Regional Estimation of T1 Metabolite Relaxation using 2D MRSI and a Bootstrap Approach at 1.5 T

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Introduction

In clinical spectroscopic studies, the use of short repetition times (TR) enables one to meet time constraints but also requires knowledge of accurate metabolite longitudinal relaxation time values (T1) to correct for the resulting strongly T1-weighted signals. Accounting for the metabolite T1 values in the quantification results may be very relevant when comparing patient and normal controls. We propose a new method to estimate the metabolite T1, at 1.5T, using MR spectroscopic imaging (MRSI) data. The use of MRSI data enables us to process many small voxels (1 cc), while considering their gray matter and white matter contents. This approach can increase the accuracy of the results as compared to large, likely heterogeneous, single-voxel studies[1]. It also enables regional analysis. The very low signal to noise ratio problem is tackled by using an approach combining Principal Component Analysis (PCA) denoising [2], bootstrap-like data averaging, and quantitation results quality assessment. A gray matter (GM) versus white matter (WM) contribution to the T1 estimation is investigated.

Method

Seven healthy volunteers were scanned on a GE 1.5T clinical imager. 2D MRSI data sets (12×12) using a PRESS volume selection and an echo time (TE) of 35 ms were acquired. Oblique Fast Spin Echo images were used to guide the positioning of the spectroscopic box just above the ventricles. Five acquisitions using different repetition times (TR) and different NEX were acquired (TR/NEX=0.850sec/3,1/2,2/1,4/1,8/1) on 7 healthy volunteers. To assess applicability to studying multiple sclerosis, 3 patients were scanned, using the same protocol except only 3 TR's were acquired (TR/NEX = 1/3, 2/1, 8/1). The processing entailed:

1) PCA denoising [2] and frequency shifting using a reference spectrum, the N_{total} signals belonging to the selection box.
2) Segmenting the T1-weighted images using the Automated Segmentation Tool FAST[3] and calculating the percentage of GM/WM within the N_{total} spectroscopic voxels.
3) Randomly averaging N_{boot} signals among the N_{total} signals, N_{art} times. This approach, similar to a bootstrapping method, enables one to artificially obtain N_{art} less noisy signals. We tested N_{boot}=1,2, 4 and 6 and fixed N_{art} to 300. The resultant percentages of GM and WM of the combined voxels were also computed.
4) Metabolite relative amplitudes were quantified for the N_{art} signals for each TR using the QUEST [4] quantitation method from the jMRUI package. The metabolite basis set used was simulated with the NMR-SCOPE toolbox from the same package. N-Acetyl Compounds (NA=NAA+NAAG, 2.02ppm), Creatine (Cr-CH_3, 3.03 ppm), and Choline compounds (3.21ppm) were the metabolites of interest in the study.
5) For each TR, linear regressions were performed several times on several sets of (1-5%) N_{art} randomly chosen voxels to determine the concentration of the metabolite for assumed pure white matter and pure gray matter content [5]. Before the linear regression the quantitation results were selected regarding the additional damping factor found by QUEST[4] compared to the "ideal" linewidth used in the basis set (LW=4 Hz). When the final linewidth was too large the quantitated value was rejected. In the linear regression, the voxels for which the quantitation results presented large Cramér Rao Lower Bounds were penalized.
6) Estimating the metabolite T1 for pure WM and pure GM contents using a home-made M-Estimation mono-exponential fitting procedure.

Results

The output of the method is the T1 values for each metabolite and each tissue (WM/GM). A regional analysis can also be done by restricting the third step of the method to specific regions. In our study we split the spectroscopic slice into anterior and posterior regions and compared the results when using all the voxels in the slice (All), or only those pertaining to the Anterior or Posterior part. Figure 1 shows the results we obtained for NA testing the method using N_{boot}=1, 2, 4, 6. When N_{boot}=1 a clear distinction between WM and GM results can be seen, but this distinction is reduced while N_{boot} increases. However, we notice that the increase of N_{boot} also induces a general reduction of the standard deviation. It is obvious in the anterior part results. This is due to the increase of the apparent SNR with N_{boot} (SNR=5.59 for N_{boot}=1 SNR=9.34 for N_{boot} =6). The SNR was calculated from the amplitude of the NAA singlet over the standard deviation of the noise. Table 1 gives T1 estimated value for the 3 metabolites. Generally the anterior part presents better reproducibility than posterior part and greater T1 values for the 3 metabolites. T1's of NA were statistically different between the anterior part and the posterior part (p=0.01) in the WM (N_{boot}=6), as well as Choline T1's anterior versus posterior in the GM (p=0.02). As for the Cre T1's no significant difference was found between the anterior part and the posterior part. Choline compounds T1's showed greater standard deviation. For the 3 MS patients, a smaller mean T1 value for NA in WM was found in the anterior region 1.32 ± 0.09 for N_{boot}=6 compared to healthy volunteers (1.47± 0.09)

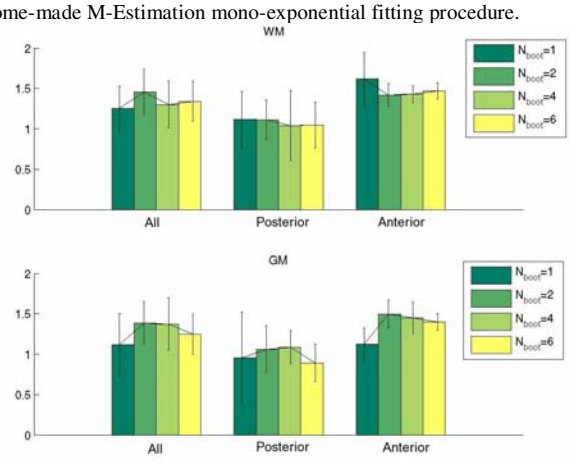

Figure 1: NA T1 values results in second for WM (top) and GM (bottom), analyzing All the voxels (left), the voxels in the posterior (center) and in the anterior part (right) for different N_{boot}

	NA T1 (s)			Cre T1(s)			Cho T1(s)		
	All	Post,	Ant	All	Post,	Ant	All	Post,	Ant
WM N_{boot}=1	1.25 ± 0.27	1.11 ± 0..35	1.61 ± 0.32	1.13 ± 0.14	1.07 ± 0.29	1.44 ± 0.29	1.27 ± 0.69	1.16 ± 0.58	1.20 ± 0.37
GM N_{boot}=1	1.31 ± 0.28	1.36 ± 0.51	1.12 ± 0.20	1.43 ± 0.42	1.21 ± 0.39	1.12 ± 0.39	1.37 ± 0.44	1.51 ± 0.90	0.95 ± 0.57
WM N_{boot}=6	1.39 ± 0.15	1.25 ± 0.27	1.47 ± 0.09	1.21 ± 0.13	1.22 ± 0.28	1.34 ± 0.25	1.13 ± 0.22	1.28 ± 0.42	1.04 ± 0.28
GM N_{boot}=6	1.32 ± 0.17	1.47 ± 0.35	1.40 ± 0.10	1.25 ± 0.20	1.21 ± 0.33	1.25 ± 0.24	1.11 ± 0.21	1.49 ± 0.57	0.89 ± 0.20

Table 1: NA, Cho and Cre T1 estimated values for WM and GM, N_{boot}=1 and 6, for analyzing All the voxels, the voxels in the Anterior and the voxels in the Posterior part of the brain.

Discussion and Conclusion

At 1.5T, we proposed to randomly average the data to increase the SNR and facilitate the quantification of MRSI data before the final T1 estimation. The results already found for N_{boot}=6 are in good agreement with the literature, slightly higher for NA when considering only the anterior part. However, averaging the data too much tended to gather all the N_{art} voxels in the same position in the percentage of WM-percentage of GM space. As a result, the linear regression failed for N_{boot} too high (typically 10) and the distinction between WM and GM is no longer meaningful. A better averaging allowing only to mix voxels with similar WM/GM content can be a future improvement of this method. Results on myo-inositol T1 require more research. To extend the study to evaluating differences between healthy subjects and patients with MS, more patients and further developments needs to be done to confirm the results. In conclusions this work introduced a new way of evaluating metabolite T1's using MRI and MRSI data, allowing a regional analysis and a GM/WM discrimination.

References : [1] Ethofer et al, MRM 50:1296-1301, 2003 [2] Zhu et al, MRM 50:474-482, 2003 [3] Zhang et al, Trans. on Medical Imaging, 20(1):45-57, 2001 [4] Ratiney et al, NMR in Biomed 16:1-13, 2005 [5] Noworolski et al, MRM 41:21-29, 1999