Quantization of ME-COSI Data With Prior Knowledge Fitting

G. Verma[1], N. Wilson[2], S. L. Lipnick[2], N. Rajakumar[3], M. A. Thomas[3], and
[1]Biomedical Engineering, UCLA, Los Angeles, CA, United States, [2]Biomedical Physics, UCLA, Los Angeles, California, United States, [3]Radiological Sciences, UCLA, Los Angeles, California, United States

Introduction: Multi-Echo enhanced Correlated Spectroscopic Imaging (ME-COSI) (1) combines two-dimensional Magnetic Resonance Spectroscopy (2D MRS) with 2D spatial encoding. 2D MRS improves over 1D MRS by allowing detection of "cross peaks" due to J-coupling interactions and resolving such peaks from other co-resonant metabolites (2). While ME-COSI has been introduced and evaluated qualitatively, data generated by such fast 4D MRSI techniques have typically lower resolution than conventional sequences and have yet to be quantified. The goal of this study is to quantify metabolite ratios in ME-COSI data through ProFit (3), a prior knowledge fitting algorithm. Analogous to LC Model (4) and VarPro, ProFit fits acquired data to a prior-knowledge basis set and works in both the time and frequency domains using parameters such as field strength and bandwidth.

Materials & Methods: A gray matter phantom containing 16 metabolites at physiological concentrations was studied to evaluate the effectiveness of ProFit quantization. Eighteen scans were performed with ME-COSI on a Siemens 3T Tim-Trio scanner running on the VB15 platform. Scan parameters were as follows: TE/TR= 30ms/1500ms, 80x80mm field of view, 40mm thickness, 4.0ml voxel volume, 512 complex points, 2000Hz bandwidth, 100 Δt_1, one average. Each scan took 40 minutes and the data array size was (512x8x8x100). Water suppression was applied through the Water Elimination through T_1 effects (WET) scheme.

Acquired data were post-processed with a custom MATLAB-based program, which applied spatial Hamming and spectral apodization filters to smooth the data. Prior knowledge fitting was applied to processed data extracted from a central voxel with the ProFit algorithm. This program calculates metabolite ratio with respect to the 3.0 ppm creatine peak (S/S_{Cr}), and the Cramer-Rao Lower Bound (CRLB), a measure of the performance of the fitting technique.

Results & Discussion: Table 1B shows the average ratio of various metabolite concentrations to that from the 3.0 ppm peak of creatine. Also shown are the standard deviation (SD) of this ratio and average CRLB for each metabolite. Figure 1A is a plot of the coefficient of variation (CV) for various metabolites across the 18 studies. Metabolites with higher physiological concentration including glutamate/glutamine (Glx), n-acetyl aspartate (NAA) and myo-inositol (mI), which all show cross peaks due to J-coupling (5), all had CRLBs between 0.28 and 0.4 and CVs between 2–8%. ProFit consistently overestimated the concentration of Glx, yet maintained a low CRLB, suggesting it may have incorporated a larger nearby peak into its estimate of the peak signal. This may be exacerbated by low F_2 spectral resolution (4 Hz/point) in ME-COSI due to the constraints of T_2 loss on readout time per echo. Lower concentrated metabolites like aspartate, glutathione and phosphoethanolamine, had CVs between 12-21% and CRLBs between 1.0 and 5.0. Lactate, whose concentration in the phantom was 400 μM, was observed to have the poorest fit, as indicated by its CRLB of 16.5, and consequently showed the highest CV at 36%.

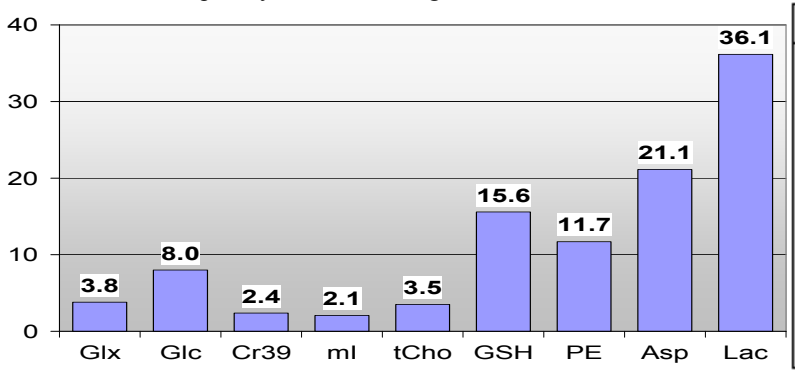

Figure 1A: Coefficients of Variation for various metabolites observed across eighteen scans of the gray matter phantom

Metabolite	Symb	S/S_{Cr}	SD	CRLB
Glutamate/Glutamine	Glx	2.648	0.10	**0.51**
n-Acetyl Aspartate	NAA	0.964	0.08	**0.28**
Creatine	Cr39	0.816	0.02	**0.28**
Myo-Inositol	mI	0.803	0.02	**0.40**
Choline	tCho	0.240	0.01	**0.34**
Glutathione	GSH	0.184	0.03	**1.23**
Phosphoethanolamine	PE	0.172	0.02	**3.08**
Aspartate	Asp	0.137	0.03	**5.02**
Lactate	Lac	0.036	0.01	**16.47**

Table 1B: Metabolite ratio (S/S_{Cr}), standard deviation and CRLB for various metabolites in a gray matter phantom.

Conclusion: Prior knowledge fitting has been implemented with *in vitro* data acquired with the ME-COSI sequence. However, it is expected that broader peak widths associated with *in vivo* studies, and artifacts like motion and thermal noise will necessitate further improvements in signal quality. This may require larger voxel size, multiple averages or moving to higher field strengths, where chemical shifts are higher and metabolite peaks are better separated.

References

1. Verma G, Ramadan S, Lipnick S, Rajakumar N, Liu X, Thomas MA, ISMRM 2008 #1602
2. Thomas MA, Hattori N, Umeda M, Sawada T, Naruse S, NMR Biomed 2003:245-251
3. Schulte R, Boesiger P, *NMR Biomed* 2006; 19:255-263
4. Provencher S, *NMR Biomed* 2001; 4:260-264
5. Velan S, Lemieux R, Raylman W, Boling G, *Magn Reson Med* 2007; 265:409