Regularized, Joint Estimation of $T_1$ and $M_0$ Maps

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Introduction

Fast and accurate quantification of spin-lattice relaxation time $T_1$ and proton density $M_0$ have been a longstanding goal in MRI research. The physical meaning of $T_1$ maps can serve as a biomarker for subtle changes in pathology. Accordingly, relaxometry has recently gained attention as a method for monitoring the progression of disorders such as Parkinson’s disease, epilepsy, and multiple sclerosis.

Classical methods such as inversion recovery (IR) and saturation recovery (SR) produce simple $T_1$ estimates, but suffer from lengthy acquisitions. By contrast, steady-state pulse sequences are faster, but depend on more complex functions of both desired and nuisance parameters, causing naïve least-squares estimators to exhibit systematic error in low-signal regions. To improve $T_1$ mapping precision, we propose a novel, model-based approach to this nonlinear estimation problem. Here, we focus on the Driven Equilibrium Single Pulse Observation of $T_1$ (DESPOT1) sequence [1], though our statistical considerations can be adapted to other relaxometry techniques as well.

Theory

We propose a model-based reconstruction framework for accurate $M_0$ and $T_1$ mapping from a DESPOT1 sequence. DESPOT1 repeats a spoiled gradient-recalled echo (SPGR) sequence over multiple flip angles, holding $T_R$ and $T_E$ constant. The steady-state signal model is given by

$$y_i = \frac{M_0}{1 - E_1} \sin \alpha_i (1 - E_1) + \epsilon_i = f(M_0, E_1, \alpha_i) + \epsilon_i,$$

where $y_i$ is the SPGR image data for the $i$th flip angle $\alpha_i$; $E_1 \approx e^{-\gamma B_0^2 \tau_1}$; $\epsilon \sim CN(0, \sigma^2)$ is complex white Gaussian noise; and $(i)$ indexes a specific voxel, without which the corresponding variable labels indicate vectorized versions across all voxels. Conventional methods typically neglect the noise term and recast this model into a linear form for least squares fitting. Unfortunately, this causes noise amplification in low-signal regions. We instead investigate $T_1$ mapping as the following joint optimization problem:

$$\hat{M}_0, \hat{E}_1 = \arg\min_{M_0, E_1} \frac{1}{N} \sum_{i=1}^N \| y_i - f(M_0, E_1, \alpha_i) \|^2 + \beta_1 \sum_{i=1}^N \psi_k(|(CM_{0,i})_L|) + \beta_2 \sum_{i=1}^N \psi_k(|(CE_{1,i})_L|)$$

where $y_i, M_0 \in C^N, \alpha_i, E_1 \in R^N, N$ is the number of voxels; $C \in R^{N \times N}$ is a 2D spatial finite differencing matrix; $\psi_k$ is a hyperbolic, edge-preserving potential function; $k$ indexes the total $K$ differencing operations; and $\beta_1, \beta_2 \in R$ are regularization parameters that control the level to which roughness in $M_0$ and $E_1$ is penalized, respectively. We iteratively solve this problem using an alternating minimization approach.

Experiments and Results

We evaluated our method with data synthesized from the BrainWeb digital phantom [2]. Ground truth maps were converted to noise-corrupted data at a range of flip angles, including the two “ideal” angles postulated in [1], with $T_R = 22.1\text{ms}, T_E = 5.1\text{ms}$. We first reconstructed the data with the conventional method [1], and then used this estimate to initialize the proposed reconstruction (Fig. 1). Comparisons with the ground truth are made in a normalized root mean-squared error (NRMSE) sense over voxels where $M_0 > 0$. Figure 2 shows that the proposed method reduces NRMSE of both $M_0$ and $T_1$ estimates over a wide range of SNR values and flip angle combinations (not shown).

We also provide in vivo results (Fig. 3) from an 8-channel receive array head coil in a 3T GE MRI scanner. We repeated an SPGR sequence at 5, 10, 20, 30, and 45 degree flip angles, with $T_R = 19.8\text{ms}, T_E = 5.1\text{ms}$. We acquired 10 axial slices at 5mm thickness, with a 24cm FOV (256x256 matrix size). We reconstructed the data by both the conventional DESPOT1 and proposed model-based approaches. We selected several regions of interest for comparing parameter estimates. From the conventional method, $T_1$ was measured as 734±54ms and 990±105ms in white and grey matter, respectively. With the proposed method, $T_1$ was measured as 802±17ms and 1181±29ms in white and grey matter, respectively. These numbers highlight that the proposed method achieves higher precision within tissue types, while preserving high contrast across tissue types.

Conclusions

We have described a statistical approach for joint reconstruction of $M_0$ and $T_1$ maps from DESPOT1 sequences. Our model-based method uses regularization to reduce conventionally common noise amplification issues. The proposed technique dramatically improves mapping precision and quality, both for synthetic and in vivo data, at a wide range of thresholds and flip angle combinations.

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References