# Convex optimisation for partial volume estimation in compressive quantitative MRI

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Abstract—Based on the recently proposed compressive sensing framework for quantitative MRI, a new approach for partial volume reconstruction is developed in this abstract. We first formulate a convex optimisation problem for the recovery of a sparse matrix of coefficients in a dictionary of measured temporal fingerprints associated with specific combinations of quantitative parameters of interest. Each column of the sought matrix represents a voxel in the volume under investigation and the sparsity of this column represents the number of active dictionary elements or partial volumes. In a second step, we employ the weighted k-means algorithm to cluster the recovered coefficient matrix in parameter space and obtain the quantitative parameter maps. The proposed approach was validated through simulations, and its performance is competitive when compared to a state of the art algorithm.

### I. INTRODUCTION

Quantitative Magnetic Resonance Imaging (qMRI), aiming to produce voxel-wise quantitative maps of parameters related to the tissues under investigation such as  $T_1$  and  $T_2$  relaxation times, remains challenging due to its prohibitively long acquisition time. Inspired by the recent growth of Compressed Sensing (CS) techniques in MRI, Magnetic Resonance Fingerprinting (MRF) was introduced to accelerate qMRI [1]. A full CS strategy was then formulated in [2] including an iterative projection algorithm that imposes consistency with the Bloch equations, namely BLoch response recovery via Iterative Projection (BLIP). It has been shown that BLIP outperforms the MRF technique proposed in [1] especially with a shorter magnetization sequence.

Nevertheless, both algorithms work with the assumption that there is only one tissue in each voxel. As a result, voxels that contain signal from multiple tissues may be incorrectly assigned. In order to address this partial volume problem, a new approach based on the CS framework in [2] is proposed.

### II. PROPOSED METHOD

We first reformulate the acquisition model in [2] as  $Y = \mathcal{A}(X) + \eta$ , where  $Y \in \mathbb{C}^{L \times M}$  represents the measurements,  $\mathcal{A} : \mathbb{R}_+^{d \times N} \to \mathbb{C}^{L \times M}$  is a linear operator,  $X \in \mathbb{R}_+^{d \times N}$  stands for the proton density coefficient matrix, and  $\eta \in \mathbb{C}^{L \times M}$  is Gaussian noise with standard deviation  $\sigma_n$ . We should note that the magnetization sequence is defined as  $\bar{X} = \Phi X \in \mathbb{C}^{L \times N}$ , where  $\Phi \in \mathbb{C}^{L \times d}$  is a dictionary with d atoms and L acquisition instances. The operator  $\mathcal{A}$  is defined row-wise as  $Y_l = \Phi_l X F P^{(l)}$ , for l = 1, ..., L, where  $\Phi_l$  is the l-th row of  $\Phi$ ,  $F \in \mathbb{C}^{N \times N}$  is the two dimensional Fourier transform, and  $P^{(l)} \in \mathbb{R}^{N \times M}$  (with  $M \ll N$ ) are the random echo-planar imaging (EPI) undersampling masks for different acquisitions. Since each voxel is expected to contain only a few dictionary atoms (tissues), X is naturally sparse. We thus reformulate the reconstruction problem as a convex minimization task:

$$\min_{X \in \mathbb{R}_{+}^{d \times N}} ||X||_{1} \quad \text{subject to} \quad ||Y - \mathcal{A}(X)||_{2} \le \epsilon, \tag{1}$$

where  $\epsilon$  is related to  $||\eta||_2$ . This kind of convex problem can be efficiently solved by various kinds of algorithms. We hereby employ the Forward-Backward Primal-Dual method to find the optimal solution [3]. The method is implemented in the same way as in [4], which allows to divide the data in multiple blocks to exploit parallelism.

Since the non-zero values are not limited in each column of X, (1) allows us to reconstruct the quantitative parameter maps with multiple tissues voxels. In a second step, we put each column of X in the parameter space and use the weighted k-means algorithm [5] in order to constrain the maximum number of tissues in a single voxel. The quantitative map can then be obtained according to the centroid of each cluster. We should note that the continuity of these centroids in fact allows us to achieve a better resolution than the dictionary used in the minimisation.

### III. EXPERIMENT AND RESULTS

In order to test the proposed method, a phantom with multiple tissues in each voxel (2 tissues at most in this experiment) was defined. The phantom was created by increasing the size of the voxel in the original phantom in [6] by a factor of 4. For each voxel, the two tissues with biggest proton density were chosen. The input noise was set to 50dB, L=200 and 1/16 of the data was acquired. The dictionary used for the proposed method was composed of 676 atoms, while 22500 atoms were used for BLIP. As seen in Fig. 1-2 and Table I, the proposed method is capable of partial volume reconstructions and performs significantly better than BLIP, which assumes that each voxel contains only one tissue. An important remark is that the proposed method can achieve good results even with a small dictionary by using the coherence of the dictionary in the reconstruction. We should also mention that BLIP is less computationally expensive than the proposed method, but has a higher demand for a fine dictionary.

# IV. CONCLUSION

In this abstract a new approach for partial volume reconstruction in qMRI was proposed based on the CS framework in [2]. The two key points of this approach are a problem re-formulation that considers multiple tissue voxels, and a post-processing clustering. Simulation results have shown the ability of the proposed method to reconstruct quantitative maps with multiple tissue voxels. Our future work will mainly focus on further simulations/experiments on real data and computational optimization of the proposed algorithm.

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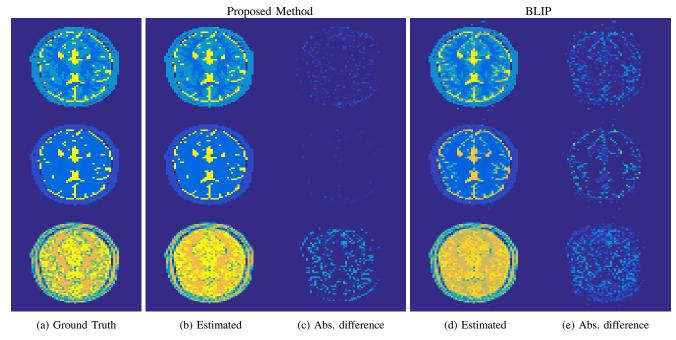


Fig. 1: First Element results (First row  $T_1$ , second row  $T_2$  and third row  $\rho$ ).

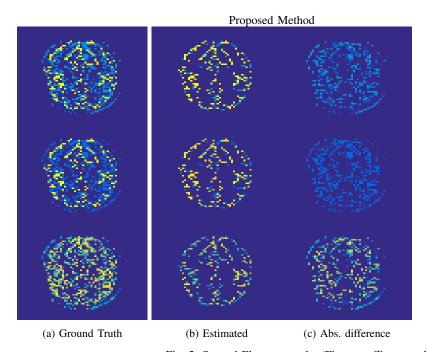


Fig. 2: Second Element results (First row  $T_1$ , second row  $T_2$  and third row  $\rho$ ).

		First Element SNR			Second Element SNR		
	$\bar{X}$ SNR	T1	T2	ρ	T1	T2	ρ
BLIP	22.31	13.24	8.96	15.54	N/A	N/A	N/A
$\ell_1$	48.74	23.31	32.28	15.07	9.46	13.05	2.84

TABLE I: Results

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