Iterative k-t PCA with motion corrected training regularization for 3D myocardial perfusion imaging

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Introduction: Various scan acceleration methods for dynamic imaging exploit redundancy in the data using sparsifying transformations. For example, principal component analysis (PCA) in the time-domain may be used [1]. Using k-t PCA [2] up to 10-fold nominal undersampling in 3D first-pass cardiac perfusion imaging has been demonstrated [3]. However, breathholding or shallow breathing is required for artifact-free image reconstruction since Nyquist replicas in the sparse transform domain smear out and hence have larger overlaps if significant respiratory bulk motion occurs during data acquisition. To address this issue, additional motion information may be used to transform the data back into a sparse representation [4-6].

In this work, an iterative k-t PCA algorithm is proposed where an additional spatial transformation is used to further sparsify the data. Training data based regularization is performed in a motion corrected x-pc domain where each time frame is warped to a reference respiratory position. Spatial transformations are derived from frame-by-frame composite images using atlas-based image registration. Using 3D perfusion data acquired in vivo it is demonstrated that this approach successfully corrects for incomplete unfolding due to respiratory bulk motion.

Methods: In k-t PCA, k-space is sampled over several dynamics on an undersampled sheared grid which is cycled each time frame [7]. Reconstruction is performed in the x-pc domain where the time-domain is Fourier transformed and converted to a principal component basis. Regularization with fully sampled, low-resolution training data is employed to unfold the signal replicas:

$$\underset{i}{\operatorname{argmin}} \| \mathbf{E}\boldsymbol{i} - \boldsymbol{d} \|_2^2 + \lambda^2 \| ({}^{\text{x-pc}}\mathbf{M})^{-1} \mathbf{B}_{f->pc} \mathbf{F}_{t->f} \boldsymbol{i} \|_2^2, \qquad \text{(k-t PCA)}$$

where ${}^{\text{x-pc}}\mathbf{M}^2$ is calculated from the signal covariance of the training data in x-pc domain as in [2]. Motion corrected k-t PCA (k-t PCA^{mc}) performs an additional spatial transformation **T** and regularizes in a motion corrected Tx-pc domain:

$$\underset{i}{\operatorname{argmin}} \| \mathbf{E}\boldsymbol{i} - \boldsymbol{d} \|_2^2 + \lambda^2 \| ({}^{\text{Tx-pc}}\mathbf{M})^{-1} \mathbf{B}_{f->pc} \mathbf{F}_{t->f} \mathbf{T}_{x->Tx} \boldsymbol{i} \|_2^2. \quad \text{(k-t PCA}^{\text{mc}}\text{)}$$

The spatial transformation fields are estimated by image registration [8] of frame-by-frame SENSE including all acquired data points per time frame. To avoid misregistration due to contrast uptake, a b-spline transformation model is used to constrain several predefined image regions to follow affine motion. To this end, heart, liver, chest wall, and back are defined by an atlas based on an exemplary segmented multi-slice survey (Figure 1). Reconstruction was implemented in MATLAB (Mathworks, Nattick, MA, USA) using a Quasi-Newton minimization (L-BFGS [9]) with 60 iterations. To speed up convergence, a diagonal preconditioner was incorporated similar to [10].

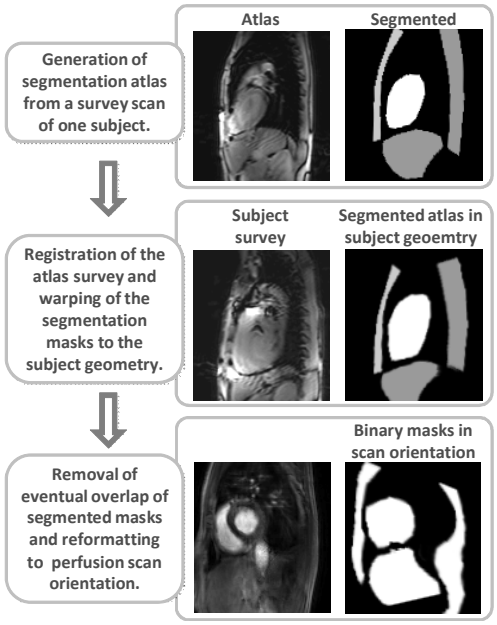

Figure 1: *Constrained motion estimation using segmentation atlas: Anatomical compartments are defined on the survey scan obtained in each individual subject using an atlas-based approach. Each compartment is allowed to undergo affine motion in the subsequent image registration step.*

Three-dimensional contrast enhanced first-pass myocardial perfusion data were acquired with 10-fold nominal undersampling in five healthy subjects on a Philips 3T Ingenia system (Philips Healthcare, Best, The Netherlands). In all subjects, a saturation-recovery gradient echo sequence was used with following parameters: TR/TE: 2.2/1 ms, flip angle = 15°, spatial resolution: 2.3x2.3x10 mm^3, saturation prepulse delay: 150 ms, acquisition window: 210 ms, 30 dynamics, Gadovist, 0.05 mmol/kg b.w. The subjects were asked to start breathing half-way through the scan to simulate incomplete breathholding. The motion-corrupted data were reconstructed with standard k-t PCA and k-t PCA^{mc} with regularization in the motion compensated Tx-pc domain and compared to a breathheld scan in the same geometry.

Results: Figure 2 shows a comparison of image quality and signal intensity curves for a motion corrupted cardiac perfusion scan reconstructed with standard k-t PCA and k-t PCA^{mc}, relative to a breathheld reference. Image quality of the motion corrected scan was found comparable to the breathheld scan while image quality from data without motion correction was clearly inferior. Peak signal and upslope of signal intensity curves in the myocardium (Figure 2b) were well recovered with k-t PCA^{mc}.

Discussion: It has been shown that respiratory motion artifacts due to incomplete unfolding in accelerated 3D myocardial perfusion imaging can be retrospectively corrected for using a data-driven non-rigid motion model. In general the method is applicable to data acquired during incomplete breathholds or during free-breathing. Larger studies are now indicated to demonstrate the diagnostic benefits of the technique in particular in non-compliant patients who are unable to sustain the standard breathhold procedure.

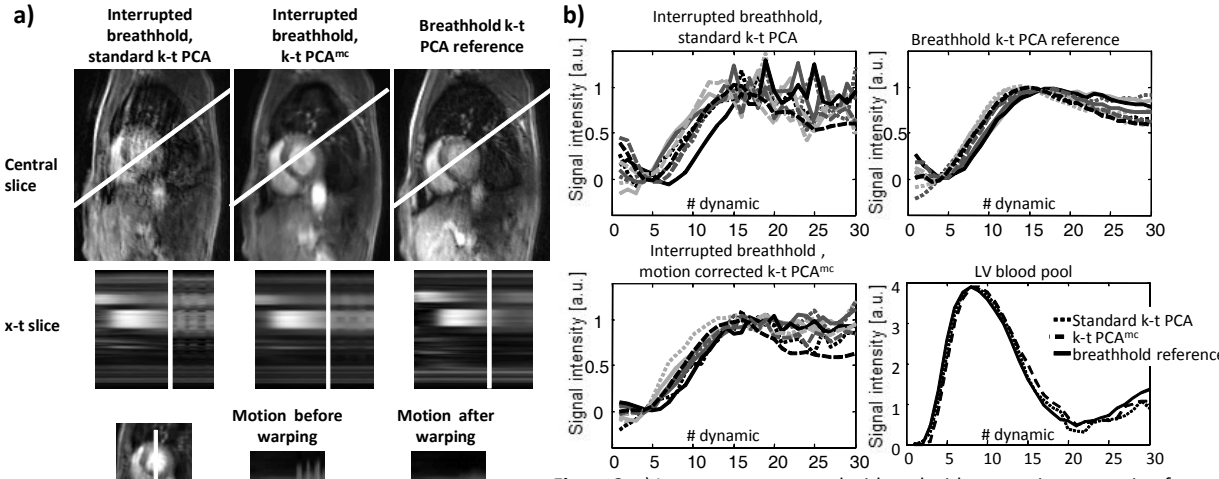

Figure 2: a) Images reconstructed with and without motion correction for a contrast enhanced myocardial perfusion scan with incomplete breathhold and a breathhold reference scan. The white lines indicate the orientation of the profiles shown in the lower row and vice versa

b) Signal intensity from three slices through three myocardial sectors (dotted: inferoseptal, dashed: inferolateral, solid: anterior) for standard k-t PCA reconstruction (top left), motion corrected k-t PCA^{mc} (bottom left) and the breathhold reference (top right). Signal intensity curves for the left ventricular blood pool are shown for all reconstruction types in the graph on the bottom right.

References:

[1] Liang,ISBI (2007)
[2] Pedersen H,MRM,62 (2009)
[3] Vitanis V,MRM,65 (2011)
[4] Jung H,MRM,61 (2009)
[5] Otazo R, Proc. ISMRM (2011)
[6] Usman M,MRM,68 (2012)
[7] Tsao J, MRM,58 (2003)
[8] Klein S,Staring M, IEEE Trans on Med Imag,29 (2010)
[9] Liu DC,Math Program,45 (1989)
[10] Hansen MS,MRM,55(2006)