A random projection approach to highly efficient GRAPPA reconstruction

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INTRODUCTION:
In GRAPPA [1], 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 [2,3]. In this paper, we tackle the complexity problem from a different prospective. We propose to use random projections [4,5] to reduce the dimension of the problem in the calibration step. Similar to compressed sensing, by projecting the data to lower dimensions using some random matrices satisfying the restricted isometry property (RIP) [6], the useful information is still preserved in the reduced data. Experimental results show that randomly projecting the data onto a lower-dimensional subspace yields results comparable to those of traditional GRAPPA, but is computationally less expensive.

THEORY AND METHOD:
In GRAPPA, auto-calibration signals (ACS) are acquired and used to estimate the reconstruction coefficients. Let $\mathbf{b}_{m\times l}=\mathbf{A}_{m\times n}\mathbf{x}_{n\times l}$ represents the GRAPPA calibration process, where $\mathbf{A}$ represents the matrix comprised of the acquired data, $\mathbf{b}$ denotes the vector of the targeting calibration data, and $\mathbf{x}$ represents the unknown coefficients. The least-squares method is commonly used to calculate the coefficients: $\hat{\mathbf{x}} = \min_{\mathbf{x}} \|\mathbf{b}-\mathbf{A}\mathbf{x}\|^2$. Since there are usually much more ACS data than the number of unknown equations, the problem is well over-determined ($l<<n$). To reduce the computational cost of the calibration process, we exploit random projection [4,5] to reduce the dimension. Specifically, we use a compressed sensing matrix $\mathbf{R}$ which satisfy the RIP to project both $\mathbf{b}$ and $\mathbf{A}$ to lower dimensions $\mathbf{R}_{k\times m}\mathbf{b}_{m\times l}=\mathbf{R}_{k\times m}\mathbf{A}_{m\times n}\mathbf{x}_{n\times l}$, where k is the reduced dimension and is chosen to be (2~4) times of n; each element of $\mathbf{R}$ is drawn from I.I.D. Bernoulli distribution. That is, we linearly combine a subset of equations in a random fashion to form a new set of equations. In this way, we have a high probability to maintain the important information in the lower dimensional space after the projection. If commonly used parameters are used in calibration, it can be calculated theoretically [7] that the computational expense ratio between GRAPPA and the randomly-projected GRAPPA (RP-GRAPPA) is about 6, suggesting a saving of 6 in time.

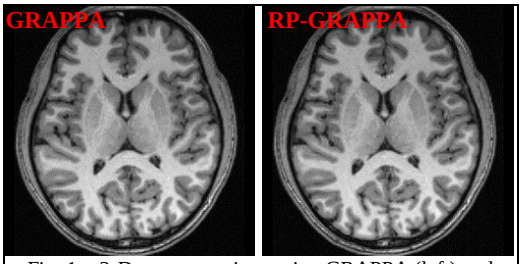

Fig. 1. 2-D reconstructions using GRAPPA (left) and RP-GRAPPA (right)

RESULTS AND DISCUSSION:
The proposed method was tested on a set of *in vivo* data. 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 = 256×256, 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. All code are written in MATLAB and run on a PC with 1.7GHz CPU and 512MB memory. The computational time is measured in CPU time from MATLAB. Fig. 1 shows the 2-D reconstructions for GRAPPA (left) and RP-GRAPPA (right) with an ORF of 2 and 32 ACS lines. The normalized mean squared errors (NMSE) 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. We define a factor $\lambda=k/n$, which represents how over-determined the new equation is after dimension reduction. 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 $\lambda>2$, while the CPU time increases only approximately linearly with λ. 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 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.

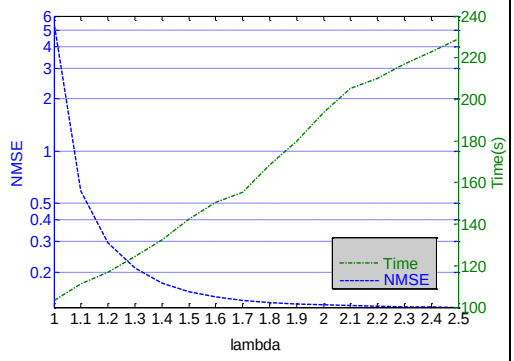

Fig.2. NMSE and CPU time of RP-GRAPPA versus λ

CONCLUSION:
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.

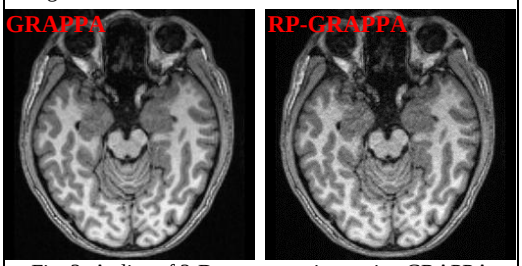

Fig. 3. A slice of 3-D reconstructions using GRAPPA (left) and RP-GRAPPA (right).

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