

In-vivo Volumetric T1 and T2 Quantitation using Single Acquisition

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Introduction:

The quantification of MR relaxation times has always been of interest. Indeed, there have been recent efforts to obtain – within a single scan – multiple relaxation parameters (1, 2). This abstract describes the development of a novel 3D acquisition method for “simultaneous” T1 and T2 quantitation; all the data required for T1 and T2 relaxometry are acquired in a single scan. T1 and T2 values obtained using this new scheme were compared to known values in both phantom and *in-vivo*.

Methods:

A 3D FSE stack of spiral sequence was modified to obtain images for both T1 and T2 quantitation. As shown in Figure 1, this new sequence consists of 3 distinct modules: magnetization reset, T1 quantitation, and T2 quantitation. Spiral readouts were kept at the same resolution for both acquisition modules. The imaging parameters were kept constant for both modules: effective spatial resolution=1.8x1.8x4mm, FOV=22-24cm, number of locs=24-28, nex = 1. The number of locations was adjusted to get maximum coverage of the brain while keeping the scan times reasonable. The modules were repeated for each z phase encoding and spiral interleaf. The total scan time for this prescription was ~9 min.

T1 quantitation module: A 3D saturation recovery Look-Locker sequence (3) was implemented for T1 quantitation. A magnetization reset pulse train, similar to CHESSE pulse described in (4) was played out to saturate the magnetization. To minimize signal saturation effects, subsequent T1 recovery was then sampled using low flip angle excitation pulses (10°). Six equidistant samples were obtained during saturation recovery.

T2 quantitation module: The T2 quantitation module is played out immediately after the T1 quantitation module. The T2 quantitation module consisted of a 90° tip down pulse followed by a train of equally spaced 180° pulses. The spacing between the 180° pulses was adjusted to sample the T2 decay curve effectively. Six time points were collected during T2 decay.

Processing: Using a custom software tool, ROI's were placed on each phantom of interest or, in the case of *in vivo* experiments, each tissue of interest. A mono-exponential fit of the sampled points was then calculated for each ROI. The custom software was also used to generate T1 and T2 maps for the regions of interest.

Phantom experiments: Phantom experiments, using a Eurospin test object (Diagnostic Sonar, Scotland) with known T1s and T2s (The T1 values ranged from 400-1200ms and T2 values from 50-250ms). Figure 2 shows the MR image of the test object with 10 different phantoms. Experiments were done to verify the feasibility of the new sequence and accuracy of calculated T1 and T2 values. The spacing between the echoes for both T1 and T2 quantitation was adjusted independently to sample the longest T1 and T2 available in these phantoms. All scans were done on a 1.5T GE Signa HDx scanner (Waukesha, WI).

In-vivo experiments: Following informed consent, volunteer head scans were performed with this sequence on a 1.5T GE Signa HDx scanner (Waukesha, WI). The T1 and T2 values of Gray Matter (GM), White Matter (WM) were measured and compared to values in the literature. ROIs were also placed on different slices to assure that obtained values were consistent across the volume.

Results:

Phantom: Calculated vs known T1 and T2 values of certain phantoms marked in Fig 2 are given in Table 1. Overall, a difference of $\pm 10\%$ was noted between the measured and known values of T1 and T2.

In vivo: Figure 3 shows the T2 (3a) and T1 (3b) maps for a slice from in-vivo experiments. Figure 3c shows the ROI drawn on GM and WM areas to measure their respective T1 and T2 values. The T1 and T2 values for GM was 902 ms and 101ms respectively. For WM T1 and T2 values were 647 and 78ms respectively. The measured values were off by ~5% from values reported in the literature. Finally, a variation of <1% was seen in the T1 and T2 values of GM and WM across the slices.

Discussion and Conclusion:

We have successfully developed a 3D scan that enables T1 and T2 quantitation from images acquired during a single scan. *In-vivo* and phantom experiments demonstrated the accuracy of our proposed approach. Numerous improvements are proposed to increase this sequences scan-time efficiency: make use of spiral-in spiral-out readouts (5), leverage parallel imaging. Future studies will also include other areas of the body (e.g. MSK) where quantitative methods are critical for diagnosis and therapy monitoring.

References:

- (1) Wamtijs JB et al. MRM 60(2):320-329, 2008, (2) Wamtijs JB et al. MRM 57(3):528-37, 2007, (3) Look DC et al. The review of scientific instruments, 41, 2, 1970, (4) Haase A et al. Phys Med Biol 30(4):341. (5) Glover GH et al. MRM 35(3):299-308. 1996.

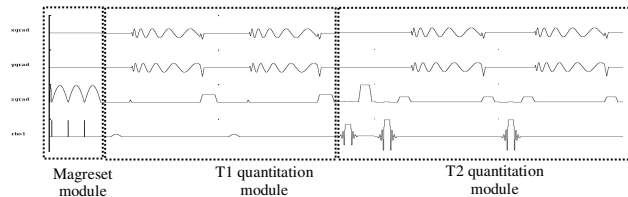


Figure 1: Sequence diagram of the new pulse sequence to acquire simultaneous T1-T2 acquisition scheme. Note that the magnetization reset pulse-train allows the sampling of T1 recovery curve at the same point. The sequence here is shown for 2 echoes.

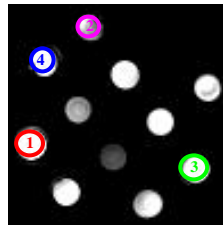


Figure 2: This shows one slice from the phantom experiments. The T1/T2 values of the numbered phantoms are shown in Table 1.

	Known value (1.5T)		Measured value	
	T1	T2	T1	T2
Phantom 1	442	154	401	146
Phantom 2	1149	214	1043	201
Phantom 3	959	223	860	214
Phantom 4	199	52	181	48

Table 1: This table shows the comparison of measured values for both T1 and T2 and the known values for the phantoms shown in Figure 2. There was, on an average, a 10% difference in the measured values from the known ones.

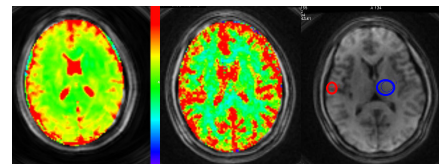


Figure 3: In-vivo results. This shows one slice from a 3D volume with overlay of (a) T2 map (b) T1 map. (c) shows the ROI's from where the T1 and T2 values were measured for WM (blue) and GM (red).