K-t PCA GROWL: Sequential Combination of Partially Parallel Imaging and K-t PCA

Haikun Qi¹, Feng Huang², Xiaoying Cai¹, Dan Zhu¹, Feiyu Chen¹, Chun Yuan^{1,3}, and Huijun Chen¹

¹Center for Biomedical Imaging Research, Tsinghua University, Beijing, Beijing, China, ²Philips Healthcare, Florida, United States, ³Department of radiology, University of Washington, Seattle, WA, United States

Target Audience: Scientists interested in high spatiotemporal cardiac cine imaging.

Purpose: The k-t principal component analysis (k-t PCA) technique [1] has been successfully applied for high spatiotemporal resolution dynamic MRI. When multichannel coil is used for data acquisition, partially parallel imaging (PPI) can be combined with k-t PCA to improve the accuracy of reconstruction [2]. In the original paper of k-t PCA method, k-t PCA/SENSE was presented by incorporating sensitivity encoding, but the performance of this method depends on the accuracy of sensitivity maps and could be computationally expensive. In this work, more accurate and computationally more efficient combination of PPI and k-t PCA is proposed, which is called k-t PCA GROWL (GRAPPA Operator for Wider readout Line) [3]

Theory: In k-t PCA reconstruction for R-fold undersampling of k-t space on a sheared grid, the aliased signals in x-f space at spatial position x ($\rho_{alias,x}$) is given by $\rho_{alias,x}$ =Ew_x (Eq. [1]) ^[1], where E is the signal encoding matrix constructed by extracting columns of matrix of temporal basis functions according to the undersampling pattern, and vector w_x is the unknown weightings at R aliasing positions related to x. The solution to Eq. [1] can be given by any least squares method. By applying GROWL before k-t PCA reconstruction, extending each readout line to three lines, another two sets of undersampled k-t space data sets can be obtained without loss of temporal resolution at the cost of slightly higher noise level. By applying k-t PCA method to the three undersampled k-t space, more equations can be obtained based on the multiplexed SENSE method used in MUSE [4]. Consequently, the unknown weightings w_x can be more accurately solved, which follows better reconstruction accuracy.

Methods: Using a 32-channel cardiac coil (Invivo Corp., Gainesville, FL) with electrocardiography gating (ECG), one Cartesian cardiac cine data set was acquired on a Philips 1.5 T system (Philips, Best, The Netherlands). A healthy volunteer was scanned using balanced TFE sequence in single 23s-long breath-hold. The acquisition parameters were: FOV 320×320 mm², matrix size 312×158, number of phases 15, TR 3.4 ms, TE 1.72 ms, flip angle 60°, slice thickness 8 mm, and number of averages 1. The k-t PCA GROWL reconstruction was performed channel by channel using acceleration factors 3-10 on artificially down sampled k-t space. The kernel size was set to 1×7 and each line was extended to three lines in GROWL. Thirteen training profiles were used for GROWL and to calculate temporal basis functions. As a comparison, coil by coil reconstructions by k-t PCA and k-t PCA/SENSE were also performed with the same training profiles, and the direct current was used for relative sensitivity map calculation. After coil by coil reconstruction, images of different coils can be combined by means of square root of sum-of-squares reconstruction (SOS) method. For accuracy evaluation, both error map and RMSE at ROI defined in Fig. 1a were calculated and the images reconstructed using the full k-space were used as the

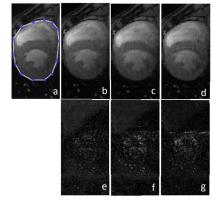


Fig.1. Comparison of reconstructed ROI at 6x acceleration. a: The reference image. b-d: Images reconstructed by k-t PCA GROWL, k-t PCA, and k-t PCA/SENSE. e-g: The error maps of b-d.

reference images. The RMSE was calculated by $\sqrt{\sum |I_{ref} - I_{recon}|^2/\sum |I_{ref}|^2}$, where I_{ref} is the reference image and I_{recon} is the reconstructed image with undersampled k-space data.

Results: Fig. 1 shows the reference image, reconstructions of three methods with 6x acceleration as well as the corresponding error maps. For better visualization, the images are zoomed to ROI and all error maps are scaled 5-fold. It can be seen from the error maps that k-t PCA GROWL resulted in lower artifacts level than k-t PCA and k-t PCA/SENSE. Fig. 2 shows the RMSE at ROI for all time frames at acceleration factor 6. The overall performance of k-t PCA GROWL can also be seen for other accelerations, as indicated by the average RMSE at ROI of all time points in Table 1. K-t PCA GROWL method resulted in much lower error level than k-t PCA and k-t PCA/SENSE when acceleration was high. For the 32-channel cardiac cine data, the total reconstruction time of k-t PCA GROWL was 8-18 min, while in k-t PCA/SENSE it was 33-44 min. All the reconstructions were performed using Matlab on a 64-bit quad core workstation.

Table 1. Comparison of mean RMSE at ROI

k-t PCA 6.6% 7.34% 8.7% 9.2% 11.1% 11.4% 12.4% 13.6%	Acceleration factor Method	3	4	5	6	7	8	9	10
	k-t PCA GROWL	5.8%	6.4%	7.5%	7.8%	9.2%	9.8%	10.5%	11.7%
1 - DCL (GENIGE 5.00	k-t PCA	6.6%	7.34%	8.7%	9.2%	11.1%	11.4%	12.4%	13.6%
K-t PCA/SENSE 5.3% 6.8% 7.6% 9.8% 11.0% 15.8% 15.9% 16.4%	k-t PCA/SENSE	5.3%	6.8%	7.6%	9.8%	11.0%	15.8%	15.9%	16.4%

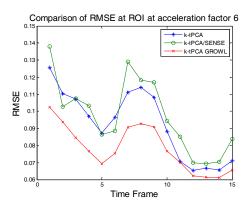


Fig.2. RMSE at ROI for all time frames with 6x acceleration

Discussions and Conclusion: In this study, a sequential combination of GROWL and k-t PCA method, k-t PCA GROWL, was proposed. Compared with k-t PCA and k-t PCA/SENSE on artificially down sampled cardiac cine data, the proposed method had the lowest error level. Assuming time-invariant sensitivity encoding, k-t PCA/SENSE did not result in lower error level than k-t PCA at high acceleration factors. On the contrary, k-t PCA GROWL consistently resulted in lower RMSE than k-t PCA. This is because of sequential combination scheme used in k-t PCA GROWL as explained in [5]. Moreover, k-t PCA GROWL is simple to implement and the speed for GROWL is fast, since GRAPPA operators use small convolution kernel. In conclusion, the proposed k-t PCA GROWL is a more efficient and more accurate scheme to combine k-t PCA and parallel imaging compared with k-t PCA/SENSE.

References: [1] Pedersen et al. MRM 2009, [2] Otazo et al. MRM 2010, [3] Lin et al. MRM 2010, [4] Chen et al. NeuroImage 2013, [5] Huang et al. MRM 2012.