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High resolution 3D cardiac perfusion imaging using compartment based k-t PCA

Viton Vitanis*[1], Robert Manka[1], Peter Boesiger[1], Henrik Pedersen[2] and Sebastian Kozerke[1]

Address: [1]Institute for Biomedical Engineering, ETH Zurich, Zurich, Switzerland and [2]Functional Imaging Unit, Glostrup Hospital, Glostrup, Denmark

* Corresponding author

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Introduction

k-t PCA [1] was recently introduced as an expansion of *k-t* SENSE, aiming at improving the temporal fidelity of accelerated dynamic MRI. Its advantage originates from the fact that it decomposes the training and undersampled data using optimized temporal basis functions, leading to better temporal fidelity in the reconstructed data.

Purpose

A modification of *k-t* PCA is presented that aims at circumventing errors in the calculation of the temporal basis set as a result of partial-volume effects in the training data [2,3].

Methods

k-t PCA is based on the assumption that the unaliased signal is a linear combination of temporal basis functions with corresponding spatial weightings (Eq.1). The temporal basis functions are derived by the low-resolution training data (Eq.2), where the spatial weightings are calculated by solving Eq.3.

According to theory, the fidelity of reconstruction is dependent on the accuracy of the matrix B. Since this matrix is derived from low spatial resolution training data, partial-volume effects can compromise its accuracy. In perfusion imaging, signal contamination from the right ventricle can lead to erroneous signal intensities in the septal wall (Fig. 1a), for example. In order to eliminate these effects, four compartments (LV/RV/Septum/Background) are defined based on a bolus arrival map computed automatically. Subsequently, the perfusion curves of the septum are derived. Pixels that display partial-volume effects are automatically excluded (Fig. 1b) and B matrices for each compartment are calculated. In solving the reconstruction equation, B matrices are dynamically reassigned based on compartment index. To test the method, high-resolution 3D perfusion data were acquired with 10-fold undersampling on a 3 T Philips system and subsequently reconstructed using the original *k-t* PCA and its compartment based variant.

Results

Fig 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. Fig. 3 demonstrates the corresponding upslope bull's-eye plots. 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.

Discussion

The presented compartment based *k-t* PCA reconstruction addresses inaccuracies associated with the coarse spatial resolution of the training data. Excluding certain training voxels from the calculation of the temporal basis func-

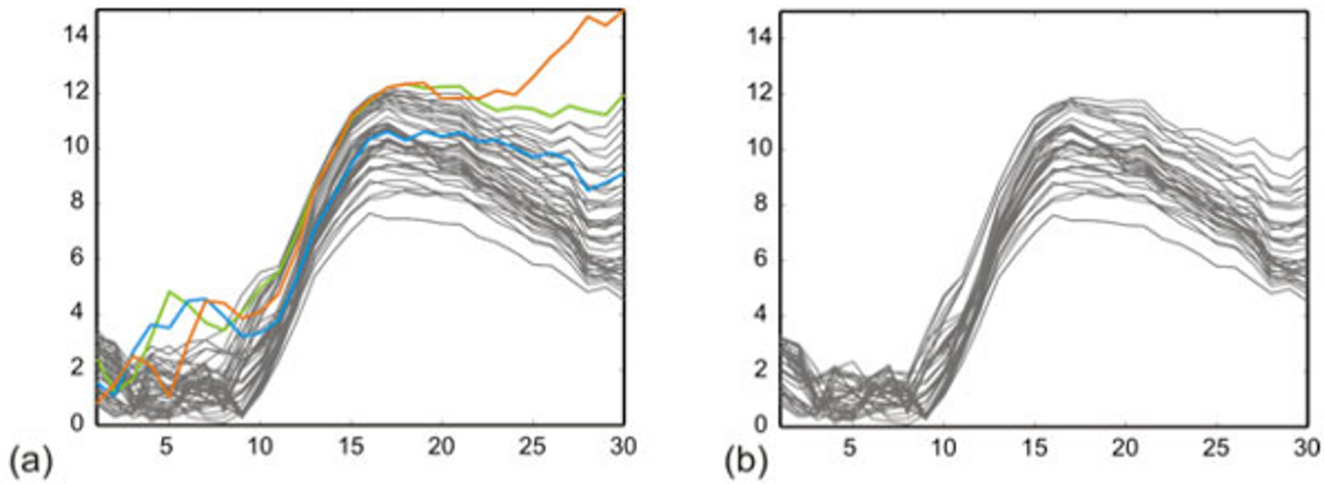

Figure 1
(a) Perfusion curves from training data voxels on the myocardium. The "spilling" due to partial-volume effects (e.g. on the septum) is evident in the perfusion curves illustrated in color. (b) The same perfusion curves after excluding the voxels that are affected by partial-volume effects.

tions can improve reconstruction, leading to more accurate perfusion curves and subsequently to more reliable semi-quantitative perfusion analyses.

References

1. Pedersen H, *et al.*: *MRM* 2009:62.
2. Plein S, *et al.*: *MRM* 2007:58.
3. Vitanis V, *et al.*: *MRM* 2009:63.

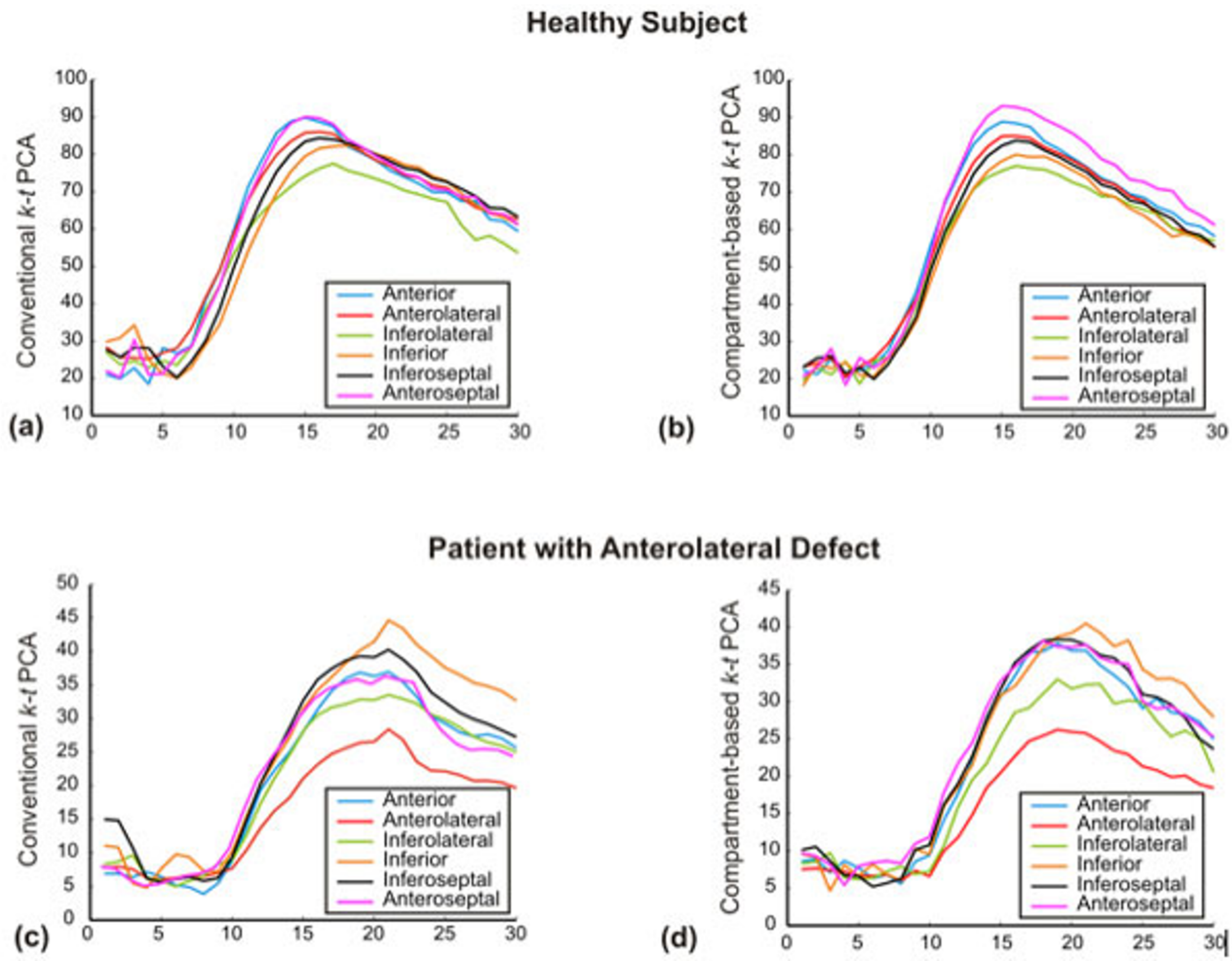

Figure 2

Perfusion curves extracted from a midventricular slice of a 3D dataset. (a) Conventional and (b) compartment-based *k-t* PCA reconstruction in a healthy subhect. The deviation between the six curves is reduced using the proposed method. (c) Converntional and (d) compartment-based k-t PCA reconstruction in a patient with anterolateral ischemis. Using compartment based *k-t* PCA the remaining "spilling" on the inferior segment and the temporal blurring (sinusoidal behaviour) on the inferoseptal segment could be corrected.

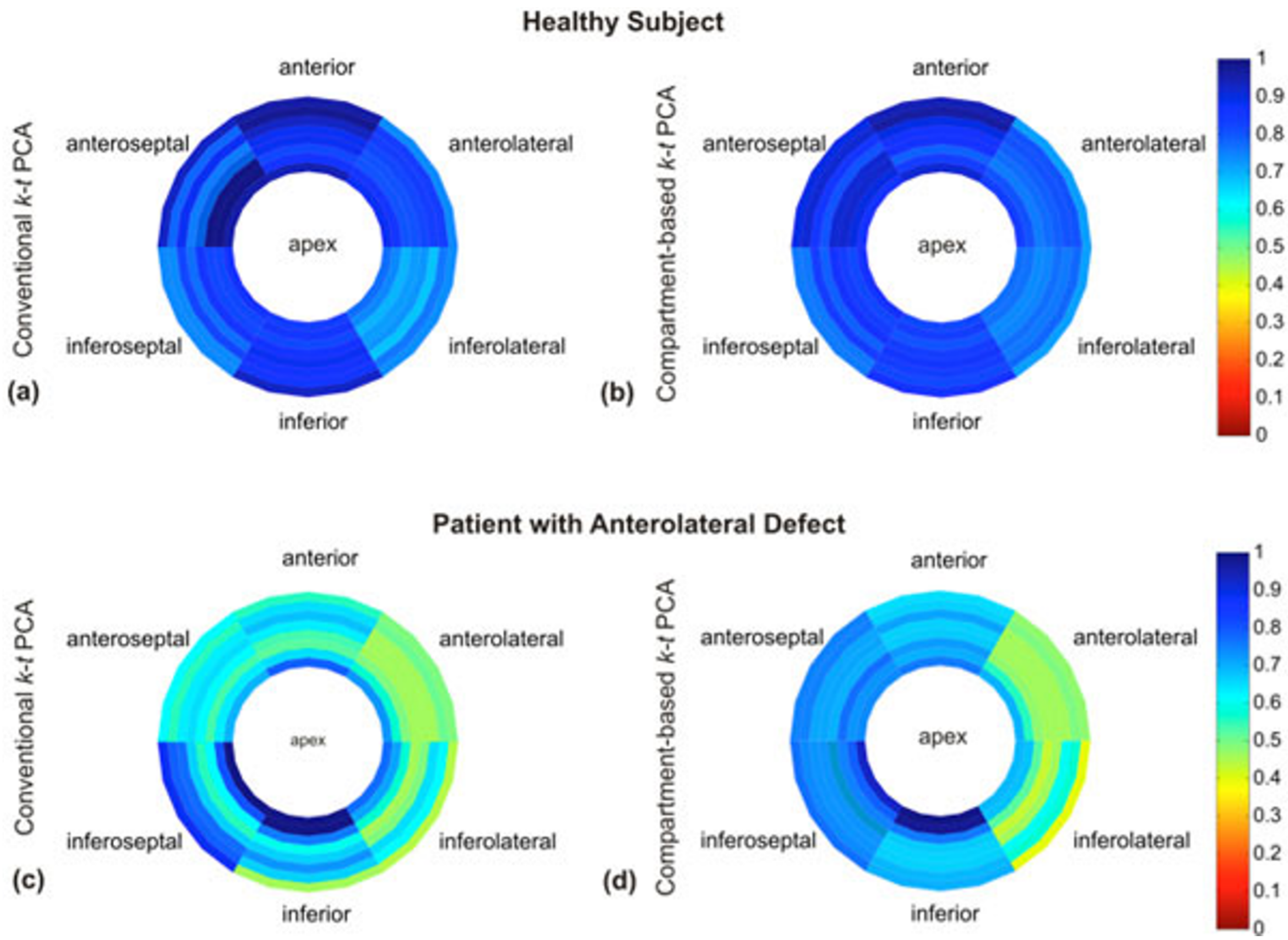

Figure 3
Bull's eye plots representing perfusion curve upslopes for 8 slices of a healthy subject (upper row), and a patient with anterolateral ischemis (lower row). On the healthy subject, the upslopes are mor uniformly distributed when the proposed method is used (b) compared to conventional K-t PCA (a). The same hold true for the healthy segments of the patient dataset (d compared to c).