Signal Normalization for MR Spectroscopic Imaging Using an Interleaved Water-Reference

A. A. Maudsley[1], and C. Domenig[1]
[1]Radiology, University of Miami, Miami, FL, United States

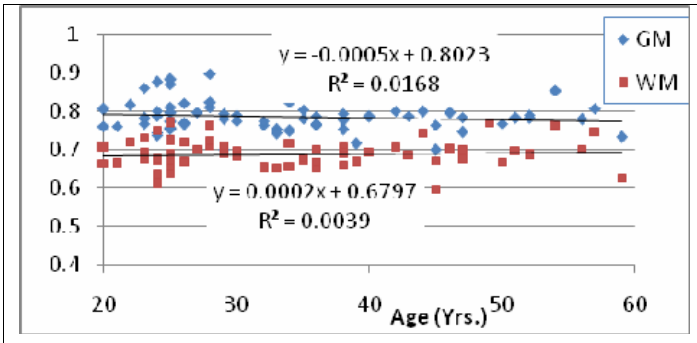
INTRODUCTION:

Since MRS signal intensities are uncalibrated the data analysis requires that a signal normalization procedure be applied. In addition, MRS signals in the brain vary according to location and a number of subject and acquisition variables, which must therefore also be accounted for. The use of tissue water as an internal reference for signal normalization in MRSI has been previously described, as well as the correction for partial volume contribution from CSF[1], and in this report this approach is further developed to account for differences in tissue water content between individuals; implemented using an interleaved water SI acquisition to provide the signal reference; and analyzed in conjunction with spatial normalization.

METHODS:

MRSI data was obtained using volumetric EPSI at 3 T with TE of 70 ms; voxel volume 0.6 ml; acquisition over a 14 cm slab covering the cerebrum; and an interleaved water SI acquisition[2]. Metabolite image reconstruction was carried out using automated parametric spectral fitting and the MIDAS package[3]. Following reconstruction a signal intensity normalization procedure was implemented as follows: 1) MRI tissue segmentation using FSL/FAST[4]; 2) Calculation of the fractional water content of grey-and white matter by a procedure that minimizes the difference between a simulated MRI, based on the tissue segmentation images, and the proton density MRI; 3) Estimation of the bias-field for the MRSI by subtraction between the acquired water-reference SI and a simulated data set based on the previously determined tissue water fractions and literature values of tissue water; 4) Bias field correction and scaling of the metabolite images using a factor previously determined from a calibration measurement in a phantom.

The results of the tissue water fraction estimation and the intra- and inter-subject variability of the normalized metabolite images were evaluated using data from 70 normal subjects, aged 19 to 59, and with data from one subject (age 24) scanned 5 times. The coefficient of variance (COV) for the metabolite image results was then calculated for the single-subject data after rigid registration of all studies; for the spatially-normalized voxels over the group data; and following tissue regression analyses by brain region following spatial normalization.



Calculated tissue factors for grey- and white-matter as a function of subject age.

	Frontal		Temporal		Parietal		Occipital		Average
	GM	WM	GM	WM	GM	WM	GM	WM	%
NAA	10	11	10	13	10	12	9	12	11
Cre	11	12	13	12	12	11	12	11	12
Cho	16	14	18	16	18	14	13	15	15

Variance, by brain region, in %, of the tissue regression analysis following intensity- and spatial-normalization of metabolite images for subjects aged 20 to 30 y.o.

RESULTS AND CONCLUSIONS:

The calculated tissue factors for grey- and white-matter for all subjects are shown in the Figure. The mean values were 0.78 for grey-matter and 0.68 for white-matter, with 5% variance over the whole group. The intra-subject COV was 9%, 10%, and 12% for NAA, Cr, and Cho respectively, and 5% for the water reference image. The average voxel-based COV calculated for a subject group of 20 to 30 y.o., in a central white matter region, was 15% for NAA, 15% for Cr, and 16% for Cho. The COV of the tissue regression analysis results, which averages data over a larger region, are shown in the table, obtained using data from 33 subjects aged 20 to 30. These analyses also indicated a grey- to white-matter ratio of 1.06 for NAA; 1.34 for Cr; and 0.87 for Cho.

The proposed intensity normalization procedure results in variances comparable to previously published results; however, comparisons between intra- and inter-subject analyses indicate that the variability of the individual subject analysis still represents a significant fraction of the variability seen across a group of subjects. Accounting for the variability of tissue water content between individuals is of benefit. Finally, the use of spatial normalization for MRSI provides a powerful approach for analysis of metabolite variations across subject groups.

ACKNOWLEDGEMENTS: This work is supported by NIH BRP grant, R01EB0822.

REFERENCES: 1) C. Garparovic et al. *Magn Reson Med*. 55:1219 (2006). 2) A. Ebel and A.A. Maudsley, *Magn Reson Med*. 53:465 (2005). 3) A.A. Maudsley, et al., *NMR Biomed*., 19:492 (2006). 4) www.fmrib.ox.ac.uk/fsl.