Improved Single-shot MR Relaxometry using Principal Component Analysis

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Introduction: Quantitative MR parameter mapping techniques are of strong clinical interest, as they provide a potential for evaluating pathology using absolute tissue characteristics [1]. However, quantitative MRI has not yet found widespread clinical adoption, mainly due to long scan times required to map the various parameters of interest. Principal Component Analysis (PCA) has previously been used to reconstruct dynamic data from an undersampled time series [2,3]. Furthermore, it has been demonstrated that the dynamics during an IR TrueFISP experiment can be described in good approximation by only a very small number of principal components [4], allowing for high acceleration factors. The IR TrueFISP sequence allows for the simultaneous quantification of spin-density, T_1 and T_2 [5]. This sequence consists of an inversion pulse followed by a series of TrueFISP acquisitions. The signal follows a quasi-relaxation towards the steady-state. Spin-density, T_1 and T_2 can then be obtained from a mono-exponential fit to the image series. In this work, we present a novel PCA aided reconstruction technique, allowing for MR parameter mapping from a single-shot radial IR TrueFISP scan.

Methods: All experiments were performed at 1.5 T with a 32-channel head array on a healthy volunteer with informed consent. After non-selective adiabatic inversion, the return to equilibrium was observed with a radial TrueFISP sequence with golden-ratio based profile order [6] (TA=4.9s, TR=3.98ms, 256 matrix, FoV=220x220 mm², 6mm slice thickness). In total, 96 time frames were reconstructed using the proposed method. Prior to the actual reconstruction process a principal component basis was determined from a synthetic training data set consisting of exponentials, artificially generated from a physiologically relevant range of T_1 and T_2 combinations. For each frame, 13 projections were then gridded to a Cartesian k-space using GROG [7]. Missing k-space data were reconstructed using the framework of partially separable functions [2], however solving the problem with an iterative method: In a first step, the time-series was transformed back and forth to the PCA domain using only the first three principal components, effectively compressing the temporal dynamics of the data set. After this step, data consistency was ensured by reinserting the acquired data into the reconstruction. After a certain convergence threshold was reached, the image time series was then obtained from a simple FFT of the iteratively reconstructed k-space data. For comparison, the time series was additionally reconstructed using an optimized k-space weighted image contrast (KWIC) filter [8]. The experiment was repeated with segmentation (TA=31s, 4 segments, with relaxation delay=4s in between). A reference time series was reconstructed from this experiment using 144 projections per frame, resulting in a total of 26 frames (6.6 frames/s). Spin-density, T_1 and T_2 were then obtained for all three relaxometry data sets from a mono-exponential 3-parameter fit [5].

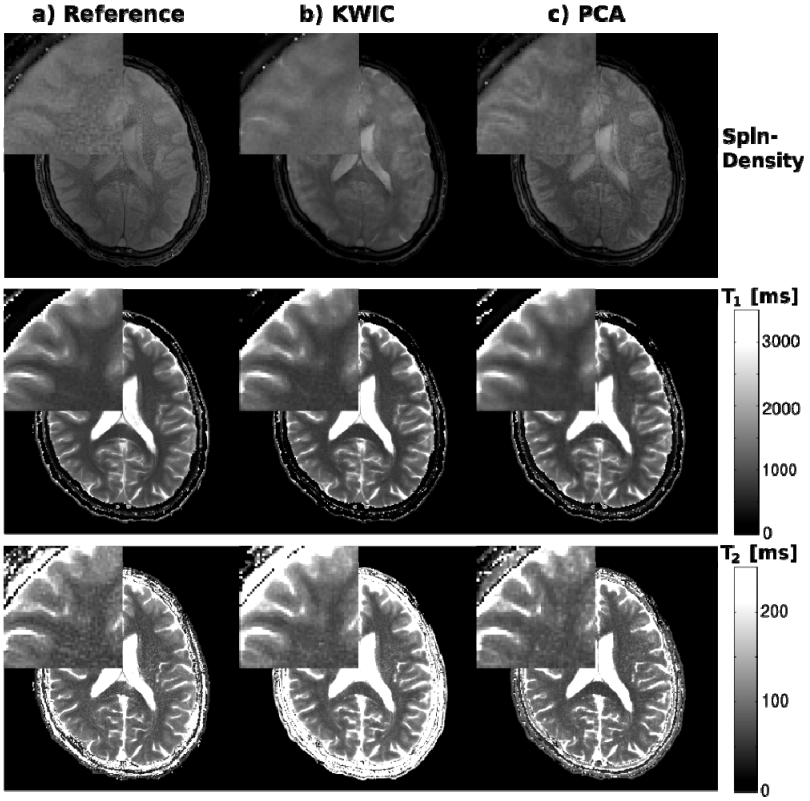

Fig. 1: Spin-density, T_1, and T_2 maps for a) the reference scan, and a single shot scan reconstructed using b) KWIC and c) PCA. In case of KWIC filtering, CSF seems to penetrate into surrounding areas in the T_2 map due to temporal blurring.

Results: Figure 1 shows parameter maps from a) the segmented reference and b-c) the single-shot scan reconstructed using KWIC and PCA, respectively. Small spin-density and T_1 differences in CSF can be explained by incomplete relaxation in the reference data set due to the relatively short relaxation delay.

Discussion & Conclusion: In this work, we propose a new PCA based method for the reconstruction of undersampled relaxometry data. This method allows the quantification of T_1, T_2 and spin-density from a single IR TrueFISP experiment in under 5 s per slice. By gridding the radial projections to Cartesian k-spaces prior to PCA reconstruction, overlap of projections in the center of k-space is fully utilized without the need of filtering or repetitive and time-consuming gridding/transforming operations. Undersampling artifacts were completely removed and the results were comparable to a segmented fully-encoded reference. Compared to view-sharing (in the form of KWIC), the PCA results show less temporal blurring in both spin-density and T_2. Results for T_1 are very similar for all three methods.

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Acknowledgements: Bavarian Ministry of Economic Affairs, Infrastructure, Transport and Technology (BayStMWIVT).