Magnetic Resonance Fingerprinting with compressed sensing and distance metric learning

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ABSTRACT

Magnetic Resonance Fingerprinting (MRF) is a novel technique that simultaneously estimates multiple tissue-related parameters, such as the longitudinal relaxation time T_1, the transverse relaxation time T_2, off resonance frequency B_0 and proton density, from a scanned object in just tens of seconds. However, the MRF method suffers from aliasing artifacts because it significantly undersamples the k-space data. In this work, we propose a compressed sensing (CS) framework for simultaneously estimating multiple tissue-related parameters based on the MRF method. It is more robust to low sampling ratio and is therefore more efficient in estimating MR parameters for all voxels of an object. Furthermore, the MRF method requires identifying the nearest atoms of the query fingerprints from the MR-signal-evolution dictionary with the $\mathcal{L}_2$ distance. However, we observed that the $\mathcal{L}_2$ distance is not always a proper metric to measure the similarities between MR Fingerprints. Adaptively learning a distance metric from the undersampled training data can significantly improve the matching accuracy of the query fingerprints. Numerical results on extensive simulated cases show that our method substantially outperforms state-of-the-art methods in terms of accuracy of parameter estimation.

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1. Introduction

Quantitative multiparametric acquisition in magnetic resonance imaging has long been the goal of research because it provides means of evaluating pathology using absolute tissue characteristics rather than contrast-based approaches [1]. It involves quantification of longitudinal relaxation time T_1, transverse relaxation time T_2, off resonance frequency B_0, proton density and other relevant parameters at each voxel of the scanned object. In most previous work, T_1 and T_2 are determined in separate scans [2–7]. Some recent methods can simultaneously estimate several parameters [8–10] but are restricted to only a limited set of parameters.

The Magnetic Resonance Fingerprinting (MRF) method recently proposed by [11] has the potential to quantitatively examine more than 4 magnetic resonance parameters simultaneously. The MRF method is based on the Inversion recovery-balanced SSFP (IR-bSSFP) [12] sequences. It has been reported that MRF outperforms the widely used DESPOT1 and DESPOT2 [7] methods for T_1 and T_2 estimation. It can also be used to directly estimate the combination proportions of different types of tissues at every single voxel. This may lead to new diagnostic methodologies.

The key idea of the MRF method is similar to matching a person's fingerprint to a database: once a match is made, additional information about the person can be obtained simultaneously. The MRF method generates unique signal evolutions by scanning a slice of the object for T times with randomized system-related parameters. After applying the inverse Fourier transformation, the T-dimensional vector at every voxel location represents its characteristic signal evolution and is called its Magnetic Resonance Fingerprint [11]. Different tissues (such as white matter, gray matter, and cerebrospinal fluid) are assumed to have their own unique magnetic resonance fingerprints. These fingerprints can be easily distinguished by matching them to a predefined dictionary, which is generated using the well-known Bloch equation. The dictionary can be seen as a natural discretization of the Bloch response. It contains fingerprints of all foreseeable combinations of materials and system-related parameters. Each fingerprint corresponds to a vector of parameters to be estimated (such as T_1, T_2, B_0 and proton density). A nearest-neighbor based method is used to select the dictionary atom that best represents the observed fingerprint of a query voxel. All the magnetic resonance parameters corresponding to this dictionary atom can then be retrieved simultaneously. In this way, a set of MR parameters are estimated at every voxel location. The same procedure can be repeated to obtain MR parameter maps of all slices of the scanned object.

However, the MRF method still suffers from two problems: (1) in order to balance the accuracy and the scanning time, the MRF method significantly undersamples data in the k-space. Thus the reconstructed images exhibit extreme aliasing artifacts, which propagate to the estimated MR parameter maps. (2) The MRF method selects the best atom whose parameters are closest to the query fingerprint with the $\mathcal{L}_2$ distance. However, we observed that the $\mathcal{L}_2$ distance is not always appropriate for retrieving the correct fingerprint from the dictionary.

Recent developments in compressed sensing (CS) theory [13,14] show that it is possible to reconstruct signals from highly undersampled data, which provides plausible solutions for the first problem. So far, CS has been successfully applied to various domains in medical imaging, e.g., MR Imaging [15,16], shape modeling [17–19] and optical coherence tomography denoising [20].

Methods in [15,21] performed optimization with L_1 and TV norm regularizations by the Conjugate Gradient decent algorithm. These two methods could effectively reconstruct MR images with a sampling ratio around 20 %. Other methods like L_p quasi-norm ($p < 1$) regularized optimization [22,23] tolerate lower compression ratios, but these non-convex algorithms do not always recover global optima and are relatively slower. Ref. [24] adaptively learned the sparsifying transform (dictionary) and thereby favoring higher sparsity and consequently higher sampling ratios. Their reconstructions can achieve higher undersampling ratios with tolerable errors. However, all these algorithms lead to aliasing artifacts if they are applied to the MRF method with a sampling ratio of only around 3%.

To our knowledge, two previous methods [25,26] were proposed to integrate a CS algorithm into the MRF framework. Ref. [25] proposed to apply CS to reconstruct the image at each sampling time. But the sampling ratio cannot be less than 70%. Ref. [26] adopted a CS solution based on the iterative projection algorithm by [27] which imposes consistency with the Bloch response manifold. At each iteration, every voxel would be replaced by its nearest atom in the dictionary. Then the whole image at each sampling time was updated by the Projected Landweber Algorithm (PLA). This method is called BLIP (BLoch response recovery via Iterated Projection), and is efficient and effective in removing the aliasing artifacts.

Moreover, all the previous works [11,25,26] used inner-product for calculating the similarities between the query fingerprint and the dictionary atoms, which is equivalent to using the $\mathcal{L}_2$ distance as the distance metric. However, we observe that if the distance metric is learned in a supervised manner, then the performance of the nearest-neighbor based dictionary matching can be significantly improved.

In this work, we propose a compressed sensing framework for simultaneously estimating multiple MR parameter maps with distance metric learning. Instead of treating each voxel individually, we assume that each image is sparse in some transform domain. The problem of estimating MR parameter maps is then formulated as a compressed sensing problem, where we make use of the spatial information of the image sequence. For each voxel, its fingerprint is then matched to its nearest atom in a predefined dictionary with a learned distance metric. Such a learned metric is more accurate in MR fingerprint matching. Furthermore, a novel sampling strategy based on Cartesian sampling is proposed. Our strategy makes the aliasing noise as incoherent as possible with the fingerprint itself, thus making it easier to be removed. Extensive experiments were conducted on simulated MR images to evaluate the performance of the proposed method. Numerical results show that it outperforms state-of-the-art methods in estimating multi-parametric MR maps of scanned objects.

In real scenarios, the ground truth MR parameter maps for distance metric learning can be obtained by applying standard MR imaging approaches to volunteers or phantoms. The learned metric can then be used for future scans under the same experimental setting.

Our main contribution is three-fold: (1) we propose a compressed sensing framework based on MRF that is more robust to estimate multiple MR parameter maps of a scanned object at low sampling ratios. It makes use of the spatial information of the image sequence and is therefore accurate in estimating the MR parameters when the sampling ratio is very low. (2) We improve the accuracy of the dictionary matching process by replacing the $\mathcal{L}_2$ distance with a learned distance metric. The proposed metric can be learned in a supervised manner. (3) In order to make the undersampling errors and the MR fingerprints as incoherent as possible, we design a novel sampling strategy with which the sampling mask at time t is conditional on the one at time $t - 1$. It generates aliasing noise that is easier to be removed by dictionary matching.

2. Methodology

In this work, we propose a novel framework to simultaneously estimate multiple MR parameters for every voxel of a scanned object based on the MRF method. In Section 2.1, the MRF method and notation is introduced. In Section 2.2, we introduce a compressed sensing framework for MRF to reduce errors. In Section 2.3, we present adaptively learning a distance metric for dictionary matching. A novel sampling strategy is proposed in Section 2.4 which further removes the aliasing noise.

2.1. Magnetic Resonance Fingerprinting (MRF)

The key underlying assumption in MRF is that different materials or tissues have their own unique signal evolutions or fingerprints. The magnetization at a given voxel location at time t depends on its magnetic resonance parameters and the system-related parameters, including the flip angle FA, repetition time TR and others, at time $t - 1$. For illustration purposes, we explain the estimation of MR parameter maps of only a single slice in Section 2.

Let $X \in \mathbf{C}^{N \times T}$ denote multiple scans of one slice of the object of interest, where N is the total number of voxels in the slice and T is the sequence length. Let $X_t^i \in \mathbf{C}$ denote the ith voxel of the scanned slice at time t, $X^i \in \mathbf{C}^{1 \times T}$ denote the signal evolution or fingerprint at voxel i at all times, and $X_t \in \mathbf{C}^{N \times 1}$ denote the scanned image of the slice at time t.

Given the initial magnetization, the signal evolution or fingerprint at voxel i can be written as

$$X^i = \rho_i \mathcal{B}(\theta_i; FA, TR), \tag{1}$$

where ρ_i is the proton density – one of the magnetic resonance parameters to be estimated, θ_i is the collection of other magnetic resonance parameters at voxel i, and $\mathcal{B}$ is the Bloch equation dynamics.

Since the possible range of θ_i of the object is known in advance, we densely sample each MR parameter and use the Bloch equation to create the dictionary $D \in \mathbf{C}^{K \times T}$, where K is the number of dictionary atoms. Each dictionary atom is normalized so that $\|D^k\|_2 = 1$, for $k = 1, 2, \ldots, K$. The same set of system-related parameters FA and TR is used for both creating the dictionary and obtaining the scanning data X. Given a query fingerprint, it is matched to its nearest atom in the predefined dictionary with the $\mathcal{L}_2$ distance. The index of the nearest dictionary atom for the fingerprint X^i is denoted as $\tilde{k}_i$, and is obtained as

$$\tilde{k}_i = \arg\min_k \|X^i / \|X^i\|_2^2 - D^k\|_2 \tag{2}$$

$$\tilde{k}_i = \arg\max_k \left\{ real\langle X^i / \|X^i\|_2^2, D^k \rangle \right\}, \tag{3}$$

where $real$ is the operation to extract the real part of a complex number and $\langle \cdot, \cdot \rangle$ is the inner product operation. The corresponding