K-t-Space Accelerated Myocardial Perfusion

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Introduction: Dynamic first-pass contrast-enhanced myocardial perfusion MRI is an important clinical tool that greatly benefits from acceleration in data acquisition in terms of spatial resolution or number of slices to acquire per heartbeat. Advanced dynamic parallel imaging techniques have been introduced such as k-t-SENSE and k-t-BLAST [1], k-t-GRAPPA [2], and PEAK-GRAPPA as an extension of k-t-GRAPPA [3] to reduce total acquisition time or to increase spatiotemporal resolution. Recently, k-t-SENSE was introduced to myocardial perfusion measurements [4]. K-t-BLAST is typically used to accelerate imaging of objects with quasi-periodic motion such as the heart, i.e. more localized in x-f-space and thus optimally suited for image reconstruction [1]. In this patient study an application of a k-t-space related GRAPPA technique to myocardial perfusion as non-periodic motion has been investigated.

Methods: Myocardial perfusion measurements were performed in 11 patients with known myocardial infarction on a 1.5 T Siemens Espree system using a 12 channel thorax coil. Three short axis slices (basal, midventricular, apical) were acquired per heartbeat with a matrix size of 78 × 256 using a FLASH sequence (TR = 3 ms, flip angle = 15°). Scan duration after contrast agent injection covered a period of 50 heartbeats. Since diagnosis was focused on delayed enhancement images no application of stress inducing substance was performed.
Image reconstruction was performed in Matlab (The Mathworks). For conventional GRAPPA and PEAK-GRAPPA reconstructions k-space lines were removed retrospectively from the full acquired k-space data with incrementally shifted phase encoding amplitudes for subsequent time frames and a pre-defined number of N_{ACS} reference lines resulting in a ky-t-space sampling pattern as illustrated in Fig. 1.
PEAK-GRAPPA uses a uniform 3D kernel (two encoding kx, ky directions and one temporal dimension) for each reduction factor R [3]. The coil weights are independently determined for each time frame and subsequently averaged to generate a single set of coil weights for the reconstruction of the entire k-t-space. PEAK-GRAPPA reconstruction included 24 reference (ACS) lines and 26 lines for conventional GRAPPA due to a kernel width by=25. Hence, the true acceleration factor is smaller than the reduction factor (for R=6, 78 ky-lines and 24 reference lines the acceleration factor is 2.4). Reference lines were copied back into the data matrix after reconstruction to preserve the temporal dynamics already existent in the acquired data.
Signal time courses in a basal slice were evaluated in three different ROI's in the blood pool of the left and the right ventricle as well as an area in the myocardium of the left ventricle. Correlation analysis was performed between the full acquired k-space reconstruction and PEAK-GRAPPA data for the signal time courses in the three different ROI's for all patients.

Results: Fig. 2 shows the perfusion images in a basal slice before the arrival of the contrast agent bolus in the heart (A), after the bolus arrival in the right ventricle (B) and the left ventricle (C), and the signal enhancement of the myocardium (D). The three columns show the images reconstructed with the full acquired k-space (left), with PEAK-GRAPPA R=6 (middle), and with conventional GRAPPA R=6 (right). The exemplary signal time courses in a patient in Fig. 3 demonstrate the dynamics of the contrast agent bolus within the three different ROI's in the right ventricle, the left ventricle, and the myocardium. For each ROI the time courses are plotted for the full acquired k-space, for PEAK-GRAPPA R=6, and for conventional GRAPPA R=6. Fig. 4 presents the difference of the signal time courses in a patient after myocardial infarction in two small ROI's in the infarcted myocardium with a lack of perfusion (see arrows) and in the healthy myocardium. Time courses are plotted the full acquired k-space data and for the PEAK-GRAPPA data with R=6 again demonstrating an excellent agreement within these two small ROI's. Fig. 5 shows correlation plots of all patients (50 temporal values × 11 patients = 550 data points) between the full acquired k-space and PEAK-GRAPPA data for the signal time courses within the myocardial ROI. The good agreement is corroborated by the fit parameters and the correlation values R2 of the linear regression.

Discussion: Results of this study demonstrate that the combination of the recently introduced k-t-space related PEAK-GRAPPA method with time-resolved myocardial perfusion MRI provides robust image quality and high SNR efficiency for high reduction factors. The integration of the temporal domain into the 3D PEAK-GRAPPA kernel helps preserving dynamics within the signal time courses and thus permits accurate quantification of perfusion parameters such as time-to-peak, mean-transit-time, or the slope of signal increase even for high acceleration factors. Due to the small matrix size (limited due to the acquisition of the full k-space data) the true acceleration factor stays small beside the high reduction factor of R=6 in the outer k-space regions. Nevertheless, the higher acceleration permitted by PEAK-GRAPPA can be used to increase spatial resolution in myocardial perfusion images resulting in a higher true acceleration factor.

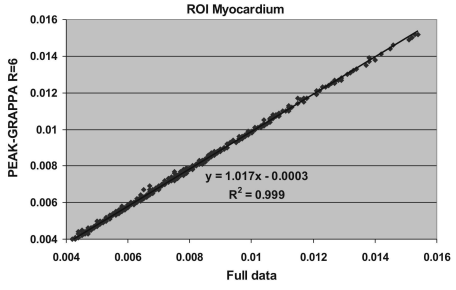

Fig.5 Correlation between the full acquired k-space data and PEAK-GRAPPA data for the signal time courses in the myocardial ROI for all 11 patients.

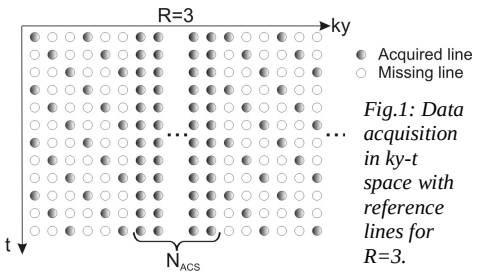

Fig.1: Data acquisition in ky-t space with reference lines for R=3.

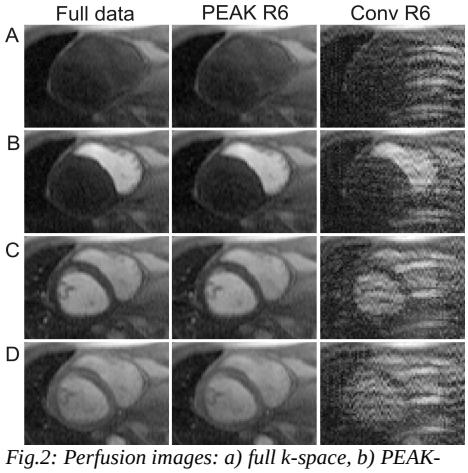

Fig.2: Perfusion images: a) full k-space, b) PEAK-Grappa R6, c) conventional Grappa R6.

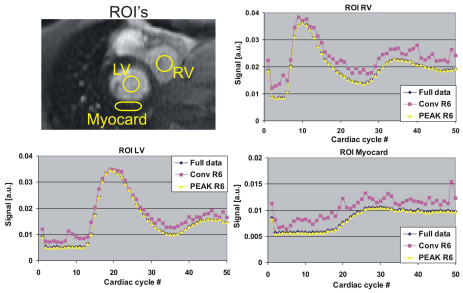

Fig.3: SNR behavior in three different ROI's for conventional Grappa and PEAK-Grappa.

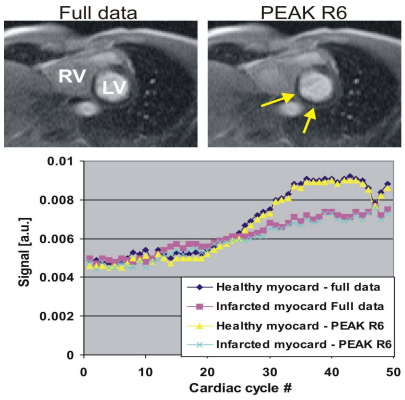

Fig.4: Signal time courses in a patient after myocardial infarction in two small ROI's in the infarcted and in the healthy myocardium.

References:
[1] Tsao et al. MRM 2003;50:1031-42. [2] Huang et al. MRM 2005;54:1172-84.
[3] Jung et al. Proc ISMRM 2007; p.748. [4] Plein et al. MRM 2007; p.777-85.