Robust T_1 mapping in the presence of partial volume effects

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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. To date, several techniques have been proposed for measuring it (e.g. [1,2]). Most of them are based on modeling monoexponential behavior for individual voxels.

Even though brain tissue is considered to exhibit monoexponential T_1 behavior, deviations from this are expected both due to partial volume effects and tissue changes due to disease. This is bound to lead to errors in T_1 estimation unless multiple exponentials are taken into account. However, fitting multiple exponentials is well-known to be a mathematically ill-defined problem [3], requiring high signal to noise ratios.

This study addresses partial volume problems when a voxel contains both cerebrospinal fluid (CSF) and another tissue type, as it occurs in the cortical ribbon and periventricular white matter. With a T_1 value in the order of 4400 ms at 3.0T, CSF interference can cause significant errors in T_1 estimation. Here, a new pulse sequence is presented that allows measuring T_1 while keeping the signal from substances with CSF-like T_1 values suppressed, thus minimizing interference and estimation error.

Theory & Methods: The proposed sequence is shown in figure 1. It starts with a saturation pulse, followed by an inversion pulse at time t_a and an imaging 90º pulse at time t_b. Single-shot echo planar imaging (EPI) is chosen for the image acquisition.

Based on the Bloch equations, signal amplitude after the imaging pulse can be calculated as:

$$Signal = M_0\left[1+\left(1-2e^{t_a/T_1}\right)e^{-t_b/T_1}\right] \quad (1)$$

If we assume that the CSF signal can be represented by an average T_1=$T_{1,CSF}$, then it is possible to suppress the CSF signal if we choose

$$t_b = T_{1,CSF}\ln\left(2e^{t_a/T_{1,CSF}}-1\right) \quad (2)$$

Hence, for every t_a there is a t_b that keeps the CSF signal suppressed. By acquiring the signal values for different values of (t_a, t_b) it is possible to fit Eq. 1 to the experimental data so as to obtain the T_1 value of the tissue under examination.

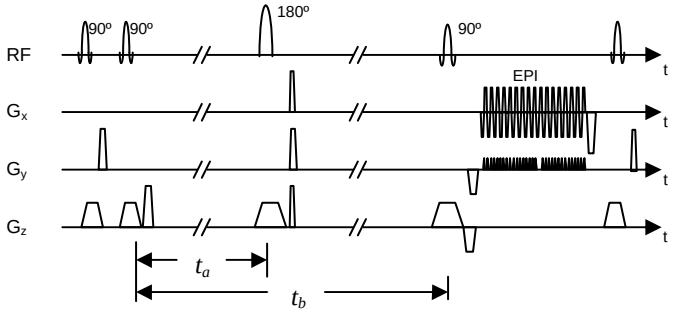

Figure 1: Diagram of the proposed pulse sequence

Selection of a set of sampling points (t_a, t_b) was the result of an optimization process. A cost function was created by modeling the fitting process based on a D-optimum design [5], which was extended into a Bayesian model in order to cover a T_1 range of interest between 900 and 2100 ms. The optimization process was repeated for different numbers of sampling points for a total sequence duration of 3 minutes.

Monte Carlo simulations were used to assess the stability of the fitting scheme over a range of T_1 values, both for the target tissue as well as for the "interfering" tissue.

The proposed sequence was implemented on a 3.0 T GE scanner. Adiabatic FOCI pulses were used for the inversion pulses. Saturation pulses were implemented as a series of two 90º pulses separated and followed by spoiler gradient pulses in order to minimize effects of transmit B_1 variations.

Results: The optimization process showed that gains from additional sampling points leveled at approximately 35 points (figure 2); a 40-point implementation was selected as a trade-off between signal-to-noise ratio and implementation complexity. The combination of the time constrain and the Bayesian nature of the cost function made the final design deviate from the two-point optimal designs for exponential fitting, giving the following set of t_as:

{1285, 1374, 1380, 1474, 1487, 1499, 1512, 1534, 1557, 1558, 1565, 1565, 1570, 1583, 1596, 1606, 1620, 1648, 1648, 1664, 1687, 1690, 1692, 1706, 1715, 1720, 1733, 1736, 1777, 1798, 1924, 2296, 9021, 9404, 9593, 9717, 9786, 10087, 10114} ms.

Figures 3 and 4 show the precision and the accuracy of the proposed method compared to an inversion recovery (IR)-based technique with 12 exponentially-spaced fitting points. In terms of precision, the proposed sequence is comparable up to 1500 ms and acceptable up to 2100 ms; however in terms of accuracy it clearly outperforms single-exponential IR fitting even if misestimating the interfering T_1 .

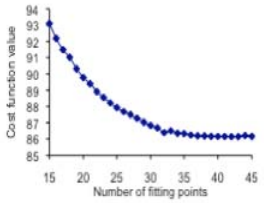

Figure 2: Cost as a function of the number of sampling points

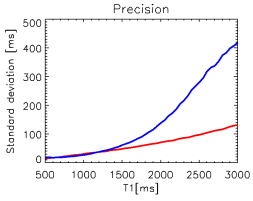

Figure 3: Fitted T_1 standard deviation as a function of T_1 for the proposed technique (blue) and IR fitting (red) (acquisition SNR=30)

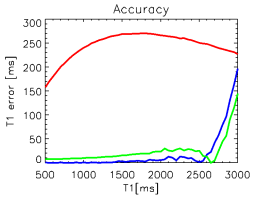

Figure 4: Estimation error at 20% partial volume for interfering T_1 at 4400 ms (blue) and 4000 ms (green) and IR fitting (red)

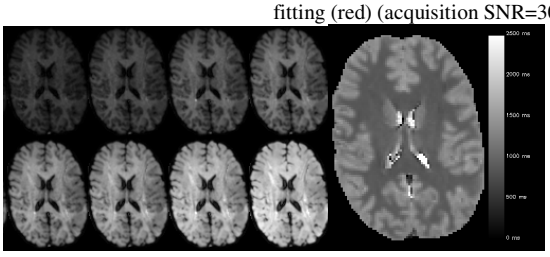

Figure 5: Sample images for different values of (t_a, t_b) and T_1 map obtained with the proposed method. CSF signal, as seen in the ventricles, is suppressed, resulting in minimal interference in the estimation of cortical T_1

Figure 5 shows data obtained from a healthy human volunteer at 3.0 T. Mean measured white matter T_1 was 839±26 ms, cortical gray matter T_1 1400±68 ms, while caudate T_1 was 1246±47 ms (data from 3 healthy volunteers), which is consistent with previously published values [6]. Mean standard deviation between 6 subsequent scans in the same areas was 10 ms for the white matter and 13 ms and 27 ms for the caudate and the cortical gray matter respectively, confirming the increase in standard deviation with T_1 expected from the simulation results.

Discussion & Conclusion: Partial volume effects can present a serious problem in T_1 measurement in the interfaces between brain tissue and CSF, especially in the cortex and the periventricular regions. As shown, T_1 estimation using single exponential fitting of the IR curve shows significant error even for a moderate percentage of partial volume contamination.The presented method gives a reliable measurement over a range of T_1 values normally expected in the human brain. It provides an easy way to minimize partial volume induced error if there is an estimation for the T_1 of the second tissue type.

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