A Novel Approach for T1 Relaxometry Using Constrained Reconstruction in Parametric Dimension

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Introduction: Knowledge of the longitudinal relaxation time T_1 is necessary in many quantitative MRI applications. T_1 mapping using variable flip angle SPGR acquisitions is an attractive choice due to its accuracy [1]. Critical to the efficiency of the method is the choice of flip angles. A pair of optimized angles, *ideal angles*, may be easily computed for a single T_1 value [1]. However, more angles may be necessary for optimized performance over range of T_1 values observed in both healthy and pathological tissues and different tissue types. Recently, a weighted genetic algorithm was used to optimize estimation accuracy for a single T_1 value yielded a 10 flip angle design with improved performance over a wider T_1 range [2]. For an accurate estimation of T_1 values, each of the acquired images should have low noise and artifact level necessitating full sampling of the *k*-space data and increasing scan time. In this work, we propose to reduce the total scan time dramatically by using the correlation between images in parametric dimension (flip angle dimension) with a final goal to accelerate T_1 relaxometry by means of high undersampling of data without compromising the accuracy of T_1 estimation.

Theory and Methods: The SPGR signal equation is given by $S = M_0 (1 - E_1) \sin\alpha / (1 - E_1 \cos\alpha)$, where M_0 is equilibrium longitudinal magnetization, α - excitation flip angle, T_R - repetition time, and $E_1 = e^{-T_R/T_1}$. The dependence of the signal intensity on flip angle value is described by a smoothly varying function that can be closely approximated by piecewise linear functions. Therefore, the second derivative of such function nearly vanishes at most points. We used this observation to design a constrained reconstruction approach from incomplete data from multiple flip angles. The series of images is obtained as the solution of the following minimization problem:

$$\overline{\mathbf{f}} = \arg\min_{\overline{\mathbf{f}}} \left(\left\| \overline{\mathbf{E}}\overline{\mathbf{f}} - \overline{\mathbf{m}} \right\|_2^2 + \lambda \Phi\left(\mathbf{L}\overline{\mathbf{f}} \right) \right), \tag{1}$$

where $\overline{\mathbf{E}}$ is the encoding matrix for the image series composed of Fourier terms and coil sensitivity values, $\overline{\mathbf{f}}$ and $\overline{\mathbf{m}}$ are solution and acquired data vectors, respectively, and λ is the regularization parameter. $\mathbf{L}$ is a sparsifying transform based on the 2nd difference in the flip angle dimension, and $\Phi(.)$ is the hybrid l_1/l_2 norm to provide both SNR optimization (via l_2 norm) and to promote sparsity (via l_1 norm). The norm is given by $\Phi(\mathbf{x}) = \sum_k \left(\sqrt{1 + (x_k/\sigma)^2} - 1 \right)$, where $\sigma = 0.6 \text{std}(x)$ [3]. A similar approach to dynamic image reconstruction was previously described in [4].

Fully sampled datasets were acquired using hybrid radial (in-plane)/Cartesian (through-plane) SPGR sequence (TR = 5.5 ms, BW = 125kHz, 20 slices, 8 coil receivers) for a set of 12 flip angles FA=[2°,3°,4°,5°,6°,7°,8°,9°,10°,12°,14°,16°] in a single scan session on a 3T scanner (MR 750, GE Healthcare; Waukesha, WI). The acquired data for a single central slice was retrospectively undersampled to simulate an interleaved undersampled radial acquisition with an acceleration factor of 20. The twelve interleaves were scheduled according to bitreverse ordering. The images were obtained from the undersampled data by solving Eq. (1). The algorithm was implemented using iteratively reweighted least squares approach [5] with 10 reweightings and 20 conjugate gradient iterations per reweighting. For comparison purposes, we also reconstructed images from the undersampled data using gridding with density compensation and iterative SENSE. Also, we used a pair of ideal flip angles for this case (calculated to be 3° and 16°) and the number of projections that could be acquired within the same scan time (100 projections per image) to assess the improvement in T_1 estimation accuracy for the given scan time. As a reference, images from fully sampled data for all 12 flip angles were reconstructed. T_1 values were then estimated from each set of the reconstructed images using non-linear minimization [1].

Results: Results of R_1 ($1/T_1$) estimation are given in Fig. 1. The proposed approach provided the best accuracy due to lower noise level, better artifact reduction and higher spatial resolution in the reconstructed images. The increase in the standard deviation measured in a region in white matter was measured to be 2.13 times for the proposed reconstruction versus 3.82 in the SENSE reconstruction from 2 ideal flip angles (both relative to the reference fully sampled data).

Discussion and Conclusions: Our preliminary results indicate that the proposed constrained method of image reconstruction from undersampled multiple flip angle data for T_1 estimation is a promising technique for improving T_1 estimation accuracy from undersampled data within a limited scan time. This method uses a novel concept of regularization in parametric dimension and may be important for acceleration of other quantitative MRI techniques.

References: [1] Deoni SCL, et al. MRM 2003, 49, 515. [2] Deoni S, et al. MRM 2004, 51:194. [3] Bube KP, et al. Geophysics,1997:62:1183. [4] Velikina JV, Samsonov AA, MR Angio Club, 2009, East Lansing, MI. [5] Wohlberg B, et al. IEEE SPL 2007;14:948.
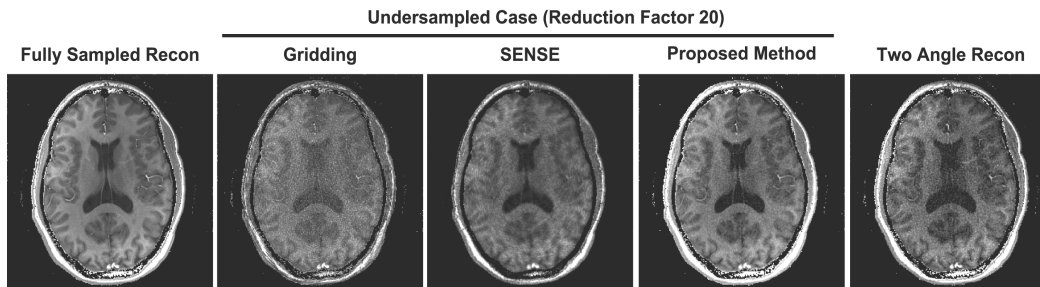
Undersampled Case (Reduction Factor 20)

| Fully Sampled Recon | Gridding | SENSE | Proposed Method | Two Angle Recon |

Figure 1. Reconstruction of T1 maps using different methods including proposed reconstruction and scan time equivalent two flip angle approach. The proposed method allows significant improvement of image quality compared to peer approaches including improved noise performance (gridding, two angle recon) and resolution (SENSE)