

# High Resolution 3D Cardiac Perfusion Imaging Using Compartment-Based $k$ - $t$ PCA

V. Vitanis<sup>1</sup>, R. Manka<sup>1,2</sup>, H. Pedersen<sup>3</sup>, P. Boesiger<sup>1</sup>, and S. Kozerke<sup>1</sup>

<sup>1</sup>Institute for Biomedical Engineering, ETH Zurich, Zurich, Switzerland, <sup>2</sup>German Heart Institute Berlin, Berlin, Germany, <sup>3</sup>Functional Imaging Unit, Glostrup Hospital, Glostrup, Denmark

**INTRODUCTION**  $k$ - $t$  PCA [1] was recently introduced as an extension of  $k$ - $t$  BLAST and  $k$ - $t$  SENSE [2], aiming at improving the temporal fidelity of accelerated non-periodic dynamic MR images. The advantage of the method originates from the fact that  $k$ - $t$  PCA decomposes the training and undersampled data using optimized temporal basis functions, therefore constraining the temporal content of the image series and improving the conditioning of the reconstruction problem.

In this work, a modification of the method is presented that aims at circumventing errors in the calculation of the temporal basis that originate from partial-volume effects in the training data [3,4], thus improving the temporal fidelity.

$$1. \rho(x_i, f_i) = B(f_i) \cdot w(x_i) \quad 2. \rho_w(x_i, f_i) = B(f_i) \cdot w_w(x_i) \quad 3. w_x = \Theta E^H (E \Theta E^H + \lambda \Psi)^{-1} \rho_{alias} \quad 4. \Theta = \text{diag}(|w_{tr,x}|^2)$$

**THEORY**  $k$ - $t$  PCA [1] is based on the assumption that the unaliased signal  $\rho$  is a linear combination of temporal basis functions ( $B$ ) with corresponding spatial weightings ( $w$ ) (Eq.[1]). The temporal basis functions are derived from low-resolution training data by performing Principal Component Analysis (PCA) (Eq.[2]). The spatial weightings  $w$  are calculated by solving Eq.3. Here,  $\Theta$  is the diagonal signal covariance matrix calculated from the weightings of the training data ( $w_{tr}$ ) (Eq. 4), whereas the encoding matrix  $E$  is constructed from copies of  $B$  that are shifted according to the sampling point spread function.  $\rho_{alias}$  is the aliased signal and  $\Psi$  the noise covariance matrix.

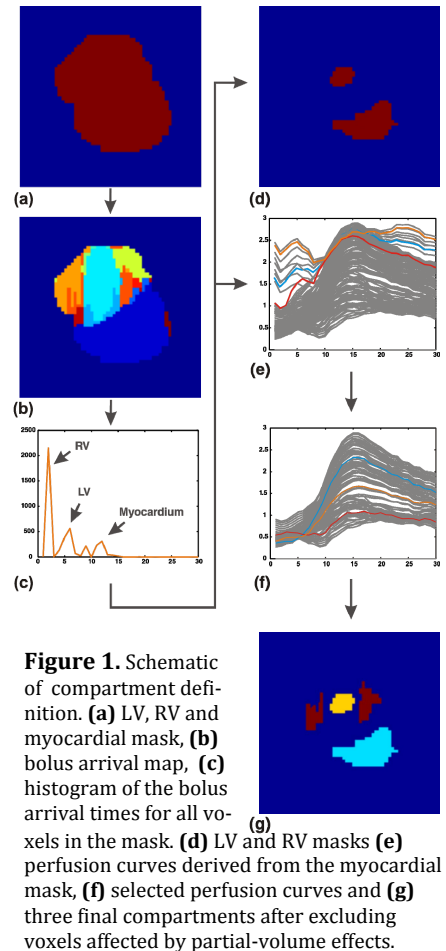
**METHODS** According to theory, the fidelity of the reconstruction result is highly dependent on the accuracy of the basis functions  $B$ , which define the temporal constraints. Since matrix  $B$  is derived from the training data, the calculation can suffer from partial-volume effects. For instance, the large voxels of the septal wall contain temporal information from both the septal wall and the two ventricles, compromising the accuracy of the  $B$  matrix. In order to eliminate these effects, a dataset containing the sliding window reconstruction of the undersampled and the training data is constructed. On those data, four compartments (LV, RV, Septum, rest) are automatically defined based on the variance along the temporal dimension (Fig 1a) and the bolus arrival times (Fig 1b, c). Subsequently, the perfusion curves of the myocardium are derived (Fig. 1e), the pixels that display a certain temporal behavior due to partial-volume effects are automatically excluded (Fig. 1f) and  $B$  matrices for each compartment are calculated. The voxel exclusion is based on the bolus arrival times and the gradients and deviations of the perfusion curves. Finally, the reconstruction problem is solved using different  $B$  matrices for each compartment.

The method was tested on perfusion images acquired with 10-fold undersampling on a 3T Philips Achieva scanner (Philips Healthcare, Best, The Netherlands) with a 6-element phased array, using a saturation-recovery gradient echo sequence. Imaging parameters include  $T_R=1.8\text{ms}$ ,  $T_E=0.7\text{ms}$ , flip angle= $15^\circ$ , spatial resolution  $2.3 \times 2.3 \times 5\text{mm}^3$ , 30 dynamics, acquisition time per heart beat = 250ms, saturation using a WET pulse with delay 150ms.

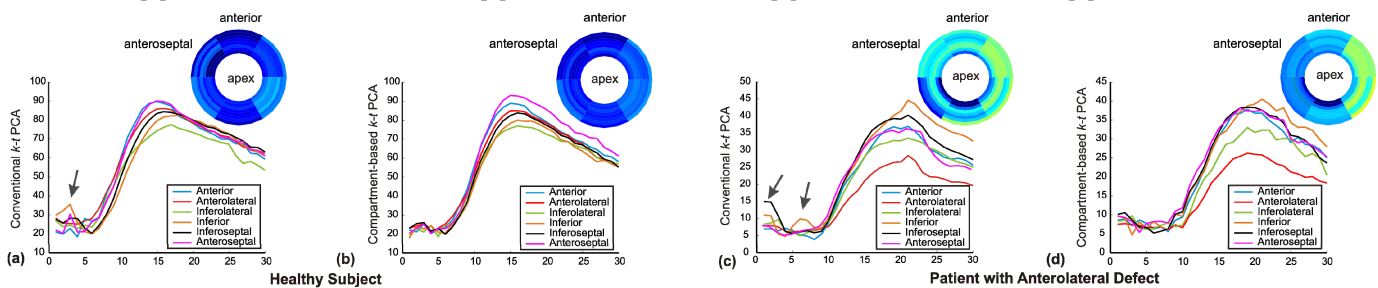
**RESULTS** Figure 2 shows perfusion curves calculated for a midventricular slice of a 3D dataset using the conventional  $k$ - $t$  PCA and the compartment based method for a stress scan of a healthy subject and a patient. Upslope bulls-eye plots are also displayed. It is seen that the proposed method eliminates temporal blurring seen in the perfusion curves and results in a more uniform distribution of upslope values in the healthy segments of the datasets considered. Figure 3 demonstrates perfusion images from a healthy subject during myocardial enhancement.

**DISCUSSION** The presented compartment based  $k$ - $t$  PCA reconstruction addresses inaccuracies associated with the coarse spatial resolution of the training data. Excluding certain voxels from the calculation of the temporal basis functions can improve reconstruction, leading to more accurate perfusion curves and subsequently to more reliable semi-quantitative perfusion analyses. The method holds great potential for highly accelerated, high-resolution 3D perfusion imaging of the heart.

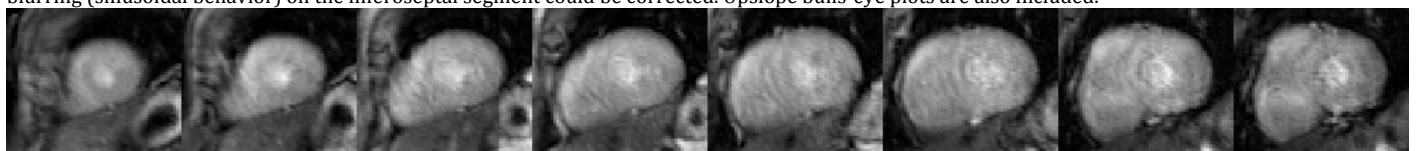
**REFERENCES** [1] Pedersen H. et al., MRM 2009, 62, [2] Tsao J. et al., MRM 2003, 58, [3] Plein S. et al., MRM 2007, 58, [4] Vitanis V. et al., MRM 2009, 62



**Figure 1.** Schematic of compartment definition. (a) LV, RV and myocardial mask, (b) bolus arrival map, (c) histogram of the bolus arrival times for all voxels in the mask. (d) LV and RV masks (e) perfusion curves derived from the myocardial mask, (f) selected perfusion curves and (g) three final compartments after excluding voxels affected by partial-volume effects.



**Figure 2.** Perfusion curves extracted from a midventricular slice of a 3D dataset. (a) Conventional and (b) compartment-based  $k$ - $t$  PCA reconstruction in a healthy subject. The deviation between the six curves is reduced using the proposed method. (c) Conventional and (d) compartment-based  $k$ - $t$  PCA reconstruction in a patient with anterolateral ischemia. Using the proposed method the remaining “spilling” on the inferior segment and the temporal blurring (sinusoidal behavior) on the inferoseptal segment could be corrected. Upslope bulls-eye plots are also included.



**Figure 3.** Perfusion images (8 slices) from a healthy subject during myocardial enhancement.