TEST-RETEST REPRODUCIBILITY OF T1RHO 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.

Methods

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 $T_{1\rho}$-weighted images were acquired using a fluid attenuated variable flip angle 3D turbo spin echo technique (TE/TR/TI=20/4800/1650ms, matrix size 140×140×100, spatial resolution 1.8×1.8×1.8mm^3) [4]. Images were acquired with a spin lock frequency of 500Hz and spin lock durations of 0, 20, 40, 60, 80 and 100ms, with a total scan duration of 14min. Each $T_{1\rho}$ map was calculated based on a weighted linear least squares fit to a single exponential to the coregistered $T_{1\rho}$-weighted images. The $T_{1\rho}$ map was then itself coregistered to a T_1-weighted anatomical scan. Using unified segmentation [5] (SPM8) of the T_1-weighted image, the $T_{1\rho}$ 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 $T_{1\rho}$ data acquisition was repeated on the same person and identical processing was performed. For histogram analysis $T_{1\rho}$ differences more than 10 standard deviations from the mean were not included in calculations.

Results

High SNR images free of artifacts were produced using this sequence, resulting in high quality $T_{1\rho}$ maps (Figure 1, left) with clear WM/GM differentiation. 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 1, 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.

	ROI Δ $T_{1\rho}$ (ms)				Whole-brain Histogram of Δ $T_{1\rho}$ (ms)	
Subject	WM Tracts	Cortical GM	Juxtacortical WM	Whole Brain	Mean	Standard 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 $T_{1\rho}$.

Discussion and Conclusions

Previous patient studies [1-3] produced $T_{1\rho}$ maps which suffered from noise to a degree where WM/GM contrast was not discernable in brain due at least partly to large possibly random $T_{1\rho}$ 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 $T_{1\rho}$ values ~90ms. 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 $T_{1\rho}$ values in the healthy human populations (and possibly in patient populations) may be small enough to allow differentiation of pathologic $T_{1\rho}$ 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 $T_{1\rho}$ difference seen in cortical and juxtacortical ROIs, and suggests that it is technically feasible to study $T_{1\rho}$ changes in these and possibly other regions in the brain.

References

1. Borthakur A, et al. T1rho MRI of Alzheimer's disease. *NeuroImage.* Jul 15 2008;41(4):1199-1205. **2.** Haris, M., et al., T1ρ MRI in Alzheimer's Disease: Detection of Pathological Changes in Medial Temporal Lobe. *Journal of Neuroimaging*, 2011 **3.** Haris M, et al. T1rho (T1ρ) MR imaging in Alzheimer's disease and Parkinson's disease with and without dementia. *J Neurol.* 2011 Mar;258(3):380-5. **4**. Watts R, et al, *In vivo* Whole-Brain T1ρ mapping across adulthood - Normative values and age dependence, (submitted). **5.** Ashburner J, Friston KJ. Unified segmentation. *NeuroImage.* Jul 1 2005;26(3):839-851. **6.** Wakana S, et al. Reproducibility of quantitative tractography methods applied to cerebral white matter. *NeuroImage.* Jul 1 2007;36(3):630-644.

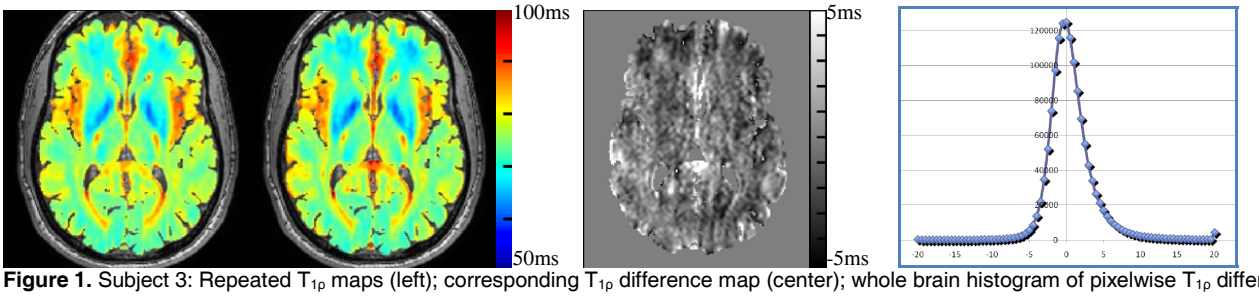

Figure 1. Subject 3: Repeated $T_{1\rho}$ maps (left); corresponding $T_{1\rho}$ difference map (center); whole brain histogram of pixelwise $T_{1\rho}$ differences (right).

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