The Impact of SNR on the Reliability of LCModel and QUEST Quantitation in ^{1}H-MRS

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Introduction: The accuracy and precision of automated spectral quantitation and metabolite identification methods are strongly dependent on the signal-to-noise ratio (SNR). Here, we examine the effect of SNR on the reliability of the frequency-domain LCModel (1) and time-domain QUEST (2) quantification methods for spectra from the human brain.

Methods: Data were collected from healthy adults on a 1.5 T Siemens Magnetom Sonata MRI system. The spectroscopy examinations included STEAM (TE/TM/TR=10/10/5000 ms, VOI~ 6-8 cm^3, NEX=256, 2500 Hz spectral width, and 2048 complex points), a water reference (NEX=8), and a progressive TR T_2 experiment (3,4). Data were processed offline to create a set of 256 spectra representing a running average from 1 to 256 averages (Fig 1). All data were quantified with LCModel and QUEST using the water reference for quantitation. NAA, Glx, Cre, Cho, and mI were identified, and the SNR calculated for each metabolite in the time and the frequency domain. Validity of the noise in the SNR calculations was verified by assessing the linearity of noise vs $1/N^{1/2}$ (N = averages). A running measure of the coefficient of variation (CV) was used to examine the reliability and stability of the measurements.

Results and Discussion: R^2 for linear fits to all noise plots were 0.99 or better, thus anomalies in the concentration plots can be reliably attributed to the spectral models.
NAA and Cr: For these relatively strong signals (Fig. 2), both LCModel and QUEST show strong reliability and stability; however, the running CV indicates that the stability of the fits is better with LCModel. Thus, the number of averages necessary to achieve a reliable fit is lower when quantifying with LCModel as opposed to QUEST.
Cho: Surprisingly, this signal exhibited extremely poor reliability with LCModel for all participants, where increases in SNR and averaging had little effect on the concentration stability. In comparison, the stability with QUEST was much better (Fig. 2).
*mI:* While the stability of fits was very good for both LCModel and QUEST, the running CV measure indicated that QUEST provided slightly more reliable and stable fits and with fewer averages than LCModel.
Glx: For this complex multiplet, the stability of fits was good using QUEST, whereas with LCModel, there appeared to be no direct relationship between SNR and concentration. Thus, Glx is more precisely fit using QUEST instead of LCModel.

Conclusion: Based on the stability of the concentration values, these results indicate that NAA and Cr are best fit with LCModel, while Glx, Cho, and mI are best fit with QUEST. The extremely poor performance of LCModel in quantifying Cho was unexpected, particularly because the Cho 3.23 ppm singlet would appear to be an easily identifiable peak. However, based upon this data and in the absence of pathology - as in this study - LCModel would appear to be completely unreliable for quantifying Cho at 1.5T. This data strongly suggests that most reported Cho concentrations measured at 1.5T are suspect. Finally, this data clearly shows that the reliability of metabolite concentration measurements is not only a function of SNR, but is also a function of the domain, time versus frequency, in which the data is quantified. The ideal quantitation methodology should thus combine time and frequency domain fitting algorithms.

References: (1) Provencher S, Magn Reson Med 1993; 30:672-9. (2) Ratiney H et al., MAGMA 2004; 16:284-96. (3) Knight-Scott J et al, J Magn Reson 2005; 173:169-74.(4) Knight-Scott J, Proceedings of ISMRM 2007, 202.

Figure 1. Data (black) and corresponding fits (red) as a function of SNR, i.e. averaging.
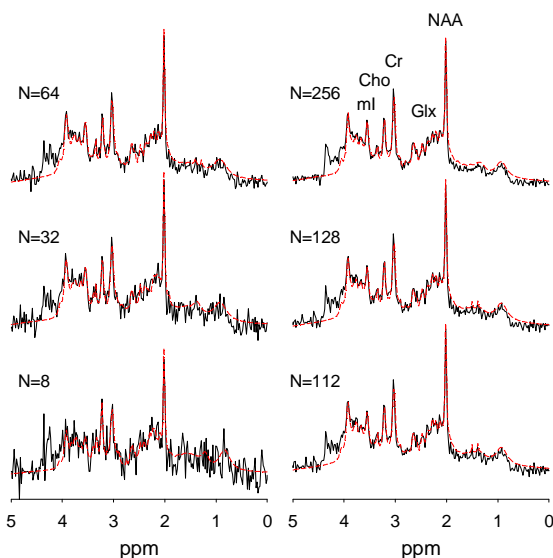
Figure 2. Concentration vs SNR plots for QUEST (A, D) and LCModel (B,E) demonstrate the stability and reliability of the quantitation algorithms for NAA and Cho, while strong similarities with respective concentration vs √N (shown for LCModel) (C,F) prove that the large concentration variations for Cho are a result of the fitting algorithm rather than the SNR calculations.