Water as an Internal Reference for Spectroscopic Imaging: Errors Due to Inacurrate Water Relaxation Times

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The unsuppressed 'internal' water signal was introduced as a concentration reference for single-voxel proton magnetic resonance spectroscopy (^{1}H-MRS) of the brain over a decade ago (1). However, to our knowledge, a detailed description of how this method could be applied to spectroscopic imaging (SI) or an examination of its potential sources of error has yet to be reported. Here we examine the potential errors due to inaccurate estimates of water proton relaxation rates in white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF) that may arise when using this method with partial volume information from image segmentation.

Theory

In numerous single-voxel ^{1}H-MRS studies on regions of brain without CSF, the metabolite concentration has been estimated from the ratio of the metabolite (S_M) and parenchymal water signals ($S_{H2O\_GM/WM}$) scaled by the relaxation attenuation factors appropriate to each signal, R_M and $R_{H2O\_GM/WM}$, respectively, the number of protons giving rise to each signal, #H$_M$ and 2, respectively, and the concentration of pure water [H2O] (55.5M):

$$[M] = \frac{S_M \times R_{H2O\_GM/WM}}{S_{H2O\_GM/WM} \times R_M} \times \frac{2}{\#H_M} \times [H_2O] \qquad [1]$$

where $R_M = \exp[-TE/T2_M](1-\exp[-TR/T1_M])$ and $R_{H2O\_GM/WM} = \exp[-TE/T2_{H2O\_GM/WM}](1-\exp[-TR/T1_{H2O\_GM/WM}])$ (2). The relaxation times in the latter factor are either the GM, the WM, or the averaged GM and WM water proton T1 and T2 times, depending on whether the voxel is considered mostly GM, mostly WM, or a mixture of both. Hence, Eq. [1] ignores that the observed water signal from a voxel may arise from a combination of the GM, WM, and CSF water fractions, each weighted by different relaxation times. This situation is likely to occur in SI studies on the brain, where the region of interest generally covers a broad and heterogeneous region of parenchyma and CSF. The following expression for calculating [M] from SI voxels takes into account the possible presence of CSF in the spectroscopic voxel as well as tissue differences in water relaxation rates:

$$[M] = \frac{S_M \times (f_{GM} \times R_{H2O\_GM} + f_{WM} \times R_{H2O\_WM} + f_{CSF} \times R_{H2O\_CSF})}{S_{H2O}(1 - f_{CSF}) \times R_M} \times \frac{2}{\#H_M} \times [H2O] \qquad [2]$$

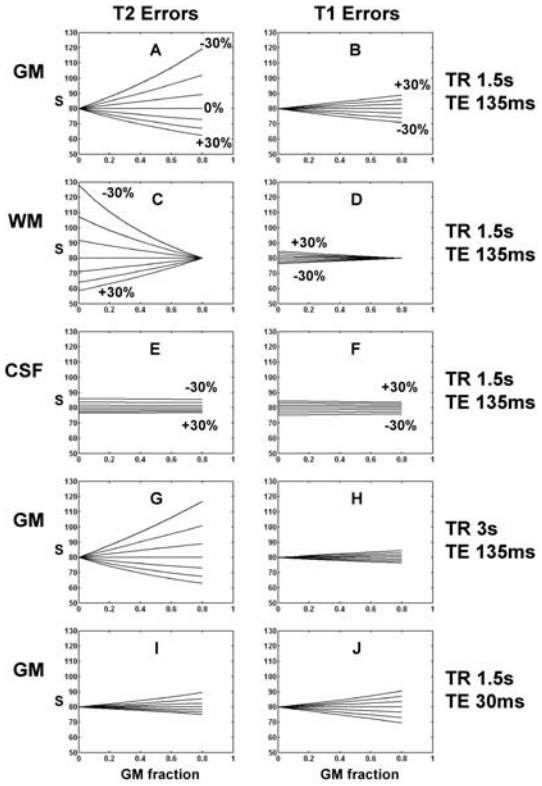
where S_{H2O} is the total water signal, f_{GM}, f_{WM}, and f_{CSF} are the volume fractions of water in GM, WM, and CSF, respectively, determined by image segmentation and the tissue water densities, and R_{H2O_GM}, R_{H2O_WM}, and R_{H2O_CSF} are the appropriate relaxation factors associated with each water pool. To obtain the concentration of a metabolite in either "pure" GM or WM, one can apply a statistical regression method (3) to [M] versus fractional GM in the parenchyma, extrapolating the regression line to GM=1 to estimate the concentration in pure GM and to GM=0 to estimate the value in pure WM.

Estimates of the Error due to Inaccurate Relaxation Times

The major potential sources of error in Eq. [2], aside from those inherent in acquiring the MRS signals and the estimate of the metabolite relaxation attenuation factor common to all SI methods, are the estimates of the various tissue fractions of water and relaxation times associated with them. Here we examine potential errors due to inaccurate estimates of the water proton T1 and T2 times in GM, WM, and CSF, which, judging from the range of values reported in the literature for normal appearing tissue alone, may differ by 10% or more from the true relaxation times (4-6). Furthermore, increases in water relaxation times in regions of edema, tumors, plaques, or brain lesions may be as high as 20% (6). To this end, we altered the T1 or T2 values used to calculate R_{H2O_GM}, R_{H2O_WM}, and R_{H2O_CSF} by 0 to ±30% in steps of 10% from values at 1.5T found in published reports (GM: T1=1.304, T2=0.093 (4); WM: T1=0.660, T2=0.073 (4,5); CSF: T1=2.93, T2=0.23 (5)).

Results and Discussion

Figure 1 displays a sampling of the results of such an analysis based on a TR of 1.5s, a typical SI TE of 135ms, and an f_{CSF} of 0.2, a fraction of CSF that might be encountered in SI voxels along the inter-hemispheric midline in a typical transverse SI slice above the lateral ventricles. Evident in these plots of GM fraction v.s. the estimated relaxation-corrected parenchymal water signal is the relatively high sensitivity of the estimates to errors in GM or WM water T2, which scale nearly linearly with the fraction of GM or WM, respectively. The sensitivity to WM water T1 error is less than that to GM water T1 error, owing to the much shorter T1 of water in WM, and errors in the CSF relaxation parameters lead to only small errors in the estimated signal, due to the relatively long T2 and low fraction of CSF water protons in this example. It would not be practical to show every permutation of the errors in the six relaxation times over a range of TE, TR, and CSF fractions, but the major implications of such an analysis can be drawn from these plots. Generally, and as expected, simultaneous errors in the various relaxation times will have either cumulative or offsetting effects, depending on the direction of the error. Also, this sensitivity is greatly reduced at short TE (Fig. 1I, 1J). Lengthening TR, on the other hand (Fig. 1G, 1H), does reduce the sensitivity to T1 errors, but from a level that was relatively low to begin with. Since lengthening TR undesirably lengthens the total SI scan time, while shortening TE does not, the strategy suggested by this analysis for reducing sensitivity to relaxation time errors when using water as an internal reference is to acquire the data with the shortest TE possible.



References

1.) Kreis R et al.. Absolute quantitation of water and metabolites in the human brain. 2: metabolite concentrations. J Magn Res Series B 1993;102(1):9-19.

2.) Barker PB et al.. Quantitation of proton NMR spectra of the human brain using tissue water as an internal concentration reference. NMR Biomed 1993;6(1):89-94.

3.) Hetherington HP et al.. Quantitative 1H spectroscopic imaging of human brain at 4.1 T using image segmentation. Magn Reson Med 1996;36(1):21-29.

4.) Vymazal et al.. T1 and T2 in the brain of healthy subjects, patients with Parkinson disease, and patients with multiple system atrophy: relation to iron content. Radiology 1999;211(2):489-495.

5.) Ibrahim MA et al.. Magnetic resonance imaging relaxation times and gadolinium-DTPA relaxivity values in human cerebrospinal fluid. Invest Radiol 1998;33(3):153-162.

6.) Nitz WR, Reimer P. Contrast mechanisms in MR imaging. Eur Radiol 1999;9(6):1032-1046.