Fast MR Parameter Mapping using k-t PCA

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INTRODUCTION: Quantification of MR-Parameters plays an increasing role in clinical applications. Simultaneous acquisition of quantitative T1, T2 and spin-density maps normally requires 2-3 min for one slice using a segmented Inversion Recovery IR-TrueFISP Sequence [1]. An additional reduction in acquisition time can be achieved by undersampling k-space, resulting in aliased signals that can be separated by various reconstruction concepts (e.g. [2]). Recently, k-t PCA [3] has been presented for dynamic imaging to speed up data acquisition by undersampling k-space over time. The k-t PCA algorithm is used for the reconstruction of the aliased signals by utilizing temporal basis functions (principle components) tailored to the training data in combination with the k-t BLAST concept.

In this work, we demonstrate that the dynamics along the relaxation curve can be described by only a small number of principal components and thus the k-t PCA concept is a promising candidate for significantly accelerating quantitative parameter mapping. In-vivo IR-TrueFISP experiments for quantitative T1, T2 & M0 parameter mapping acquired with up to 8-fold acceleration by using the k-t PCA concept are presented.

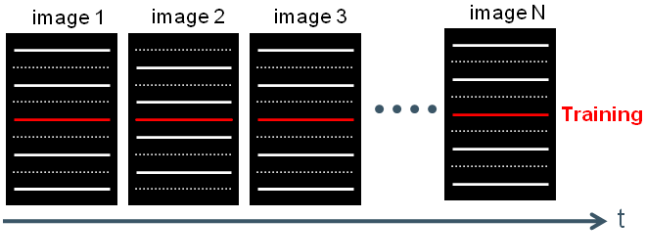

Fig.1 : exemplary sampling pattern for a 2x undersampled dataset including the trainingdata (red)

METHODS: Imaging was performed on a MAGNETOM Avanto 1.5 T (Siemens Medical Solutions) using a 12 channel head array and a modified segmented Inversion-Recovery TrueFISP Sequence [4] which allows significant scan time reduction by eliminating undesired waiting-times between the individual segments. The fully encoded acquisition consisted of non-slice selective inversion pulses, 16 segments, 120 images along the relaxation curve, TR = 5.4ms and a matrix size of 192x160. Undersampling was performed retrospectively (see Fig. 1) with various acceleration factors (Acc). Image reconstruction was performed as described in [3]. However, the principal component analysis was performed only on the central k-space line along the relaxation curve, which contains the dynamics of the relaxation process (M0, T1 and T2) and can be described by only 3 or 4 principal components (PCs). The reconstructed time series of images was fit on a pixel by pixel basis to a 3 parameter mono exponential model, based on the parameters T1, T2 and M0 [1].

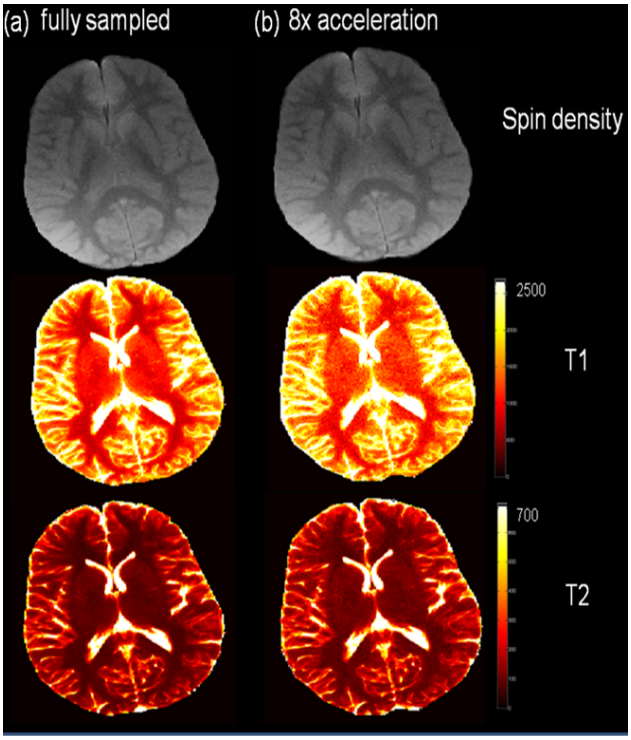

Fig. 2: Quantitave parameter maps derived from a fully sampled segmented (16 segments) (a) and a 8x accelerated (2 segments) k-t PCA (b) modified IR-TrueFISP aquisition

RESULTS: In Figures 2a) –b) T1, T2 and M0 Maps derived from a fully encoded dataset and the reconstructed 8x accelerated dataset using the k-t PCA concept with only 3PCs and one training data line along time for image reconstruction are shown. The parameter maps appear with slightly lower SNR, but no visible artifacts. The reconstruction provides good image quality for acceleration factors 2, 4, 6 and 8 with only small decrease in SNR.

CONCLUSION: MR parameter mapping can be performed up to 8- times faster using the information contained in the basis functions of the central k-space line fully sampled over time. Due to the simple temporal dynamics in relaxometry and in contrast to the application of k-t PCA in dynamic imaging only one extra training data line needs to be acquired (Fig. 1). Using PCA with only a few principal components to extract the main dynamics of an undersampled dataset will shorten particularly time consuming measurements with only little loss of image quality for any process with simple temporal dynamics. In future work, this concept will be combined with parallel MRI for potentially allowing for further scan time reductions. In summary, k-t-PCA has been demonstrated to be a promising acceleration technique for MR relaxometry studies and might be an ideal candidate for providing 3D parameter maps of the entire brain with high isotropic resolution within clinically acceptable imaging times.

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