SELF-CONSISTENT GRAPPA RECONSTRUCTION WITH CLOSE-FORM SOLUTION

Yu Ding[1], Hui Xue[2], Ti-chiun Chang[3], Christoph Guetter[3], and Orlando Simonetti[1]

[1]*Dorothy M. Davis Heart and Lung Research Institute, The Ohio State University, Columbus, OH, United States,* [2]*siemens corporate research,* [3]*Siemens Corporate Research*

Introduction: Parallel MRI (pMRI) reconstruction techniques reduce scan time by undersampling k-space; in real-time cine imaging this directly improves temporal resolution. GRAPPA, a k-space based pMRI technique, is widely used clinically for dynamic cardiac MRI because of its robustness [1]. It reconstructs the missing k-space by solving a set of linear equations using an implicit assumption: the missing k-space lines are uncorrelated with the sampled lines. In reality, however, all k-space lines are correlated. The correlation can be estimated easily, and we expect that incorporating this correlation into the image reconstruction algorithm will improve the image quality by reducing the noise.

Several new algorithms have been proposed to take advantage of k-space correlations, such as SPIRiT[2] and PRUNO[3]. However, these methods have no closed-form solutions, and can only be solved using computationally-intensive iterative methods. We propose a new k-space based pMRI technique, SC-GRAPPA (self-consistent GRAPPA) by including an extra set of linear equations utilizing the intrinsic correlation between skipped k-space points. SC-GRAPPA combines the linear equations of traditional GRAPPA with these additional equations to solve for the missing k-space data. SC-GRAPPA utilizes a least-square solution of the linear equations, and therefore has a closed-form solution without any free parameters.

Theory: The multiple-channel MRI k-space data has local correlations. Therefore, there exists a null space N, for every vectorized local k-space data k, and $c \in N$: we have: $c \cdot k = 0$. Since every vector in null space N has this property, we have a matrix equation:

$$\boldsymbol{A}k = 0 \qquad (1)$$

Every row of matrix A is a vector in null space N. The matrix $\boldsymbol{A}$ can be estimated from a fully sampled k-space, i.e. the ACS lines of the GRAPPA reconstruction. We adopt the algorithm proposed by Zhang [3]. In the SC-GRAPPA algorithm, there are two sets of linear equations. The first set is the GRAPPA reconstructed k-space. This is a priori estimation of k-space. The second set is the null-space constraint, as in Equation (2).

$$k = k_0 + w \qquad (2.a)$$

$$0 = \boldsymbol{A}k + v \qquad (2.b)$$

where w and v represent the random noise terms. To simplify the results, let's assume that w and v have no correlations, with the same variance. The least-square solution of Equation (2) is:

$$k = k_0 + A^T(I + AA^T)^{-1}(Ak_0) \qquad (3)$$

This is a closed form solution in matrix form. It is a multiple-kernel convolution in k-space, which can be computed efficiently using pixel wise multiplication in image space.

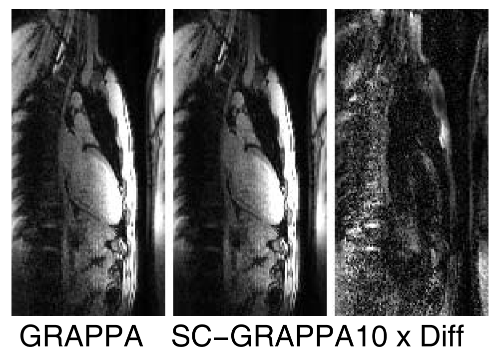

Figure 1. GRAPPA reconstruction, SC-GRAPPA reconstruction, and the 10 times the difference. The low SNR region has significant difference.

Methods: SC-GRAPPA was tested in multiple cardiac views in a single healthy volunteer. MR real-time cardiac cine images with acceleration rate 6 were reconstructed using both GRAPPA and SC-GRAPPA. We acquired SSFP real-time cine images on a 3.0T MR scanner (MAGNETOM Trio, Siemens Healthcare, Germany) using TGRAPPA with parallel acceleration rate = 6, in vertical and horizontal long-axis and four short-axis views. Imaging parameters were: 192 × 96 matrix reconstructed from 192 x 16 acquired matrix, 6 mm thick slice, flip angle=48^o, TE/TR = 1.0/2.56 ms, pixel bandwidth=1447 Hz/pixel, FOV = 380 × 285 mm^2. A total of 256 images were acquired per image series to support statistical analysis. The reconstruction is computed in k-space. The image SNR reconstructed by both methods was evaluated using the MP-law method based on the random matrix theory [4].

Results: SC-GRAPPA showed more than 10% global signal-to-noise ratio (SNR) gain over GRAPPA. More significant (> 20%) noise level reduction was observed in low-SNR regions (near the spinal cord, where the signal penetration is poor) in the images, see Figure 1. The image reconstruction time was more than 10 times slower than GRAPPA reconstruction when computed in k-space.

Discussion and Conclusion: We proposed a new k-space pMRI method, the SC-GRAPPA algorithm. It combines the traditional GRAPPA reconstruction and the recently described k-space self-consistency condition. The new method has a closed-form solution. Compared to the iterative self-consistent reconstruction methods [2,3], SC-GRAPPA has two advantages: the computation load is very low, and the robustness is high. There are no ad hoc assumptions about the image content or free parameters to estimate. The self-consistent condition can be derived from the standard ACS lines used by GRAPPA and therefore the method can be utilized in any scenario where GRAPPA can be applied. The convolution operation in Equation (3) can instead be computed in image space as pixel-wise multiplication to avoid the time-consuming k-space convolution approach and increase the speed of reconstruction. In conclusion, SC-GRAPPA offers improved SNR over GRAPPA and should provide advantages in situations where high acceleration rates are needed.

References: [1] Griswold MA, et al, Magn Reson Med, 47 (2002), 1202. [2] Lustig M. et al, Magn Reson Med, 64 (2010), 457. [3] Zhang J, et al. Magn Reson Med, 66 (2011), 1241. [4] Ding Y et al, Magn Reson Med 63: 782 (2010)