LCModel analysis: How do simulated macromolecular resonances affect the metabolite concentrations ?

G. Jost[1], I. Harting[1], S. Heiland[1]

[1]Department of Neurology, Division of Neuroradiology, University of Heidelberg Medical Center, Heidelberg, Germany

INTRODUCTION:

The quantification of short TE spectra is generally difficult due to the overlapping metabolite signals and contributions of macromolecular components. The LCModel quantification (1) is only slightly influenced by the SNR and the peak width of the MR-spectra (2), but strongly depends on the prior knowledge, e.g. on the basisset used. Previous studies have shown, that the use of simulated basis spectra, which account for broad macromolecular components, improves the quality of the LCModel quantification (3). This results in a flat baseline and in reduced Cramér-Rao lower bounds (CRLB). On the other hand, this may systematically affect the metabolite concentrations. We therefore examined the effect of including macromolecular components in the basisset on the LCModel quantification of metabolites in a group of volunteers.

MATERIAL AND METHODS:

Thirteen healthy volunteers were examined on a clinical 1.5 T MR unit (Siemens Symphony), using a single voxel STEAM sequence (TE = 20 ms, TR = 4500 ms, NSA = 96). For each volunteer a voxel was placed in the centrum semiovale and in the white matter of the cerebellum, respectively. For each voxel position one additional spectrum without water suppression (NSA = 8) was acquired. This was used for eddy current correction. The LCModel (Version 6.0) analysis was performed using a basisset acquired at our institute. The spectra were analyzed in the frequency range between 0.7-4.2 ppm. All other LCModel-parameters remained on their default values. In a second step the analyses were repeated, using the default LCModel simulated macromolecular basis spectra in addition to the metabolite basisset.

RESULTS:

The inclusion of simulated macromolecular basisspectra results in a clear but nonuniform change of metabolite concentrations and their corresponding CRLB (Tab.1). This affects not only the metabolite signals that are explicitly superimposed with macromolecular resonances, such as NAA, NAAG, Lactat, Alanin, Glutamin, Glutamat, but also all other metabolites, even if they do not overlap with macromolecular resonances, e.g. Cholin, Taurin, myo-Inositol and scyllo-Inositol. Only the determined Creatin-concentrations are nearly independent from the use of simulated macromolecular model spectra. The most important difference was observed for the NAA+NAAG signal, which significant concentration differences of 14,9 % and 16,3 % and an increase of CRLB using the extended basisset. This is mainly based on the reduced NAAG signal, which is a result of the macromolecular components around 2 ppm (MM20). The use of the extended basisset results further in an significant reduction of Glu-resonances, whereas Gln-resonances increased. We observed also an obvious increase of the Alanin concentration and an strong decrease of Lactat. The total sum of all metabolite signals was 3,9 % and 8,3 % lower. This is due to the additional macromolecular resonances and demonstrates that the basline spline fit alone cannot account completely for macromolecular resonances. However, with our experiments we can also not exclude an partial overestimation of macromolecular resonances using the extended basisset

	Centrum semiovale		Cerebellum	
	Δ C	Δ CRLB	Δ C	Δ CRLB
Creatin	-1,4 %	-7,1 %	1,0 %	-10,0 %**
Choline	-0,3 %	-14,4 %*	2,0 %	-17,2 %**
NAA+NAAG	-16,3 % **	38,2 %	-14,9 % **	64,8 %**
NAA	3,1 % *	-20,0 %*	6,2 % **	-3,9 %
myo-Inositol	1,5 %	-16,0 %**	-3,8 %	-15,4 %**
Glu+Gln	-5,7 %	-20,1 %**	-6,3 %	-24,6 %*
Glutamt (Glu)	-16,7 % **	26,0 %	-11,9 % **	15,9 %
Glutamin (Gln)	17,0 %	-21,9 %	3,5 %	-12,1 %*
Glucose	6,8 %	-40,9 %	-12,6 %	-5,7 %
Alanin	41,5 % *	-20,0 %	88,8 % *	-19,6 %*
scyllo-Inositol	-11,6 %	80,5 %	-8,6 %	2,5 %
GABA	-24,0 % *	46,9 %	-13,6 %	12,0 %
Taurin	-15,7 %	3,6 %	-32,4 % *	18,0 %
NAAG	-75,4 % **	241,8 %	-49,9 % **	419,1 %
Aspartat	41,4 %	43,1 %	16,8 %	-29,4 %
Lactat	-39,8 %	131,8 %*	-75,3 % *	24,3 %

Tab.:1 Relative differences of mean metabolite concentrations and CRLB between LCModel-analysis including and excluding macromolecular components in the basisset (dependent t-test; significance level: *p < 0.05, **p < 0.01).

CONCLUSION:

The additional use of simulated macromolecular components in the LCModel analysis improves the quantification quality, because the majority of the metabolites showed an decrease of CRLB. The obvious changes of the metabolite concentrations demonstrate the influence of the basisset on the quantification. This have to take into account to avoid misinterpretations when comparing metabolite concentrations analysed with different components in the basisset. The simulated macromolecular components have to be validated in pathological MR-spectra.

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