





Test-Retest Reproducibility of T_{1p} Mapping in Brain at 3T

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Introduction

Recent studies have demonstrated $T_{1\rho}$ differences in the brains of patients with Alzheimer's disease [1-3] and Parkinson's disease [3] compared to normal controls at 1.5T. Unfortunately these studies have produced $T_{1\rho}$ maps which suffer from noise and their reproducibility is not reported. Since the reported differences between $T_{1\rho}$ for controls and diagnosed patients are small (4-9%) [2], accuracy and reproducibility is especially important in such studies. The current study evaluates the test-retest reproducibility of a novel fluid-suppressed 3D acquisition with high resolution at 3T to assess its potential utility in patient studies.

Results

The $T_{1\rho}$ -weighted images were free of gross artifacts using this sequence. In addition, the signal and contrast were sufficient to create high quality $T_{1\rho}$ maps (Figure 2, color maps) with clear WM/GM differentiation which visually matched anatomy seen in the corresponding slice of the anatomical reference image. Reproducibility was high for all ROIs (Table 1), generally with repeated measures differences in the mean $T_{1\rho}$ of approximately 1ms or less. Histograms (Figure 2, bottom right) of the pixelwise differences of $T_{1\rho}$ over the entire brain parenchyma showed an average difference between the two scans of less than 1ms in every case (representing possible bias), while the standard deviation (reflecting noise in the data throughout the whole brain) was less than 3ms in all cases.

Discussion and Conclusions

The current methods incorporate several improvements over previously published methods: full brain coverage in a clinically realistic time using a 3D sequence, larger range of spin locking times (compared to [3]), and the use of T2 prep train designed to improve SNR by reducing T1weighting [7]. Previous patient studies [1-3] produced T_{10} maps which suffered from noise to a degree where WM/GM contrast was not discernible in brain, due at least partly to large possibly random T_{10} variations throughout the image [1, Figure 3] even in controls. This may be partly due to the fact that spin lock times in that study were no higher than 40ms to estimate T_{10} values ~90ms. In one such study the range of ROI T_{10} values for hippocampus in controls ranged from ~60ms to ~120ms [3, Figure 2]. One previous study [2] reported population standard deviations of 4.4ms and 5.2ms in the medial temporal lobe for GM and WM respectively in their elderly control subjects. Using the current technique we have recently reported corresponding GM and WM population standard deviations of 1.2ms and 1.3ms respectively [4]. This further suggests that the actual inherent range of T_{10} values in the healthy human populations (and possibly in patient populations) may be small enough to allow differentiation of pathologic T_{1o} values in individual patients compared to normative values of healthy controls. Also, earlier patient studies have been limited to single slice scans typically covering the hippocampus. With whole brain coverage it was possible in this study to perform robust registration and atlas-based segmentation of many regions. This is supported by the low repeated measure T₁₀ difference seen in cortical and juxtacortical ROIs, and suggests that it is technically feasible to study T_{10} changes in these and possibly other regions in the brain.

Methods



Figure 1. 3D proton density weighted variable flip angle turbo spin echo with fluid suppression inversion pulse and T2 preparation.

4 healthy volunteers with no history of neurological disease were recruited in this IRB-approved study. Data was acquired using a Philips 3T Achieva TX scanner and an 8-channel head coil. Whole-brain T_{10} -weighted images were acquired using a proton density weighted fluid attenuated variable flip angle 3D turbo spin echo technique (Figure 1): TE/TR/TI=20/4800/1650ms, matrix size = 140 140 100, spatial resolution 1.8 1.8 1.8mm3, spin lock frequency = 500Hz, spin lock durations (TSL)= 0, 20, 40, 60, 80 and 100ms, total scan duration = 14min [4]. Each T_{10} map was calculated based on a weighted linear least squares fit to a single exponential to the coregistered T_{10} -weighted images. The T_{1o} map was then itself coregistered to a T1-weighted anatomical scan. Using unified segmentation [5] (SPM8) of the T1-weighted image, the T_{10} maps were segmented into white matter (WM) and gray matter (GM) and spatially normalized to MNI space. Major WM tracts were defined using the JHU atlas [6], while cortical GM and juxtacortical WM were defined by an intersection of the Harvard-Oxford cortical atlas (dilated by 5mm) with the subject-specific GM and WM masks respectively. 2-6 months after the first scan session, the T_{10} data acquisition was repeated on the same person and identical processing was performed. For histogram analysis T_{10} differences more than 10 standard deviations from the mean were not included in calculations.



Figure 2. Subject 3: T1W anatomical reference (top); Repeated $T_{1\rho}$ maps (middle); $T_{1\rho}$ difference map (bottom left); whole brain histogram of pixelwise $T_{1\rho}$ differences (bottom right).

	ROI ΔT _{1ρ} (ms)				Whole-brain Histogram of $\Delta T_{1\rho}$ (ms)	
	WM	Cortical	Juxtacortical	Whole		Standard
Subject	Tracts	GM	WM	Brain	Mean	Deviation
1	1.1	1.1	0.4	0.8	0.8	2.2
2	-0.8	-0.7	-0.6	-0.6	-0.5	1.9
3	-0.3	0.2	1.2	0.6	0.5	3.0
4	1.2	0.5	-0.1	0.2	0.3	2.4

Table 1. Difference of mean repeated measure estimates of T1ρ.

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