T_1 measurements at 7T with application to tissue specific imaging

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Introduction: The longitudinal relaxation time (T_1) plays an important role in MRI experiments. Apart from its diagnostic value, it is a major contrast modifier for anatomical imaging, and affects NMR signal sensitivity. Therefore, knowing baseline T_1 values and their expected range of variation is important when optimizing the parameters of MRI experiments. This creates an additional challenge when porting pulse sequences to different field strengths.
T_1 values are measured by fitting exponential curves to the inversion recovery or the saturation recovery curves (e.g. [1-3]). Fitting exponential decays is an extensively studied problem, since it is descriptive of many natural processes, and it is known to be ill-conditioned [4-6]. In this study, we present an application of a logarithmic sampling scheme, known to improve stability, and T_1 measurements at 7T.

Theory & Methods: From a mathematical point of view, there are three factors that affect stability of the exponential curve fitting problem. These are the SNR of the data, the spacing of the sampling points, and the range of times at which the curve is sampled [5,6]. It has been suggested that the use of non-linearly spaced sampling points can be beneficial for the fitting stability [5]. Thus, we tried a scheme with sampling points forming a logarithmic progression, following an $t_i = t_1 a^{i-1}$ with minimal sampling time set to 30 ms after the inversion pulse and maximum set to 8000 ms. A minimum distance between subsequent acquisitions was taken into account, so as to allow for multislice acquisition, as proposed in [2], where multislice imaging is used to acquire all slices after a single inversion, and the order of slice acquisition is varied over subsequent inversion cycles, so as to acquire all slices at all time points. The inversion recovery sampling scheme was preceded by a reference EPI acquisition without inversion, with the rationale of providing an estimate of signal value at full relaxation, thus increasing the timing sampling range. The proposed sampling scheme was implemented on a GE 7.0 T scanner. Adiabatic FOCI pulses were used for the inversion pulses. Total imaging time for 12 slices (2mm thickness, 6 mm gap) at 7.0 T was 195 s.
Fitting of a single exponential curve was performed on the magnitude data using the Powell optimization algorithm [7]. The variables to fit were proton density, T_1 and inversion pulse flip angle. Since the TR for the inversion sampling cycle was set to 15 s, additional modeling for the incomplete relaxation of the cerebrospinal fluid (CSF) was incorporated in the cost function used for the fitting both in the simulations and in the experimental data.
Region of interest (ROI) analysis was employed to obtain average T_1 values over white matter (WM), cortical gray matter (CGM), striatum and CSF. ROIs were manually selected so as to be as large as possible, but on the same time avoid regions with partial volume effects or obvious artifacts. The results were confirmed with the T1 histograms of the whole brain.
The measured T1 values were used to optimize a double inversion recovery sequence (tissue specific imaging –TSI [8]) for application on 7T. For sequence TR of 8900 ms, the sequence consisted of three imaging pulses at times 0 ms, 5551 ms and 8455 ms with flip angles 67º, 23º and 76º respectively, combined with two inversion pulses at times 4743 ms and 7783 ms. The imaging pulses were followed by EPI acquisition trains, as described in [8].

Results: Eight healthy normal volunteers (5 male / 3 female, ages 22-41) were scanned after giving informed consent under an IRB approved protocol.
Table 1 shows the results of the ROI analysis, averaged over the eight volunteers.
The spread of the values can be understood by examining the corresponding T_1 histograms. Histograms are reproducible between different volunteers. They show a relatively narrow peak for white matter, but a much wider peak for gray matter, reflecting partial volume effects and inherently different values between different types of gray matter. The ill-defined CSF peak shows a big spread, but a consistent mean value.
Figure 3 shows a set of TSI images obtained at 7.0T based on the measured T_1 values.

	Mean T_1 [ms]	Min T_1 [ms]	Max T_1 [ms]
White matter	1357 (±22)	1126 (±75)	1559 (±31)
Cortical GM	2007 (±45)	1560 (±140)	2391 (±91)
Striatum	1730 (±66)	1418 (±81)	2086 (±128)
CSF	4636 (±31)	3352 (±248)	5574 (±160)

Table 1: Results of the ROI analysis. Standard deviations reflect differences in mean, maximum and minimum values between different volunteers

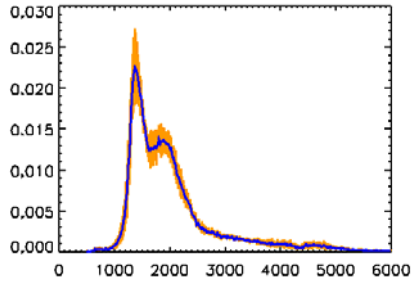

Figure 1: Whole brain *T_1 distribution in the human brain at 7.0 T (Voxel occurrence fraction vs T_1 in ms) . Blue line shows mean values and orange area standard deviation over the 8 volunteers*

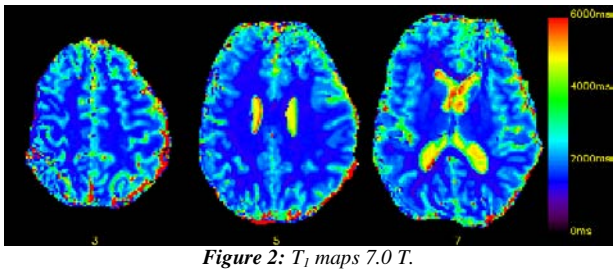

Figure 2: *T_1 maps 7.0 T.*

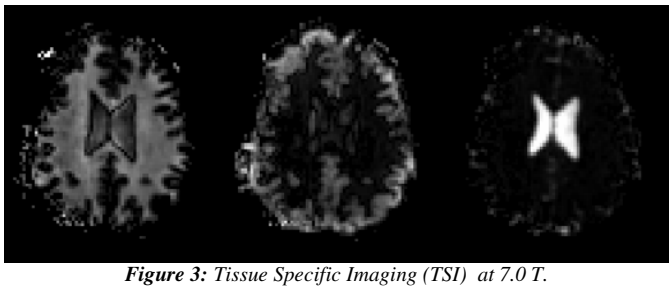

Figure 3: *Tissue Specific Imaging (TSI) at 7.0 T.*

Discussion & Conclusion: We have presented an application of a geometrically spaced sampling scheme for fitting a single exponential on the inversion recovery curve. Using an additional acquisition without inversion pulse aided the stability of the fitting, even when fitting magnitude data and taking a finite TR into account.
T1 values were measured at 7.0 T. The values presented are similar to previously published report [9]. They were used to calculate timings and flip angles for a TSI sequence. The latter was used in order to obtain single tissue type images at 7.0 T.

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