

# Improved Compressed Sensing using Parallel Imaging: TGRAPPA-PRISM for Cardiac Cine MRI

Da Wang<sup>1</sup>, Stanislas Rapacchi<sup>2</sup>, Hao Gao<sup>3</sup>, and Peng Hu<sup>2</sup>

<sup>1</sup>Biomedical Physics/Radiological Sci, UCLA, Los Angeles, CA, United States, <sup>2</sup>UCLA, Los Angeles, CA, United States, <sup>3</sup>EMORY University, Atlanta, GA, United States

**Introduction:** Cardiac cine MRI is routinely used to assess cardiac function but limitations in acquisition speed require a compromise between spatial and temporal resolution. A novel compressed sensing MRI reconstruction method has been proposed for dynamic MRI using Prior Rank, Intensity and Sparsity Model (PRISM) [1][2]. By using a low rank decomposition, PRISM can extract the stationary background component from dynamic images to further promote sparsity of the motion component for L1 norm minimization. An incoherent under-sampling pattern is used in k-t space. The combination of parallel MRI methods like GRAPPA[3] and TGRAPPA[4] with compressed sensing methods has shown great potential[5][6][7] to improve the reconstructed image quality and acceleration rate. We propose to further improve PRISM compressed sensing algorithm by using TGRAPPA to fill in additional data lines in the k-space before feeding to the PRISM algorithm.

**Theory:** PRISM reconstruction is formulated as the following optimization problem:  $(X_L, X_S) = \underset{(X_L, X_S)}{\operatorname{argmin}} \frac{1}{2} \|AX - Y\|_2^2 + \lambda_* \|X_L\|_* + \lambda_1 \|WX_S\|_1 +$

$\lambda_t \|WX\|_*$ . Matrix  $X$  represents dynamic MR images, where each column vector is all sorted spatial pixels for one temporal frame in the dynamic images.  $X$  can be decomposed into low-rank background component  $X_L$  and the sparse motion component  $X_S$ .  $X = X_L + X_S$ . The first term is the data fidelity term,  $A$  represents 2D Fourier transform (temporal direction is not transformed),  $Y$  represents randomly under-sampled k-space data that is acquired,  $\| \cdot \|_*$  represents the nuclear norm i.e. the sum of its singular values,  $\| \cdot \|_1$  represents L1 norm.  $W$  represents tight framelet sparsifying transform, but wavelet can potentially be used as well. Based on the randomly under-sampled k-t-space data (Fig.1), we used TGRAPPA to fill in additional k-space lines in a sliding window under-sampling pattern in center k-space and missing lines adjacent to the acquired paired lines in outer k-space, as shown in Fig. 1. We then perform PRISM reconstruction based on the resulting TGRAPPA-recovered k-space data.

**Methods:** Full-sampled cine cardiac MRI data were acquired by TRUFI sequence on SIEMENS Avanto 1.5T scanner with a multi-channel surface coil. The data were acquired along the 3 slices orientations (vertical long axis VLA, horizontal long axis HLA, and short axis SA), using 14-30 frames per cardiac cycle depending on heart rate. We retrospectively decimated the k-space lines in phase encoding direction to generate net acceleration factors  $R=4, 6$  and  $8$  using following under-sampled patterns: 40% of the chosen lines were located in the center k-space region with a  $R_c=3$  sliding window under-sampling pattern; The remaining 60% lines were paired and randomly distributed in outer k-space region. A sliding window of  $3 \times R_c$  nearest frames of each frame were merged to a complete center k-space, which was used as the auto-calibration signals (ACS) lines for the frame's TGRAPPA reconstruction in center k-space and GRAPPA reconstruction for recovering 2 missing adjacent lines to each paired lines in outer k-space, as shown in Fig. 1. The pairing of the k-space lines has been shown to reduce eddy current effects in SSFP sequences [8] and would therefore be helpful for prospective implementation of the under-sampling.

**Results:** We use retrospectively decimated data sets (404\*120 pixels for fully-sampled data, 12-19 channels) of cardiac cine images to test the proposed method. After TGRAPPA reconstruction, PRISM will have a better starting point for reconstruction. The effective acceleration factor for the PRISM stage of the reconstruction was further decreased by TGRAPPA and the proposed method reconstructs images with better image quality (Fig.2). TGRAPPA-PRISM was able to improve image sharpness in diastole frames (red arrows) and reduce temporal blurring artifacts in systole frames (blue arrows).

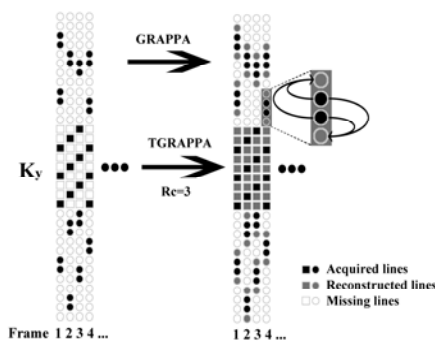


Fig. 1: Local TGRAPPA reconstruction on a randomly under-sampled 2D dynamic MRI dataset. Gray boxes show

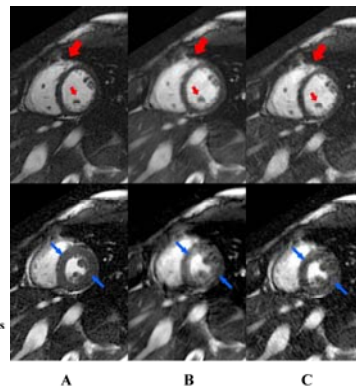


Fig. 2: SA slice reconstruction from 6-fold under-sampled datasets: A) Reference Image (no under-sampling). B) 6x-PRISM. C) 6x-TGRAPPA-PRISM. Upper images are diastole, lower images are systole.

**Discussion:** In this work, we demonstrate that by inserting an additional parallel imaging step before PRISM algorithm can improve the image quality of our reconstruction by reducing blurring effects and artifacts. The low rank structure of PRISM induces temporal blurring but improves greatly reconstructed image quality. Whereas TGRAPPA exploits correlation between coils and reduces the actual acceleration factor for the PRISM reconstruction stage alone. The combination of TGRAPPA and PRISM proves to be superior to PRISM alone. We note that TGRAPPA reconstruction increases the background noise level due to geometric factors. The amount of SNR degradation and its spatial distribution remains to be further investigated because in this case the TGRAPPA kernels are only applied at partial regions rather than on the full k-space as is the case for conventional parallel imaging reconstruction.

**References :** [1] Gao H., et. al. Inverse Problems. 2011; 27: 115012 [2] Gao H., et. al. ISMRM 20. 2012. p2242 [3]Griswold MA., et. al. MRM, 2002; 47: 1202-1210 [4] Breuer, F., et. al. MRM, 2005, 53: 981-985 [5] Huang F., et. al. ISMRM 19. 2011. p2860 [6] Weller DS, et. al. ISMRM 18. 2010. p4880 [7] Liang D., et. al. MRM, 2009; 62: 1574-1584 [8] Bieri O., et. al. MRM, 2005; 54: 129-137