

## Automated partial volume calculation in single voxel $^1\text{H}$ -MRS

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**Introduction** In proton magnetic resonance spectroscopy ( $^1\text{H}$ MRS), low abundance of the chemical compounds requires enhancement of signal detection by performing single voxel  $^1\text{H}$ MRS at a relatively coarse spatial resolution, making partial volume effects inevitable. Also substantial uncertainty is introduced in metabolite concentration calculations when water is used as an internal reference. The present study focuses on methodological aspects pertaining to mapping the  $^1\text{H}$ MRS voxel onto the corresponding anatomical scan. Both automated and manual voxel placement were performed, and results are compared on the basis of positional accuracy, positional reliability, and metabolite concentration estimates.

**Method:** A total of 26 participants (age range 41 -79 years 13 normals and 13 lung cancer patients) underwent MRI imaging as a part of ongoing IRB approved larger longitudinal study to investigate the cerebral metabolic status of lung cancer patients vs normal controls; some participants were scanned twice. A total of 48 scanning sessions were performed on a 3.0T Siemens(25 sessions) and 3T Philips (23 sessions) whole body scanners. At each session, a T1W high resolution sequence (1x1x1mm) was acquired sagittally followed by a single voxel PRESS  $^1\text{H}$ MRS scan in the parietal and occipital lobes with following parameters TR/TE/2000ms/30~32ms, receiver bandwidth=1200/2000Hz, number of points=1024/2048, and average =256/128. Water unsuppressed scans were also performed as an internal reference for concentration calculation. Manual  $^1\text{H}$ MRS voxel placement was performed by translating and rotating a binary mask. Computerized reconstruction of a  $^1\text{H}$ MRS voxel was performed by mapping the voxel onto the anatomical scan using transformation matrices derived from directions of cosines, Euler angles, or Euler parameters. Tissue volume fractions were then calculated by using SPM8, and water concentration was subsequently corrected for varying tissue volume composition including T1 and T2 effects. Metabolites (tNAA, tCh, tCr, tGlx, mI) concentrations were quantified by LC model.[1~3]

**Result** Manual vs automated method: Figure 1 depicts overlays of manually placed voxels, reconstructed voxel, and screen display at the scanner console. Excellent agreement between the screen display and reconstructed voxel is evident from the figure. Spatial overlaps (Dice metric) between the manually and reconstructed method in 48 scans were  $0.71\pm0.13$  (occipital lobe) and  $0.69\pm0.12$  (parietal lobe), respectively. Nearly 30% positional discrepancy led to only  $2.5\pm2.2\%$  (occipital) and  $1.8\pm1.2\%$  (parietal) differences in metabolite concentrations. However it was statistically significant only in the parietal lobe as determined by means of a paired t-test. Repeated visit: Reliability of voxel positioning and metabolites concentrations over two visits (~30 days) among healthy subjects were analyzed using reconstructed voxel positions. Spatial overlaps (Dice metric) between the two visits were  $0.66\pm0.15$  (occipital lobe) and  $0.57\pm0.12$  (parietal lobe). As for metabolites concentrations over the two visits, coefficients of variance (COV) in the parietal lobe were  $4.3\pm4.0\%$  (tNAA),  $5.6\pm4.6\%$  (tCr),  $10.5\pm8.9\%$  (tGlx),  $4.9\pm3.7\%$  (tCh),  $5.2\pm5.6\%$  (mI), and in occipital lobe, they were  $5.9\pm4.3\%$  (tNAA),  $3.7\pm2.5\%$  (tCr),  $7.2\pm0.5\%$  (tGlx),  $5.0\pm4.8\%$  (tCh),  $9.9\pm9.4\%$  (mI), consistent with the estimate of CRLB from LC Model.

Correlation with tissue volume: Correlations between the metabolites

(tNAA, tCho, tCr, Glx, and mI) concentrations and GM tissue volume fractions among healthy subjects were evaluated. In the parietal lobe, GM volume fractions and metabolite concentrations were significantly correlated with tCr( $r=0.84$  Figure 2b), Glx( $r=0.64$ ), tNAA( $r=0.79$ ). In the occipital lobe, GM volume fractions and metabolites concentrations were significantly correlated with tCr( $r=0.48$  Figure 2a), tNAA( $r=0.56$ ), and tCho( $r=0.42$ ).

**Discussion** The present study focused on methodological aspects pertaining to partial volume calculations. Computerized and manual placement methods yielded metabolite concentrations well below COV, indicating that either method is acceptable, at least in the two regions investigated in this study. We also found significant correlation between metabolite concentrations and GM tissue volume fractions confirming previous studies.[4~6]

**References** 1. Ashburner et al. Neuroimage (2005) 2. Gasparovic et al. MRM (2009) 3. Provencher MRM (1993) 4. Posse et al. MRM (2007) 5. Baker et al. JMRI (2008) 6. Degaonkar et al. JMRI (2005)

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