# Free-breathing first-pass 3D perfusion imaging of the heart

Johannes F.M. Schmidt<sup>1</sup>, Lukas Wissmann<sup>1</sup>, Robert Manka<sup>1,2</sup>, Peter Boesiger<sup>1</sup>, and Sebastian Kozerke<sup>1</sup>

<sup>1</sup>Institute for Biomedical Engineering, University and ETH Zurich, Zurich, Switzerland, <sup>2</sup>Department of Cardiology, University Hospital Zurich, Zurich, Switzerland

**Introduction:** Scan acceleration methods have proven invaluable for dynamic contrast-enhanced perfusion imaging enabling increased spatial resolution and coverage [1-3]. Among the various methods available k-t PCA [4] has shown great promise and has facilitated 3D perfusion imaging with whole-heart coverage [5]. Besides the progress, one practical issue relates to the requirement of breathholding or shallow breathing which cannot be ensured under all circumstances in clinical routine exams. Recently, retrospective non-rigid motion correction techniques [6] have successfully been implemented for whole-heart, cardiac cine and fully sampled contrast enhanced scans [7-9] by extending the image encoding matrix with motion operators.

In the present work, an extended k-t PCA algorithm is proposed which corrects for non-rigid frame-to-frame motion based on motion operators derived from two pencil-beam navigators for feet-head and anterior-posterior motion detection and from the fully sampled, low-resolution training images inherently contained in the k-t PCA data sets. It is demonstrated that this approach successfully corrects for respiratory motion artifacts and hence enables free-breathing 3D cardiac perfusion MRI.

## Methods:

<u>Theory</u>: In k-t PCA, k-space is sampled over several dynamics on an undersampled sheared grid which is cycled each time frame [10]. 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 used to unfold the signal replicas. In order to account for object motion, the k-t PCA encoding matrix can be extended with an image warping matrix upon transformation into the x-t domain:  $\mathbf{E} = \mathbf{\Xi}_{k,t} \mathbf{F}_{x->k} \mathbf{STF}_{f->t} \mathbf{B}_{pc->f}$ 

Matrix T represents the relative motion from a reference state

to the respiratory states in each dynamic frame.  $\Xi$  denotes sampling in k-t space, F the Fourier transform, S weighting with coil sensitivities and B the basis transformation from the x-pc to the x-f domain.

## Implementation:

The major motion components in feet-head and anterior-posterior direction are derived from two pencil beam navigators (Figure 1) acquired directly after the image acquisition in each heart cycle. Non-rigid registration of the fully sampled k-t PCA training images was performed with the ITK based elastix framework [11] using the navigator displacements in image coordinates as initial transformation. The image reconstruction framework was implemented in Matlab (Mathworks, Natick, USA) and was performed on standard dual CPU computer hardware. The underdetermined system of linear equations given by the extended encoding matrix and the measured data was solved iteratively and regularized with training data and a Tikhonov regularizer consisting of the identity matrix.

## In-vivo experiments:

Three-dimensional perfusion data were acquired with 10-fold nominal undersampling in three 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: 2.02ms, TE: 0.65ms, flip angle: 15°, spatial resolution:

2.3x2.3x10mm<sup>3</sup>, 30 dynamics, acquisition window: 220ms, saturation delay: 150ms. Pencil beam navigators of 20 mm diameter and an axial resolution of 1 mm were placed in feet-head direction on the heart-liver interface and in anterior-posterior direction on the chest wall next to the heart. For each subject, a free-breathing contrast enhanced scan was reconstructed with and without motion correction 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 free-breathing scan with and without motion correction and a breathhold reference scan for a given subject. Image quality of the motion corrected free-breathing scan was found comparable to the reconstruction of the breathhold scan while image quality from free-breathing data without motion correction was clearly inferior. Peak signal and upslope of signal intensity curves through the myocardium (Figure 2, right) were well restored with motion corrected k-t PCA. The frame-by-frame registration with motion corrected k-t PCA also serves perfusion quantification as it inherently aligns the 3D volumes acquired over time.

**Discussion:** It has been shown that respiratory motion artifacts in accelerated 3D myocardial perfusion imaging can be retrospectively corrected for using a non-rigid motion model derived from pencil-beam navigator guided image registration of k-t training data. The navigator displacement aids the non-rigid registration to handle the strong contrast changes in the low-resolution training. A potential shortcoming relates to the limited and anisotropic resolution in the training data sampled with Cartesian methods. To this end, undersampled radial and spiral trajectories appear most promising and remain to be studied in future work.









References:
1] Kellmann P, MRM,51(2004)
2] Plein S, MRM,58(2007)
[3] Shin T, MRM,63(2010)
4] Pedersen H,MRM,62(2009)
[5] Vitanis V,MRM,65(2011)
[6] Batchelor PG,MRM,54(2005)
7] Odille F,MRM,60(2008)
[8] Odille F,MRM,63(2008)
9] Filipovic M,MRM,64(2010)
10] Tsao J, MRM,58(2003)
11] Klein S, Staring M, IEEE Trans
on Med Imag 29(2010)

### Figure 2:

Images on the left: Images reconstructed with and without motion correction for a free-breathing myocardial perfusion scan and a breathhold reference scan. The dashed white lines indicate the orientation of the profiles shown in the lower row and vice versa. The graph on the right shows signal intensity curves for mycoardium and left ventricular blood pool.