Detection Strategies at 7 Tesla Using Clinical MRS Pulse Sequences

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Introduction: The contributions of *in vivo* MR spectroscopy as a clinical research tool continue to increase in impact in parallel with increases in static magnetic field. Whereas a handful of methyl groups from abundant molecules such as N-acetylaspartate, creatine, and choline are detectable at 1.5 Tesla, migration to higher fields has made the measurement of less concentrated and coupled resonances more feasible (e.g. GABA and glutamate). However, MRS at high fields e.g. 7 Tesla is challenged by technical problems such as increased inhomogeneities in the static magnetic field and the uniformity and performance of RF pulses. In an effort to contribute to the solution of these problems systematically and comprehensively across the range of detectable metabolites, we have calculated and assembled a database of Cramer Rao Lower Bounds (CRLBs), which enable comparisons and predictions of the performances of systematic and comprehensive variations of PRESS single and multiple echo acquisitions.

Methods: Density matrices were propagated with custom programs (C++ with GAMMA libraries [1]). Spin-systems were taken from Govindaraju et al. [2] and CRLBs were calculated following the expression given in Cavassila [3] and validated with Monte Carlo methods. The spectra were scaled to incorporate transverse relaxation effects across T2's ranging from Cre (T2 = 109 ms) and NAA (T2 = 158 ms) [4] at 7 T. *In vivo* spectra were collected for the optimal echo-time from the anterior cingulate cortex of two healthy volunteers in accordance to Vanderbilt University Institutional Review Board.

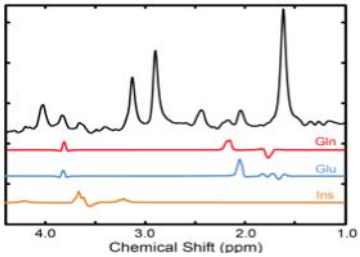

Figure 2. *In vivo* spectrum with 3 spectral bases (Glu, Gln, mI) at the echo time optimum for Gln and Glu (109 ms).

Results and discussion: We find that the trends in CRLBs can be approximately subdivided according to echo-time into 3 phases and further by 3 dominant structural motifs. Measurement precision varies inversely with echo-time to a CRLB peak at ~50 ms for most metabolites. In the second major trend, methylene spins begin to refocus and amino acids (Glu, Gln and GABA) reach a CRLB trough (peak in precision) near 110 ms (Figure 1). CRLBs for inositol compounds (mI and sI) on the other hand increase from 30-50 ms followed by a gradual decrease in CRLB to a trough at 78 ms. Methyl-bearing molecules display the expected T2-dominated CRLBs which increase approximately monotonically and do not impact strategy, but simultaneous and optimal detection for Glu and Gln in conjunction with mI is not feasible at a single echo (Figure 2). For Glu and Gln, Figure 2 illustrates that measurement precision becomes less sensitive to resolution near the turning points (TE > 90 ms) in a regime where mI CRLBs will require increasingly sharp increases in resolution to maintain a constant precision. Two dimensional acquisitions and prior-knowledge fits would be sufficient to ameliorate this condition but are not widely available on clinical systems. In the absence of elaborate editing or multidimensional acquisitions, these results suggest a beneficial and simple strategy available across clinical scanner platforms is to add echoes from the respective minima. Given the small number of trends in echo times and molecular structure, we show that this amounts to combining optimal values for mI and Glu/Gln. Hence, over the clinically relevant range of 30-120 ms (PRESS echo times), 30 and 109 ms should be co-added for maximum combined precision, and, compared to single acquisitions, streamlines the protocol and removes the overhead of starting a new scan.

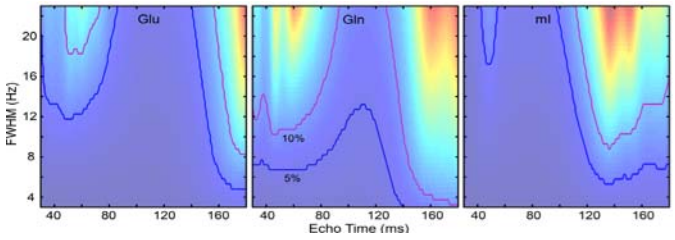

Figure 2. CRLBs of Glu (left), Gln (center), and mI (right) as a function of resolution (FWHM) and echo time at a proton frequency of 300 MHz (7 T). Isolines for 5 and 10% CRLB are shown in blue and purple

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