High Resolution T1 Mapping of the Human Brain with an Acquisition Time of 19 Seconds per Slice

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Introduction: During recent years, several methods for quantitative T_1 mapping of the human brain have been suggested. Methods based on EPI imaging [1,2] provide whole brain coverage within a few minutes. However, the in-plane resolution is usually restricted to 2mm [2]. Moreover, EPI images may suffer from distortions. Methods based on magnetization-prepared FLASH imaging [3,4] are able to provide T_1 maps with an in-plane resolution of 1mm [5,6]. Most of these sequences apply the Look and Locker (LL) concept [7], monitoring T_1 relaxation after spin inversion by acquiring an image series. To achieve a sufficient temporal resolution on whole body scanners, images usually have to be segmented in k space. However, the acquisition is considerably slowed down by the necessary relaxation delays between segments. A way of overcoming this problem is to introduce saturation pulses followed by delays τ before each inversion [5,6]. However, this lowers the SNR, because the dynamic range is reduced and the delays τ cannot be used for acquisition. In the current work, a multislice version of the original inversion recovery method [4] is proposed. In contrast to previous methods, relaxation delays can be used for data acquisition because inversion and excitation pulses are slice-selective. An improved fitting algorithm, employing smoothed flip angle maps, enhances the quality of the T_1 maps. The method was validated *in vivo* and *in vitro*. T_1 maps of a human brain with an in-plane resolution of 1mm and a slice thickness of 4mm have been acquired on a 1.5T scanner. 30 contiguous slices covering the whole brain could be acquired in only 9min39s.

General theory of segmented LL sequences: A series of N_{IMG} images with reduced number of k-space lines is acquired after spin preparation. This process is repeated N_{SEG} times [5]. An effective relaxation time $T_1^*<T_1$ is observed, and the magnetization approaches a saturation value $M_0^*<M_0$ (equilibrium value) with $M_0^* = M_0 \cdot T_1^*/T_1$ [4]. For a 3-parameter fit according to $M(t)=A+B\cdot\exp(-t/T_1^*)$, the equations $A=M_0^*$ and $B=M_S-M_0^*$ hold, where M_S is the starting value. After inversion, M_S equals $-M_0$, so T_1 follows from $T_1 = -T_1^* \cdot (1+B/A)$ [4,5]. Even in the absence of inversion pulses T_1 fitting is still possible: in this case, M_S equals M_0, and T_1 follows from $T_1 = T_1^* \cdot (1+B/A)$.

Methods and Materials: Experiments were performed on a 1.5T Sonata whole body scanner (Siemens Medical Systems, Erlangen, Germany) using a whole body transmit coil and a head receive coil. Imaging parameters were: matrix 256x192, in-plane resolution 1mm, 30 contiguous 4mm slices, $N_{IMG}=8$, $N_{SEG}=8$, TR/TE/BW = 12.52ms/4.39ms/29kHz. Interleaved slice sampling with an acquisition time of 36s per interleave was chosen to avoid crosstalk between adjacent slices. The adiabatic inversion and the excitation pulses were optimised to achieve full inversion across the whole profile of the excitation pulse. RF sidelobes did not extend beyond the adjacent slices, thus avoiding crosstalk. The method was tested *in vitro* and *in vivo*. The phantom consisted of tubes filled with different aqueous concentrations of Gd-DTPA, resulting in T_1 values between 400ms and 3s. T_1 mapping was performed 7 times with different flip angles α_0, ranging from 4° to 16°. To check for accuracy, control values were measured by acquiring a series of 10 single-slice inversion recovery EPI images with TI values ranging from 50ms to 10s. The *in vivo* experiment was performed on a healthy volunteer using $\alpha_0=12°$. Data analysis was based on a 3-parameter fit as explained above to calculate T_1 maps and α_0 maps. The latter were smoothed and used as prior information for a subsequent 2-parameter fit, as proposed in the literature [6]. The two resulting T_1 maps were compared qualitatively and quantitatively. To check that the off-centre inversion pulses caused neither imperfect inversions [8] nor magnetisation transfer effects, the *in vivo* scan was repeated on the same volunteer without inversion pulses and analysed as described in the Theory section.

Results: *Phantom Experiment:* There was very good agreement between T_1 values obtained with the new method and the EPI control values. The best results were achieved with $\alpha_0=12°$ where T_1 values in the range from 400ms to 1s deviated by less than 1% from the control values. For the longest T_1 of 3s, the deviation was 5.5%. For low α_0, T_1 maps were noisier. For large α_0, there were deviations for the longest T_1 (9% at 14°, 13% at 16°), an effect also reported by other researchers [6]. *In vivo experiment:* Figure 1 shows a single slice of the T_1 map. Values for various regions of interest are: Genu: 566±49ms, Splenium: 575±42ms, Frontal white matter: 590±35ms, Occipital white matter: 600±34ms, Putamen: 900±60ms, Caudate Nucleus: 1020±60ms. These values are in excellent agreement with the literature [9,10]. The two reconstruction methods yielded almost identical T_1 maps. However, for short T_1 values, e.g. in the fat layer, the T_1 maps were less noisy for the method based on smoothed α_0 maps (Fig. 2). The acquisitions with and without inversion pulses yielded the same T_1 values. It can thus be concluded that the method is not susceptible to imperfect inversion or magnetization transfer effects.

Fig. 1: Single slice of the quantitative T_1 map.

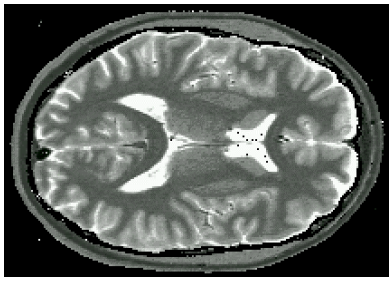
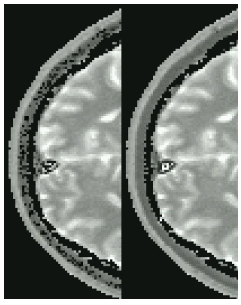


Fig. 2: Comparison of T_1 maps calculated with the 3-parameter fit (left) and a 2-parameter fit based on smoothed flip angle maps (right).



Conclusion and References: The method presented in this work generates quantitative T_1 maps with an in-plane resolution of 1mm, a slice thickness of 4mm, and whole brain coverage in a clinically acceptable imaging time of about 19s per slice. It has an increased dynamic range due to the lack of saturation pulses. All relaxation delays are used for data acquisition. These advantages allow for an accuracy comparable to values reported using a sequence with twice the slice thickness [6].

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