

Spatiotemporal acceleration of dynamic MR imaging without training data: prior-data-driven k-t PCA

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Introduction: One major limitation of k-t BLAST [1] and k-t PCA [2] is the fidelity of training data. Training data acquired in a separate scan may not exactly follow the same spatial location of the real acquisition. In the presence of patient motion, whereas variable density k-t sampling pattern in a single acquisition reduces the motion problem but presents a tradeoff between the actual acceleration ratio and the quality of training data. In this work, we propose to solve the reconstructing problem using an approach similar to k-t PCA but without additional acquisition of training data, by exploiting a prior-data-driven method to obtain the prior knowledge of the imaged object. The method uses the idea that each x-f profile can be transformed into a linear combination of features, which are the principal components of the distribution of x-f profiles. The principal components, instead of from the training data on the same subject, can be extracted from multiple sets of pre-existing images acquired at similar anatomical locations representing a more homogenous distribution of the x-f pattern (which we shall call the “homogeneous data”), hence eliminating the need for training data acquisition. We demonstrate its feasibility with numerical simulations of cine cardiac imaging. The results show that the proposed method can simultaneously achieve increased temporal resolution and reduced reconstruction errors even from substantially down-sampled k-space data.

Theory: k-t PCA resolves the underdetermined problem in k-t BLAST by approximating each x-f profile using a weighted sum of the “best” principal components (PCs) (i.e., those that have largest eigenvalues). [2] The reconstructing problem is basically over-determined if the number of the best PCs is small enough, such that the process of unfolding aliasing depends slightly on the signal covariance of training data. The quality of the best PCs, that is the compressive level of energy by projecting x-f profiles onto those PCs, accounts for the reconstructing performance in a deterministic manner. As shown in Fig. 1, PCs extracted from a set of pre-existing homogeneous data are more representative than those extracted from low-resolution training data of the imaged object. Using these best PCs, aliasing can be solved using least square method: $w_x = E^H (EE^H + \lambda I)^{-1} P_{alias,x}$, where w_x denotes the weightings of the best PCs of each unaliased x-f signal, E is the encoding matrix with the best PCs from a set of homogeneous data, and $P_{alias,x}$ is the aliasing x-f profile for specific spatial position x , respectively.

Materials and Methods: Nine sets of cine cardiac imaging data from five different subjects were acquired on a Philips Achieva 3T scanner and a Siemens Trio 3T scanner with distinct acquisition parameters. Four sets of data were used to generate under-sampled data set by a given accelerating factor for reconstruction with sampling pattern in k-t domain depicted in Fig.2 (the “to-be-reconstructed” data). Ten principal components were extracted intentionally from the other five cine cardiac imaging of different experiments. There were totally 28040 x-f profiles selected for principal component analysis (PCA). Fig. 3 shows the two categories of data. Results from different acceleration factors were compared with their original k-t PCA counter-parts using 20 central k lines for training data [2] for benchmarking.

Results and Discussion: The reconstructed images from one subject (short-axis 2D FLASH with ECG gating on Siemens 3T, matrix size 192x192, 25 cardiac phases, 12° flip angle, and 6mm slice thickness) are illustrated in Fig.4. Images reconstructed by k-t PCA and the proposed method both revealed slightly blurring in the myocardium in the both systolic and diastolic phases, with our method preserving more details as shown in the absolute value of reconstructing error. In addition, our method preserved more temporal changes for myocardium dynamics, than k-t PCA (arrows). Root mean square (RMS) error plotted in Fig.5 shows that our proposed method provided improved reconstruction when compared with k-t PCA even from substantially down-sampled k-space data. Moreover, the net accelerating ratio is higher than k-t PCA since no training data acquisition was needed.

Conclusion: A robust prior-data-driven method for reconstructing dynamic images without training data was presented in this study. The experimental results indicate that the proposed method can achieve improved temporal resolution with reduced errors even from substantially down-sampled k-space data. The principle can theoretically be extended to other dynamic imaging, such as functional MRI or dynamic contrast-enhanced MRI and is not restricted to cardiac applications.

References: [1] J Tsao et al., Magn Reson Med, 2003; 50:1031-1042, [2] H Pedersen et al., Magn Reson Med, 2009; 62:706-716

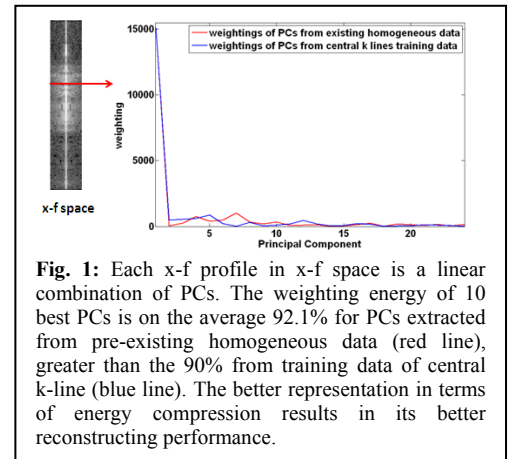


Fig. 1: Each x-f profile in x-f space is a linear combination of PCs. The weighting energy of 10 best PCs is on the average 92.1% for PCs extracted from pre-existing homogeneous data (red line), greater than the 90% from training data of central k-line (blue line). The better representation in terms of energy compression results in its better reconstructing performance.

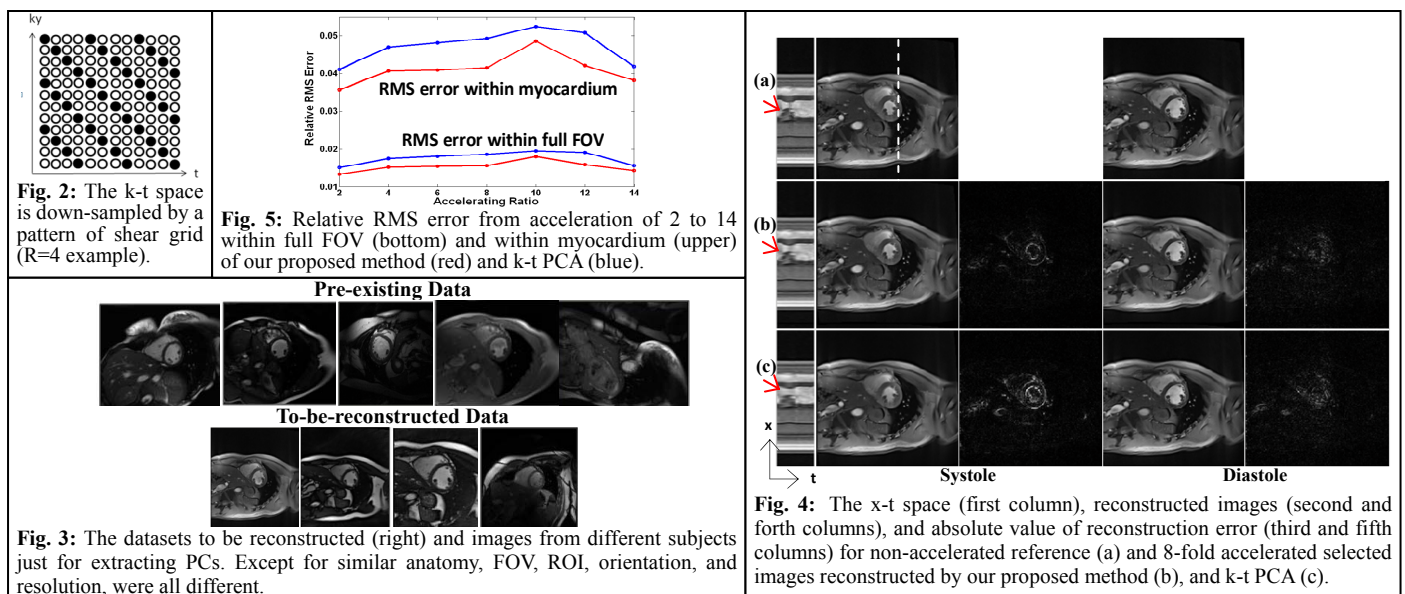


Fig. 2: The k-t space is down-sampled by a pattern of shear grid (R=4 example).

Fig. 5: Relative RMS error from acceleration of 2 to 14 within full FOV (bottom) and within myocardium (upper) of our proposed method (red) and k-t PCA (blue).

Fig. 3: The datasets to be reconstructed (right) and images from different subjects just for extracting PCs. Except for similar anatomy, FOV, ROI, orientation, and resolution, were all different.

Fig. 4: The x-t space (first column), reconstructed images (second and forth columns), and absolute value of reconstruction error (third and fifth columns) for non-accelerated reference (a) and 8-fold accelerated selected images reconstructed by our proposed method (b), and k-t PCA (c).