Saturated T_2 Curves for Relaxometry-Based Compartmental Analysis in Localized ^{1}H MRS

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Introduction

Recently we introduced a rapid relaxometry-based compartmental analysis method for *in vivo* single-voxel ^{1}H MRS *(1)*. The method employs short recovery times, multiple relaxation curves, and a variable echo time T_2 technqiue in conjunction with progressive saturation. This method has been shown to replicate results of the standard T_2 experiment with equal or better precision *(1)*. As currenlty implemented, the method halves the experiment time while nearly doubling the sampling density, compared to a standard ^{1}H MRS T_2 technique with full recovery of the longitudinal magnetization between acquisitions. The rapid relaxometry technique was originally optimized for sensitivity in order to separate the signal contributions of a two-compartment model: CSF and tissue water. In this work, we explore improving the speed of the technique by optimization of the sampling of the T_2 curves, specifically, reducing the sampling density.

Method

T_2 analysis was performed on nine sets of ^{1}H MRS water relaxometry data acquired from healthy adults ranging from 21 to 68 years of age (top figure). The data were collected on a 1.5 T MRI system (STEAM, TD: 1.6 and 3.2 seconds, TE: 10-1500 ms, 24 points per curve, 2500 Hz spectral width, volume ~ 6 cm^3). Each curve was decimated to 20 points, 16 points, 12 points, and 8 points. The shortest and longest TE in each new curve, 10 and 1500 ms, respectively, were fixed so that all curves had identical dynamic range. We created one case where the dynamic range was reduced; the original curve was decimated to remove all TE acquisitions above 400 ms. This shorten TE technique is used by some research groups to reduce the T_2 experiment time, while not reducing the dynamic range for the tissue component of the water signal. All curves were fit with the bi-exponential model:

$$S(TE,TD) = S_{O\_tis}\left\{\exp\left(-\frac{TE}{T_{2\_tis}}\right)\left[1-\exp\left(-\frac{TD}{T_{1\_tis}}\right)\right]\right\} + S_{O\_csf}\left\{\exp\left(-\frac{TE}{T_{2\_csf}}\right)\left[1-\exp\left(-\frac{TD}{T_{1\_csf}}\right)\right]\right\}$$

Results and Discussion

Compared to a standard T_2 technique, the rapid technique yields T_1 values in addition to the signal intensities and T_2 values for each compartment (see Eq above). The CSF metrics have been proven to be unreliable, even for the standard T_2 method, so we confined our analysis to the tissue water metrics: S_{0_tis}, T_{1_tis}, and T_{2_tis}. Surprisingly, the tissue metrics were relatively insensitive to the data reduction when the dynamic range was preserved (e.g., middle Figs: S_{0_tis} & T_{2_tis}); although, the variability was consistently, if only slightly, worse for results calculated from the 8-point curves (bottom Fig). In comparison, truncation of the decay curves resulted in large errors for all three metrics (see middle and bottom Fig) - even though the sampling density was fairly high: 17/18 points per curve. Thus, the supposition that only the dynamic range for the tissue signal need be considered when sampling the decay curve does not apply in this case.

Relaxometry-based compartmental analysis is a standard *in vivo* ^{1}H MRS technique used to minimize the effects of CSF partial voluming within the localized volume-of-interest. Because the time required for the standard T_2 method is prohibitively long, metabolite ratios are often preferred to absolute quantitation methods that rely on accurate separation of the water compartments. With errors typically less than 2%, our analysis suggest that sparsely sampled saturated T_2 curves might provide the reliability and speed needed for the clinical environment. Currently, our standard is two 16-point curves that take a total of 2:39 minutes. The analysis here suggests that 12- or 8-point curves may be sufficient, thereby reducing the total acquisition time to 90-100 seconds.

Conclusion

Analysis of variously sampled relaxation curves suggests that sparsely sampled saturated T_2 curves may be a robust and fast method for relaxometry-based compartmental analysis in localized spectroscopy.

Reference: (1) Knight-Scott J et al. J Magn Reson 2005; 173:169-74. (2) Knight-Scott J et al. Magn Reson Imag 2002; 681-689.