Magnetic Resonance Fingerprinting by exploiting Low Rank

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Abstract—**Magnetic Resonance Fingerprinting (MRF) is a relatively new approach that provides quantitative MRI measures using randomized acquisition. Extraction of physical quantitative tissue parameters is performed off-line, based on acquisition with varying parameters and a dictionary generated according to the Bloch equations. MRF uses hundreds of radio frequency (RF) excitation pulses for acquisition, and therefore high under-sampling ratio in the sampling domain (k-space) is required for reasonable scanning time. This under-sampling causes spatial artifacts that hamper the ability to accurately estimate the tissue's quantitative values. In this work, we introduce a new approach for quantitative MRI using MRF, called magnetic resonance Fingerprinting with LOw Rank (FLOR). We exploit the low rank property of the concatenated temporal imaging contrasts, on top of the fact that the MRF signal is sparsely represented in the generated dictionary domain. Experiments on real MRI data, acquired using a spirally-sampled MRF FISP sequence, demonstrate better resolution compared to other compressed-sensing based methods for MRF at 5% sampling ratio.**

I. INTRODUCTION

Recently, an approach for quantitative MRI (QMRI), estimating the T1 and T2 tissue's relaxation time constants and the proton density (PD) maps called magnetic resonance fingerprinting (MRF) has been proposed [1]. MRF uses pseudo-randomized acquisitions to generate many different imaging contrasts, acquired at a high under-sampling ratio. It exploits the different acquisition parameters over time to produce a temporal signature, a "fingerprint" for each tissue under investigation. By matching this unique signature to a pre-generated set of simulated patterns, the quantitative parameters can be extracted off-line. This approach saves scan time compared to previous methods for accelerated QMRI [1]. Figure 1 demonstrates the MRF scheme.

An initial work describing the implementation of a low-rank model for MRF has been developed recently [2] and has also been presented by us in [3]. Here, we apply an improved reconstruction algorithm, together with under-sampling using spiral trajectories. Moreover, we show that our algorithm, called FLOR, increases the accuracy of the resulting parameter maps from highly under-sampled data, compared to previous CS-based methods.

II. METHOD

MRF data consists of multiple frames, where each column of $\mathbf{Y}$ is an under-sampled Fourier transform of an image frame, $\mathbf{X}_{:,i}$:

$$\mathbf{Y} = [F_u\{\mathbf{X}_{:,1}\}, ..., F_u\{\mathbf{X}_{:,L}\}] \tag{1}$$

where $F_u\{\cdot\}$ denotes an under-sampled 2D Fourier transform. The row $\mathbf{X}_{j,:}$ represents the temporal signature of a single pixel (assumed to correspond to a single tissue). The signature depends on the tissue's relaxation times, T1 and T2, and its PD. Each column, $\mathbf{X}_{:,i}$ represents

a response image acquired at a single time point with different acquisition parameters: the repetition time (TR), the time to echo (TE) and the flip angle (FA) of the RF pulse.

Recovery is performed by defining a dictionary $\mathbf{D}$ of dimensions $M \times L$ that consists of simulating the signal generated from M tissues using the Bloch equations (represented as M different combinations of T1 and T2 relaxation times), and L is the sequence length. The PD is not simulated in the dictionary, as it is the gain used to match the Bloch simulation performed on a single spin to the signal obtained from a pixel containing multiple spins. After successful recovery of $\mathbf{X}$, each row in $\mathbf{X}$ is matched to a single row in $\mathbf{D}$, and T1 and T2 are estimated as those used to generate the matched dictionary row.

In our approach the low-rank property of $\mathbf{X}$ can be exploited for improved reconstruction using the following optimization problem:

$$\underset{\mathbf{X} \in \mathbb{D}}{\text{minimize}} \quad \frac{1}{2}\sum_i \|\mathbf{Y}_{:,i} - F_u\{\mathbf{X}_{:,i}\}\|_2^2 + \lambda \|\mathbf{X}\|_* \tag{2}$$

where $\|\mathbf{X}\|_*$ is the nuclear norm and $\mathbb{D} = \{\mathbf{X} : \mathcal{N}(\mathbf{X}) \supseteq \mathcal{N}(\mathbf{D})\}$ is the subspace spanned by the dictionary signatures. This equation is solved iteratively by using the incremental subgradient proximal method [4] which includes a gradient step, followed by a projection into the dictionary sub-space and a singular value thresholding. After the iterations a matched filter calculation matches pixel of $\mathbf{X}$ to a single signature of $\mathbf{D}$.

III. RESULTS

Reference data was generated by acquisition of Fast Imaging Employing Steady-state Acquisition (FIESTA) and Spoiled Gradient Recalled Acquisition in Steady State (SPGR) images, at 4 different flip angles (3°, 5°, 12° and 20°), and implementation of the well known DESPOT1 and DESPOT2 [5] algorithms, after improvements as described in [6], to generate T1,T2 and PD quantitative maps. The FISP pulse sequence was simulated with constant TE of 2ms, random TR values in the range of 11.5-14.5 ms, and a sinusoidal variation of RF pulses in the range of 0-70 degrees [7]. To simulate noisy samples, we added complex Gaussian zero-mean noise with standard deviation of $\sigma = 0.5$. Data was then under-sampled to acquire only 5% of the k-space in each TR with spiral sampling. We generated the dictionary using Bloch equations, in a range that covers the relaxation times values that can be found in a healthy brain scan [8].

Figure 2 shows the resulting maps for the recovery of T1, T2 and PD obtained with FLOR, wavelet-based approach [9] and BLIP [10] against the gold-standard (left).

IV. CONCLUSION

We presented FLOR, a method for high quality reconstruction of quantitative MRI data using MRF, by utilizing the low-rank property of MRF data. We provide results that are comparable to fully sampled MRF, using only 5% of the data. In addition, comparison against CS-based methods for MRF shows the added value of low-rank based reconstruction.
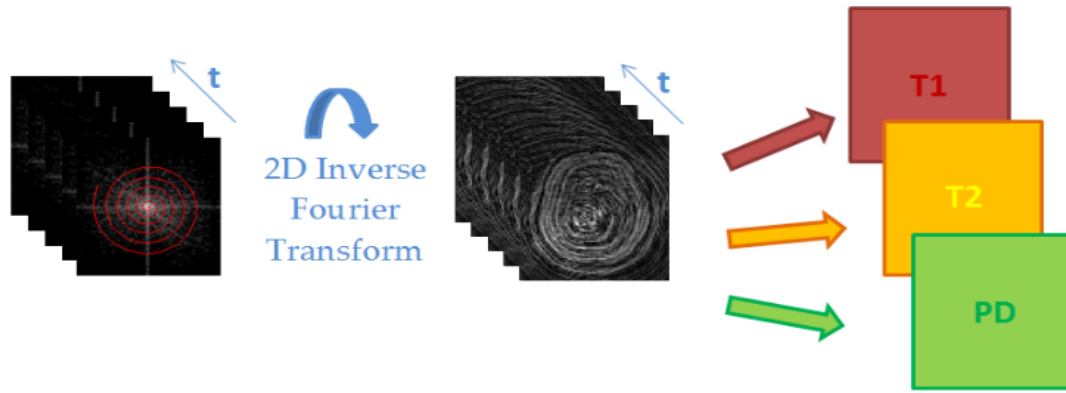
Fig. 1. Illustration of the MRF scheme. Left to right: Data is acquired in the k-space domain resulted in low resolution temporal images. Matched filtering against a simulated dictionary leads to quantitative maps.
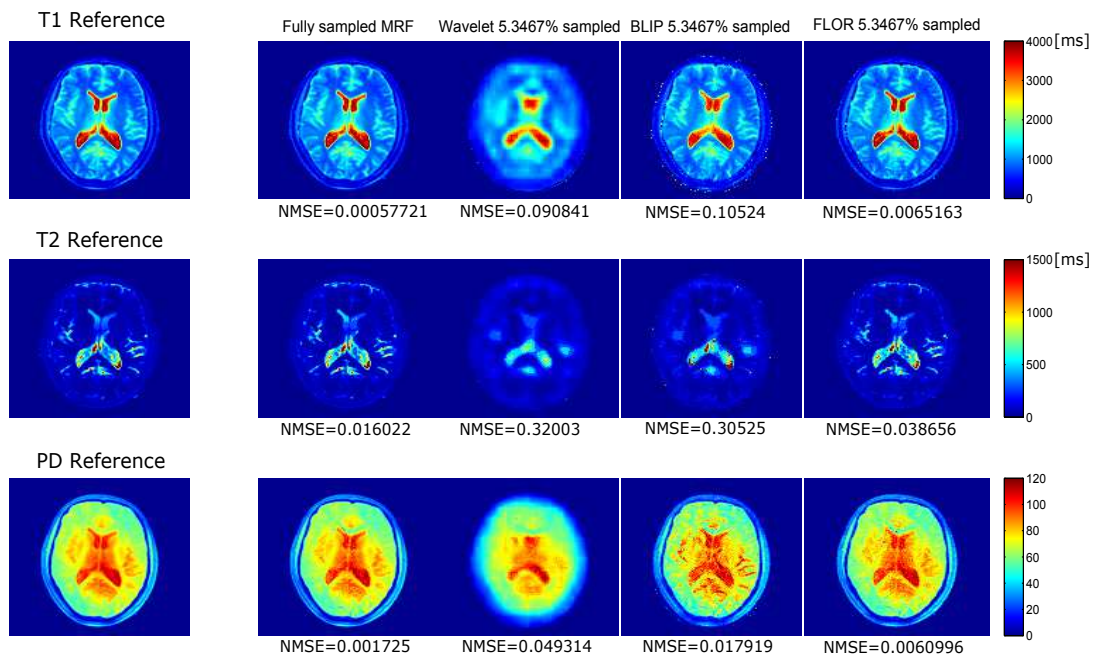

Fig. 2. Results of T1, T2 in milliseconds and PD in arbitrary units reconstructions. Left: Reference, reconstruction using conventional MRF from 100% of the data, followed by wavelet based algorithm, BLIP, low-rank MRF reconstruction with acceleration from 5% of the noised data.

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