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 and has 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 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.
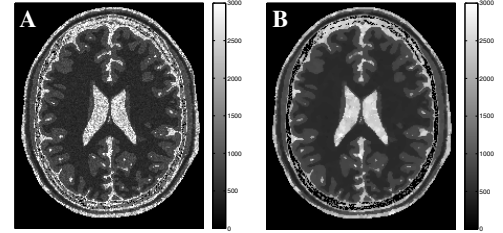

Fig. 1: T_1 maps for simulated data at 40dB SNR, for "ideal" flip angles 5 and 30 degrees. [A] conventional. [B] proposed.

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

$$y_l^{(j)} = \frac{M_0^{(j)} \sin \alpha_l^{(j)} \left(1 - E_1^{(j)}\right)}{1 - E_1^{(j)} \cos \alpha_l^{(j)}} + \epsilon_l^{(j)} \triangleq f\left(M_0^{(j)}, E_1^{(j)}; \alpha_l^{(j)}\right) + \epsilon_l^{(j)},$$

where $y_l^{(j)}$ is the SPGR image data for the lth flip angle $\alpha_l^{(j)}$; $E_1^{(j)} \triangleq e^{-T_R/T_1^{(j)}}$; $\epsilon_l \sim \mathbb{CN}\{0, \sigma^2\}$ is complex white Gaussian noise; and (j) 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:

$$\{\widehat{M}_0, \widehat{E}_1\} = \underset{\{M_0, E_1 \in (0,1)\}}{\operatorname{argmin}} \frac{1}{2} \sum_{l=1}^{L} \|y_l - f(M_0, E_1; \alpha_l)\|_2^2 + \beta_1 \sum_{k=1}^{K} \psi_k([CM_0]_k) + \beta_2 \sum_{k=1}^{K} \psi_k([CE_1]_k),$$

Fig. 2: NRMSE versus SNR of simulated data at "ideal" flip angles. Using more flip angles yields similar improvements.

where $y_l, M_0 \in \mathbb{C}^N$; $\alpha_l, E_1 \in \mathbb{R}^N$; N is the number of voxels; $C \in \mathbb{R}^{K \times N}$ is a 2D spatial finite differencing matrix; ψ_k is a hyperbolic, edge-preserving potential function; k indexes the total K differencing operations; and $\beta_1, \beta_2 \in \mathbb{R}$ 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 $T_R = 22.1$ms, $T_E = 5.1$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 $T_R = 19.8$ms, $T_E = 5.1$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 noise thresholds and flip angle combinations.

References

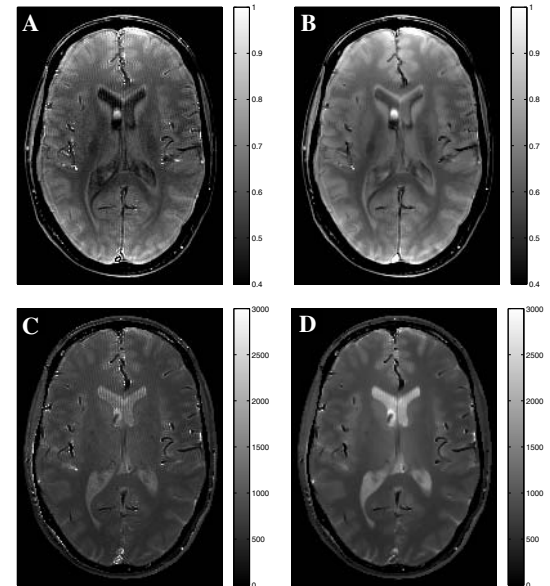[1] Deoni et al., MRM 49(3):515-26, 2003. [2] Collins et al., IEEE TMI 17(3):463-8, 1998.
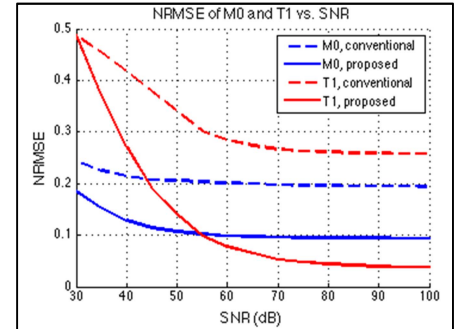
Fig. 3: Reconstructions from DESPOT1 sequence. [A] M_0, conventional. [B] M_0, proposed. [C] T_1, conventional. [D] T_1, proposed. Regularized estimation yields piecewise-smooth images. This translates to an increase in parameter mapping precision over the conventional methods.