Fast T1 Mapping in Human Brain Using Inversion Recovery EPI with GRAPPA at 3T and 7T

J. Grinstead[1], and W. Rooney[2]

[1]Siemens Medical Solutions USA, Inc., Portland, Oregon, United States, [2]Advanced Imaging Research Center, Oregon Health & Science University, Portland, Oregon, United States

Introduction

Quantitative ^1H_2O T_1 techniques find a wide range of applications in biological NMR; from molecular dynamic measurements to characterization of tissue structure and physiology. The major drawback of these techniques is that they are slow. This is because for most *in vivo* applications sampling requirements are high, not only must the T_1 recovery be well sampled, but also spatial encoding is usually desired. Separately, each requirement is time demanding. Together, they are prohibitive using conventional acquisition techniques. This work investigates the combination of echo-planar and parallel imaging techniques for high-speed acquisition of quantitative T_1 [$\equiv R_1^{-1}$] data sets in human brain at 3T and 7T.

Methods

An inversion recovery (IR) EPI sequence with slice reordering was used, similar to the approach of Clare and Jezzard [2]. For each repetition period TR, a non-selective inversion pulse is followed by *N* slices acquired with single-shot gradient echo EPI. Because of the multi-slice nature of the acquisition, each slice has its own effective inversion time (TI), equal to the time from the inversion pulse to the read pulse for that slice. By shuffling the slice acquisition order relative to the inversion pulse for each TR, multiple TI points are measured for each slice. **Figure 1** illustrates this for *N*=4 slices for the case of sequential slice ordering, where the slice order for *N* measurements is [1,2,3,4; 2,3,4,1; 3,4,1,2; 4,1,2,3]. For *N*=4 interleaved slices the slice ordering would be [1,3,2,4; 3,2,4,1; 2,4,1,3; 4,1,3,2]. To minimize changes in the effective TR for each slice it is important not to rearrange the slices in a right cyclic permutation, such as [1,2,3,4; 4,1,2,3, …], which would make the repetition time for the *N*th slice short relative to the other slices.

Healthy controls and subjects with several cerebral pathologies were studied after obtaining informed consent. All data were acquired using 3 T and 7 T MRI instruments (Trio a Tim System, and MAGNETOM 7T, Siemens Medical Solutions) using phased array RF coils. The number of slices (and TI values) was varied between 12 and 24. A single-shot gradient recalled 2D EPI sequence was used to acquire axial slices of 2-3 mm thickness. An interleaved slice excitation order was used and the slice thickness was 2-3 mm. A $(128)^2$ matrix acquired typically over a $(256\ mm)^2$ FOV with $0.034 \le TI \le 7$ s, FA90, 1600 Hz/pixel, and TR=10s resulted in total acquisition times of 120-240 s, depending on the number of slices (and TI values). To minimize T_2 weighting, image distortion, and intravoxel dephasing, a minimum TE value was selected, which typically was 27 ms for standard acquisitions, and 18 ms for parallel acquisitions (GRAPPA=2). Parametric T_1 maps were produced by voxel-wise fitting of the signal intensity to a single exponential inversion recovery function, $S(TI) = S_0|(1-2e^{-TI/T1})|$, using a gradient expansion algorithm. To reduce processing time, images were masked to remove the scalp and extra-cranial regions prior to T_1 fittings.

Results

The magnitude images over a range of inversion times from a control subject at 3 Tesla are shown in **Figure 2**. The inversion times range from 34 ms at the top left to 5.8 s at the bottom right. In **Figure 3** are shown 3T inversion recovery behaviors of single voxels of mostly white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF). The T_1 histograms and T_1 maps in **Figure 4** contain data from a healthy control, a multiple sclerosis (MS) subject, and another with mild cognitive impairment (MCI). Table I contains the calculated T_1 values for several brain tissue types at 3T and 7T.

Discussion and Conclusion

A difference in our data acquisition to [2] was the use of a non-selective IR pulse instead of a multi-block approach with slab-selective IR pulses for each block of slices. This was done to minimize any inflow effects. Our approach increases the number of TI points measured allowing more precise fitting, but reduces the number of slices that can be acquired in the same scan time. The use of GRAPPA, however, allows more slices (and hence TI points) for a given TR. Whole-brain coverage was not needed for our purposes so slice coverage was adequate while maintaining a scan time short enough to be easily added to most exams.

The T_1 values in Table I are in agreement with literature values from normal human brain [1], and show the expected increase in brain ^1H_2O T_1 with field strength for tissues with protein-bound water. Significant shifts in the T_1 histograms are observed for the MS and MCI subjects relative to control (**Fig. 4**).

The combination of EPI and parallel image reconstruction provides a high speed flexible acquisition strategy with excellent signal to noise and accuracy, and is demonstrated here at 3T and 7T.

References

[1] Rooney et al., MRM, 2007; 57:308-318. [2] Clare and Jezzard, MRM, 2001; 45:630-634.

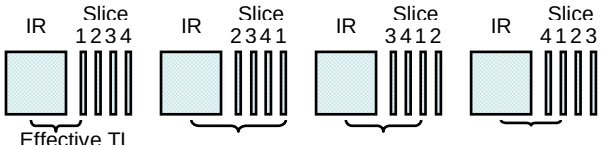

Fig. 1. Slice ordering scheme for *N*=4 sequentially ordered slices. The braces show the effective TI for slice 1 over each TR.

	WM	Putamen	Caudate	Thalamus	CSF
7T	1.18 (0.04)	1.46 (0.05)	1.58 (0.03)	1.60 (0.07)	4.3 (0.8)
3T	0.86 (0.03)	1.22(0.04)	1.37(0.03)	1.23 (0.06)	4.3 (0.3)

Table I. T_1 values in sec (±SD)

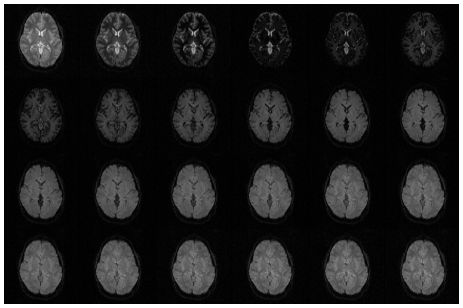

Fig. 2. Images from 3T with TI ranging from 34 ms at the top left to 5.8 s at the bottom right.

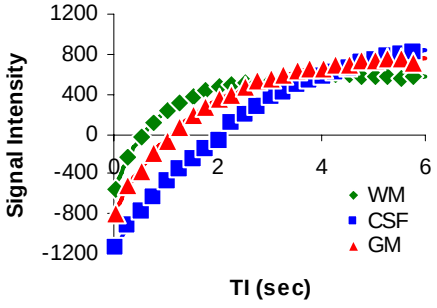

Fig. 3. 3T inversion recovery of ^1H_2O signal intensity for single voxels of containing mostly GM, WM, or CSF from a healthy control.

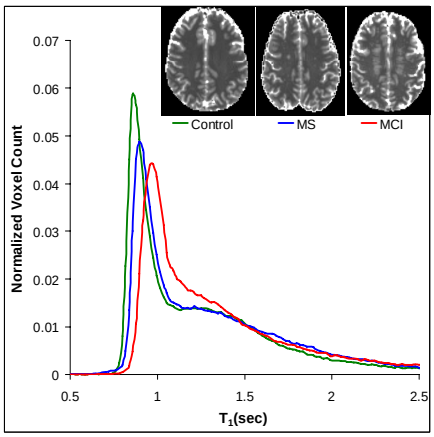

Fig. 4. 3T T_1 histograms and maps from a healthy control, a multiple sclerosis (MS) subject, and a subject with mild cognitive impairment (MCI).