

Automatic Kernel Selection For Optimal GRAPPA Reconstruction

R. Nana¹, T. Zhao¹, and X. Hu¹

¹Biomedical Engineering, Georgia Institute of Technology / Emory University, Atlanta, Georgia, United States

Introduction

GRAPPA [1] has emerged to be a popular k-space-based parallel imaging reconstruction technique. GRAPPA procedure involves a block-wise reconstruction in which multiple k-space lines from all coils are combined to fit a missing line for each single coil. Recent work has suggested the incorporation of acquired k-space points in both phase encoding (PE) and frequency encoding (FE) directions in the reconstruction [2]. Two main types of error exist for GRAPPA [3]: model error and noise-related error. The model error arises from the use of a limited (or truncated) size of the k-space subset, or kernel, to fit each missing datum. The noise-related error results from the noise amplification during the estimation of the fitting coefficients (weights) which is accomplished through an inversion of a linear equation and during the application of these weights in the estimation of the missing data. While a larger kernel reduces the model error, it increases the noise-related error. The choice of the optimal kernel, which balances these two errors, constitutes a challenge that has not been fully addressed. It has been shown that the optimal kernel depends on the coil array configuration, noise level in the acquired data, imaging field-of-view (FOV) orientation, and the auto-calibrating signals (ACS) lines [3,4]. Therefore, the use of a fixed kernel for all situations, as it is the case for common implementation of GRAPPA, is sub-optimal.

The present work presents a method based on cross-validation (CV) [5] for selecting the optimal kernel support for GRAPPA reconstruction. Cross-validation is one of the most popular methods for the selection of linear regression model among an appropriate class of model candidates. Our method explicitly uses the k-space locality criterion [6] to efficiently and automatically select the optimal kernel which minimizes the CV error and therefore yields the balance between the conflicting demand of accuracy of fit and stability. Results on human images are demonstrated and compared to an ordinary GRAPPA reconstruction which uses a fixed 4 x 5 (blocks on PE x columns on FE) kernel based on locality criterion. Because this method is simple and robust, it can be incorporated into most GRAPPA routines.

Methods

Cross-validation (CV) is a resampling technique to overcome overfitting and has been proven to be effective for model selection in linear regression. In our implementation of CV for model selection in GRAPPA, the available samples (ACS lines) are divided into k approximately equal size disjoint sets; kernel weights for each model are determined k times, each on a different combination of $k-1$ partitions and tested on the remaining partition. The cross-validation error for the given kernel is simply the mean of the k prediction errors. The case where k is equal to the size of the sample is referred as leave-one-out cross-validation. In our current implementation, leave-one-block-out cross-validation is used where a block comprises of one acquired line and its corresponding $R-1$ missing lines (R is the acceleration factor).

Assuming that the optimal kernel only contains the signals nearest to a given missing datum (k-space locality criterion), the method uses the brute-force search strategy to find the kernel size that generates the minimum cross-validation error. The search starts from the minimum kernel size (1 x 1) to a sufficiently large size. In the current implementation, the search extends up to the kernel size of 10 x 9. For certain kernel sizes, the source signals may have a symmetric or asymmetric arrangement around the missing datum. In the case of asymmetric arrangement, all possible configurations that can be formed within the data set are taken into account during the search. The effectiveness of this method is demonstrated on in vivo data and its performance is compared with GRAPPA reconstruction using a fixed 4 x 5 kernel.

Experiments were performed on a 3T Siemens Trio whole-body MR scanner using a 12-channels volume coil for both transmission and reception. Human brain data were acquired using a gradient-echo sequence (GRE) (TR = 300 ms, TE = 2.56 ms, flip angle = 80°, slice thickness = 5 mm, FOV = 256 mm) in axial scans. Unaccelerated multi-coil imaging was first performed with a matrix of 256 x 256 and later decimated to emulate the parallel imaging acquisition procedure. Three parallel imaging data sets were synthesized with acceleration factors of 2, 3, and 4, respectively. Correspondingly, the numbers of ACS lines used were 2, 6, and 9. All algorithms were implemented in MATLAB programming environment on a Pentium 4 CPU 2.00 GHz computer with 1GB RAM.

Results and Discussion

Figure 1 shows 1D projection plots of CV error (a) and mean square error (MSE) (b) vs. kernel size along PE direction for acceleration factor of 2 taking at kernel size of 3 along FE direction. The MSE was estimated between the reconstructed images and the unaccelerated images. The CV error decays to a minimum and is in a good agreement with the results of the MSE error. Similar results were obtained using different acceleration factors, coil geometries, noise levels in the data, FOV orientations, and numbers of ACS lines. The good correspondence between the CV error and the MSE validates the use of the CV as a measure to identify the optimal kernel. Figure 2 illustrates the reconstructed human brain images using (a) a fixed 4 x 5 kernel and (b) the CV method. It can be seen that the images reconstructed using automatically determined kernels are virtually free of ghosting artifacts as compared to the ones reconstructed using the fixed kernel. Limited number of ACS lines was intentionally used to demonstrate the effectiveness of the method although our method also performs well when more ACS lines are available. The searching part of the algorithm took 53 - 91 seconds to execute. Investigation to further optimize this searching time is underway.

Conclusion

This work demonstrates a simple and robust method that efficiently and automatically selects the kernel that balances the conflicting demand between accuracy of fit and stability in GRAPPA reconstruction. The method can be incorporated into most GRAPPA routines.

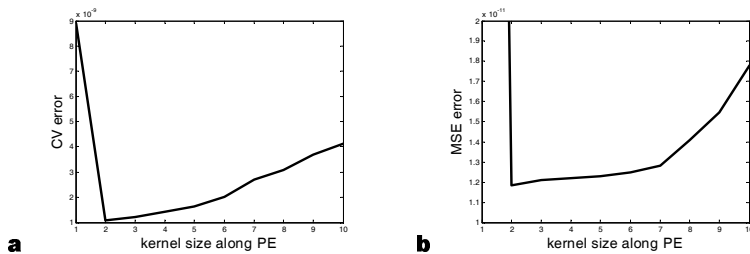


Fig.1 (a) CV error and (b) MSE error plots vs. kernel size along PE for kernel size along FE = 3, and R = 2.

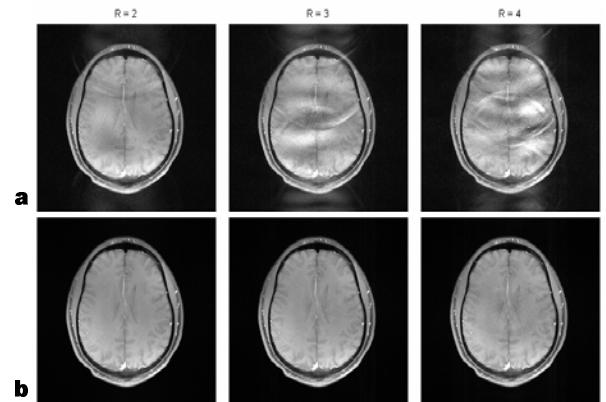


Fig.2 axial human brain images reconstructed using (a) fixed 4 x 5 kernel and (b) CV selected optimal kernel, for acceleration factors of 2, 3, and 4.

References

1. Mark A. Griswold, et al., MRM 47:1202-1210, 2002.
2. Ze Wang, et al., MRM 54 :738-742, 2005.
3. F. Huang, et al. ISMRM 2006, #2468.
4. Peng Qu, et al., JMR 174: 60-67, 2005.
5. M. Stone, J. Roy. Statist. Soc. B36: 111-147, 1974.
6. Ernest N. Yeh, et al., MRM 53:1383-1392, 2005.

Acknowledgements: This work was supported in part by the National Institutes of Health (RO1EB002009) and Georgia Research Alliance.