Automating Kernel Size Selection in MRI Reconstruction via a Transparent and Interpretable Search Approach

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Abstract. GeneRalized Autocalibrating Partial Parallel Acquisition (GRAPPA) is a clinical Magnetic Resonance Imaging (MRI) reconstruction method. The kernel size in GRAPPA directly controls the image quality and the optimal kernel size can be manually selected through comparing multiple reconstructed images. However, the optimal kernel size is often impractical to be manually selected in clinical settings. To resolve this issue, we propose an automated kernel size selection method utilizing grid search, which maintains GRAPPA's transparent and interpretable nature in a linear interpolation process. This strategy redefines kernel size selection as an exhaustive search problem and tests all potential kernel sizes within a predefined hyperparameter space. Experimental results, evaluated through both qualitative and quantitative metrics, demonstrate the effectiveness of our method in consistently identifying the optimal kernel size. The proposed approach significantly enhances the efficiency and utility of GRAPPA reconstruction for ensuring high image quality pivotal in accurate clinical diagnoses and treatment plans.

Keywords: Magnetic Resonance Imaging, Clinical Imaging, Grid Search.

1   Introduction

GeneRalized Autocalibrating Partial Parallel Acquisition (GRAPPA) [1] is a renowned method utilized in clinical imaging, specifically within the field of Magnetic Resonance Imaging (MRI). One of the distinguishing features of GRAPPA is its use of Autocalibration Signals (ACS) data, which enables the system to estimate interpolation coefficients. This characteristic eliminates the necessity for external training data, making GRAPPA an efficient and self-sufficient method for accelerating imaging speed. When comparing GRAPPA to deep learning-based MRI reconstruction methods [3], a significant advantage becomes apparent: GRAPPA employs a linear interpolator, making it transparent and interpretable. This transparency ensures that GRAPPA's workings can be thoroughly analyzed, providing a clear understanding of how the imaging results are achieved. Consequently, GRAPPA's use in clinical MRI continues to be a preferred choice for many practitioners due to its blend of efficiency, autonomy, and interpretability.

While GRAPPA offers several advantages, it also presents certain challenges, particularly related to kernel size optimization [2]. Generally, kernel size, which directly influences the quality of the reconstructed image, is manually optimized in GRAPPA. However, in practical, fast-paced clinical settings, manual selection and adjustment of the kernel size are often infeasible, leading to a potential compromise in the quality of the reconstructed images. This limitation underscores the need for an automated approach to kernel size selection. By automatically searching for the optimal kernel size, the imaging process could become more streamlined and efficient. Moreover, it would ensure consistently high image quality, vital for accurate clinical diagnoses and treatment plans, making the overall process more suited to the demanding needs of clinical applications.

In the context of GRAPPA's image reconstruction process, the selection of the optimal kernel size, which directly impacts the resultant image quality, can be redefined as a search problem. Considering GRAPPA's linear and transparent nature, the method used to find the optimal kernel size should similarly be interpretable. In this regard, grid search as a straightforward and exhaustive exploration of all combinations of predefined hyperparameters may be a suitable choice. Its simplicity lies in systematically testing all potential kernel sizes until the best one is identified, contributing significantly to achieving optimal image quality. Through its simple principle of testing all combinations in a predefined hyperparameter grid, grid search could be an efficient solution for automatic kernel size selection in GRAPPA, especially considering its linear and interpretable nature. This shift from manual selection to automated kernel size determination via grid search can substantially improve the efficacy and convenience of GRAPPA in clinical settings.

In this study, we introduce an innovative approach for automatic kernel size selection in the GRAPPA imaging method. Our proposed method is designed with a focus on achieving the highest possible quality in reconstructed images, therefore significantly enhancing the effectiveness and utility of GRAPPA in clinical imaging applications. The structure of the paper is as follows: the first part provides an introduction, setting the context and presenting the problem at hand. This is followed by the second part, where we discuss related works and the current landscape of solutions. The third section delves into the details of our proposed method for automatic kernel size selection. In the fourth section, we present the experimental results that demonstrate the efficacy of our proposed method, followed by the fifth and final section which provides a conclusion, summarizing our findings and their implications for GRAPPA imaging and potentially highlighting future avenues for further research.

2   Related Work

Functioning as a linear parallel MRI reconfiguration, GRAPPA [1] addresses the inverse issue by resolving a set of linear equations. Additionally, GRAPPA reconstruction can be depicted as

$$S_j\left(k_y - m\Delta k_y\right) = \sum_{l=1}^{L} \sum_{b=0}^{N_b-1} n\left(j,\, b,\, l,\, m\right) S_l\left(k_y - bA\Delta k_y\right) \qquad (1)$$

In the formula, the weights used in the linear combination are shown by $n(j, b, l, m)$. N_b represents the number of blocks and A represents the acceleration factor in the reconstruction. Index l and b count through the individual coils and individual reconstruction blocks respectively [4]. The initial regression evaluation in GRAPPA can be substituted with other linear or nonlinear techniques to approximate the linear or nonlinear correlation [5-9] between the undersampled points and their adjacent captured points. A more precise calculation of the missing k-space data can be achieved, surpassing the original GRAPPA technique. As a result, reduced artifacts and an enhanced signal-to-noise ratio (SNR) in the reconfigured images can be secured.

As per machine learning theory, the generalization error is broken down into three components:

$$E = bias^2(x) + var(x) + \varepsilon^2 \tag{2}$$

, which represent bias, variance, and noise, respectively. Variance tends to increase as a larger number of features are employed to learn a linear or nonlinear mapping from raw to reconstructed data. The quality of the reconstruction may be subject to the Bias-Variance Tradeoff (BVT) [10] when a linear or kernel-based learning approach is utilized. Owing to BVT, concurrently reducing bias and variance poses a challenge. Ensemble methods are commonly adopted to lessen variance while maintaining low bias, thereby enhancing quality and stability. Diversity, an essential element for a successful ensemble method, signifies the difference among multiple individual learners. A collective result derived from a group of diverse learners is theoretically assured to accomplish a T-factor error reduction, given that the learners are independent [11], where T represents the ensemble size. Ensemble learning is not a single algorithm, but it accomplishes the learning task by creating and merging multiple diverse learning methods, striving for stable and accurate results. These multiple learning methods are viewed as the individual base or component learners, which can be assembled into homogeneous or heterogeneous ensembles. In the context of MRI reconstruction, diversity can be observed in the different sets of parameters used by a reconstruction method or the distinct reconstruction strategies. To search for the best reconstruction quality, a search algorithm is needed with optimal kernel size selection.

3 Proposed Method

3.1 Influence of Kernel Sizes on Image Quality

We assume each interpolator is a learner in machine learning and needs to be trained using original ACS data. Since multiple interpolators use different kernel sizes for convolution, they are trained with multiple different views, respectively. As shown in the figure below, a small and a large kernel containing small and larger numbers of neighboring k-space data points are used by these two interpolators for interpolating the target k-space signals. Each neighboring k-space data point represents one feature for interpolating the target signal: 6 features (6 black dots) for the small kernel (small view) and 16 features (16 black dots) for the large kernel (large view). Each view represents a feature set. In the calibration step of GRAPPA, two learners trained from these two views have different generalization performance, so that one learner is more

accurate and another one less accurate. This observation is also consistent with Reference [2], which showed that the optimal view (optimal kernel size) needs to be manually observed and selected.
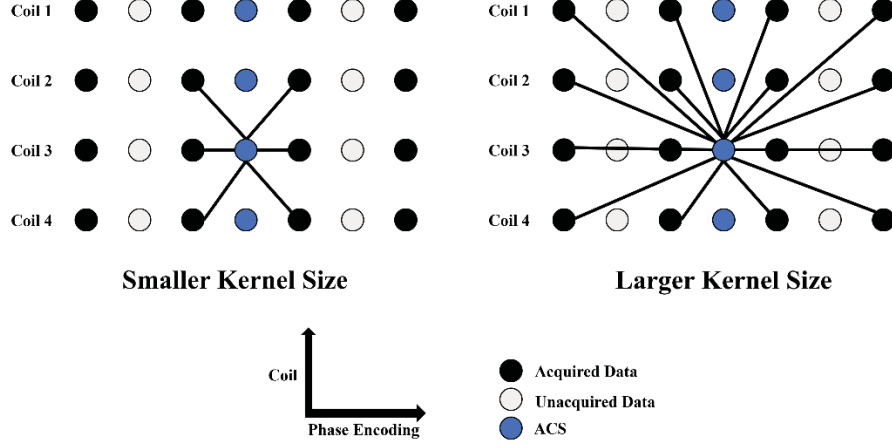

Fig. 1. Different kernel sizes for interpolating missing k-space data in the GRAPPA method. A larger kernel size contains more parameters in the interpolation process while a smaller kernel size includes fewer parameters in the interpolation. BVT is applied to different kernel sizes. An optimal kernel size is searched for to obtain an optimal quality of a reconstructed image.

In the interpolator size determination process, overfitting (interpolation size is too large) and underfitting (interpolation size is too small) problems may appear. For different k-space datasets, the optimal interpolator sizes have also deviated, so manual determination case-by-case is also time-consuming and infeasible in clinical settings. Quantitatively determining an interpolator's accuracy (e.g., using quantitative metrics like NMSE, SSIM, or PSNR) for the whole k-space is difficult without using the fully sampled k-space data. The proposed method cannot determine an interpolator's absolute value of accuracy but try to use the difference between two interpolators' accuracy for reducing the underfitting and overfitting issues.

3.2 Analysis of Kernel Size in GRAPPA Reconstruction

The association between acquired and unacquired k-space data can be divided into two categories: linear and nonlinear relationships. Commonly used in clinical routines, GRAPPA [1] operates as a linear relationship approach that establishes a linear correlation within auto-calibration signals (ACS), followed by utilizing this correlation to recover missing data in peripheral k-space. The linear shift-invariant property enhances the interpretability of GRAPPA, surpassing that of nonlinear relationship techniques. Thus, the impact of reconfiguration parameters, such as the size of the interpolation kernel on the quality of the image, can be quickly discerned. Deep learning uses nonlinear relationship strategies that offer intricate associations between acquired and unacquired k-space data. These strategies excel over their linear coun-

terparts by reducing artifacts and noise. The interpretability of intricate networks, however, remains elusive despite their high accuracy, a result of the accuracy-interpretability trade-off [10] in machine learning theory. Unstable image reconstruction [13] might also occur during deep learning-based MRI reconfiguration, and it becomes challenging to determine the factors responsible for inconsistent performance. Alterations within the training and testing domains can potentially impede generalization performance, consequently impairing image quality [8]. The ability to have consistent and interpretable MRI reconfigurations could assure medical practitioners and patients of the reliability of learning-based medical imaging methodologies [12]. The resilience of reconstruction when employing the low acceleration factor typically surpasses that of reconstruction using the high acceleration factor.

3.3   Grid Search for Optimal Kernel Size

GRAPPA is a renowned parallel MRI reconstruction technique, where the kernel size plays a pivotal role in determining the quality of the reconstruction of missing k-space data. Optimizing this parameter is crucial, and one efficient and systematic approach to do this is through the utilization of the grid search method [14,15]. Grid search is a hyperparameter tuning technique that offers an exhaustive search over a manually specified subset of hyperparameter values. In the context of GRAPPA, we aim to identify the optimal kernel size that will lead to the best possible reconstruction of the missing k-space data. To initiate this process, we first establish a set of possible kernel sizes that can be adjusted and scrutinized. The range and increments of this set must be chosen carefully, bearing in mind that a larger range or smaller increments will result in a more comprehensive search but will also demand more computational resources. Once this predefined set of kernel sizes is established, we proceed with the iterative process of k-space reconstruction. For each kernel size in the set, the GRAPPA algorithm is employed to perform a reconstruction of an undersampled k-space. The kernel size essentially determines how many neighboring k-space lines are used to estimate the missing k-space data. The choice of kernel size is a critical balance – a smaller kernel might lead to a less accurate estimation due to limited data, while a larger kernel could introduce errors due to the assumption of linearity over a larger region. One reconstruction with a selected kernel size can be shown in Figure 2.
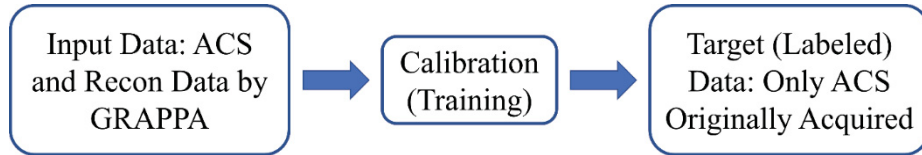

Fig. 2. One reconstruction using a selected kernel size by GRAPPA. ACS data are used as the target or labeled data in this training process of the reconstruction. Once the reconstruction is completed, its performance metrics are evaluated in comparison to the reference image with full sampling. Missing k-space data are interpolated using the estimated kernel coefficients. Next reconstruction selects another kernel size from the pre-defined set and repeats the three steps above. Note that only ACS data are

used for grid search because ACS data represent the real acquired data from a MRI scanner.

Following the reconstruction process in Fig. 2, the performance of each reconstruction is then evaluated. This evaluation involves objective quantitative metrics that assess the quality of the reconstruction against a known ground truth or a fully sampled data set. We used the fully sampled k-space-based reconstruction as the ground truth for evaluating all reconstructed images by different kernel sizes. In this case, we leveraged metrics such as the Normalized Mean Square Error (NMSE), Structural Similarity Index Measure (SSIM), and Peak Signal-to-Noise Ratio (PSNR). NMSE provides a measurement of the overall error in the reconstruction. SSIM, on the other hand, assesses the perceived change in structural information, offering insight into the visibility of the artifacts, while PSNR measures the peak noise error. Each of these metrics brings a unique perspective to the evaluation, and together, they provide a comprehensive understanding of the reconstruction performance. Upon completion of this evaluation for each kernel size in the predefined set, we find ourselves in a position to select the kernel size that yields the best performance. This optimal kernel size is typically chosen based on a compromise among the NMSE, SSIM, and PSNR values, as the perfect balance between these metrics often leads to the most satisfactory reconstruction results.

The proposed grid search method provides a systematic and robust approach to identifying the optimal kernel size for the GRAPPA algorithm. This technique takes advantage of the benefits of exhaustive search and cross-validation to yield a kernel size that enhances the reconstruction quality of missing k-space data. However, it's important to remember that while this method may provide the best solution within the predefined range, it might not be the absolute optimal solution. Regular refinements and reconsiderations of the range of kernel sizes, as well as advancements in algorithmic design and hardware capabilities, may lead to further optimization of the GRAPPA algorithm.

3.4 The Effects of Search Space on Reconstruction Quality

Grid search isn't without its limitations. In some cases, grid search may fail to identify the best optimal kernel size due to inadequacies in the pre-established set of kernel sizes or the increments chosen. If these predetermined choices do not encapsulate the true optimal value, the grid search will, quite understandably, be unable to locate it. To counteract this drawback and bolster the reconstruction performance, one of the first steps could be to refine the search space. This might involve either broadening the range of possible kernel sizes under consideration or reducing the increment steps between the values in the search grid. Tuning these aspects would permit a more detailed exploration of potential kernel sizes and increase the probability of stumbling upon the optimal value.

Refining the search space may not always be sufficient, and the conventional grid search might need to be substituted with more sophisticated methods. Two such alternatives could be adaptive grid search [16] and random search [17]. An adaptive grid

search method brings a certain dynamism to the process - it identifies promising regions within the grid and narrows down the search to that region, thereby improving the efficiency and effectiveness of the search. On the other hand, a random search method provides a solution to the exhaustive nature of grid search. By selecting random combinations of hyperparameters for evaluation, it can sometimes uncover optimal values that might be overlooked in a regular grid search. The influence of human expertise [2] can be utilized in this process. Particularly for something as specialized as MRI reconstruction, the experience of an MRI technologist could be invaluable. Their experience and intuition about the plausible range of optimal kernel sizes could help in defining the search space more accurately and efficiently.

While grid search remains a powerful tool in hyperparameter tuning, its effectiveness is dependent on various factors, such as the defined search space and the increment steps. In situations where it falls short, alternative methods like adaptive grid search [16] and random search [17], and the application of human expertise [2], can offer more nuanced and effective strategies to locate the best kernel size for the GRAPPA algorithm. Ultimately, the goal is to enhance the reconstruction performance, and sometimes that means going beyond the conventional methodologies and embracing more flexible and sophisticated techniques.

4 Experimental Results

4.1 Reconstruction Datasets

Two datasets are used to evaluate the reconstruction performance of the proposed grid search-based GRAPPA method. The first dataset was acquired on a GE 3T scanner (GE Healthcare, Waukesha, WI) with an 8-channel head coil. In the first dataset, a uniform water phantom was scanned using a gradient echo sequence (TE/TR = 10/100 ms, 31.25 kHz bandwidth, matrix size = 256 × 256, FOV = 25 cm^2). The third set of coronary brain data was acquired using a 2D gradient echo sequence (slice thickness = 3.0 mm, matrix size = 256 × 256, FOV = 24 × 24 cm^2, and TE/TR = 2.29/100 ms).

4.2 Reconstruction Performance

The phantom dataset was subject to undersampling by an outer reduction factor of 5, with the ACS lines set at 30. The block number for the interpolation kernel size was established at 2, and the column values varied in a range from 3 to 35, using only odd numbers. These 17 distinct kernel sizes facilitated the creation of a diversified search space for the recovery of k-space data. Subsequently, we applied the grid search to identify the best reconstruction quality. In Fig.3, we present the reconstructed images produced by using manual selection (3 columns) and automatic determination by grid search (17 columns), respectively. It is seen that the reconstruction generated through the optimal kernel size searched surpasses the reconstructions by manual selection in terms of quality. This method notably suppresses noise and aliasing artifacts, leading to clearer images. In terms of quantitative metrics, the reconstruction utilizing grid

search demonstrated commendable performance with an NMSE of 0.903095e-04, PSNR:4.358909e+01, and SSIM: 9.540220e-01. Grid search-based reconstruction reinforces its capacity for efficient noise and artifact suppression. For the reconstruction using 3 columns manually selected, NMSE:1.221693e-03, PSNR:3.655454e+01, and SSIM: 7.769426e-01.
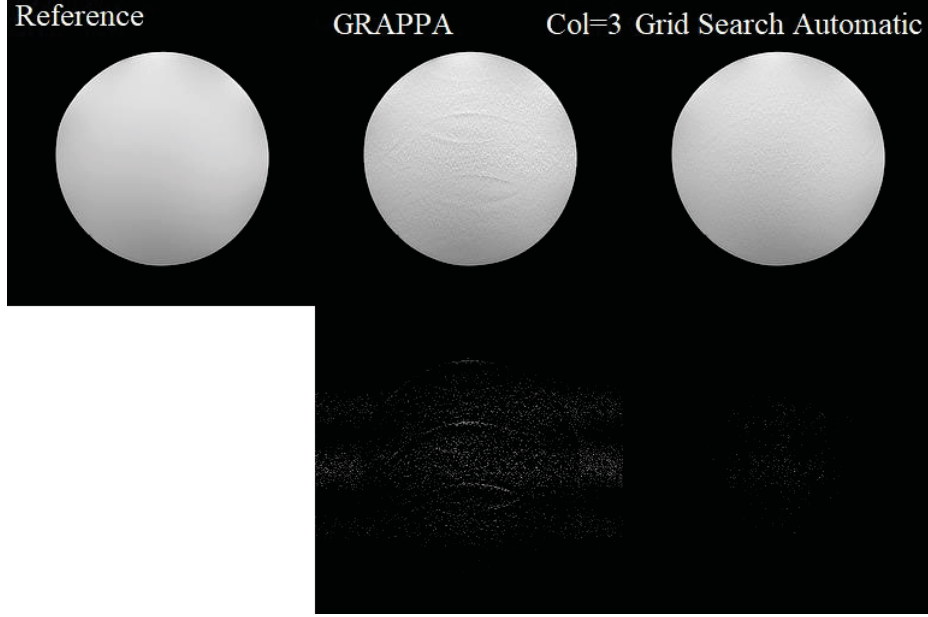

Fig. 3. Phantom reconstruction using the optimal kernel size by grid search. For each reconstruction, the k-space data is recovered by using an interpolation kernel size. For the kernel sizes, the block number is set as 2, and column numbers range from 3 to 35. Manually selected column number 3 is used to show the reconstructed phantom images. Optimal kernel size is identified in the grid search process and it is used to reconstruct missing k-space data and final image.

Moreover, Figure 4 portrays the NMSE values generated from individual reconstructions based on all columns (indicated by the green curve). A bias-variance trade-off can be observed with a "U" shape. When less parameters are used in a smaller kernel size and more parameters are used in a larger kernel size, NMSE errors are high. On the bottom of the "U" shape, optimal kernel size (in this dataset, the kernel size of 2 blocks by 17 columns is optimal) can be obtained.
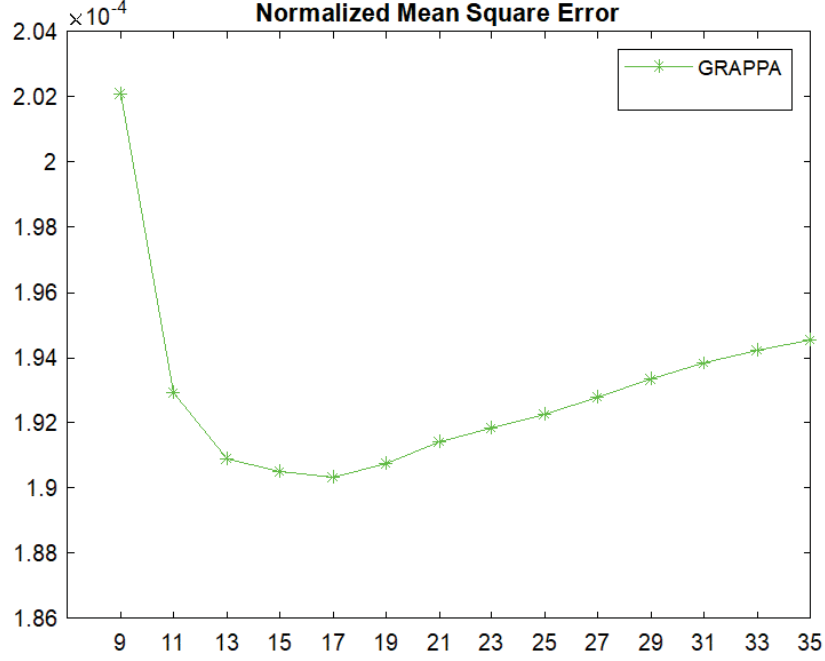
Fig. 4. Bias-variance tradeoff curve for the GRAPPA reconstructions using different columns ranging from 9 to 35. The optimal kernel size-based GRAPPA reconstruction has the lowest NMSE errors which locate at the bottom of the "U" shape.

In the second dataset, we employed 30 ACS lines and the outer reduction factor 6 for undersampling k-space data. In the search space of columns 9 to 23, grid search can identify the best quality of image reconstruction with kernel size 2 blocks by 9 columns. From the different maps shown in Fig.5, the optimal kernel size-based reconstruction has less noise than other reconstructed images. The quantitative metric values are shown in Table 1. It is seen that the kernel size identified by the grid search has the lowest value of NMSE and the highest values of PSNR and SSIM. The grid search can effectively find the GRAPPA reconstruction kernel size with the best quality in this search space with 8 kernel sizes.

Table 1. Quantitative Metric Values for Evaluating Reconstructions of Coronary Brain Data.

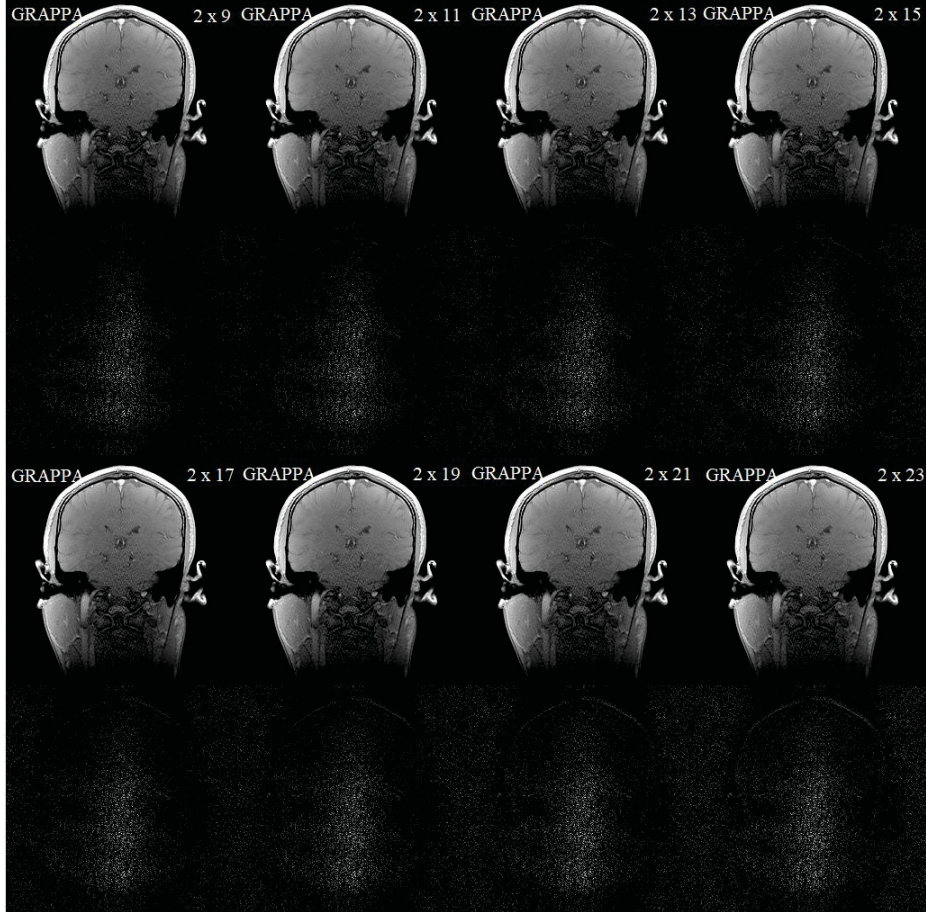| Kernel Size	NMSE	PSNR	SSIM
2 x 9	**1.491039e-01**	**4.137814e+01**	**9.525026e-01**
2 x 11	1.568932e-01	4.118346e+01	9.493362e-01
2 x 13	1.678597e-01	4.092436e+01	9.451885e-01
2 x 15	1.818892e-01	4.061941e+01	9.400285e-01
2 x 17	1.983778e-03	4.028633e+01	9.343896e-01
2 x 19	2.185512e-03	3.991481e+01	9.277394e-01
2 x 21	2.442428e-03	3.949184e+01	9.197368e-01
2 x 23	2.738180e-03	3.905595e+01	9.110834e-01

Fig. 5. A coronary brain image reconstruction results using different kernel sizes. The proposed grid search method can identify the best reconstruction quality in a search space.

5   Conclusion

In conclusion, we have introduced a grid search approach to automate the identification of the optimal GRAPPA reconstruction quality. Our proposed methodology has demonstrated its effectiveness in discerning the optimal kernel size. This has been substantiated through experiments on in-vivo MRI datasets, which affirm the method's ability to accurately pinpoint the best kernel size within a predefined search space. As a future course of action, we aim to enhance the search space by leveraging prior knowledge, thereby refining and optimizing the outcomes of clinical MRI even further.

Acknowledgment

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