

# Context Based GRAPPA Reconstruction Using a Small Kernel

B. Kanberoglu<sup>1</sup>, L. J. Karam<sup>1</sup>, and J. P. Debbins<sup>2</sup>

<sup>1</sup>Electrical Engineering, Arizona State University, Tempe, AZ, United States, <sup>2</sup>Keller Center for Imaging Innovation, Barrow Neurological Institute, Phoenix, AZ, United States

## Introduction

GRAPPA (GeneRALized Autocalibrating Partially Parallel Acquisitions) [1] is a frequency domain parallel imaging reconstruction method which fills in missing k-space data using a weighted combination of the neighboring data points. These weights are determined through autocalibration signals (ACS) which are extra lines acquired in the center of the k-space. GRAPPA uses these extra lines to set up an over-determined system of equations and determines the weights by using a least squares solution. However, only one set of weights is obtained and used to calculate the whole k-space. In this paper, context based clustering method with a small GRAPPA kernel for the ACS data is proposed. The proposed method allows the adaptation of the weights to the local characteristics of the k-space data. Using the k-means clustering method, it is possible to obtain multiple sets of weights to fill in the missing k-space data. This presents advantages for small ACS data sets, or when using smaller size kernels.

## Theory and Methods

The well known k-means algorithm [2] was used to cluster the ACS data. k-means algorithm attempts to iteratively partition  $p$  observations (a vector) into  $k$  clusters so that each vector belongs to the nearest cluster mean. In this case, observations are the vectors created from the neighboring data points of target point in the ACS data. After collecting all the vectors, k-means is performed to divide the vectors into  $k$  clusters. For each cluster, a set of weights is generated using the least squares method. During the reconstruction of a missing data point, a vector is formed from its neighboring data points and then the vector is assigned a cluster. After the cluster is determined, the corresponding set of weights for that cluster is used to reconstruct the missing point

In order to obtain a reliable set of weights, each cluster needs to have a minimum number of elements that exceeds the total number of the weights to satisfy the over-determined system of equations. Because of this reason, *merging* is also implemented in the k-means algorithm. If a cluster has less elements than the required number, that cluster is merged with the nearest cluster. Different GRAPPA kernel sizes and geometries are implemented to compare the results.

All experiments were performed on a GE 3T long bore scanner using eight-channel head coil. Images were acquired using a GRE pulse sequence. The imaging parameters were FOV=22x22 cm, 256x256 matrix, TR=6976 ms, TE=2680 ms, slice thickness = 3mm. The proposed reconstruction and simulations are implemented in MATLAB programming environment (The Mathworks, Natick, MA). Subsampled k-space data with ACS data is simulated by subsampling, using an acceleration factor of 2, a full k-space dataset and keeping the ACS data untouched. In this way, the original data was preserved and used to compare the results. The mean squared error (MSE) is used as the error norm.

## Results and Conclusion

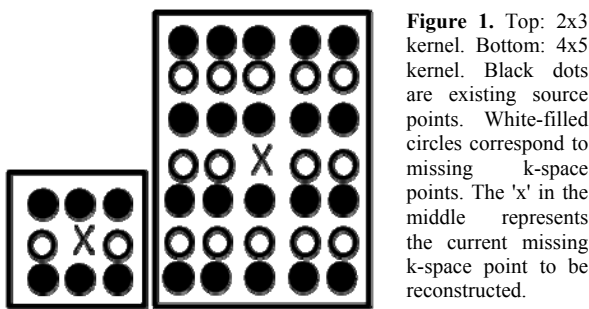
Two of the kernel geometries used are shown in Fig. 1. The results obtained using a 4x5 kernel without clustering (traditional GRAPPA) were compared to the results obtained using the 2x3 kernel with the proposed context-based clustering. It should be noted that the 4x5 kernel requires more than 160 (8 coil images with 20 points in each of them) equations to solve for the weights, while the 2x3 kernel requires a nominal 48 equations in order to get a reliable set of weights. When the 4x5 GRAPPA kernel was compared to the 2x3 GRAPPA kernel without clustering (traditional GRAPPA), the 4x5 kernel produced 5% better MSE than the 2x3 kernel. This is expected due to the increased number of weights available with the larger kernel, with the tradeoff being processing speed and complexity.

Using the proposed context-based clustering and context-based weight computation, which we refer to as context-based GRAPPA, with the 2x3 kernel, the 2x3 GRAPPA kernel with clustering was able to produce close MSE results when compared to the 4x5 GRAPPA kernel without clustering (traditional GRAPPA). Fig. 3 demonstrates a case where the proposed context-based GRAPPA with the smaller 2x3 kernel produces visually better results (Fig. 3b) as compared to the traditional GRAPPA (no clustering) with the larger 4x5 kernel (Fig. 3a). In this example (Fig. 3), only 4 ACS lines were used. Even though an over-determined system of equations was used for computing the weights corresponding to the 4x5 kernel, the traditional GRAPPA method with the 4x5 kernel could not produce a reliable weight set that could be used throughout the whole image. The same 4 ACS lines were sufficient to produce two sets of reliable weights (2 clusters) using the proposed context-based GRAPPA with the smaller 2x3 kernel size.

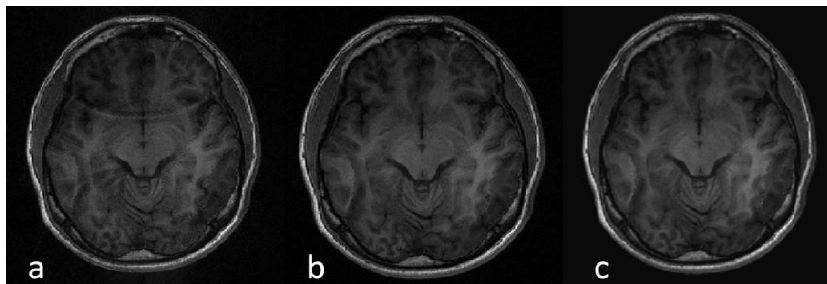
Context-based clustering for small GRAPPA kernels can be added to the existing GRAPPA algorithm to improve the MSE or speed up the acquisition by collecting less ACS data. In addition, the proposed context-based GRAPPA can produce better or same quality with smaller kernel sizes as compared to traditional GRAPPA with much larger kernel sizes. Our current non-optimized MATLAB implementation of the k-means algorithm tripled the computation time compared to traditional GRAPPA; however, the proposed context-based clustering could be implemented very efficiently in other programming environments or hardware.

## References

[1] Griswold MA, et al, MRM 2002, 47:1202-20. [2] Duda RO, Hart PE and Stork DG 'Pattern Classification' 2nd Ed. 2001, p.526-8.



**Figure 1.** Top: 2x3 kernel. Bottom: 4x5 kernel. Black dots are existing source points. White-filled circles correspond to missing k-space points. The 'x' in the middle represents the current missing k-space point to be reconstructed.



**Figure 3.** a) GRAPPA reconstruction, kernel size 4x5. b) GRAPPA with clustering, kernel size 2x3. c) GRAPPA reconstruction, kernel size 2x3.

**Figure 2.** MSE comparisons.

