THE EFFECT OF SOFTWARE PROCESSING PIPELINES ON 7T MRS METABOLITE QUANTIFICATION

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Introduction: 1H Magnetic resonance spectroscopy (MRS) can be used to quantify in vivo differences in brain metabolites using a linear combination of model spectra. Commercial, academic and freeware software packages are available which are based on the same model spectra, but use different implementation strategies involving a set of additional parameters that may vary between the tools or sites. Currently, it is not known to what extent the analysis pipeline used to process the MRS data affects the outcomes. To investigate whether metabolite levels of identical MRS scans are influenced by the applied software, we compared two software packages LCModel (Provencher, CA, USA)[1] and NMRWizard, a similar linear combination of model signals software implemented in Matlab[2].

Methods: 46 scans were collected in 23 healthy subjects during two different scan sessions on the same day. 1H-MRS experiments were performed using a semi LASER sequence(TE=30ms, TR=6s, 32Avg, no OVS) on the same 7Tesla whole body MR system (Philiphs,Cleveland,OH,USA). A birdcage transmit head coil was used and driven in dual transmit in combination with a 32 channel receive coil (both Nova Medical, INd., Burlington, MA,USA). Voxels(2x2x2cm^3) were located in the medial prefrontal cortex voxel. Non water suppressed spectra were obtained in order to calculate absolute concentrations of metabolites. Spectral fitting was performed with LCModel and NMRWizard using basissets simulated for the semi LASER sequence. One of the main differences between the two packages was that LCModel used a polynomial order baseline versus no baseline in NMRWizard. To illustrate the impact of the software pipeline, in this study we only report the correlation between the LCModel and NMR wizard of the highest and least overlapping resonances: total NAA, glutamate, total creatine and glutamate concentrations using Spearman regression modelling (R version 3.1.0).

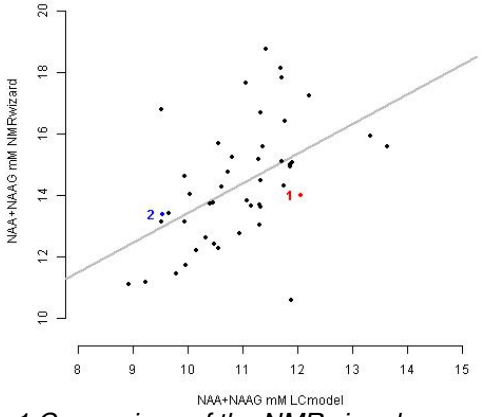

Figure 1 Comparison of the NMRwizard versus LCModel NAA concentration for all 46 scans. The grey line denotes the correlation. The fits of the two labeled scans are displayed in figure 2.

Results and discussion: Correlation (rho) ranged between 0.20 for glutamate (p=0.16) to 0.53 for total NAA (p<0.001, see figure 1). These analyses show a discrepancy between the measured metabolite concentrations between LCModel and NMRWizard, even though the fits are of similar quality (figure 2).This indicates that the processing steps used in the analysis pipeline have a major effect on the measured outcomes. While the origin of the discrepancy can be caused by the many variables included in the fits as well as processing parameters, we also expect differences to derive from the polynomial baseline used by LCModel, as this can vary between subjects (see figure 2B+2D).

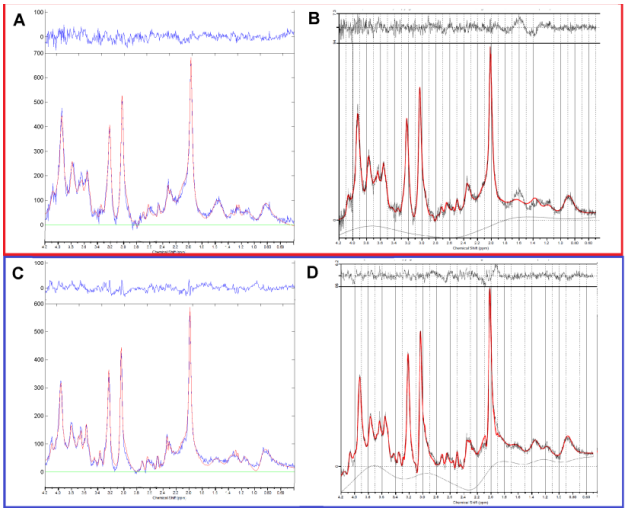

Figure 2 NMRwizard (left) and LCModel (right) fits for two selected subjects.

Conclusion: While absolute quantification of metabolites with ^{1}H-MRS would facilitate group comparisons, it must be realized that the values obtained through model fitting are severely biased by the parameters used. Even accurate fits and low CRLB does not imply accurate quantification. In this work we demonstrated that even for the most prominent signals in MRS obtained at 7T, still a systemic difference and a standard deviation of 20% is obtained by comparing two fitting settings on the same data.

References:

1. Provencher SW. *Estimation of metabolite concentrations from localized in vivo proton NMR spectra.* Magn Reson Med 1993;30(6):672-679.
2. De Graaf R.A. *NMR Processing Software for Spectroscopy, Imaging and Spectroscopic imaging.* 1999.