

Quantitative T_1 estimation using Tissue Specific Imaging

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Introduction

The longitudinal relaxation time (T_1) of tissues plays an important role both as a contrast mechanism for anatomical imaging and as a disease marker. While several dedicated T_1 measurement techniques exist, they require additional imaging time, so it would be beneficial if equivalent information could be extracted from other diagnostic imaging sequences. Tissue Specific Imaging (TSI-[1]) has been previously applied for the characterization of Multiple Sclerosis (MS) lesions [2] and white matter integrity [3]. TSI can be considered a variant of Double Inversion Recovery, used for the detection of cortical lesions in MS [4]. This study addresses the potential application of TSI for the measurement of T_1 .

Theory and Methods

TSI uses a combination of two inversion pulses and three 3D EPI acquisitions to produce three different T_1 weighted images whose linear combination results in three single tissue type images (figure 1); imaging time is approximately 10 minutes for whole brain coverage. The same TSI raw images can be used to estimate tissue T_1 as follows: assuming single experimental behavior, it is possible to calculate, based on the Bloch equations and knowledge of the sequence parameters, the expected signal levels for each image as a function of T_1 and M_0 using the following equation: (M_z is calculated after the N^{th} pulse, and M_z^{eq} is the equilibrium magnetization as described in [1]).

$$M_z(t) = M_0 \left[1 + \left\{ \sum_{i=1}^{N-1} [(\cos(\phi_i) - 1) \left(\prod_{j=i+1}^N \cos(\phi_j) \right) e^{t_i/T_1}] + (\cos(\phi_N) - 1) e^{t_N/T_1} + (M_z^{eq} - 1) \prod_{i=1}^N \cos(\phi_i) \right\} e^{-t/T_1} \right]$$

We applied least squares fitting to calculate T_1 and M_0 of each voxel. B_1 information is used to correct for the flip angle variation on a voxel-by-voxel basis. While simulated signal levels are real signed numbers, TSI data as acquired from magnet are complex. Real values are calculated based on signal magnitude, and sign information is estimated by the sign of the inner product of each voxel by the respective one in the first TSI raw image.

Accuracy and precision of the proposed technique were estimated using the Monte Carlo simulation and varying levels of white Gaussian noise. SNR was calculated as M_0 divided by the standard deviation of noise; signal levels were adjusted for TE=35ms. Results were compared to DESPOT1 [5], with SNR levels adjusted for both echo time and bandwidth. We used the technique in order to estimate T_1 from previously acquired TSI (as described in [1]) and B_1 mapping [6] data from 5 healthy volunteers.

Results

Figure 2 shows an estimation of precision of the presented technique as a function of T_1 for SNR of 250 and 500, corrected for T_2^* relaxation time. Monte Carlo simulation results show that the precision is comparable to that of DESPOT1 for SNR of 500 and 1000 (adjusted for bandwidth) for T_1 values corresponding to healthy tissue. Mean estimation error was less than 1% for normal tissue T_1 values. Figure 1 shows TSI image and the resulting T_1 map. Average T_1 values for white matter, gray matter (ROI placed in the head of the caudate nucleus) and cerebrospinal fluid were 822(21) ms [mean (standard deviation)], 1399(48.24) ms and 4065(282) ms respectively.

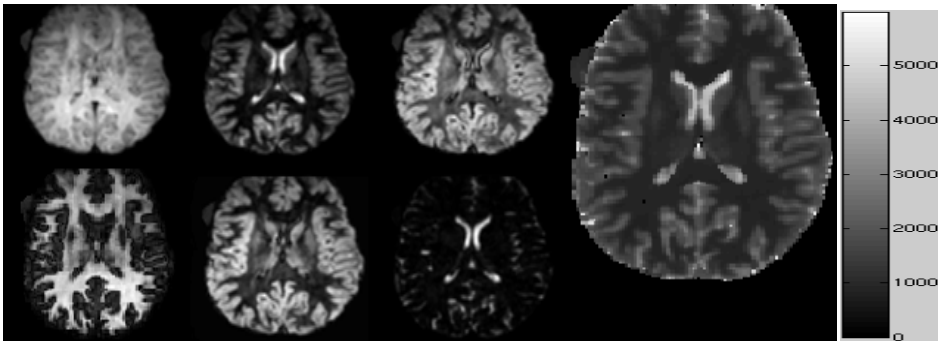


Figure 1: Raw (first row) and synthesized (second row) TSI images, and resulting T_1 map

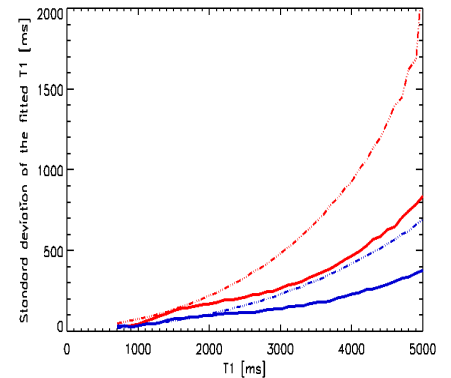


Figure 2: Monte Carlo generated standard deviation of estimated T_1 values using the proposed method (solid line) and DESPOT1 (dashed line) of equivalent SNR levels (red-1000/500, blue-500/250)

Conclusion

We have shown that TSI can be used for quantitative estimation of tissue T_1 , with results comparable to DESPOT1 over the normal T_1 range for healthy tissue. Possibly due to a longer TR of 6 ms, it shows good stability for longer T_1 values (figure 1), making it an attractive solution for estimation of longer T_1 values, such as the ones encountered in advanced MS lesions.

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