EFFICIENT GRAPPA RECONSTRUCTION USING RANDOM PROJECTION

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ABSTRACT

As a data-driven technique, GRAPPA has been widely used for parallel MRI reconstruction. In GRAPPA, a large amount of calibration data is desirable for accurate calibration and thus estimation. However, the computational time increases with the large number of equations to be solved, which is especially serious in 3-D reconstruction. To address this issue, a number of approaches have been developed to compress the large number of physical channels to fewer virtual channels. In this paper, we tackle the complexity problem from a different prospective. We propose to use random projections to reduce the dimension of the problem in the calibration step. Experimental results show that randomly projecting the data onto a lower-dimensional subspace yields results comparable to those of traditional GRAPPA, but is computationally significantly less expensive.

Index Terms— GRAPPA, Dimension Reduction, Random Projection, Restricted Isometry Property

1. INTRODUCTION

Generalized autocalibrating partially parallel acquisitions (GRAPPA) [1] has been widely used for reconstructing MR images from reduced acquisitions with multiple receivers. It reconstructs the missing *k*-space data by a linear combination of the acquired data, where the coefficients for combination are estimated using some additionally acquired auto-calibration signal (ACS) lines. A high acceleration can usually be achieved when a larger number of channels are used in acquisition [2]. A lot of work has dedicated to developing phased array coils with many channels [3]. However, such an increase in channel numbers also increases the computational burden significantly at the same time. Most existing work attempts to address this issue by reducing the effective number of channels using hardware-based approaches or software-based ones. In the hardware-based approach [4], a hardware RF signal combiner inline was placed after preamplification and before the receiver system to construct an eigencoil array based on the noise covariance of the receiver array. Optimal SNR and similar reconstruction quality can be achieved with such a channel reduction. However, the requirement of additional hardware can be cumbersome. In contrast, the software-based channel reduction methods are more flexible. For example, principal component analysis (PCA) has been used to compress large array coils [5-8]. The coil compression process generates a new set of fewer virtual channels which can be expressed as a linear combination of the physical channels. In addition, several studies [9-11] have investigated to synthesize a single target channel for *k*-space-based reconstruction techniques. These methods combine data from multiple channels prior to calibration so that the convolution-based calibration and unaliasing only need to be performed once instead of for each channel and significant computation gain can be achieved.

Random projection is another useful method in data dimension reduction [12,13]. The concept of random projection is related to compressed sensing, a topic that has attracted a lot attentions recently. By projecting the data to lower dimensions using some random matrices with certain properties, the useful information is still preserved in the reduced data. Since GRAPPA calibration involves solving a large well-over-determined equation, we expect random projection would help reduce the equation to a slightly over-determined equation without compromising the information.

In this paper, we propose to use random projection to reduce the dimension in GRAPPA calibration. Random matrices that have been proved to satisfy the restricted isometry property [14] are used as the projection matrices. As a result, the over-determined equation in GRAPPA calibration can be solved in a lower dimension and thereby in a shorter time. Our experiment results demonstrate that the proposed method can achieve the same reconstruction quality with only 1/6 the computation time of the conventional GRAPPA.

2. COMPLEXITY OF GRAPPA

The GRAPPA reconstruction can be represented as

$$S_j\left(k_y + r\Delta k_y, k_x\right) = \sum_{l=1}^{L}\sum_{b=B_1}^{B_2}\sum_{h=H_1}^{H_2} w_{j,r}\left(l,b,h\right) \times S_l\left(k_y + bR\Delta k_y, k_x + h\Delta k_x\right) \quad (1)$$

where the unacquired *k*-space signal S_j on the left-hand side is obtained by a linear combination of the acquired *k*-space

signals on the right-hand side. Here *w* denotes the coefficient set, *R* represents the reduction factor, *j* is the target coil, *l* counts all coils, *b* and *h* transverse the acquired neighboring *k*-space data in k_y and k_x directions respectively, and the variables k_x and k_y represent the coordinates along the frequency- and phase-encoding directions, respectively. The formulation of GRAPPA can be simplified as a matrix equation

$$\mathbf{b}_{m\times l} = \mathbf{A}_{m\times n}\mathbf{x}_{n\times l}, \quad (2)$$

where **A** represents the matrix comprised of the acquired data, **b** denotes the vector of the missing data, and **x** represents the coefficients. In general, the coefficients depend on the coil sensitivities and are not known a priori. In GRAPPA, some auto-calibration data are acquired and used as the vector **b** to estimate the coefficient vector **x** based on the shift-invariant property. In this case, the least-squares method is commonly used to calculate the coefficients:

$$\hat{\mathbf{x}} = \min_{\mathbf{x}} \left\|\mathbf{b} - \mathbf{A}\mathbf{x}\right\|^2 . \quad (3)$$

Since there are usually much more ACS data available to set up Eq. (2) than the number of unknown equations, the problem is well over-determined and the solution is given by:

$$\mathbf{x} = (\mathbf{A}^H\mathbf{A})^{-1}(\mathbf{A}^H\mathbf{b}) \quad (4)$$

In summary, there are two parts in the GRAPPA reconstruction process: the calibration process and the synthesis process. The computational expense of each part can be estimated using matrix multiplication and inversions. The calibration part requires $mn^2 + 2lmn + n^3$ complex-valued multiplications. Assuming *R* is the outer reduction factor (ORF), N_p is the number of phase-encoding lines that are possible fit locations along the phase-encoding direction, N_x is the number of points along the frequency encoding direction, N_c is the total number of all channels for the original k-space data, and d_x and d_y are the convolution size of GRAPPA along the frequency-encoding and phase-encoding directions respectively, then $m = N_p N_x$, $n = d_x d_y N_c$ and $l = (R-1)N_c$ [15]. Furthermore, in the synthesis step of GRAPPA, $N_u N_x N_c^2 d_x d_y (R-1)$ complex-valued multiplications are needed, where N_u is the number of phase-encoding lines to be synthesized at a particular phase-encoding offset location. Therefore, the total computational expense for GRAPPA reconstruction is approximately on the order of $N_p N_x (N_c d_x d_y)^2 + 2N_p N_x N^2{}_c d_x d_y (R-1) + (N_c d_x d_y)^3 + N_u N_x N_c^2 d_x d_y (R-1)$. If we adopt the commonly used 32 ACS lines and reconstruction parameters [15] N_{acs} = 32, N_x = 256, d_x = 13, d_y = 4, R = 2, N_u = 112, N_c = 8, *SlideBlock* = 4, $N_p \approx N_{acs} \times (R-1) = 32$, the ratio between the calibration and synthesis processes are $\frac{N_p d_x d_y}{N_u (R-1)} \approx 16$, which suggests the calibration process dominates the total computational time. Reduction of the calibration cost would reduce the total cost directly.

3. PROPOSED DIMENSION REDUCTION METHOD FOR GRAPPA

3.1 Random Projection

Random projection has been shown to be very useful in data dimension reduction [12,13]. In random projection, an original *m*-dimensional data is projected to a *k*-dimensional (*k*<<*m*) subspace, using a random *k*×*m* matrix **R**, with a dimension reduction factor *m*/*k*. The key idea of random mapping arises from the Johnson-Lindenstrauss lemma [16]: if points in a vector space are projected onto a randomly selected subspace of suitably high dimension, then the distances between the points are approximately preserved.

LEMMA *(Johnson and Lindenstrauss, 1984) Suppose we have an arbitrary matrix* $\mathbf{A} \in \Re^{n\times m}$. *Given any* $\varepsilon > 0$, *there is a mapping* $f : \Re^m \to \Re^k$, *for any* $k \geq 12\frac{\log n}{\varepsilon^2}$, *such that for any two rows* $u, v \in \mathbf{A}$, *we have*

$$(1-\varepsilon)\left\|f(u)-f(v)\right\|^2 \leq \left\|u-v\right\|^2 \leq (1+\varepsilon)\left\|f(u)-f(v)\right\|^2 \quad (5)$$

The theorem states that we can find such an *f* for any matrix **A**, but does not state how to find such an *f*. Apparently the criterion in Eq. (5) shares similarity with the well-known restricted isometry property (RIP) in compressed sensing [17]. Many studies have investigated linear transformations that satisfy the RIP. These matrices can be used for *f* as long as *k* is greater than $12\frac{\log n}{\varepsilon^2}$. Random matrices from certain distributions have been shown to satisfy RIP. Therefore random projections using these matrices are good for dimension reduction. In particular, when the computational complexity is of concern, random matrices with only 0 and 1 elements are especially useful because no multiplication is needed when computing the projection.

3.2 Dimension reduction for GRAPPA

To reduce the computational cost of the calibration process in GRAPPA, we exploit random projection to reduce the dimension. Specifically, we multiply a random matrix **R** on both sides of Eq. (2):

$$\mathbf{R}_{k\times m}\mathbf{b}_{m\times 1} = \mathbf{R}_{k\times m}\mathbf{A}_{m\times n}\mathbf{x}_{n\times 1}, \quad (6)$$

where *k* is the reduced dimension and is chosen to be (2~4) times of *n*. For the same number of unknowns *n*, the number of equations have been reduced to be about (2~4) times of that of unknowns. Each element of **R** is independent random variables from the following distribution [18]:

$$R_{(i,j)} = \sqrt{3}\begin{cases} 1 & p = 1/6 \\ 0 & p = 2/3 \\ -1 & p = 1/6 \end{cases}. \quad (7)$$

With such a sparse binary projection matrix, a subset of equations are linearly combined in a random fashion to form a new set of equations, and with a high probability the important information is maintained in the lower dimensional space after the projection.

Since the sparse matrix has only 0s and ±1s, the computational expense of random projection can be neglected because only additions are needed. If we assume k is $2n$, and the commonly used GRAPPA parameters are used, then the size of the equation is reduced from 8,192×416 in Eq. (3) to 832×416 in Eq. (6). The calibration process has a saving of approximately 10 times. Now the ratio between the computation time of the calibration and synthesis processes becomes 2.3. The computational expense ratio between GRAPPA and the randomly-projected GRAPPA (RP-GRAPPA) is 5.1, suggesting a saving of 5.1 times.

4. EXPERIMENTAL RESULTS

The proposed method was tested on a set of *in vivo* data downloaded from http://www.nmr.mgh.harvard.edu/~fhlin/codes/mprage_8ch_slice20.mat. The data was acquired on a 3T SIEMENS Trio system using 3-D MPRAGE sequence (TE = 3.45 ms, TR = 2530 ms, TI = 1100 ms, Flip angle = 7°, slice = 20, matrix = 256 x 256, slice thickness = 1.33 mm, FOV = 256 mm^2) and an 8-channel head array coil. The data was acquired in full and then manually undersampled retrospectively to simulate the accelerated acquisition. Both the conventional GRAPPA and randomly-projected GRAPPA (RP-GRAPPA) were used to reconstruct the final image from reduced acquisition. All code are written in MATLAB and run on a PC with 3.4GHz CPU and 16GB memory, except that for Figure 2.

For the proposed randomly-projected GRAPPA, the random projection matrix has elements drawn from a Bernoulli distribution and reduces the dimension of the calibration equation from m to k. We define a factor $\lambda = k/n$, which represents how over-determined the new equation is after dimension reduction. The smaller the λ is, the less the equation is over-determined.

To measure the accuracy of the proposed dimension reduction method, we compare reconstructions with and without dimension reduction both visually and quantitatively using normalized mean squared error (NMSE). The computational time is measured in CPU time from MATLAB.

4.1 2-D GRAPPA Results

The savings by the proposed method was first evaluated in 2-D reconstruction with 1-D undersampling. An ORF of 2 with 32 ACS lines was used with a net acceleration of 1.78. A single slice of the 3-D image is reconstructed. In both GRAPPA and RP-GRAPPA methods, the number of blocks d_y is 4 and the number of columns d_x is 13. Figure 1 shows the reconstructions for GRAPPA (left) and RP-GRAPPA (right). The NMSEs of GRAPPA and RP-GRAPPA are 0.035 and 0.041 respectively, and the CPU times are 27.7 s and 4.6 s, respectively. The CPU time ratio between GRAPPA and RP-GRAPPA is $T_{GRAPPA} / T_{RP-GRAPPA} = 27.7/4.6 \approx 6$. Such a saving in computation time roughly agrees with our theoretical analysis. It is seen from the results that the proposed RP-GRAPPA has an NMSE about the same as the conventional GRAPPA, but saves about 6 times in the computational cost.

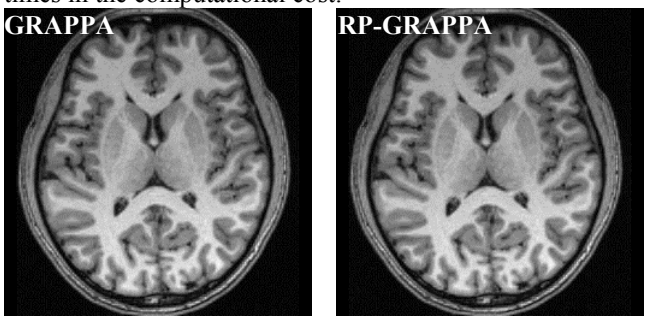

Fig. 1 2-D reconstructions using GRAPPA (left) and RP-GRAPPA (right)

In order to show the relationship between λ and the computation time, Fig. 2 shows the curves of NMSE and CPU time for RP-GRAPPA as λ increases from 1 to 2.5, with a step of 0.1. It is seen that the NMSE decreases rapidly (approximately in exponential) as λ increases and becomes sufficiently low for λ>2, while the CPU time increases only approximately linearly with λ. It should be noted that the results shown in Figure 2 were obtained from a PC with 1.7GHz CPU and 512MB memory to show the increment in time with λ more clearly.

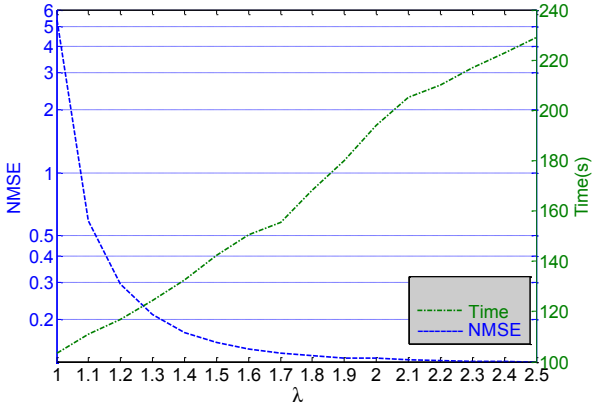

Fig. 2 NMSE and CPU time of RP-GRAPPA versus λ

4.2 3-D GRAPPA Results

We also evaluated the performance of the proposed method in 3-D reconstructions with 1-D undersampling (only along

the phase direction). An ORF of 3 with 32 ACS lines were used. In both methods, the number of blocks d_y and d_z are 4 and 2, respectively. The number of columns d_x is 11. In Fig. 3, a single slice of the 3-D reconstructions using GRAPPA and the proposed method are compared. The NMSEs for the 3-D images are 0.38 for GRAPPA and 0.40 for RP-GRAPPA. The CPU time for GRAPPA is 16834 s, while RP-GRAPPA is 1616 s, corresponding a saving of about 10 times. Compared with GRAPPA, RP-GRAPPA saves hours in calibration time without compromising the image quality.

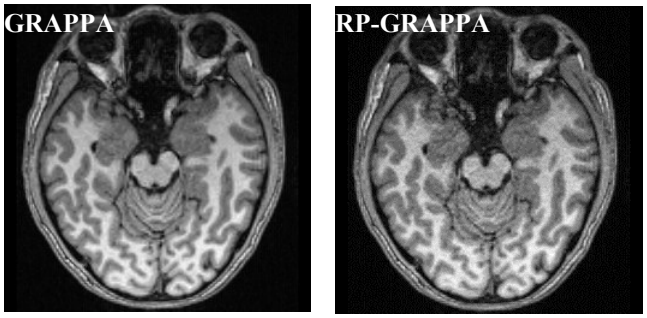

Fig. 3 A slice of 3-D reconstructions using GRAPPA (left) and RP-GRAPPA (right).

5. CONCLUSION

In this paper, a random project method is used to reduce the dimension of the over-determined equations in GRAPPA and thus save the computation time. Experimental results demonstrate that random projection can reduce the execution time by a factor up to 6 for 2-D GRAPPA and 10 for 3-D GRAPPA without compromising the reconstruction quality. The method is expected to be especially useful for large array systems with 32 or more channels.

6. ACKNOWLEDGEMENT

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