TOWERS: T-One With Enhanced Robustness and Speed

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Introduction

T1 mapping has a multitude of technical and clinical applications including sequence optimization and diagnosis. The inversion recovery (IR) sequence is regarded as the gold standard for measuring T1; however, this approach suffers from a long acquisition time that limits its practical use. Alternatives have been developed by several groups. Among these methods, an echo-planar imaging (EPI)-based Look-Locker sequence is one of the fastest, providing a 3-second scan per slice using 12 samples on the recovery curve [1]. Nevertheless, this method is prone to noise-related problems in estimation due to the low signal-to-noise ratio (SNR) inherent to the low flip-angle acquisitions. Other multislice T1 mapping sequences with inversion times (TI) of a given slice being altered from repetition to repetition [3, 4] have also been proposed. In this study, we proposed a rapid whole brain T1 mapping method, the **T-O**ne **W**ith **E**nhanced **R**obustness and **S**peed (TOWERS). This new method combines both the inversion recovery (IR) and saturation recovery (SR) together with slice shifting to efficiently sample the T1 recovery process. Phantom and in vivo results show the promise of the method.

Methods

The image acquisition scheme is illustrated in Figure 1. Firstly, TOWERS consists of two segments that are completely separated in spin history which helps reset the magnetization of the system should motion occur in the first segment. Secondly, the inversion recovery loops were prepended by a single-repetition of saturation recovery to yield a high SNR sample that approximates the M_0 of especially the white and gray matter voxels; however, the fitting procedure does not regard this volume as the true M_0, but rather keeps track of the partial recovery. Finally, TOWERS collects 32 samples per slice for a 60-slice acquisition in 2 min 20 sec as opposed to 12 samples per slice in 3 min again for 60 slices [2] or 6 samples per slice in 6 min 32 sec for 12 slices [3]. The high number of samples improves estimation through the inherent averaging effect.

Various concentrations of Gadodiamide were prepared in 15-ml tubes since increasing concentrations of Gadolinium causes a linear increase in $R_1 = 1/T_1$ over a certain range [4]. Acquisition parameters for TOWERS for the phantom were as follows: TE/TR = 13 ms/4000 ms., PF = 6/8, FOV = 200x200mm, Matrix size = 128x128, GRAPPA R = 4, #slices = 48, # repetitions = 26, shifting 4 slices per repetition. The changing parameters for IRSE-EPI were TE/TR = 20/45000 ms., # slices = 1, # repetitions = 200. The first two TI values were 18 ms., all other TIs obeying TI(n) = 18 + 100 x (n-2) ms for $n \geq 3$. Acquisition parameters for TOWERS *in vivo* were the same as those for the phantom except the TE = 17 ms, GRAPPA R = 2, # slices = 60, # repetitions = 32.

During fitting, modulus data were used with no polarity restoration since the spin history was mathematically tracked and the conventional negative-to-positive IR curve graph is no longer in place. The Levenberg-Marquardt-Fletcher routine was used for the nonlinear least-squares fitting of T_1 and M_0.

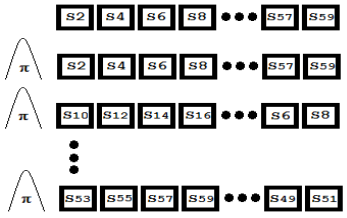

Figure 1 - First segment of 60-slice acquisition. Second segment works on a grid that is shifted by 2 slices to more uniformly sample recovery

Gadodiamide Concentration [mM]	T1 [ms] (IRSE)	T1 [ms] (TOWERS)
0.2	1029±80	978±17
0.1	1331±77	1345±29
0.05	1916±77	1952±35
0 (Water)	2947±76	3181±139

Table 1 – Results for phantom

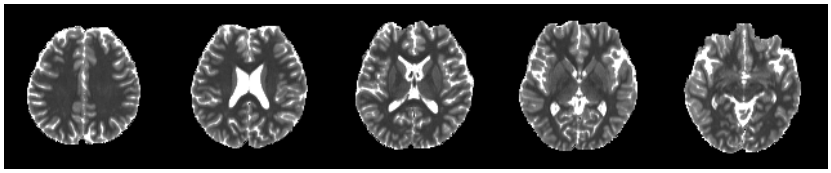

Figure 2 – Results *in vivo*

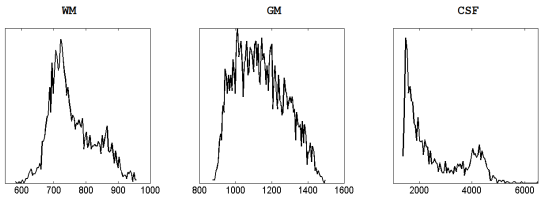

Figure 3 – Tissue T_1 histograms

Results

Table 1 lists the results of the phantom experiments for various concentrations of Gadodiamide. Figure 2 shows sample slices from a whole brain TOWERS scan and Figure 3 plots the histogram of T_1 values within white matter, gray matter and CSF where the segmentation of the tissues was performed via FMRIB's Automated Segmentation Tool (FAST) [5].

Discussion and Conclusions

The phantom results in Table 1 shows that TOWERS agrees very well with the gold standard IRSE sequence. In addition, the *in vivo* results demonstrate the clear separation of white matter, cortical gray, deep gray, putamen and CSF. It is worth noting that no low-pass filtering was applied to the images prior to curve fitting. The high SNR in the fitted T1 maps is an expected outcome of as many as 32 T1 recovery sampling points. Finally, the histograms of Figure 3 agree with the literature-reported values [6].

In conclusion, TOWERS is a rapid T_1 mapping sequence that comes with a number of advantages. Firstly, the two independent IR segments separated by an SR scan that resets spin history, make the proposed approach less sensitive to motion. Secondly, comprising an SR acquisition at the beginning of the segments, it acquires two high-SNR samples that resemble the external M_0 acquisitions to improve the accuracy of T1 measurements when the TI's that are not sufficiently long. In summary, we have demonstrated that an accurate whole brain T1 mapping can be achieved in 2 minutes and 20 seconds.

References

1. Gowland et al., *MRM 1993;* 30: 351-354, **2.** Clare et al., *MRM 2001;* 45: 630-634 **3.** Zhu et al. *MRM 2001;* 54: 725-731 **4.** Wang et al., *Invest Radiol. 1990 Sep;* 25 Suppl 1:S44-5. **5.** Zhang et al. *IEEE Trans. on Medical Imaging 2001*, 20(1):45-57 **6.** Wright et al., *Magn Reson Mater Phy 2008;* 21:121–130