Cerebrospinal Fluid Partial Volume Correction in Quantitative Short TE Magnetic Resonance Spectroscopic Imaging

E. A. Yoshimoto Ninamango[1], A. Van Der Kouwe[2], F-H. Lin[2,3], L. Wald[2], and S. Posse[1,4]

[1]Department of Electrical and Computer Engineering, University of New Mexico, Albuquerque, NM, United States, [2]A. A. Martinos Center, Massachusetts General Hospital, Charlestown, MA, United States, [3]Institute of Biomedical Engineering, National Taiwan University, Taipei, Taiwan, [4]Department of Neurology, University of New Mexico, Albuquerque, NM, United States

Introduction

Magnetic resonance spectroscopic imaging (MRSI) is a powerful tool to map brain metabolites relevant to brain diseases [1]. Low spatial resolution, outside lipid contamination and model dependence of spectral quantification of MRSI data represent technical challenges that can compromise the accuracy of metabolite concentration values measured in different tissue compartments [2,3]. Absolute spectral quantification requires correction for signal loss due to cerebral spinal fluid (CSF) partial volume, which is sensitive to errors in tissue segmentation and correction for signal relaxation effects [4]. In this study we investigate the effects of CSF fraction on absolute quantification as a function of spatial resolution for voxel sizes of 0.3, 1.2 and 4.8 cc.

Methods

Data in 3 healthy volunteers were obtained on a 3 T TIM Trio scanner equipped with 32 channel head array RF coil. T1-weighted Magnetization Prepared Rapid Gradient Echo (MP-RAGE) scans and multi-slice T2-weighted turbo spin-echo data were obtained for tissue segmentation and spatial coregistration. Water suppressed data (WS) were acquired from a supraventricular axial slice using the PEPSI sequence with 8-slice outer volume suppression along the perimeter of the brain [4] (TR: 2 s, TE: 15 ms, spatial matrix: 64x64, FOV: 286x286 mm^2, slice thickness: 15 mm, number of averages: 16, acquisition time: 34 min). Data were reconstructed as described previously [5] using only mild spatial apodization (Fermi filter: R= 0.9, D=0.1) to preserve spatial resolution. Constrained spectral fitting in reference to a non-WS (NWS) scan was performed using LCModel with simulated basis sets of 18 metabolites [5]. Correction for relaxation attenuation and partial-volume effects (PVC) [5] was performed using tissue segmentation with FSL. In addition, the 64x64 matrix data were donwsampled in k-space to 32x32 and 16x16 matrices.

Results

The sensitive volume (no. of voxels with CSF fraction below threshold) strongly decreases with decreasing CSF fraction threshold (Figs.1 and 2). Except for the largest voxel size, increasing CSF fraction increases pure GM concentrations while reducing WM concentrations (Fig.2). Increasing spatial resolution reduces CSF contamination, increases sensitive volume and improves the estimation of the slope of metabolite concentration vs. GM fraction (Fig 2). The pure WM and GM metabolite concentrations as a function of CSF fraction are approximated by 1st order polynomial fit when the CSF fraction is greater than 60%, 30% and 10% for 4.8 cc, 1.2 cc and 0.3 cc respectively (fig. 2). The metabolites concentrations are in the range of literature values [3, 4, 5] for voxel sizes of 0.3 and 1.2 cc, but not for 4.8 cc. (Table 1)

	Voxel size								
	4.8 cc.			1.2 cc.			0.3 cc.		
Metabolite	1	2	3	1	2	3	1	2	3
Ins	2.34	0.21	2.39	1.4	1.5	1.4	1.34	1.40	1.44
Cr+PCr	2.10	1.14	2.42	1.4	1.5	1.4	1.50	1.47	1.45
NAA/G	2.41	0.30	1.62	1.1	1.3	1.2	1.09	1.15	1.22
Glu+Gln	1.78	1.70	1.75	2	2.4	1.8	2.14	1.86	1.91
Cho	1.61	0.38	1.71	1	1.5	1.2	0.97	1.36	1.28
MM20	6.51	1.02	1.88	1.6	1.3	1.5	1.69	1.34	1.28

Table 1. Pure GM versus pure WM concentration ratios for different voxel sizes at 20% CSF fraction.

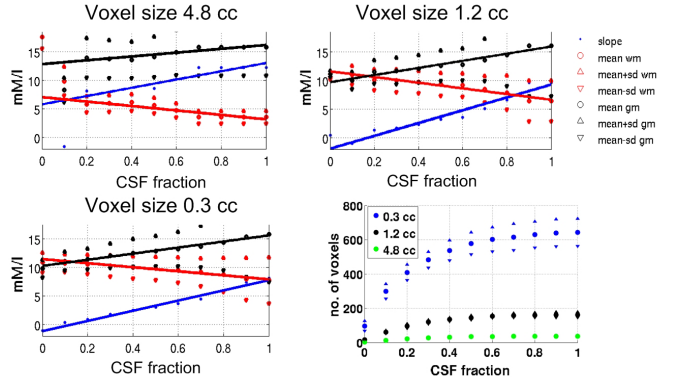

Figure 2. NAA/G concentration in pure WM (red) and pure GM (black) and slope of the fitted NAA/G concentration versus GM fraction (blue) as a function of CSF fraction for different voxel sizes. Sensitive volume (no. of voxels below threshold) versus CSF fraction (bottom-right plot).

Discussion and conclusion

Metabolite quantification is highly sensitive to CSF and peripheral lipid contamination in the spectroscopic voxel, leading to bias in GM/WM concentration estimates. This bias decreases with increasing spatial resolution, which reduces CSF contamination and constrains peripheral lipid contamination. Increasing spatial resolution also improves delineation of GM, WM and CSF structures in metabolite maps and reduces sensitivity to partial volume correction when assessing metabolic changes in focal brain lesions and in normal appearing WM and GM.

References [1] Maudsley et al. Magn Reson Med 2009, Mar;61:548-559, [2] Gasparovic et al. Magn Reson Med 2009 Sep;62(3):583-90, [3] Ernst et al. Magn Reson B 1993; 102:1-3 [4] Gasparovic et al. Magn Reson Med 2006;55:1219-1226, [5] Posse S et al. Magn Reson Med 2007;58: 236-244.

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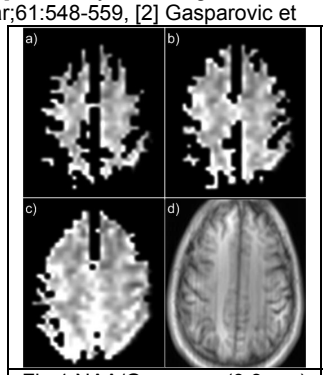

Fig.1:NAA/G maps (0.3 cc) thresholded at: a) 10%, b) 20% and c) 40% CSF fraction. D) MPRAGE scan averaged across the MRSI slice.