Published in final edited form as:

Magn Reson Imaging. 2010 January ; 28(1): 119–128. doi:10.1016/j.mri.2009.05.047.

Data Consistency Criterion for Selecting Parameters for k -space Based Reconstruction in Parallel Imaging

Roger Nana¹ and Xiaoping Hu¹

¹The Wallace H. Coulter Department of Biomedical Engineering, Georgia Institute of Technology / Emory University, Atlanta, GA 30322

Abstract

k -space based reconstruction in parallel imaging depends on the reconstruction kernel setting, including its support. An optimal choice of the kernel depends on the calibration data, coil geometry, and signal-to-noise ratio as well as the criterion used. In this work, data consistency, imposed by the shift invariance requirement of the kernel, is introduced as a goodness measure of k -space based reconstruction in parallel imaging and demonstrated. Data consistency error (DCE) is calculated as the sum of squared difference between the acquired signals and their estimates obtained based on the interpolation of the estimated missing data. A resemblance between DCE and the mean square error in the reconstructed image was found, demonstrating DCE's potential as a metric for comparing or choosing reconstructions. When used for selecting the kernel support for generalized auto-calibrating partially parallel acquisition (GRAPPA) reconstruction and the set of frames for calibration as well as the kernel support in temporal GRAPPA reconstruction, DCE led to improved images over existing methods. DCE is efficient to evaluate, robust for selecting reconstruction parameters, and suitable for characterizing and optimizing k -space based reconstruction in parallel imaging.

Keywords

parallel imaging; GRAPPA; kernel support selection; TGRAPPA; calibrating data frames selection; reconstruction error; image reconstruction; artifact reduction

Introduction

Fundamentally, parallel MRI reconstruction in k -space assumes that only a limited number of acquired k -space data contribute to the synthesis of a missing datum [1]. For Cartesian sampling, it is further assumed that the reconstruction kernel (or simply kernel) is shift invariant in the k -space. Given a parallel imaging data set including calibration data, the reconstruction performance strongly depends on the selection of kernel support which could vary in both size and configuration and strongly influence the kernel [2-6]. For example, small kernels may be inadequate in representing the complexity needed in k -space synthesis while large kernels tend to be overly sensitive to errors in the data and both could result in poor reconstruction. A proper choice of kernel support size (or simply kernel size), which has been shown to depend on coil

Corresponding Author: Xiaoping Hu, Ph.D., Dept. of Biomedical Engineering, 101 Woodruff Circle, Suite 2001, Atlanta, GA 30322, phone: 404-712-2615, fax: 404-712-2707, email: xhu@bme.emory.edu.

Publisher's Disclaimer: This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final citable form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

array configuration, noise level in the acquired data, imaging configuration, and calibration data, should provide a suitable compromise between the two extremes. Methods for automatically determining the optimal kernel parameters for a given parallel-acquired dataset have been developed [2,5,6].

The work of Qu et al. [2] improves the generalized auto-calibrating partially parallel acquisition (GRAPPA [7]) technique using a rank-revealing QR factorization to select the most linearly independent columns of the encoding matrix formed from a large local k -space subset. The linear independence criterion there permits the selection of the kernel support configuration for a fixed kernel size, minimizing the noise amplification in the estimation of GRAPPA weights. The emphasis on the noise in the weights does not account for other errors in GRAPPA reconstruction.

Samsonov introduced an attractive formalism, SPARSE [6], in which k -space based parallel MRI reconstruction is framed as approximation of the inverse of the encoding matrix with a sparse matrix, with the error of this approximation used as a criterion for optimizing the kernel. Although SPARSE works well in many cases, it does require that the calibration data capture the complexity of the entire k -space data. In other words, the data used for SPARSE prediction error are the same data used to derive the weights, and this prediction error does not indicate how well the weights predict other acquired data that are not involved in the determination of the weights.

In a recent paper, the choice of the kernel support for GRAPPA was posed as a model selection problem, and cross-validation (CV) was used to select the optimal kernel support among a group of candidates [5]. In that approach, CV was performed via partitioning of the calibration dataset, focusing on consistency with the calibration data. Similar to SPARSE, the CV approach focuses only on the calibration data, generally localized in the low frequency. Additionally, CV can be computationally expensive, as K -fold cross-validation requires each kernel support candidate to be trained K times ($K>1$). Furthermore, the performance of cross-validation may vary with the choice of K . For example, with increasing K , the bias of the true error estimator (the estimator accuracy) decreases whereas the variance of the true error estimator increases. Selection of the optimal K is still an open question [8]. Therefore, a computationally efficient, robust and balanced metric that facilitates the selection of reconstruction kernel settings which provides a proper compromise between artifacts and SNR is still desirable.

In this work, we employ data consistency imposed by the shift invariance requirement of the kernel as a simple measure of performance of k -space synthesis for Cartesian parallel imaging. Specifically, a data consistency error (DCE) is determined from the difference between the acquired signals and their estimates obtained from the synthesis of the estimated missing data. Specifically, DCE was used to automatically select the kernel support for GRAPPA and the set of calibrating frames for temporal GRAPPA (TGRAPPA [9]). Comparison of DCE-optimized reconstruction with reconstructions derived using existing methods showed that DCE based reconstruction performs better or equally.

Theory

The formalism presented here is based on the GRAPPA interpolation procedure and can be extended to other k -space based parallel MRI reconstruction algorithms. It is assumed that the data are under-sampled along the phase encoding direction by a factor of R . In GRAPPA, a missing k -space data point in a single coil is reconstructed by linearly combining data acquired in both phase (k_y) and frequency (k_x) encoding directions from all coils. Let us now use a blockwise notation as shown Fig.1a, where a block consists of one acquired line of data and $R-1$ neighboring missing lines. In this notation, GRAPPA reconstruction can be written as [10]

$$S_j(k_y + r\Delta k_y, k_x) = \sum_{l=1}^L \sum_{b=-N_b}^{N_a} \sum_{h=-H_l}^{H_r} W_{j,r}(l, b, h) \times S_l(k_y + bR\Delta k_y, k_x + h\Delta k_x) \quad (1)$$

where S_j represents the k -space signal for the j th coil at the k -space coordinates (k_x, k_y) , and Δk_y and Δk_x are the unaccelerated sampling intervals along k_y and k_x , respectively. In the above equation, $r \leq R$, N_a and N_b are the lower and upper limits of neighboring blocks used in the reconstruction and H_l and H_r are the lower and upper limits of neighboring frequency-encoded lines used in the reconstruction, L is the number of coils in the array. In equation (1), $W_{j,r}(l, b, h)$ is the weighting coefficient for interpolating the signal located at the k -space coordinates $(k_y + bR\Delta k_y, k_x + h\Delta k_x)$ of the l -th coil to estimate the signal at the k -space coordinates $(k_y + r\Delta k_y, k_x)$ of the j -th coil. The reconstruction weights are obtained by solving equation (1) with its left side filled by auto-calibrating data.

Since GRAPPA kernel should ideally be shift invariant in the k -space, the estimated missing lines should be capable of predicting the acquired lines as depicted in Fig. 1b, allowing one to write

$$S_j(k_y, k_x) = \sum_{l=1}^L \sum_{b=-N_b}^{N_a} \sum_{h=-H_l}^{H_r} W_{j,r}(l, b, h) \times S_l(k_y + bR\Delta k_y + \Delta k_y, k_x + h\Delta k_x) \quad (2)$$

where, except for the ACS lines, S_l represents missing lines estimated using GRAPPA procedure with acquired data. Assuming that the optimal set of weights minimizes the difference between the acquired k -space data and their estimates, the optimal parameter setting m (e.g. kernel size, kernel support configuration, calibration dataset) of the reconstruction kernel minimizes the data consistency error function given by

$$\text{DCE}(m) = \|A - \tilde{A}(m)\|_2 \quad (3)$$

where $\|\cdot\|_2$ is the L2-norm, A is a column vector stacked with the k -space data acquired by all coils, $\tilde{A}$ is the estimate of A obtained using the parameter m . DCE extends the cross-validation approach [5] by taking into account both calibration data and under-sampled data in the consistency validation process.

The operational steps for determining DCE of a given setting is as follows:

- Step 1. Derive the GRAPPA weights using the calibration information,
- Step 2. Fill in the missing data of all coils according to Eq. (1),
- Step 3. Predict the acquired data using the same GRAPPA weights using (Eq. (2)),
- Step 4. Compute DCE using Eq. (3).

Methods

The utility of DCE was evaluated on experimentally obtained GRAPPA and TGRAPPA data. DCE was calculated to automatically select the reconstruction kernel setting. In both applications, the selection process started by forming the collection of kernel settings to be examined followed by the evaluation of DCE of each setting and the identification of the setting

with the minimum DCE. For comparison, GRAPPA or TGRAPPA reconstruction was also carried out for each kernel setting examined by DCE in order to compute the normalized image space root mean square error (RMSE). Here RMSE is defined by

$$\text{RMSE} = \sqrt{\frac{\sum_n^N |I(n) - I_{\text{ref}}(n)|^2}{\sum_n^N |I_{\text{ref}}(n)|^2}} \quad [3]$$

where I represents the GRAPPA or TGRAPPA reconstructed image, I_{ref} is the full-data reconstructed image, N is the total number of pixels, and n is the pixel index.

Experimental data were collected with participants' written informed consent in accordance with institutional review board policies. All algorithms were implemented in MATLAB (The Mathworks Inc., Natick MA, USA) on a Quad Core Intel Xeon CPU 2.4 GHz computer with 8GB RAM.

Application to GRAPPA

The aspect of the kernel selected here was the kernel support. The set of kernel supports to be examined by DCE was formed by following the procedure described previously [5] which considers only rectangular kernels formed according to the k -space locality criterion [3]. The kernel support that minimized DCE was taken as the optimal one.

Axial brain imaging was performed on a 3T Siemens TimTM Trio whole-body MR scanner (Siemens Medical Solutions, Malvern, PA) equipped with a 12-channel head matrix coil. Fully sampled scans were acquired from healthy adults using a gradient-echo sequence (TR = 300 ms, TE = 5 ms, flip angle = 60°, slice thickness = 2 mm, FOV = 256 mm, matrix = 256 × 256 × 12) with two different bandwidth BW = 260 Hz/pixel and BW = 1150 Hz/pixel to generate datasets with two different noise levels. The fully acquired datasets were down-sampled to emulate the parallel imaging data. Specifically, GRAPPA-type datasets were synthesized for outer reduction factors (ORF) of 2, 3, and 4, respectively, and with different numbers of ACS lines chosen within a range encountered in the literature [2,10-12].

GRAPPA reconstruction using DCE-identified kernel setting was compared to those using a 4 × 5 kernel, SPARSE-optimized kernel [6], and reference line based cross-validation kernel [5]. The coil dimension of the kernel varied in the case of SPARSE and was set to the number of coils used for data acquisition in the case of other reconstructions. As the SPARSE paper [6] does not impose a stopping criterion in the optimization process and varied the kernels along the coil dimension, the target k -space subset size was chosen to match the number of points contained in the DCE-identified kernel in order to make a proper comparison between the two methods. In each case, we verified that the SPARSE approximation error as a function of k -space subset size decreased down to the desired size (as described in Samsonov's paper [6]).

Application to TGRAPPA

In TGRAPPA [9], adjacent undersampled time frames are used as the calibration data in the GRAPPA reconstruction process of a time frame. Since different time frames may carry different sensitivity information in real time cardiac imaging, the number of calibrating frames should be, in principle as minimal as possible (i.e. equals the acceleration factor) to minimize the effect of sensitivity mismatch and temporal blurring. On the other hand, in the original TGRAPPA implementation, more than the minimum number was used to improve the SNR of the calibration data with averaging. In the present work, DCE was applied to select the number of calibrating frames and the kernel support in order to achieve an optimal TGRAPPA reconstruction. Since the procedure for the selection of kernel support was the same as described in the previous subsection, only the calibrating frames selection is described here.

It was assumed (as per original implementation of TGRAPPA) that the optimal set is comprised of consecutive frames neighboring the frame to be reconstructed. For the reconstruction of each frame, DCE was calculated for calibration data sets formed by its neighboring frames, starting from the one with the minimum number of frames needed for calibration (i.e., the parallel imaging acceleration factor including the frame under consideration) to a preset maximum. The minimum calibration data sets for $R = 2, 3$, and 4 , respectively are shown in Fig. 2a and their possible expansions are illustrated in Fig. 2b. This process was repeated for all kernel supports to be examined. The combination of kernel support and number of calibrating frames that minimized DCE was taken as the optimal kernel parameter set.

Real-time non-gated, non-breath-hold cardiac imaging was performed on a 1.5T Siemens Avanto with a 15-channel cardiac matrix coil using a trueFISP sequence. Fully sampled short-axis view cardiac data were acquired at a rate of 7 frames/s on healthy subjects ($TR = 2.29$ ms, $TE = 1.15$ ms, flip angle = 70° , slice thickness = 8 mm, $FOV = 360 \times 264.38$ mm, matrix = $256 \times 56 \times 15$) and down-sampled in a time-interleaved phase-encoding scheme as described by Breuer *et al.* [9]. Three parallel MRI datasets were synthesized with acceleration factors 2, 3, and 4, respectively. DCE-optimized TGRAPPA was compared to the original TGRAPPA which uses 6 (for $R = 2$), 9 (for $R = 3$), or 12 (for $R = 4$) calibrating frames and a 4×5 kernel. In all TGRAPPA reconstructions performed here, all the k -space calibration data were used in deriving the GRAPPA weights.

Results

Application to GRAPPA

The dependence of DCE on GRAPPA kernel size along the phase encoding direction for a range of ACS lines and ORF of 2, 3 and 4, respectively, is presented in Fig. 3a. These plots were generated from the datasets acquired with a bandwidth of 260 Hz/pixel. Corresponding RMSE plots are shown in Fig. 3b. For all plots in Fig. 3, the kernel size along the readout direction was set to three. The asymmetric “U-shape” and location of the minimum in each DCE plot virtually match those of the corresponding RMSE plot. This observation also holds for other kernel sizes along the readout direction.

Figure 4 presents GRAPPA reconstructed images using (a) a 4×5 kernel, (b) SPARSE optimized subset, (c) the cross-validation-identified kernel, and (d) the DCE-identified kernel for 24 ACS lines at ORF = 4. Beside each reconstructed image, its absolute difference from the full-data derived image is displayed, with a windowing setting that is 10 times lower than that for the reconstructed image. Interestingly, the cross-validation- and DCE-identified kernel supports are dependent on the bandwidth (i.e. noise level); they are 2×9 (along $k_y \times$ along k_x) and 2×11 , respectively, for BW= 260 Hz/pixel, and 2×7 and 2×9 , respectively, for BW= 1150 Hz/pixel. A graphical representation of these kernels is given in Fig. 4. The SPARSE-selected kernel support configurations varied also along the coil dimension and could not be represented graphically in a readily visualized form. At BW= 260 Hz/pixel, the reconstructions with SPARSE, cross-validation-, and DCE-identified kernels led to similar reconstruction, while the 4×5 kernel led to an image with larger errors. Interestingly, at the BW of 1150 Hz/pixel, the image reconstructed with the DCE-identified kernel exhibits more reduced artifacts and noise than those reconstructed by other methods as indicated by the difference images. Table 1 lists the normalized root mean square error of these reconstructions for situations with a range of ACS lines. In all cases, the DCE-selected kernel resulted in a smaller reconstruction error than other methods.

Application to TGRAPPA

Fig. 5a shows DCE as a function of kernel sizes along k_y and k_x and the number of calibrating frames for the cardiac dataset down-sampled at $R = 3$. In each plot, two variables were set to their optimal values while the other was varied. For frames 2, 43, and 75, the optimal parameters were {4, 21, 5}, {3, 23, 8}, and {4, 17, 3}, respectively. The parameters in the bracket denote the optimal kernel size along k_y , the optimal kernel size along k_x , and the optimal number of calibrating frames, respectively. Corresponding RMSE plots are shown in Fig. 5b. The DCE plots exhibit virtually identical “U-shape” and location of the minimum as their RMSE counterparts.

Figure 6 presents short-axis view cardiac images reconstructed ($R = 3$) using: (b) a 4×5 kernel support and nine adjacent calibrating frames as described in the original TGRAPPA (9) and (c) the DCE-identified numbers of calibrating frames and the DCE-identified kernel supports. Below each reconstructed image, its absolute difference from the full-data derived image (a) is displayed. A quantitative comparison of the two reconstructions in terms of RMSE is shown in Fig. 7 for three different acquisition schemes: (a) $R = 2$, (b) $R = 3$, and (c) $R = 4$, computed for all frames.

Discussion

The shift invariance requirement of the reconstruction kernel in k -space-based Cartesian parallel imaging has been essential for the development of other parallel MRI reconstruction algorithms such as GRAPPA operator formalism [13] and iterative GRAPPA [14], both of which have found several applications [15-17]. In this work, a different exploitation of this requirement is demonstrated with the purpose of optimizing and characterizing reconstructions in parallel imaging.

The root mean square error has been widely used for assessing the performance of parallel MRI reconstruction algorithms but requires the full-data reconstructed image [3,5,18,19]. The plots in Figs. 3 and 5 show a strong resemblance between DCE and RMSE, indicating that DCE is a suitable measure for characterizing errors in k -space-based parallel MRI reconstruction algorithms. Unlike RMSE, DCE does not need the full-data set, making it appropriate for optimizing reconstruction in parallel imaging.

The “U” shape of DCE and RMSE plots as a function of kernel size (Fig. 3 and Fig. 5a) reflects the conflicting demand between model accuracy and noise stability in GRAPPA reconstruction and is consistent with the results reported previously [3,5,6]. GRAPPA reconstruction using the kernel support that led to the minimum DCE shows a better tradeoff between artifact and SNR than reconstruction using other methods (Fig. 4 and Table 1).

All kernel optimization methods (SPARSE, CV, and DCE) discussed in this work bear some degree of similarity in that they minimize the norm of the residual error between actual and predicted data. The difference between them lies in which subset(s) of acquired data is (are) examined in calculating the error. For SPARSE, the data used are the same data used to derive the weights, and the residual evaluation does not give an indication of how well the optimized weights predict other acquired data (i.e. data that did not participate in the determination of the weights). For CV, the subsets are defined by cross validation partitioning, which excludes the data to be predicted from the data used to obtain the kernel, although both the training and the testing sets belong to the calibration dataset. CV considers the prediction error, but its focus is limited to the calibration data. With DCE, prediction error is computed for all acquired k -space data, making it more balanced and achieving better performance than other methods.

An alternative comparison between these methods can be made through analyzing how they minimize two main types of error present in GRAPPA reconstruction, model and noise-related errors as discussed in [3-6]. As pointed out by Samsonov [6], SPARSE does not target the noise-related errors, but focuses mainly on the reconstruction accuracy (model error). CV targets both the model and noise-related errors [5], but only within the extent of the calibration data. DCE considers both types of errors over the entire acquired k -space data set. These considerations may explain the increasing discrepancies between DCE and the other methods with the complexity of reconstruction (acceleration factor, number of ACS lines, and the noise level), as indicated by the results of Fig.4 and Table 1. The difference in k -space data used in calculating the prediction error between CV and DCE also led to a difference in the optimized kernel sizes, with DCE-derived kernel larger than its CV counterpart in a number of cases. In addition, because CV and DCE method both give a balanced emphasis on the noise in the data, their optimized kernels are also dependent on the SNR level.

The SPARSE optimized k -space subsets of sizes 216 and 264 used for the reconstructions in Fig. 4 were determined in 181 s and 267 s, respectively, using an initial k -space subset of $7 \times 18 \times 12$ (similar to that is used by Samsonov [6] with the exception of the number of coils). As a comparison, corresponding DCE-identified kernels were identified in 9 s and 11 s, respectively, with a maximum search size of 7×18 . Although these computation times should not be directly compared as the DCE method explicitly utilizes the locality criterion [3] and does not vary the kernel support with coils whereas SPARSE allows the kernel to vary along three dimensions and uses the locality criterion only when defining the search space, they are indicative of the computational efficiency of these methods. Note that the DCE-identified kernel support led to smaller reconstruction errors on all the data sets examined in this study, suggesting that the locality criterion is a good approximation.

A K -fold cross-validation ($K>1$) [5] requires a computation time of approximately $K-1$ times that of DCE search to produce results that are at most comparable. For example, with a maximum search size set to 7×18 , the kernel size searching algorithm using leave-one-out cross-validation on the data shown in Fig. 4 adds an additional time of 18-39 s to conventional GRAPPA reconstruction whereas the same search using DCE adds only 9-11 s. This time difference increases with the number of ACS lines and the maximum kernel size to be examined.

A limitation of the searching strategy adopted here is the assumptions of locality criterion [3] in forming the set of kernel candidates as described by Nana et al. [5] and the fixed configuration of the kernel along the coil dimension. Although all possible kernel configurations could be examined with DCE in principle, it is impractical due to computational burden. Given the performance of DCE approach revealed here, these assumptions are reasonable.

DCE and RMSE plots in Fig. 5 (left column) demonstrate the influence of the number of adjacent calibrating frames on TGRAPPA reconstruction performance. In most cases, the plots exhibit an asymmetric “U-shape” demonstrating a tradeoff between reconstruction accuracy and stability as a result of including different number frames in the calibration data set. The increase in the number of calibrating frames reduces the effect of noise (as a result of averaging) during the GRAPPA weight estimation but at the same time increases the error due to sensitivity mismatch between different calibrating frames. The number of calibrating frames that generated the minimum DCE corresponds to a suitable compromise between these two errors. The variation of the location of the minimum of DCE with frames indicates that the use of a fixed number of calibrating frames for all frames (as it is the case for original TGRAPPA) is unlikely optimal. The variation of the optimal number of calibrating frames with the frame number may be explained by motion such as respiration. The images reconstructed using the DCE-identified kernel support and the DCE-identified number of calibrating frames exhibit a

significant reduction in noise and artifacts compared to those using the original TGRAPPA reconstruction parameters as seen in the difference images of Fig. 6. A quantitative assessment of the performances of these three strategies using RMSE, shown in Fig. 7, clearly demonstrates that the reconstruction using the DCE-identified kernel parameters outperforms the original TGRAPPA. The significant improvement obtained with DCE for TGRAPPA may also be attributed to 1) that the kernel support was also optimized in the DCE optimized reconstruction and 2) our experimental dataset was acquired at a relatively low rate (7 frames per second), making frame to frame variations more substantial and larger possible errors due to using more frames in the reconstruction.

The data consistency error introduced here is appropriate for characterizing and optimizing other k -space based parallel MRI reconstruction algorithms that assume the kernel to be partially or totally shift invariant in k -space. For example, DCE can be applied to non-Cartesian reconstruction algorithms that divide the k -space into sectors and assume shift-invariant sector-specific reconstruction kernels [20-25]. In this case, the kernel parameters need to be optimized sector-wise and the sum of the resultant DCE values may be used.

Conclusions

In this paper, we have introduced the use of data consistency error for validating, characterizing, and optimizing k -space-based reconstruction in parallel imaging. DCE was applied to automatically select the optimal kernel support for GRAPPA reconstruction and the optimal set of frames for calibration in TGRAPPA reconstruction. The result is an optimized tradeoff between artifacts and noise in the reconstructed images. The new metric is easy to evaluate, robust for selecting reconstruction parameters, and can be applied to all k -space based parallel MRI reconstruction algorithms that assume the kernel to be partially or totally shift invariant in k -space.

Acknowledgments

This work was supported in part by the National Institutes of Health (RO1EB002009) and the Georgia Research Alliance. The authors thank Drs. Renate Jerecic, Sven Zuehlsdorff, and Brian Dale of Siemens Medical Solutions for providing the cardiac data.

References

1. Larkman DJ, Nunes RG. Parallel magnetic resonance imaging. *Phys Med Biol* 2007;52(7):R15–55. [PubMed: 17374908]
2. Qu P, Shen GX, Wang C, Wu B, Yuan J. Tailored utilization of acquired k -space points for GRAPPA reconstruction. *J Magn Reson* 2005;174(1):60–67. [PubMed: 15809173]
3. Yeh EN, McKenzie CA, Ohliger MA, Sodickson DK. Parallel magnetic resonance imaging with adaptive radius in k -space (PARS): constrained image reconstruction using k -space locality in radiofrequency coil encoded data. *Magn Reson Med* 2005;53(6):1383–1392. [PubMed: 15906283]
4. Huang, F.; Duensing, GR. A theoretical analysis of errors in GRAPPA. Proceedings of the Fourteenth Annual Meeting of the International Society of Magnetic Resonance in Medicine; Seattle, WA: ISMRM; 2006. p. 2468
5. Nana R, Zhao T, Heberlein K, Laconte SM, Hu X. Cross-validation-based kernel support selection for improved GRAPPA reconstruction. *Magn Reson Med* 2008;59(4):819–825. [PubMed: 18383295]
6. Samsonov AA. On optimality of parallel MRI reconstruction in k -space. *Magn Reson Med* 2008;59(1):156–164. [PubMed: 18058935]
7. 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]

8. Cawley, G. IEEE, Neural Networks, IJCNN '06 International Joint Conference. 2006. Leave-one-out cross-validation based model selection criteria for weighted LS-SVMs; p. 1661-1668.
9. Breuer FA, Kellman P, Griswold MA, Jakob PM. Dynamic autocalibrated parallel imaging using temporal GRAPPA (TGRAPPA). *Magn Reson Med* 2005;53(4):981-985. [PubMed: 15799044]
10. Wang Z, Wang J, Detre JA. Improved data reconstruction method for GRAPPA. *Magn Reson Med* 2005;54(3):738-742. [PubMed: 16088880]
11. Huang F, Akao J, Vijayakumar S, Duensing GR, Limkeman M. A k -space implementation for dynamic MRI with high reduction factor. *Magn Reson Med* 2005;54(5):1172-1184. [PubMed: 16193468]
12. Huang F, Li Y, Vijayakumar S, Hertel A, Duensing GR. High-pass GRAPPA: an image support reduction technique for improved partially parallel imaging. *Magn Reson Med* 2008;59(3):642-649. [PubMed: 18219633]
13. Griswold MA, Blaimer M, Breuer F, Heidemann RM, Mueller M, Jakob PM. Parallel magnetic resonance imaging using the GRAPPA operator formalism. *Magn Reson Med* 2005;54(6):1553-1556. [PubMed: 16254956]
14. Zhao T, Hu X. Iterative GRAPPA (iGRAPPA) for improved parallel imaging reconstruction. *Magn Reson Med* 2008;59(4):903-907. [PubMed: 18383282]
15. Blaimer M, Breuer FA, Mueller M, Seiberlich N, Ebel D, Heidemann RM, Griswold MA, Jakob PM. 2D-GRAPPA-operator for faster 3D parallel MRI. *Magn Reson Med* 2006;56(6):1359-1364. [PubMed: 17058204]
16. Blaimer, M.; Kellman, P.; Griswold, MA. Dynamic parallel MRI using the temporal GRAPPA-operator (TGRAPPA-Operator). Proceedings of the 15th Annual Meeting of ISMRM; Berlin, Germany. 2007. p. 3339
17. Nana, R.; Zhao, T.; Heberlein, K.; Zuehlsdorff, S.; Jerecic, R.; Hu, X.; Iterative, GRAPPA. (iGRAPPA) for dynamic parallel imaging. Proceedings of the Sixteenth Annual Meeting of the International Society of Magnetic Resonance in Medicine; Toronto, ON: ISMRM; 2008. p. 3668
18. Willig-Onwuachi JD, Yeh EN, Grant AK, Ohliger MA, McKenzie CA, Sodickson DK. Phase-constrained parallel MR image reconstruction. *J Magn Reson* 2005;176(2):187-198. [PubMed: 16027017]
19. Qu P, Wang C, Shen GX. Discrepancy-based adaptive regularization for GRAPPA reconstruction. *J Magn Reson Imaging* 2006;24(1):248-255. [PubMed: 16758468]
20. Griswold, MA.; Heidemann, RM.; Jakob, PM. Direct parallel imaging reconstruction of radially sampled data using GRAPPA with relative shifts. Proceedings of the Eleventh Annual Meeting of the International Society of Magnetic Resonance in Medicine; Toronto, ON: ISMRM; 2003. p. 2349
21. 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]
22. Heberlein K, Hu X. Auto-calibrated parallel spiral imaging. *Magn Reson Med* 2006;55(3):619-625. [PubMed: 16453323]
23. Heidemann RM, Griswold MA, Seiberlich N, Kruger G, Kannengiesser SA, Kiefer B, Wiggins G, Wald LL, Jakob PM. Direct parallel image reconstructions for spiral trajectories using GRAPPA. *Magn Reson Med* 2006;56(2):317-326. [PubMed: 16826608]
24. 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]
25. 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]

Figure 1. GRAPPA interpolation procedure with illustration of the shift invariance property of the kernel. (a) A missed line is estimated from acquired lines from all coils; (b) an acquired line should be predictable from the estimated missing lines. In this illustration, $R = 3$ and a kernel of 2×3 is used.

Figure 2.

Formation of the set of frames to be examined by DCE in TGRAPPA. The initial set (m_1) is formed with the minimum number of neighboring undersampled frames necessary to form a complete dataset for calibration, which equals R (including the frame under consideration). (a) Possible configurations of m_1 assuming that only frames neighboring the frame to be reconstructed contribute to the calibration process. (b) Formation of other sets m_i by adding one frame at a time up to the maximum number allowed by the dataset or user-defined number.

Figure 3.

Plots of (a) DCE and (b) RMSE of human brain data vs. kernel size along k_y (when the kernel size along k_x is fixed at 3) for different ORFs as indicated at the top of each figure. The legends denote the number of ACS lines used in each case.

Figure 4.

GRAPPA reconstructed brain images using (a) a 4×5 kernel, (b) SPARSE k -space subset, (c) cross-validation-identified kernel support, and (d) DCE-identified kernel support. To the right of each reconstructed image, its absolute difference with the non-accelerated image is shown. The GRAPPA data sets were synthesized for ORF of 3 and 18 ACS lines. The images on the left and right columns were derived from data acquired with different bandwidths per pixel (indicated on the top). The kernel diagrams used by the reconstructions are shown and the arrows are used to associate each kernel to the corresponding reconstruction. The configurations of the k -space subsets used by SPARSE are not shown since they vary along the coil dimension.

Figure 5. Plots of (a) DCE and (b) RMSE of dynamic cardiac data accelerated at $R = 3$ vs. number of calibrating frames (left), kernel size along k_y (center), and kernel size along k_x (right). In each plot, two variables were set at their optimal values and the other one was varied. The legends denote the frame number in each case.

Figure 6. Cardiac images at three different frames ($R = 3$). (a) Nonaccelerated images used as reference, (b) TGRAPPA reconstructed images using original parameters, and (c) TGRAPPA reconstruction using DCE-identified parameters. The absolute difference of each reconstructed image with the non-accelerated image is shown right below the reconstructed image.

Figure 7.

Quantitative comparison between TGRAPPA reconstructions using the original parameters and DCE-identified parameters. RMSE is plotted as a function of frame number in each case and for three parallel MRI settings (a) $R = 2$, (b) $R = 3$, (c) $R = 4$. All plots have the same scale.

Table 1

Comparison between image errors (RMSE) of GRAPPA reconstructions for the datasets acquired with $BW = 260$ Hz/pixel obtained using 4×5 kernel support, SPARSE k -space subset, cross-validation-identified kernel support, and DCE-derived kernel support.

ORF	# of ACS lines	RMSE (4×5)	RMSE (SPARSE kernel)	RMSE (CV kernel)	RMSE (DCE kernel)	CV-identified kernel size	DCE-identified kernel size
2	4	0.1293	0.1114	0.1097	0.1097	2×5	2×5
	8	0.1158	0.1051	0.1042	0.1042	2×7	2×7
	12	0.1011	0.1019	0.1015	0.1011	2×9	4×5
3	12	0.1399	0.1257	0.1241	0.1241	2×7	2×7
	18	0.1251	0.1223	0.1220	0.1203	2×8	2×9
	24	0.1173	0.1169	0.1173	0.1160	4×5	3×7
4	18	0.1598	0.1416	0.1379	0.1379	2×9	2×9
	24	0.1484	0.1326	0.1321	0.1310	2×9	2×11
	36	0.1363	0.1303	0.1300	0.1271	4×7	3×11

Table 2
Comparison between image errors (RMSE) of GRAPPA reconstructions for the datasets acquired with BW = 1150 Hz/pixel obtained using 4 × 5 kernel support, SPARSE-optimized k-space subset, cross-validation-identified kernel support, and DCE-derived kernel support

ORF	# of ACS lines	RMSE (4×5)	RMSE (SPARSE kernel)	RMSE (CV kernel)	RMSE (DCE kernel)	CV4identified kernel size	DCE-identified kernel size
2	4	0.3190	0.2297	0.2221	0.2206	2×3	2×5
	8	0.2099	0.2083	0.2087	0.2068	3×3	2×5
	12	0.2032	0.2016	0.2012	0.1974	2×5	2×7
3	12	0.3565	0.2548	0.2481	0.2420	2×4	2×5
	18	0.2439	0.2359	0.2347	0.2331	2×7	3×5
	24	0.2367	0.2310	0.2303	0.2303	2×9	2×9
4	18	0.4014	0.2931	0.2775	0.2765	2×6	2×7
	24	0.3121	0.2796	0.2741	0.2612	2×7	2×9
	36	0.2782	0.2539	0.2532	0.2501	2×9	2×11