points S . Thus, we can simply write the following GRAPPA equation:

$$m(t) = \sum_{j=0}^{N-1} w_j m(s_j) \quad [1]$$

The set of GRAPPA weights W is determined by inverting a system of equations consisting of target points and their corresponding source points where all signals are known, i.e. calibration data. This calibration data consists of an ordered set of target points $T = \{t_0, t_1, \dots\}$ belonging to the same coil as t . Each t_u in T has associated source points $S_u^T = \{s_{u,0}^T, s_{u,1}^T, \dots, s_{u,N-1}^T\}$ and relative shifts $\delta_u^T = \{\Delta s_{u,0}^T, \Delta s_{u,1}^T, \dots, \Delta s_{u,N-1}^T\}$ (Fig. 1a). The number of elements in the set T (denoted by $|T|$) depends on the amount of calibration data available. Using matrix notation, Eq. 1 becomes the following:

$$\mathbf{m}_T = \mathbf{M}_S \cdot \mathbf{w} \quad [2]$$

$\mathbf{m}_T$ is a column vector containing the target point signals $m(t_u)$. $\mathbf{M}_S$ is a two dimensional matrix whose elements are the source point signals $m(s_{u,j}^T)$, where $s_{u,j}^T$ is the j^{th} source point of target point t_u . $\mathbf{w}$ is a column vector of GRAPPA weights w_i from the set of GRAPPA weights W . When $\mathbf{m}_T$ and $\mathbf{M}_S$ are known, $\mathbf{w}$ can be determined by inverting the system:

$$\mathbf{w} = (\mathbf{M}_S^H \mathbf{M}_S)^{-1} \mathbf{M}_S^H \mathbf{m}_T \quad [3]$$

In order for the system of equations to be determined, the condition that the number of target points be equal to or larger than the number of weights ($|T| \geq N$) must be satisfied. In practice, because MRI data is inherently noisy, it is necessary to have additional data such that the system is overdetermined, producing reliable inversions.

In Cartesian sampling patterns, the set of the relative shifts δ_u^T is constant between different target points (Fig. 1a), which leads to Eq. 2 being typically overdetermined. In radial sampling patterns, the set δ_u^T is unique for different target points (Fig. 1b), which leads to Eq. 2 being typically underdetermined. However, δ_u^T may be approximated as constant in small local regions, allowing the inclusion of a sufficient number of target points and their source points for adequately solving Eq 2. This will be used in the following section to enable self-calibrated radial GRAPPA.

RASCAL GRAPPA Algorithm—The proposed Radial Self-CALibrated GRAPPA algorithm (RASCAL GRAPPA) consists of two basic steps: 1) Calculate the set of GRAPPA weights for each acquired target point. The resultant sets of GRAPPA weights allow estimation of acquired target points as linear combinations of their corresponding acquired source points, with associated varying relative shifts. 2) Determine the set of GRAPPA weights appropriate for estimating each unacquired target point as linear combinations of their corresponding acquired source points. Since each set of GRAPPA weights in Step 1 is associated with a unique set of relative shifts, a new set of GRAPPA weights for an arbitrary set of relative shifts can be computed through interpolation. These new sets of GRAPPA weights can then be used to reconstruct missing projections. We will now explain these two steps in detail.

Step 1: The first step is divided into 3 sub-steps as follows:

Step 1.1: Radial k-space is segmented into angular partitions, each having L_θ projections (Fig. 2a). Within each angular partition and for each coil, target points that have the same radial position are assumed to have the same set of relative shifts, i.e., their angular dependence is ignored within the partition. All subsequent GRAPPA weight calibration and interpolation is performed on each angular partition and for each coil independently, allowing global variation of the GRAPPA weights along the angular direction of radial k-space.

Step 1.2: Within each angular partition and coil, an ordered set of target points $\Psi = \{\psi_0, \psi_1, \dots\}$ with unique radial positions are selected for which unique sets of GRAPPA weights will be computed (Fig. 2a). Each ψ_i has an associated ordered set of source points

$S_i^\Psi = \{s_{i,0}^\Psi, s_{i,1}^\Psi, \dots, s_{i,N-1}^\Psi\}$, relative shifts $\delta_i^\Psi = \{\Delta s_{i,0}^\Psi, \Delta s_{i,1}^\Psi, \dots, \Delta s_{i,N-1}^\Psi\}$, and GRAPPA weights $W_i = \{w_{i,0}, w_{i,1}, \dots, w_{i,N-1}\}$ (Fig. 2b). This produces a diverse collection of discrete relative shifts for which GRAPPA weights will be computed. Here, we refer to the space of relative shifts for which GRAPPA weights are computed as the “GRAPPA-space” (Fig. 2c). The distance between each target point ψ_i along the radial axis is set to $D/\tan(\theta)$, where θ is the angle between projections, and D is a distance that is in units of $1/\text{FOV}$, where FOV denotes the field of view. This ensures that the distance between source points is approximately D ,

or $\text{abs}(s_{i,j}^\Psi - s_{i+1,j}^\Psi) \approx D$ for all $j=0, \dots, N-1$ (Fig. 2b & 2c), and defines the sampling density in GRAPPA-space. Therefore, the number of sets of GRAPPA weights that will be computed within each angular region for each coil is equal to the size of the readout divided by the spacing between target points ($512 \cdot \tan(\theta)/D$, for a readout with 512 points). As an example, suppose the distance between source points is set to $D = 1$, the number of projections in the dataset is 50, and the readout consists of 512 points. Then, the distance between target points for which GRAPPA weights are computed is $1/\tan(\pi/50)$, which is roughly equal to 16. Then, taking the total number of points along a readout and dividing by this number, we see that GRAPPA weights are computed for 32 target points along a readout. In this work, we set $D = 1$, making the sampling density of GRAPPA-space (i.e. the distance between source points for which GRAPPA weights have been calibrated) equal to that of k-space. We have repeated the proposed reconstruction while varying the value of D to validate this choice.

Step 1.3: For each target point ψ_i , the corresponding set of GRAPPA weights W_i associated with source points S_i^Ψ and relative shifts δ_i^Ψ must be computed. However, due to the nature of radial sampling, there is a lack of adequate calibration data: there exists no collection of measured target points $T = \{t_0, t_1, \dots\}$ that satisfies $|T| \geq N$, and for which the set of relative shifts $\delta_u^T = \{\Delta s_{u,0}^T, \Delta s_{u,1}^T, \dots, \Delta s_{u,N-1}^T\}$ associated with each target point t_u of the set T is equal to the set of relative shifts δ_i^Ψ . Therefore, in order to solve Eq. 2, all points belonging to a sector of length R_θ angular points and R_r radial points centered around ψ_i , such that $R_\theta \times R_r \geq N$, are selected as members of T (Fig. 2d). This sector will be referred to in the following as the calibration region. The assumption at this step is that each δ_u^T within that calibration region is equal to δ_i^Ψ . This is approximately true if the calibration region size is small. For each target point t_u of the set T , the signal $m(t_u)$ then constitutes the corresponding element of $\mathbf{m}_T$ in Eq. 3. The signal of the corresponding source points $m(s_{u,j}^T)$ comprise the rows of the matrix $\mathbf{M}_S$. Since both $\mathbf{m}_T$ and $\mathbf{M}_S$ are now defined for the target point ψ_i , Eq. 2 is determined, and the set of GRAPPA weights W_i can be computed. This is repeated for each target point ψ_i in the angular partition.

In this work, the angular size of the calibration region R_θ was chosen to be equal to L_θ . However, R_θ may be chosen to be greater than L_θ , for instance to allow small values of L_θ .

This makes a greater variation of the GRAPPA weights along the angular direction possible without hampering the ability to solve Eq. 2.

Step 2: In the second step, the goal is to estimate unacquired target points that lie on unacquired projections as linear combinations of their corresponding acquired source points. This step is also divided into 3 sub-steps, as follows:

Step 2.1: Let $\Psi^* = \{\psi_0^*, \psi_1^*, \dots\}$ be the set of unacquired target points that need to be estimated along an unacquired projection within the same angular partition and for the same coil as the set of target points Ψ . For each unacquired target point ψ_p^* in this set Ψ^* , a new set of GRAPPA weights $W_p^* = \{w_{p,0}^*, w_{p,1}^*, \dots, w_{p,N-1}^*\}$ is required that allows the target point ψ_p^* to be estimated as a linear combination of its acquired source points $S_p^* = \{s_{p,0}^*, s_{p,1}^*, \dots, s_{p,N-1}^*\}$ with associated relative shifts $\delta_p^* = \{\Delta s_{p,0}^*, \Delta s_{p,1}^*, \dots, \Delta s_{p,N-1}^*\}$ (Fig. 3a). In general, such sets of GRAPPA weights W_p^* are not available because the set of relative shifts δ_p^* associated with each does not exactly correspond to any of the sets of relative shifts δ_i^Ψ for which sets of GRAPPA weights were calibrated in Step 1. Instead, each GRAPPA weight $w_{p,j}^*$ in W_p^* is computed by interpolating among the known GRAPPA weights $w_{i,j}$ in W_i from Step 1 in the following manner (Fig. 3b):

$$w_{p,j}^* = \frac{\sum_{i=0}^{|\Psi|-1} w_{i,j} C(\text{abs}(\Delta s_{i,j}^\Psi - \Delta s_{p,j}^*))}{\sum_{i=0}^{|\Psi|-1} C(\text{abs}(\Delta s_{i,j}^\Psi - \Delta s_{p,j}^*))} \quad [4]$$

for all $j=0, \dots, N-1$, where $C(x)$ is the interpolation function (see below) and $|\Psi|$ denotes the number of target points in the set Ψ . Because of the summation over i , several calibrated GRAPPA weights calculated from Step 1 may be used for interpolation, each contributing in a different manner determined by the interpolation function and the distance between the calibrated and interpolated source points. The spacing along the radial axis between successive target points ψ_p^* in Ψ^* for which sets of GRAPPA weights must be interpolated is set to 1, so that a unique set of GRAPPA weights is interpolated for every readout point along an unacquired projection. Therefore, for a projection with 512 points, this will produce 512 interpolated sets of GRAPPA weights.

In this study, five convolution functions were evaluated for interpolation of the GRAPPA weights: 1) nearest neighbor, where the nearest GRAPPA weights are chosen without further interpolation 2) Kaiser-Bessel with width 2 and $\beta = 9$, 3) linear, 4) sinc, and 5) apodized sinc function:

$$C(x) = \text{sinc}(x) \cdot e^{-(x)^2} \quad [5]$$

where x represents the distance between the source points associated with the calibrated and interpolated GRAPPA weights.

Step 2.2: The resultant sets of GRAPPA weights from Eq. 4 are then used to reconstruct projections positioned between acquired projections within the angular region and coil, thus effectively increasing the sampling density:

$$m(\psi_p^*) = \sum_{j=0}^{N-1} w_{p,j}^* \cdot m(s_{p,j}^*) \quad [6]$$

Step 2.3: Finally, steps 1.2, 1.3, 2.1, and 2.2 are repeated across all angular partitions and for all coils to reconstruct missing projections across all of k-space.

In this study, the RASCAL GRAPPA algorithm was implemented for an acceleration factor of 2. Acceleration factors of 4 and 8 are achieved by repeated R=2 reconstructions using the output of the previous RASCAL GRAPPA reconstruction as the input for the next iteration of the algorithm (19).

Pulse Sequence Design

All scans were performed on a GE Signa 1.5T scanner (General Electric, Milwaukee, WI) using an 8 channel phased-array cardiac coil for abdominal imaging or an 8 channel phased-array head coil for brain imaging. Radial k-space was sampled using a balanced steady state free precession sequence (11,20). Gradient timing errors were measured and corrected by adjusting prewinder and rewinder gradients (12,14). Pulse sequence parameters were as follows: 512 readout points (acquiring a FOV double to that prescribed), TR 4ms, TE 1.2ms, prescribed FOV 24–40cm, receiver bandwidth 250 kHz, matrix size 256×256×16 slices at 6mm thickness. Projections were regridded onto Cartesian space using a standard regridding algorithm (21).

Experiments

This study was approved by our institutional review board and written consent was obtained from all volunteers. Five healthy volunteers (3 male, 2 female; age range 24 to 63, average 39.5) were scanned. Four volunteers were scanned in the axial plane at the liver, and one volunteer was scanned in the axial plane at the brain. In addition, a high-resolution calibration phantom was scanned in the axial plane. Data sets were acquired using 400 projections for full Nyquist sampling. From these data, undersampled data sets were simulated resulting in 200, 100, and 50 projection data sets, corresponding to undersampling factors of 2, 4, and 8, respectively. Image error for each reconstruction was defined as the total power error of the reconstructed image with respect to the standard regridding reconstruction of the fully sampled data set with 400 projections, considered as the reference image. The total power error was defined as the pixel-by-pixel sum of squared differences between the two images divided by the pixel-by-pixel sum of squares of the reference image, and was used to assess image error in prior literature (16,18,22).

First, in order to assess the influence of the size of the calibration region on the image quality of RASCAL GRAPPA, undersampled data sets with 100 (R=4) and 50 (R=8) projections from the liver images in one volunteer were reconstructed while varying the size of the calibration region in both the angular and radial dimension. In vivo data were used for this experiment since noise levels encountered in practice will partly determine optimal calibration region sizes. The angular size of the calibration regions was set to 1, 5, 10, 15, ..., and 50 projections of the undersampled data set. The radial size of the calibration regions was set to 1, 5, 10, 15, ..., and 50 readout points. In addition, the process was repeated for three different GRAPPA kernel configurations: 1) a GRAPPA kernel configuration with two neighbors being the nearest neighbor on either angular side of the target point ($N_n = 2$), 2) a GRAPPA kernel configuration with six neighbors being the nearest three radial neighbors on either angular side of the target point ($N_n = 6$), and 3) a GRAPPA kernel configuration with ten neighbors being the nearest five radial neighbors on

either angular side of the target point ($N_n = 10$). Note that the effective number of source points is the number of neighbors times the number of coil elements ($N_c = 8$ in this study). The calibration region and the GRAPPA kernel configuration that yielded minimal image error were used to reconstruct the remaining data in this manuscript.

Second, the influence of the interpolation function on image error was assessed by comparing reconstructions at an acceleration factor of 8 on a noiseless digital phantom using nearest neighbor, Kaiser-Bessel, linear, sinc, and apodized sinc interpolation functions. The region size and GRAPPA kernel configuration used are those that were determined previously to yield minimal image error. Data were simulated using a Shepp-Logan phantom with matrix size 512×512 . Coil sensitivity maps were generated by placing a 2D Fermi filter at 8 different symmetrically positioned points around the phantom. The Shepp-Logan image was multiplied with each coil's sensitivity map, and the result was Fast Fourier Transformed (FFT) and regridded onto projections, in accordance with prior literature (16,18). The different interpolation functions were compared by their effect on the image error with respect to the regridding reconstruction of the known noiseless Shepp-Logan phantom image sampled at 400 projections.

Third, we studied the dependence of image quality on the parameter D , which is approximately equal to the distance between each pair of source points $s_{i-1,j}^\Psi$ and $s_{i,j}^\Psi$ for which GRAPPA weights are calculated, with $i = 1, \dots, |\mathcal{P}|-1$ and $j = 0, \dots, N-1$. The parameter D was varied on an in vivo liver image between 0.1 and 1.2 with step size 0.1 (in units of the sample spacing along the radial dimension), while using the interpolation function and calibration region size that was previously found to produce the minimum error.

Finally, RASCAL GRAPPA was performed in the phantom, brain, and abdominal data in all volunteers. Fully sampled data sets (using 400 projections) were retrospectively undersampled by a factor of 2, 4, and 8, corresponding to 200, 100, and 50 projections, respectively. The performance of RASCAL GRAPPA was compared to radial GRAPPA reconstructions using the full 400 projection dataset as calibration data (15,18). In addition, comparisons were made to a previously described self-calibrated radial GRAPPA technique by Arunachalam et al (16). This technique constructs synthetic calibration data for each coil by multiplying the composite image with each coil's sensitivity map obtained from the fully sampled center of k-space. Henceforth, this technique will be referred to as the Fully Sampled Center (FSC) GRAPPA technique.

Partitioning of the sampled k-space into calibration regions was performed both in the angular and radial dimensions for each GRAPPA method. This represents an extension of the original radial GRAPPA (15) where partitioning only took place in the radial direction. The dimensions of calibration regions were kept constant between all GRAPPA methods relative to the k-space on which the GRAPPA weight calibration took place. This implies that for radial GRAPPA and FSC GRAPPA, the number of sets of GRAPPA weights along the angular dimension was larger than for RASCAL GRAPPA. For instance, for reduction factor $R = 2$ and for a given angular dimension of the calibration region, radial GRAPPA and FSC GRAPPA will have twice as many sets of GRAPPA weights as RASCAL GRAPPA. This is because the GRAPPA weight calibration for these two methods takes place on a k-space that has twice as many projections as the one used for GRAPPA weight calibration for RASCAL GRAPPA.

GRAPPA reconstructions were performed in MATLAB 2007a on an Apple MacBook Pro with an Intel Core 2 Duo 2.2 GHz and 4 GB of random access memory.

RESULTS

Figure 4 shows the resultant total power error (TPE) as a function of the size of the calibration region for RASCAL GRAPPA with an acceleration factor of 8, for all GRAPPA kernel configurations studied. The largest image errors were observed for small and large calibration regions, which was consistent for all GRAPPA kernel configurations studied. The smallest image error was observed between these two extremes. Fig 5 displays subtraction images displaying the reconstruction error of the RASCAL GRAPPA images with respect to the fully sampled image for various sizes of the calibration region. The calibration region that is 10 k-space samples wide in the angular direction and 45 k-space samples wide in the radial direction (abbreviated as 10×45) with a six neighbor ($N_n = 6$) GRAPPA kernel configuration yielded the minimum TPE of 0.0060, and was therefore chosen for subsequent reconstructions. Results for an acceleration factor of 4 were found to be in agreement with those for an acceleration factor of 8 and are not shown.

Figure 6 shows the image reconstruction error as a function of the interpolator used, reconstructed at an acceleration factor of 8 with a calibration region dimension of 10×45 on a digital phantom. Nearest neighbor interpolation yielded the largest TPE of 0.0282. The linear interpolation function produced the least error among those studied, and was used for all remaining reconstructions.

Figure 7 demonstrates the effects on image error while varying the distance D between source points $s_{i-1,j}^\Psi$ and $s_{i,j}^\Psi$ for which GRAPPA weights are calibrated. When $D < 1$, reconstruction times are long, and image error is approximately constant. However, when $D > 1$, image error quickly increases, while no significant benefit in reconstruction times are seen. A balance between image error and running time is seen at $D = 1$. Therefore, the distance between source points D is set to 1, corresponding to the inverse of the FOV, for the remaining experiments in the study.

Figure 8 shows the error of the RASCAL and FSC GRAPPA methods, compared to radial GRAPPA, both in phantom and in vivo. Table 1 lists the average TPE values for all methods at all acceleration factors. Image reconstructions using RASCAL GRAPPA and radial GRAPPA on a volunteer liver image are shown in Figure 9. Image reconstructions from RASCAL, FSC, and radial GRAPPA methods are shown for a volunteer brain image in Figure 10, and on a phantom in Figure 11. All methods reduced streaking artifact considerably. In general, the TPE for RASCAL GRAPPA and radial GRAPPA reconstructed images were similar for acceleration factors of 2 and 4, whereas higher TPE was observed in RASCAL GRAPPA for the acceleration factor of 8. The FSC GRAPPA method produced greater TPE compared to the other two methods for all acceleration factors. Running times are shown in Table 2. The presented RASCAL GRAPPA method for $R=8$ ran up to 40% faster than radial GRAPPA (84.2 vs 140.5 s). In addition, for $R=8$, RASCAL GRAPPA performed computation considerably faster than the FSC GRAPPA method (84.2 vs 187.9 s).

DISCUSSION AND CONCLUSION

The preliminary results presented in this study demonstrate that RASCAL (RADial Self-CALibrated) GRAPPA yields image quality comparable to conventional radial GRAPPA in less processing time and without the use of additional calibration data. In addition, the proposed technique performed faster and produced fewer image errors than a previously published self-calibrated technique that relied on coil sensitivity maps generated from the fully-sampled center (FSC) of k-space (16). The proposed approach involves only one additional GRAPPA weight interpolation step compared to the radial GRAPPA

implementation, and eliminates the need to compute coil sensitivity maps, perform image space operations, grid to Cartesian space, or generate synthetic calibration data (16–18,22) prior to the calibration of the sets of GRAPPA weights.

The increased processing time of radial GRAPPA and FSC GRAPPA in comparison to RASCAL GRAPPA is due in part because these other techniques use a larger number of angular partitions since a fully sampled or synthetic radial k-space is available for the calibration of the sets of GRAPPA weights. The difference in processing time between FSC GRAPPA and radial GRAPPA represents the additional time necessary for FSC GRAPPA to generate pseudo-fully sampled calibration data.

Additional errors found in the final reconstructed images of RASCAL GRAPPA in comparison to radial GRAPPA may be caused by the assumption of constant relative shifts within a local region, by the interpolation of the sets of GRAPPA weights, or by increased sensitivity to noise due to the reduced amount of data available for calibration. The additional error is small at lower acceleration factors and increases as the acceleration factor reaches the number of coil elements. As the amount of initial projections is reduced, the variation between sets of relative shifts in calibration regions with a fixed number of projections increases, breaking the assumption that sets of relative shifts within that calibration region are constant. As a corollary, error is dependent on the size of the calibration region used to solve the linear system for computing a set of GRAPPA weights. This is well visualized in Fig 5. Small calibration regions yield large error, as there is not enough data to robustly invert the system of linear equations for calibration. Large calibration regions yield large error as the assumption of constant sets of relative shifts over the entire calibration region breaks down. The lowest error is found between these two extremes, and the result is similar for all GRAPPA kernel configurations studied. For the purposes of this study, only three GRAPPA kernel configurations were studied. Larger GRAPPA kernel configurations may produce longer reconstruction times, but may also reduce or increase error, depending on the size of the calibration region used to solve for the set of GRAPPA weights.

The proposed method may be considered a subset of more general method, which, for a given set of relative shifts, replicates source points around each target point by resampling, and then calculates the corresponding GRAPPA weights using the resampled data (22,23). In our proposed method, the assumption that the set of relative shifts is constant within a calibration region is similar to nearest neighbor resampling for the replication of source points. The replications of source points in previous methods have been limited to the fully sampled k-space center to ensure accurate resampling (21). In contrast, the proposed method allows calibration in under-sampled areas where relative shifts of source points are close to those needed for reconstruction. For example, consider the case of a reduction factor of 8 with a 256 readout, which is 400 projections undersampled at 50 projections. The points at the periphery, 128 units away from the center, are 7 units apart between adjacent projections. However, in the fully sampled region, which is up to 40 units away from the center, k-space points are by definition at most only 1 unit apart between adjacent projections. RASCAL GRAPPA must use points beyond a radius of 64 in order to fit GRAPPA weights at a relative shift of 3.5 that will be appropriate to reconstruct the periphery of k-space to at least double the density (i.e. reach 100 projections).

The RASCAL GRAPPA method can also be conceptually explained using Figs. 2c and 3b, where all target points within an angular partition are collapsed into one single point with all source points forming a space of relative shifts around it (here called the GRAPPA-space). The spacing between source points for which GRAPPA weights are computed is not allowed to surpass the inverse of the FOV ($D=1$), since GRAPPA weights are assumed to be band-

limited by the image FOV. This assumption is consistent with our preliminary data (Fig. 7). The linear interpolation function was shown to produce optimal results among the interpolation functions studied, with the apodized sinc a close second. Prior literature has also used linear interpolation to estimate reconstruction weights (22). Nearest neighbor produced the worst results, demonstrating the need for interpolation in order to produce accurate weights. Further study on a wider variety of interpolation functions is warranted to optimize and assess the performance of the interpolation process. Such optimization of the interpolation function may require better understanding of the properties of the GRAPPA weights (24,25).

The approach taken in RASCAL GRAPPA may potentially work well for other non-uniform sampling trajectories, such as the variable density spiral trajectories (26–30), as long as the sampling trajectories provide a base collection of various k-space relative shifts.

A number of variations of the proposed RASCAL GRAPPA algorithm can be explored to further improve image quality. Overlapping calibration regions by setting $L_\theta \ll R_\theta$ may improve results by producing more sets of GRAPPA weights across the angular dimension. Interpolation may be performed in the angular dimension as well as the radial dimension. In addition, introducing regularization may improve the stability of the GRAPPA inversion problems, permitting the use of smaller regions for inversion (31). Using a set of “hyper-weights”, which are multiplied by a known matrix representing angular rotation before inversion, as a basis for the GRAPPA weights may provide both a more accurate angular fit, as well as more stable inversions, as shown in previous work (32). Coil subset selection algorithms can be used to reduce the number of GRAPPA weights to solve for, and thus further stabilize the inversion for smaller calibration regions (33). The optimization on the size and shape of the GRAPPA kernel configuration may also prove effective to reduce the number of source points necessary for reconstruction (23). In addition, as mentioned previously, source points within a calibration region can be regridded using standard regridding or GROG (34) so that relative shifts within the region are equal to the relative shifts of the target point for which GRAPPA weights are being inverted (18,22).

While the purpose of this study was to present a new method of performing self-calibrated radial GRAPPA, no conclusions can be drawn about the difference in performance or clinical utility between RASCAL GRAPPA and other parallel imaging algorithms not compared in this work. A thorough and direct comparison in a broader patient cohort and controlled phantom images with varying SNR levels would be useful to assess the advantages and disadvantages between RASCAL GRAPPA and other algorithms in literature.

In conclusion, an efficient Radial Self-CALibrated (RASCAL) GRAPPA algorithm is developed that performs all computations in k-space, without the need to compute coil sensitivity maps, perform image space operations, grid to Cartesian space, or generate synthetic calibration data prior to the calibration of the sets of GRAPPA weights. Significant reductions in aliasing artifact are achieved, generating image quality comparable to that obtained with radial GRAPPA using fully sampled training data.

Acknowledgments

This work was funded by the NIH (R01HL064647, R01HL062994). The authors would like to thank Thanh Nguyen, Bryan Kressler, Ludovic de Rochefort, Jing Liu, Tian Liu, James Codella, and Vince Siu for their insightful discussions and comments.

Abbreviations

GRAPPA	Generalized Autocalibrating Partially Parallel Acquisition
C	Calibrated
SC	Self-calibrated
GROG	GRAPPA Operator Gridding
TPE	Total Power Error
RASCAL	RAAdial Self-CALibrated GRAPPA Algorithm
FSC	Fully Sampled Center self-calibrated technique compared in this study
PARS	Parallel imaging with Augmented Radius in k-Space

References

1. Sodickson DK, Manning WJ. Simultaneous acquisition of spatial harmonics (SMASH): fast imaging with radiofrequency coil arrays. *Magn Reson Med*. 1997; 38(4):591–603. [PubMed: 9324327]
2. Pruessmann KP, Weiger M, Scheidegger MB, Boesiger P. SENSE: sensitivity encoding for fast MRI. *Magn Reson Med*. 1999; 42(5):952–962. [PubMed: 10542355]
3. Griswold MA, Jakob PM, Heidemann RM, Nittka M, Jellus V, Wang J, Kiefer B, Haase A. Generalized autocalibrating partially parallel acquisitions (GRAPPA). *Magn Reson Med*. 2002; 47(6):1202–1210. [PubMed: 12111967]
4. Jakob PM, Griswold MA, Edelman RR, Sodickson DK. AUTO-SMASH: a self-calibrating technique for SMASH imaging. *Simultaneous Acquisition of Spatial Harmonics*. *MAGMA*. 1998; 7(1):42–54. [PubMed: 9877459]
5. Theisen D, Sandner TA, Bauner K, Hayes C, Rist C, Reiser MF, Wintersperger BJ. Unsupervised fully automated inline analysis of global left ventricular function in CINE MR imaging. *Invest Radiol*. 2009; 44(8):463–468. [PubMed: 19561514]
6. Hunold P, Maderwald S, Ladd ME, Jellus V, Barkhausen J. Parallel acquisition techniques in cardiac cine magnetic resonance imaging using TrueFISP sequences: comparison of image quality and artifacts. *J Magn Reson Imaging*. 2004; 20(3):506–511. [PubMed: 15332260]
7. Meckel S, Mekle R, Taschner C, Haller S, Scheffler K, Radue EW, Wetzel SG. Time-resolved 3D contrast-enhanced MRA with GRAPPA on a 1.5-T system for imaging of craniocervical vascular disease: initial experience. *Neuroradiology*. 2006; 48(5):291–299. [PubMed: 16532336]
8. Zenge MO, Vogt FM, Brauck K, Jokel M, Barkhausen J, Kannengiesser S, Ladd ME, Quick HH. High-resolution continuously acquired peripheral MR angiography featuring partial parallel imaging GRAPPA. *Magn Reson Med*. 2006; 56(4):859–865. [PubMed: 16964615]
9. Girometti R, Furlan A, Bazzocchi M, Soldano F, Isola M, Toniutto P, Bitetto D, Zuiani C. Diffusion-weighted MRI in evaluating liver fibrosis: a feasibility study in cirrhotic patients. *Radiol Med*. 2007; 112(3):394–408. [PubMed: 17440695]
10. Zhu X, Ebel A, Ji JX, Schuff N. Spectral phase-corrected GRAPPA reconstruction of three-dimensional echo-planar spectroscopic imaging (3D-EPsi). *Magn Reson Med*. 2007; 57(5):815–820. [PubMed: 17457872]
11. Peters DC, Ennis DB, Rohatgi P, Syed MA, McVeigh ER, Arai AE. 3D breath-held cardiac function with projection reconstruction in steady state free precession validated using 2D cine MRI. *J Magn Reson Imaging*. 2004; 20(3):411–416. [PubMed: 15332248]
12. Stehning C, Bornert P, Nehrke K, Eggers H, Dossel O. Fast isotropic volumetric coronary MR angiography using free-breathing 3D radial balanced FFE acquisition. *Magn Reson Med*. 2004; 52(1):197–203. [PubMed: 15236387]
13. Stehning C, Bornert P, Nehrke K, Eggers H, Stuber M. Free-breathing whole-heart coronary MRA with 3D radial SSFP and self-navigated image reconstruction. *Magn Reson Med*. 2005; 54(2):476–480. [PubMed: 16032682]

14. Peters DC, Derbyshire JA, McVeigh ER. Centering the projection reconstruction trajectory: reducing gradient delay errors. *Magn Reson Med*. 2003; 50(1):1–6. [PubMed: 12815671]
15. Griswold, M.; Heidemann, R.; Jakob, P. Direct parallel imaging reconstruction of radially sampled data using GRAPPA with relative shifts. Proceedings of the 11th Annual Meeting of the ISMRM; Toronto, Canada. 2003.
16. Arunachalam A, Samsonov A, Block WF. Self-calibrated GRAPPA method for 2D and 3D radial data. *Magn Reson Med*. 2007; 57(5):931–938. [PubMed: 17457884]
17. Huang F, Vijayakumar S, Li Y, Hertel S, Reza S, Duensing GR. Self-calibration method for radial GRAPPA/k-t GRAPPA. *Magn Reson Med*. 2007; 57(6):1075–1085. [PubMed: 17534921]
18. Seiberlich N, Breuer F, Heidemann R, Blaimer M, Griswold M, Jakob P. Reconstruction of undersampled non-Cartesian data sets using pseudo-Cartesian GRAPPA in conjunction with GROG. *Magn Reson Med*. 2008; 59(5):1127–1137. [PubMed: 18429026]
19. Heidemann RM, Griswold MA, Seiberlich N, Nittka M, Kannengiesser SA, Kiefer B, Jakob PM. Fast method for 1D non-cartesian parallel imaging using GRAPPA. *Magn Reson Med*. 2007; 57(6):1037–1046. [PubMed: 17534925]
20. Peters DC, Korosec FR, Grist TM, Block WF, Holden JE, Vigen KK, Mistretta CA. Undersampled projection reconstruction applied to MR angiography. *Magn Reson Med*. 2000; 43(1):91–101. [PubMed: 10642735]
21. Jackson JI, Meyer CH, Nishimura DG, Macovski A. Selection of a convolution function for Fourier inversion using gridding [computerised tomography application]. *IEEE Trans Med Imaging*. 1991; 10(3):473–478. [PubMed: 18222850]
22. Samsonov AA, Block WF, Arunachalam A, Field AS. Advances in locally constrained k-space-based parallel MRI. *Magn Reson Med*. 2006; 55(2):431–438. [PubMed: 16369917]
23. Samsonov AA. On optimality of parallel MRI reconstruction in k-space. *Magn Reson Med*. 2008; 59(1):156–164. [PubMed: 18058935]
24. Liu T, Kressler B, Wang K, Wang Y. Block circulant quasi-band matrix property for the SENSE unfolding in k-space and justification for GRAPPA. *Conf Proc IEEE Eng Med Biol Soc*. 2008; 2008:1659–1662. [PubMed: 19162996]
25. Wang Y. Description of parallel imaging in MRI using multiple coils. *Magn Reson Med*. 2000; 44(3):495–499. [PubMed: 10975905]
26. Heberlein K, Hu X. Auto-calibrated parallel spiral imaging. *Magn Reson Med*. 2006; 55(3):619–625. [PubMed: 16453323]
27. Kressler B, Spincemaille P, Nguyen TD, Cheng L, Xi Hai Z, Prince MR, Wang Y. Three-dimensional cine imaging using variable-density spiral trajectories and SSFP with application to coronary artery angiography. *Magn Reson Med*. 2007; 58(3):535–543. [PubMed: 17763360]
28. Kressler B, Spincemaille P, Prince MR, Wang Y. Reduction of reconstruction time for time-resolved spiral 3D contrast-enhanced magnetic resonance angiography using parallel computing. *Magn Reson Med*. 2006; 56(3):704–708. [PubMed: 16892189]
29. Meyer CH, Hu BS, Nishimura DG, Macovski A. Fast spiral coronary artery imaging. *Magn Reson Med*. 1992; 28(2):202–213. [PubMed: 1461123]
30. Qian Y, Zhang Z, Stenger VA, Wang Y. Self-calibrated spiral SENSE. *Magn Reson Med*. 2004; 52(3):688–692. [PubMed: 15334593]
31. Peng, H.; Craig, M. BOSCO: Parallel Image Reconstruction Based on Successive Convolution Operations. Proceedings from the 14th Annual Meeting of the ISMRM; 2006.
32. Skare S, Newbould RD, Nordell A, Holdsworth SJ, Bammer R. An auto-calibrated, angularly continuous, two-dimensional GRAPPA kernel for propeller trajectories. *Magn Reson Med*. 2008; 60(6):1457–1465. [PubMed: 19025911]
33. Heberlein, K. Automated Coil Subset Selection for Improved GRAPPA Reconstruction. Proceedings from the 17th Annual Meeting of the ISMRM; 2009.
34. Seiberlich N, Breuer FA, Blaimer M, Barkauskas K, Jakob PM, Griswold MA. Non-Cartesian data reconstruction using GRAPPA operator gridding (GROG). *Magn Reson Med*. 2007; 58(6):1257–1265. [PubMed: 17969027]

Figure 1.

Depiction of calibration data used to fit sets of GRAPPA weights. A single coil with six neighbors is shown for simplicity ($N_c = 1$, $N_n = 6$). Solid lines represent acquired data. a) Cartesian case. Two elements of the set T of target points are shown, t_u and t_{u+5} 5 units away (hollow circles), along with corresponding source points (dark circles). In Cartesian sampling, relative shifts $\Delta s_{u,0}^T$ and $\Delta s_{u+5,0}^T$ are equal. b) In radial sampling, the relative shifts $\Delta s_{u,0}^T$ and $\Delta s_{u+5,0}^T$ are unique.

Figure 2.

Step 1 of the RASCAL GRAPPA algorithm. ($N_c = 1$, $N_n = 6$). a) acquired k-space projections (solid lines) are divided into angular partitions of size L_θ . A unique set of GRAPPA weights W_i is calibrated for each target point ψ_i (hollow circles) along the radial dimension in the angular partition. b) The relative shift $\Delta s_{i,2}^\psi$ between target point ψ_i (hollow circles) and source point $s_{i,2}^\psi$ (dark circle) is shown as an example. The distance between target points ψ_i and ψ_{i-1} is set to $D/\tan(\theta)$, where D is the desired spacing between the shifts $\Delta s_{i-1,j}^\psi$ and $\Delta s_{i,j}^\psi$. c) GRAPPA-space: target points are plotted at the same position in the center to better illustrate the relative shifts $\Delta s_{i,j}^\psi$ of source points $s_{i,j}^\psi$ for which GRAPPA weights $w_{i,j}$ are to be computed in Step 1 and used for weight interpolation in Step 2. d) A region of size $R_\theta \times R_r$ centered around ψ_i (marked here in gray) is used as a calibration region..

Figure 3.

Step 2 of the RASCAL GRAPPA algorithm. ($N_c = 1$, $N_n = 6$). a) Depiction of an unsampled target point ψ_p^* along an unacquired projection (dotted line), and its acquired source points $s_{p,j}^*$ (grey x). b) GRAPPA-space of source points $s_{i,j}^*$ associated with calibrated GRAPPA weights $w_{i,j}$, overlaid with source points $s_{p,j}^*$ associated with unknown GRAPPA weights $w_{p,j}^*$. In this example, the GRAPPA weight for $s_{p,2}^*$ is computed from interpolating between the calibrated GRAPPA weights $w_{i,2}$, $w_{i-1,2}$, and $w_{i-2,2}$ corresponding to source points $s_{i,2}^*$, $s_{i-1,2}^*$, and $s_{i-2,2}^*$ belonging to target points ψ_i , ψ_{i-1} , and ψ_{i-2} .

Figure 4.

Total power error (TPE) maps showing errors for a range of calibration region sizes using RASCAL GRAPPA at an acceleration factor of 8. a) TPE using the GRAPPA kernel configuration with two neighbors ($N_n = 2$), b) six neighbors ($N_n = 6$), and c) ten neighbors ($N_n = 10$).

Figure 5.

Error images for varying sizes of the calibration region an acceleration factor of 8. First numbered dimension is the angular extent, and the second dimension is the radial extent. Image intensities for error images are scaled between 0 and $1/10^{\text{th}}$ the maximum intensity of the reference image. The respective TPE is shown for each image.

Figure 6.

Digital phantom reconstructed at an acceleration factor of 8 using 5 unique GRAPPA weight interpolation methods. Image error (TPE) was calculated with respect to a 400 projection fully sampled reference reconstructed with the standard regridding method. Results from radial GRAPPA using fully sampled calibration data is also shown for comparison. Corresponding TPE is shown for each method.

Figure 7.

Image quality and running time dependence on the distance between source points $s_{i-1,j}^{\Psi}$ and $s_{i,j}^{\Psi}$ (denoted by D). a) Image reconstruction error as a function of D , using a region size of 10×45 with linear interpolation on a liver dataset. b) Corresponding plot of running times as a function of D .

Figure 8.

Resultant total power error (TPE) from both self-calibrated (SC) RASCAL and FSC GRAPPA methods, compared to the calibrated (C) radial GRAPPA method, across all acceleration factors. a) Comparison of image error between RASCAL GRAPPA and radial GRAPPA. b) Comparison of image error between FSC GRAPPA and radial GRAPPA. Please note the difference in image error scale between the two graphs.

Figure 9.

RASCAL GRAPPA in vivo abdominal results. a) Rows, top to bottom: 400, 100, and 50 projection images corresponding to acceleration factors of 1, 4, and 8, respectively. Column 1: images reconstructed using the standard regridding method. The top image in this column is fully sampled and is the reference image for the comparison in this figure. Column 2: accelerated images using RASCAL GRAPPA. Column 3: difference between the RASCAL GRAPPA image and the reference image. Column 4: accelerated images using radial GRAPPA. Column 5: difference between radial GRAPPA image and the reference image. Image intensities for error images are scaled between 0 and $1/10^{\text{th}}$ the maximum intensity of the reference image. b) Magnified regions of the liver from the acceleration factor of 8.

Figure 10.
GRAPPA in vivo brain results, acceleration factor 8. TPE is shown for each case.

Figure 11. GRAPPA phantom scan results, acceleration factor 8. TPE is shown for each case.

Table 1

Average total power error (TPE) measurements for each method.

	8X			4X			2X		
	RASCAL	FSC	C	RASCAL	FSC	C	RASCAL	FSC	C
Average	0.0088	0.0593	0.0058	0.0018	0.0165	0.0017	0.0005	0.0033	0.0005
Std. Dev.	0.0038	0.0422	0.0025	0.0009	0.0096	0.0010	0.0004	0.0017	0.0004

RASCAL = RAdial Self-CALibrated, FSC = Fully Sampled Center self-calibrated, C = Calibrated.

Table 2

Running Time for each GRAPPA method.

	Reconstruction time (s)		
	RASCAL	FSC	C
R=8	84.2	187.9	140.5
R=4	58.1	148.1	101.4
R=2	33.7	101.2	51.3

RASCAL = RAdial Self-CALibrated, FSC = Fully Sampled Center self-calibrated, C = Calibrated.