Baseline Estimation in 1H-MR Spectroscopy Imaging of the Normal Brain; A Correlation Study Between Different Regions

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Target Audience: Scientists, physicists and clinicians interested in MRS of the brain, baseline estimation

Introduction: Variations of macromolecules and lipids within any anatomical region of the brain is highly correlated with the chemical compounds and therefore, metabolites' concentrations of the same region, in both healthy and pathological conditions. There are several works about correlation between brain's anatomical regions and metabolites' concentrations **[1, 2]**. In this study, our purpose is to exhibit correlation between magnetic resonance spectroscopy (MRS) baselines of different brain's anatomical regions. Qingjia Bao *et al.*'s algorithm **[3]** has been used for the baseline estimation. Then, correlation coefficients for estimated baselines of voxels belonging to specific regions in selected cut of the brain with all voxels from same cut or other cuts have been calculated.

Material and Methods: Data Acquisition: MRS data was acquired by 3T MR scanner (Siemens MAGNETOM Tim TRIO). PRESS pulse sequence was used for multi-voxel MRS data acquisition, matrix size = 16×16, *TE* = 30 and 135msec, TR = 2500msec, sampling time = 0.833msec. In order to have data from all regions of the normal brain, data was acquired in 3 different axial cuts of the brain: upper cut, middle cut and lower cut.

Baseline Quantification: Eddy current correction and signal-to-noise ratio enhancement were performed. Qingjia Bao *et al.*'s algorithm **[3]** was used for baseline estimation. After baseline estimation, correlation coefficients between extracted baselines of all voxels belonging to the selected cut of the brain with a voxel belonging to a specific region – white matter (WM), gray matter (GM), cerebellum or CSF – of the brain were calculated using MATLAB; ranging values between -1.0 to 1.0, corresponding to black to white colors, representing weak to strong correlation values.

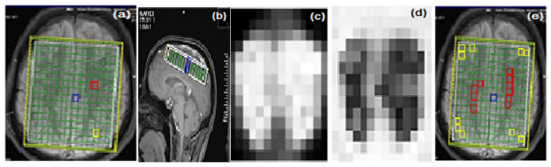

Fig.1 (a) T_2-weighted anatomical image of the upper cut (axial); (b) T_2-weighted anatomical image (sagittal); (c) Baseline correlation coefficient map between selected voxel (red voxel) from WM and all other voxels of the upper cut; (d) Baseline correlation coefficient map between selected voxel from GM (yellow voxel) and all other voxels of the upper cut; (e) Red voxels: positions of selected WM voxels; yellow voxels: positions of selected GM voxels .

Results and Conclusions: WM-GM MRS Signal Baseline Correlation**: Fig. 1 (c,d)** show gray-scale images of baseline correlation maps for all voxels with the selected voxel, either in WM or GM, as shown as either red or yellow in **Fig.1 (a)**, respectively. For better investigation, 10 WM and 10 GM voxels were selected, as shown by red and yellow colors in **Fig. 1 (e)**, respectively. For the rest of this abstract, these voxels were used to compare baseline of other tissues of the brain with WM and GM tissues. After baseline estimation of all selected voxels, correlation coefficients of theirs baseline spectra were calculated with all baselines of GM voxels, resulting in 100 correlation coefficients with the value of 0.12±0.14, showing weak correlation between baseline from WM and GM.

CSF-WM, GM MRS Signal Baseline Correlation**: Fig. 2** shows baseline correlation maps of selected voxels (pink and black voxels) from CSF tissue in the middle cut of the normal brain with other voxels of the same cut. **Fig. 2 (c-d)** are gray scale images resulted from correlation coefficients maps between MRS signal baseline of black and pink voxels, with other voxels from the same cut of the brain, respectively. Also, MRS signal baselines of 2 selected voxels from CSF were compared with baseline of voxels from the upper cut of brain, containing WM and GM tissues. **Fig. 2 (e-f)** show the correlation coefficient maps. As **Fig. 2 (e)** shows, there is weak correlation between black voxel and GM, but strong correlation with WM. **Fig. 2 (f)** shows that correlation between black voxel and WM is approximately the same as the correlation between black voxel and GM. But, for the voxels containing both WM and GM, e.g. red voxels in **Fig.2 (f)**, correlation is high. To numerically exhibit the correlation between CSF and WM-GM tissues, selected voxels from WM/GM from the upper cut of the brain were used. Correlation coefficients between CSF voxels, black and pink voxels as shown in **Fig. 2 (a)**, respectively, and selected WM-GM voxels, yellow and red voxels as shown in **Fig. 1 (a)**, respectively, were separately calculated. Calculated mean and standard deviation values are shown on **Table 1** (Rows: 1, 2, 3 and 4).

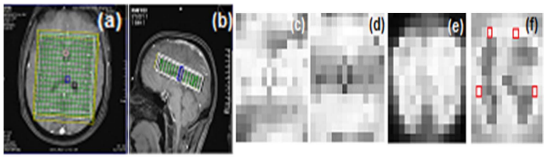

Fig. 2 (a) T_2-weighted anatomical image of middle cut (axial), black and pink voxels show position of selected voxels from CSF; (b) T_2-weighted anatomical image (sagittal); (c) Baseline correlation coefficient map between the black voxel and all other voxels of the same cut; (d) Baseline correlation coefficient map between the pink voxel and all other voxels of the same cut; (e) Baseline correlation coefficient maps between the black voxel and all voxels of the upper cut; (f) Baseline correlation coefficient map between the pink voxel and all voxels of the upper cut.

Table 1 Different Brain Regions MRS Signal Baseline Correlation

Correlation between ..... and		Correlation coefficients	Mean of Correlation Coefficients	Standard Deviation of Correlation Coefficients
White matter(yellow voxels)	CSF(pink voxel)	0.62, 0.45, 0.56, 0.80, 0.82, 0.56, 0.66, 0.48, 0.53, 0.67	0.61	0.11
Gray matter(red voxels)	CSF(pink voxel)	0.68, 0.67, 0.66, 0.65, 0.56, 0.62, 0.58, 0.71, 0.70, 0.74	0.66	0.05
White matter(yellow voxels)	CSF(black voxel)	0.94, 0.84, 0.95, 0.95, 0.93, 0.92, 0.97, 0.94, 0.90, 0.88	0.92	0.03
Gray matter(red voxels)	CSF(black voxel)	0.04, 0.03, 0.03, 0.09, 0.04, 0.07, 0.03, 0.06, 0.06, 0.2	0.07	0.06
White matter(yellow voxels)	Cerebellum (white voxel)	0.94, 0.84, 0.95, 0.95, 0.93, 0.92, 0.97, 0.94, 0.90, 0.88	0.92	0.05
Gray matter(red voxels)	Cerebellum(white voxel)	-0.05, -0.08, -0.05, -0.03, -0.02,-0.02, -0.04, -0.06, -0.06, 0.2	- 0.0236	0.0795

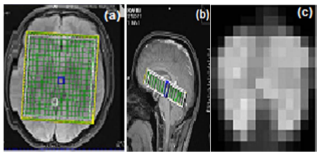

Fig. 3 (a) T_2-weighted anatomical images of the lower cut (axial); white voxel shows position of selected voxels from cerebellum; (b) T_2-weighted anatomical image (sagittal); (c) Baseline correlation coefficient maps between white voxel and all other voxels of the upper cut.

Cerebellum-WM/GM MRS Signal Baseline Correlation: **Fig. 3 (a)** shows a voxel in cerebellum in lower cut of the brain (white voxel), correlation coefficient maps between baseline in this voxel and other voxels in WM-GM, as depicted in **Fig. 3 (c)**, resulting in stronger correlation between baselines in cerebellum WM than baselines in cerebellum and GM. **Table 1** (Rows: 4, 5) numerically presents the same results, indicating that baseline from cerebellum is more similar to baseline of WM than baseline of GM.

Results indicate that such correlations, existing between the baseline spectra is useful not only for tissue segmentation, but also for accurate baseline estimation of MRS signals for different tissues, and therefore tissue quantification in heterogeneous tissue types, e.g. glial tumorous tissues in the brain, when the tissue significantly changes over a small region, obligating this capability of the baseline estimation algorithm to be adaptively adjusted to different tissue types.

References: **[1]** Barker PB *et al.*, *Magn Reson Med* 43, 348 (2000). **[2]** Hennig J *et al.*, *NMR Biomed* 5, 193 (1992). **[3]** Qingjia B *et al. JMR* 218, 35 (2012). **[4]** Golotvin S *et al. JMR* 146, 122 (2000). **[5]** Carlos C J *et al. JMR* 183, 145 (2006).