Pulse Wave Velocity Assessment in a Single Breathhold using Compartment *k-t* PCA

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Introduction: Cine phase-contrast flow measurements (PC-MRI) of the aorta have been shown to exhibit considerable spatiotemporal correlations and hence can be significantly accelerated using *k-t* undersampling methods [1-2]. The *k-t* BLAST framework [3] has recently been extended by forcing temporally constrained reconstructions [4]. Moreover, spatial compartments have been introduced to further enhance reconstruction accuracy while achieving more than 8-fold net acceleration with a single receiver coil [5]. In this work, the previously presented compartment-based *k-t* PCA method is applied in-vivo for the assessment of pulse wave velocity (PWV) during a single breathhold. Results are compared to fully sampled, free breathing acquisitions. In addition, we demonstrate that shared training acquisitions permit dual-slice phase-contrast acquisition at high temporal resolution in a single breathhold.

Methods: In compartment based *k-t* PCA [5] (termed *k-t* PCA+ hereafter), the image is decomposed into spatial compartments in each of which a temporal basis set is calculated. The basis functions are derived from low spatial but high temporal resolution training data using principal component analysis. The spatially dependent weighting coefficients are then unfolded in a regularized least-squares sense [4]. When using a balanced velocity encoding gradient scheme, the temporal evolution of each of the two encoding segments is expected to differ by its velocity related phase:

$$\varphi(x,t)_{1,2} = \pm 0.5\gamma M_1(t)v(x,t) + \gamma \Delta B(x)t$$

where $M_1(t)$ corresponds to the flow encoding first gradient moment, γ to the gyromagnetic ratio, v to the spins velocity and $\Delta B(x)t$ to the susceptibility related background phase. Assuming identical background phase in the two segments, the principle components of the first segment can serve reconstruction of the second segment and hence data acquisition of the training data for the second segment can be omitted.

On a 3T Philips Achieva system (Philips Healthcare, Best, The Netherlands), eight healthy volunteers were examined using the fully sampled, free breathing acquisition including two signal averages for partial motion compensation resulting in scan times of 2-3min per slice. Thereafter undersampled acquisitions with net acceleration factors ranging from 6 to 8 were acquired in a single breathhold per slice (nominal acceleration factor: 16, number of training profiles: 7-11 depending on cardiac frequency). Breathhold durations ranged from 10-17sec. Further, in two volunteers, shared training acquisition was used resulting in a net acceleration factor of 9-10 and permitting the acquisition of two transversal slices in a single breathhold of 15-20sec. All protocols had a temporal resolution of 8.5ms at a spatial resolution of 2.5x2.5x5mm^3. Flow encoding was performed in feet-head direction with an encoding velocity of 200cm/s. PWVs were calculated manually by finding the time to foot (TTF) point of all three flow curves [6] and by measuring the inter-slice distances through the aorta (Figure 1).

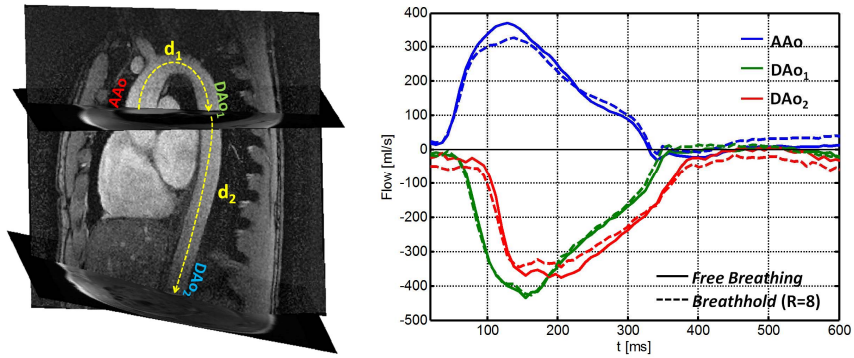

***Figure 1**: Slice orientations for PWV measurements (left). Extracted flow curves (right), through ascending (AAo), distal descending (DAo_1,) and proximal descending (DAo_2) aorta for the free-breathing and the undersampled breathhold cases. Time to foot (TTF) and distances (d_1 and d_2) were determined in order to calculate the pulse wave velocity.*

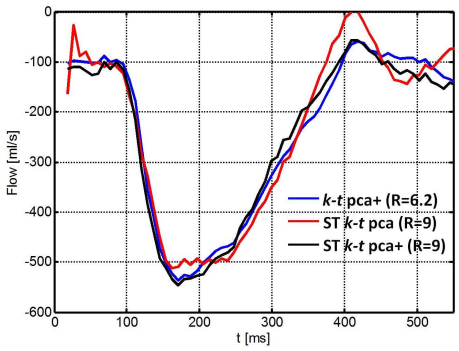

***Figure 2**: Simulated single segment training k-t PCA (ST k-t PCA) and k-t PCA+ (ST k-t PCA+) relative to dual segment training (k-t PCA+) demonstrate the feasibility of shared training data.*

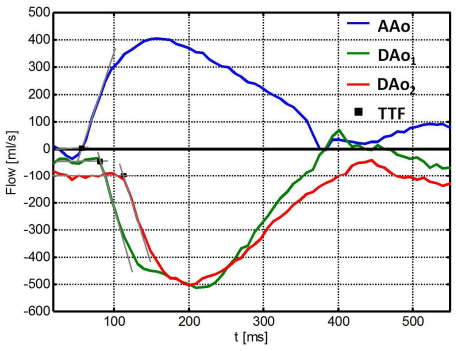

***Figure 3**: Dual-slice, single breathhold, shared training k-t PCA+ with 10-fold net acceleration. Flow curves from the ascending and descending aorta are shown along with the time to foot (TTF) time-points.*

Results: Figure 2 shows flow curves through the descending aorta obtained from data simulating shared training (ST) data acquisition and reconstructed using *k-t* PCA (ST *k-t* PCA) and *k-t* PCA+ (ST *k-t* PCA+) relative to reconstructions utilizing both training segments (*k-t* PCA+). Although the net acceleration factor increased from 6.2 to 9, flow curves reconstructed by ST *k-t* PCA+ still showed excellent agreement with the reference in contrast to ST *k-t* PCA. Figure 3 presents flow curves of the single breathhold dual-slice reconstructed using ST *k-t* PCA+. Again, flow curves show the expected patterns allowing quantification of pulse wave velocity (baseline and upslope lines as well as times to foot of the waveforms (TTF) are illustrated). In all 8 volunteers, the PWV was measured using the fully sampled dataset and using the undersampled, single breathhold acquisition. All values showed good agreement with the expected distribution in healthy subjects reported in the literature [6]. Figure 4 shows PWVs of the descending aorta measured on the free breathing and the breathheld acquisitions confirming good agreement between the methods.

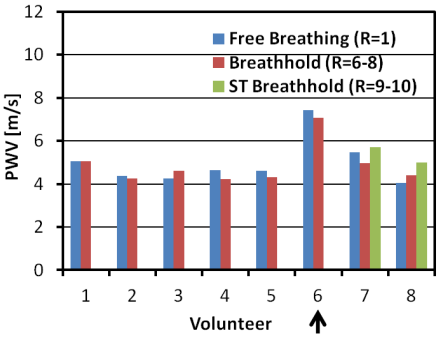

***Figure 4**: PWVs show good agreement between the reference and the proposed undersampled breathhold method. Increased PWV is observed in the eldest volunteer (66y.o., arrow). Shared training acquisition (ST breathhold) on two volunteers yielded good inter-method agreement.*

Discussion: The present work has demonstrated the feasibility of reconstructing highly undersampled PC-MRI data acquired during a single breathhold using *k-t* PCA+. PWV values in healthy volunteers were obtained and compared well with results reported in the literature. Using a balanced velocity encoding scheme it was shown that a single training data set is sufficient for *k-t* PCA+ reconstruction permitting further increase of the net acceleration factor achievable. With net 10-fold acceleration, dual slice acquisitions are considered feasible for clinical application and further studies are warranted to test the performance in patients.

References: [1]Baltes Cet.al.Magn.Reson.Med.2005;54 [2]Jung.B.et.al.Magn.Reson.Med.2008;60 [3]Tsao.J,et.al.Magn.Reson.Med. 2003;50 [4]Pedersen.H.et.al.Magn.Reson.Med.2009;62 [5]Giese.D.et.al.ISMRM'10;3699 [6]Boese J.M.et.al.Phys.Medicine.Biol.2000;45