Combining morphometry and T1 relaxometry in a single imaging protocol: measuring T1 with MPRAGE

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Introduction:

We are using morphometry and relaxometry to study brain development in children, and so it is imperative to minimize the length of the imaging protocol. MPRAGE [1] provides high quality anatomical images that can be used for quantitative morphometry, and an additional image acquired at an inversion time mid way between the null point for grey and white matter can assist in image segmentation [2]. An efficient imaging protocol for combined anatomical imaging and T1 relaxometry could be produced by acquiring MPRAGE images at additional inversion times. However the evaluation of the T1 from MPRAGE images is not trivial due to the complexity of the sequence. The aim of this work is to measure T1 with the MPRAGE sequence and to optimize the acquisition protocol in terms of SNR per unit time in the T1 map. The longitudinal relaxation times of white and cortical grey matter were measured with this approach and validated against IR EPI at 1.5, 3 and 7 T.

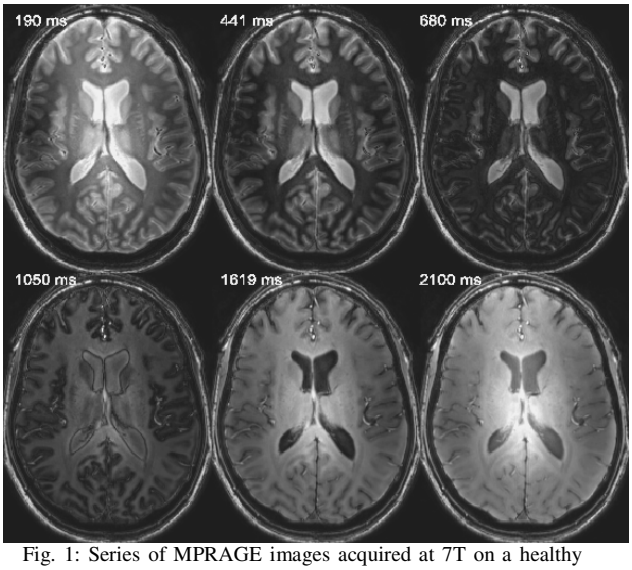

Fig. 1: Series of MPRAGE images acquired at 7T on a healthy volunteer. The Inversion Times vary from 190ms to 2100ms.

Experimental method:

Scanning was carried out using the MPRAGE sequence and the IREPI sequence on 1.5, 3 and 7 T Philips scanners. Parameters for the IREPI sequence were TE/TR 45/5000 ms, acquisition matrix size 64x64 (single shot) and a voxel size 3.12x3.12x3 mm^3. Nine inversion times of TI = 160, 200, 300, 600, 900, 1500, 2100, 3000 and 4000 ms were acquired with a total scan per TI of 15s. The parameters of the MPRAGE sequence were a readout pulse flip angle β of 8° (256 readout pulse per inversion pulse), TR/TE = 11/6.7ms, Shot to Shot Interval (SSI) = 5s and a voxel size of 0.86x0.86x1.5 mm^3. Eight inversion time TI = 160, 190, 285, 441, 680, 1050, 1619 and 2100 ms were acquired for an acquisition time of 1min 40s for 20 slices per TI. A calibration study was carrying out on two spherical phantoms with different agar concentration and also on 5 smaller phantoms with a range of different Gadolinium concentrations from 0.01 mmol/L to 0.13 mmol/L to give a range of T1 relaxation times. Five healthy subjects (33±9 years) were scanned with approval of the ethics committee. In vivo data was first motion corrected using the FSL Flirt (FMRIB, Oxford) rigid body model, with a mutual information cost function due to the different contrasts. Polarity was restored in the modulus images using the phase images from the MPRAGE data [3]. The IR EPI signals collected at each TI were fitted to: $S(TI) = S_0(1-(1-\cos(\alpha))\exp(-TI/T_1))$ with a simplex downhill method, where S_0 is the equilibrium signal and alpha is the flip angle of the inversion pulse. For the MPRAGE sequence, all the RF pulses, the recovery periods and the approach to steady state from equilibrium were simulated to model the signal acquired as a function of T1 and Mo, the longitudinal magnetization at equilibrium. In combination with a B1 map, this numerical model can be fitted to estimate T1, Mo and the flip angle of the inversion pulse. Errors on the fitting were investigated by calculating the covariance matrix, and assuming a SNR of 100. Monte-Carlo simulations were also performed to check the results of the optimizations and the performance of the fitting routine. The covariance matrix method was also used to optimize the sequence parameters (the different TI, the number of measures, the Shot to Shot interval (SSi) and the readout flip angle β).

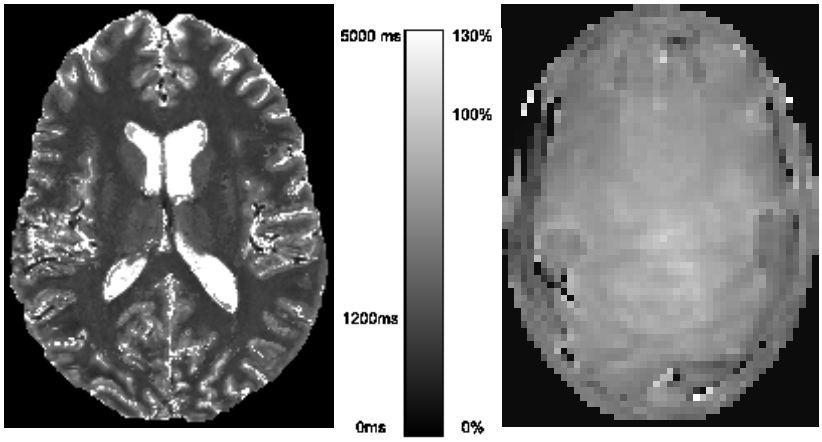

Fig. 2: The T1 map at 7T of the same slice as the Fig. 1 and its corresponding B1 map with its grey scale bar (indicating % of expected B1)

Results:

High resolution T1 maps can be produced with MPRAGE (Fig.1 and 2) and the measured values of T1 are given in the table. There was no significant difference between T1 measured with EPI and MPRAGE in the phantom or in vivo (t-test). However the MPRAGE T1 map is rather noisy and took about 15 minutes to acquire. The optimal pulse sequence at for the measurement of a T1 of 1600 ms in 15 minutes with $\beta = 8^o$ was found to have only 5 readouts at TIs of 160, 398 (high quality anatomical scan at 7T), 988, 2455 and 6102 ms and a SSI of 9s, giving a ten fold improvement in SNR. The optimum value of β was actually found to be 62^o, but this would yield images with a poor point spread function and excessive SAR at 7T. It was also found that the SNR in the T1 maps could be further increased by allowing the SSI to vary with TI, compared to keeping it fixed.

Table: Values of T1 measured with MPRAGE sequence, with standard deviation between subjects. N=4

Field (T)	GM T1 (ms)	WM T1 (ms)
1.5	1200 ± 130	650 ±30
3	1600 ± 110	840 ± 50
7	1940 ± 150	1130 ± 100

Conclusion:

T1 measurements were in agreement with those reviews in the literature [4]. Future work will be aimed at optimizing this sequence with regarded to the Point Spread Function as well as SNR in T1. This protocol that yields both quantitative images and high quality anatomical images in a reasonable imaging time will be applied to measuring relaxation time in developmental studies.

Bibliography:

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