Highly accelerated 3D spiral acquisition for whole brain myelin water mapping using a hybrid SPIRiT-PCA reconstruction

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INTRODUCTION The quantitative assessment of myelination is important for proper treatment of multiple sclerosis. Multi-component T2 relaxometry (1-3) is a promising method to measure myelin water fraction (MWF), but the clinical utility of the conventional approach is impeded by the long acquisition time of 26 min per slice (4). An SNR efficient 3D T2prep spiral gradient echo sequence has been developed to provide whole brain coverage in 24 min at 1.5T (5), but further acceleration is needed for routine MRI. Recently, a novel method called Iterative Self-consistent Parallel Imaging Reconstruction (SPIRiT) has been introduced that provides a generalized reconstruction framework for non-Cartesian k-space sampling (6) by exploiting spatial redundancy. To reduce temporal redundancy, Principal Component Analysis (PCA) has been applied in accelerated dynamic imaging (7) and MR relaxometry (8,9). Here, we propose to develop a hybrid SPIRit-PCA reconstruction method for multi-component T2 relaxometry at 3T to accelerate whole brain coverage from 24 min down to only 6.5 min.

THEORY The proposed SPIRiT-PCA method uses an image domain based formulation and solves the spiral image reconstruction problem by minimizing the energy function $\| \mathbf{DBx} - \mathbf{y}\|^2 + \lambda\|(\mathbf{G}-\mathbf{I})\mathbf{Bx}\|^2$ using the conjugate gradient algorithm. The first term enforces data consistency between the sampled spiral data **y** and the solution **Bx**, where **D** represents a series of non-uniform FFT (10) that project the image **Bx** onto the corresponding spiral trajectory. The second term represents a self-consistency constraint on the solution which uses the GRAPPA convolution kernel **G** as determined from the oversampled spiral k-space center. **I** is the identity matrix. In the PCA formulation, the images to be reconstructed over time are expressed as a linear combination of temporal basis functions **B** with unknown weights **x**. For T2 relaxometry, these functions can be obtained from a synthetic training data set consisting of exponential decay curves for T2 values within the range of interest (5-500 ms with 1 ms step in our study).

METHODS Eight volunteers were imaged with a 3D T2prep variable density spiral sequence at 3T (26 TEs between 3 and 320 ms, 1.6x1.6x5 mm^3 voxel size, 28 slices, 48 spiral leaves, 26 min scan time, 8-channel head coil). For SPIRiT-PCA reconstruction, each fully sampled data set was undersampled by a factor R=4 using a quasi-random golden ratio based sampling to maintain uniform k-space coverage across TEs. The size of the convolution kernel and calibration data, the number of principal components (PC), and the regularization parameter λ were optimized in one subject by minimizing the error between the accelerated reconstruction and the fully sampled image. T2 distributions were obtained using a regularized non-negative least squares fitting (4) for matching ROIs placed within WM regions. Voxel-wise MWF was calculated by dividing the sum of T2 components under 40 ms by the sum of all T2 components.

RESULTS The optimal kernel and calibration data size was found to be 7x7 and 15x15, respectively. Four PCs were found to provide the best compromise between temporal fidelity and undersampling artifacts. Fig.1 show the superior performance of the proposed hybrid algorithm compared to SPIRiT, especially at higher acceleration factor. Fig.2 compares images reconstructed from fully sampled spiral data (R=1, 26 min) and accelerated data (R=4, 6.5 min) by SPIRiT-PCA, demonstrating effective undersampling artifact suppression while retaining temporal fidelity of the T2 decay. Reconstruction time (using a Matlab implementation) was approximately 5 min per slice. In the healthy human brain, SPIRiT-PCA at R=4 was found to provide MWF in major WM regions comparable to that obtained with the fully sampled data (Fig.3), although there was a slight but statistically significant overestimation of about 0.7% in the splenium of corpus callosum (CC).

DISCUSSION Our preliminary data suggest that the proposed SPIRiT -PCA algorithm provides similar MWF for multi-component T2 relaxometry and enables whole brain coverage in 6.5 min at 3T. The acceleration is made possible by the synergistic benefits of spatial self-consistency constraints by SPIRiT and the reduction of high temporal redundancy in T2 relaxometry data (11) by PCA. Combined with the 3D T2prep spiral acquisition, SPIRiT-PCA may be a promising approach to bringing MWF quantification closer to clinical practice.

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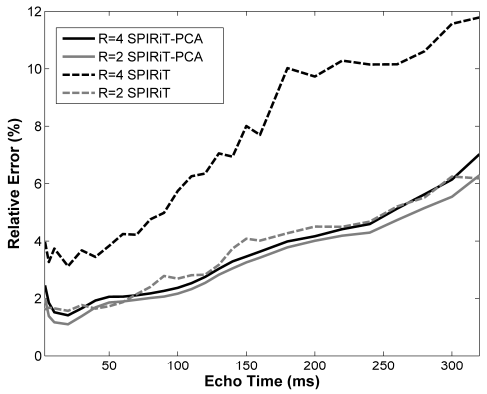

Fig.1. Relative errors of conventional SPIRiT and proposed SPIRiT-PCA reconstruction of 3D T2prep spiral brain data obtained at acceleration factors R=2 and 4.

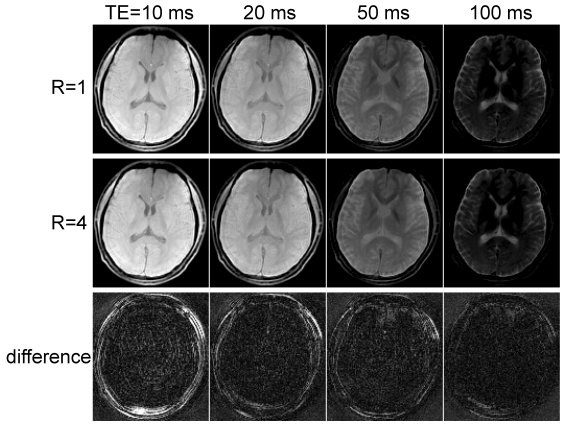

Fig.2. T2 weighted images reconstructed with fully sampled data (R=1) and R=4 acceleration. The difference images are scaled up 10x to allow better visualization.

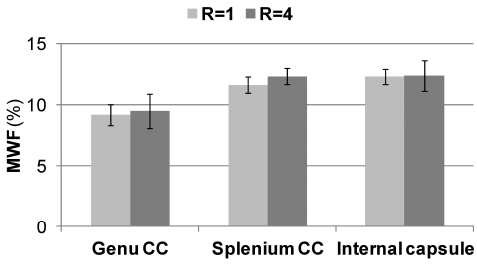

Fig.3. Comparison of MWF obtained with fully sampled (R=1, 26 min) and accelerated (R=4, 6.5 min) 3D spiral acquisition (n=8).