

# An Improved Reconstruction Method for Auto-calibrating Partially Parallel Imaging

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## Introduction

In parallel imaging, images of the scanned object are modulated by the spatially localized sensitivity map of each component coil in the array coil, resulting in strong correlations between the k-space data of all component coils. Due to these correlations partially parallel imaging (PPI)[1] can skip partial phase encoding lines ( $k_y$ ) and recover the missing information from the acquired data. In current auto-calibrating k-space PPI methods [2,3], the data recovery is a linear interpolation process supervised by several additionally acquired reference lines (ACS). Due to this supervised learning and full use of ACS, the generalized auto-calibrating approach, GRAPPA [3], one of the state-of-the-arts, has demonstrated higher performance than other methods [3,4]. However, in these methods, only the correlations between the missing data point and its same column ( $k_x$ ) neighbors are used during the data recovery, which is insufficient for high accelerated PPI, since more information is lost with an increasing acceleration factor. It's necessary to include more information from the available data to provide a high quality recovery. In this report, we described a new auto-calibrating reconstruction algorithm for PPI using multi-column multi-line interpolation (MCMLI), i.e., recovering one missing data not only from neighboring points in different acquired lines but also from different columns. And a bidirectional fitting between the acquired lines and the reference lines was used to estimate the interpolation weights.

## Materials and Methods

Fig.1 is an illustration for GRAPPA and MCMLI. To recover one missing data point (white circles), an interpolation net is first built by locating its nearest neighbors in both approaches. While GRAPPA uses a 2-dimensional net, MCMLI uses a 3-dimensional interpolation net, whose leaf nodes are the missing data point's column and line nearest acquired neighbors. For illustration purpose, only 2 line neighbors and 3 column neighbors are used in the MCMLI net shown in Fig. 1. The net weights are the interpolation weights, which are obtained by solving a linear fitting problem between the ACS (red circles) and the acquired data (cyan circles), i.e., the root node of the net is an ACS datum, and the leaf nodes are the acquired neighbor data. Denote the acceleration factor as R, one acquired line and the R-1 consecutive lines can be defined as a block. The net for each missing data point in the same ordinal lines of all blocks of one coil has the same structure, only the node values are different for different missing data. And it has different structure for different ordinal missing lines in a block. Extra training steps for estimating the net weights are got by treating the regularly acquired data in the center as reference one.

Imaging experiments were performed on a 3T Siemens Trio whole body MR scanner with an 8-channel array coil (Nova Medical Inc., Wakefield, MA) using a gradient echo sequence (TR=168 msec, TE=3.77 msec, slice thickness 6 mm, FOV=220 mm). For full-FOV imaging, the matrix was 128x128. Partial parallel acquisition (PPA) was also performed using iPAT sequence with acceleration factors of 2 and 3. Five healthy volunteers gave the written informed consent before scanning following an Institutional Review Board approved protocol. Raw k-space data were saved.

Simulations were performed using the full-FOV in-vivo data. Partially phase encoded lines were removed to simulate the partial parallel acquisition (PPA). Three PPA were simulated with acceleration factors as 2, 3 and 4. Correspondingly, the ACS lines used were 12, 16, and 18 ACS respectively. The simulated acquisitions are therefore termed the simulated PPA2, PPA3, and PPA4, respectively. The whole reconstruction procedure for simulated PPA data or true PPA data was performed off-line with custom programs written in MATLAB (Mathworks, Sherborn, MA). Four neighbor lines and 3 neighbor columns were used for MCMLI, and 4 lines and 1 column were used for GRAPPA. To reduce the reconstruction time, we only used the center part of each acquired line and ACS line to estimate the interpolation weights, since most energy of k-space data is concentrated in the center.

The root of the mean squared (RMS) distance between the simulated PPA images and full-FOV images was calculated for different acceleration factors, to assess the recovery performance of each PPI reconstruction methods.

## Results and discussions

Fig. 2 shows the simulation result. The RMS has the same scale as the MR images, 0-1200, and the mean RMS values were averaged across 5 subjects. From this figure, we can see that with increasing acceleration factor, MCMLI increasingly outperforms GRAPPA. Fig. 3 shows the same slice from the full-FOV acquired image and PPA images with different acceleration factors, reconstructed with GRAPPA and MCMLI. Compared to the full-FOV image, MCMLI reconstructed images presented smaller ghost artifacts than GRAPPA reconstructed ones, which are the main distortions of PPA images.

With MCMLI, using different number of neighbor columns could yield different reconstruction quality. As in GRAPPA [3], the final image could be a weighted averaged of different reconstructions. And in the case of high accelerated PPA, more neighbor columns can yield better reconstruction quality, with a side-effect of requiring longer reconstruction time. In this work, 4 line 3 column MCMLI took 6 times longer than GRAPPA. A similar approach has previously been reported for a 2-fold accelerated phantom image [5]. Our approach is different from this prior report in two ways. First, we can control the overall fitting precisions by including both line neighbors and column neighbors in a single recovery step. Second, only the center k-space data are used for data fitting, which can prevent estimation errors caused by high frequency noises.

## Reference

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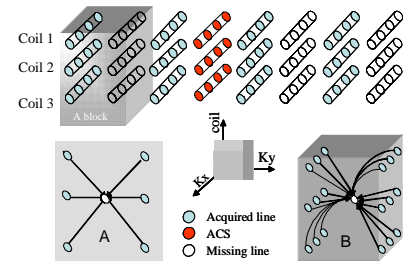


Fig. 1: Interpolation net of A) GRAPPA and B) MCMLI for a 2-fold accelerated PPI. 3 coils are used. Each circle represents one k-space data point. White circles are missing data, cyan circles are acquired data, and the red circles represent reference data.

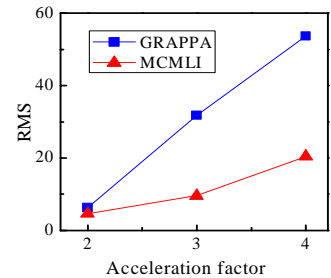


Fig. 2: RMS vs acceleration factor curves for GRAPPA and MCMLI using the simulated PPA data.



Fig. 3: Full-FOV acquired image a) and GRAPPA reconstructed PPA2 b) PPA3 c), MCMLI reconstructed PPA2 d) and PPA3 e) images.