A systematic approach for chemical quantification in MRSI: methodological considerations

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Purpose: Proton magnetic resonance spectroscopic imaging (MRSI) allows for a tremendous volume of data to be produced in a single scan, as compared to conventional single voxel spectroscopy methods. MRSI data sets, however, can contain thousands of spectra and be very cumbersome to process. In this work we evaluate a proposed systematic approach for chemical quantification in MRSI data sets that is capable of making use of the information contained in the data set to increase regional specificity was well as increase the reliability of the calculated chemical concentrations. We demonstrate the benefits of this method by applying it to quantification of lactate during sodium lactate infusion in healthy adults and comparing to the results from an alternative approach.

Methods: Data from 19 healthy control adults were included in this analysis. Imaging data was acquired on a 1.5 Tesla GE Signa whole-body MR scanner. Prior to subject entry of the MR scan suite, a catheter was inserted by an experienced anesthesiologist. High-resolution axial proton density and T2-weighted MR images covering the whole brain were acquired. These were followed by acquisition of a series of MRSI scans using a proton echo-planar imaging (PEPSI) sequence for a single axial slab that was located at the level of the lateral ventricles. In addition to the acquisition of several non-water suppressed MRSI volumes, a series of water-suppressed scans were acquired with a TE of 144 ms. Three baseline scans were acquired followed by four scans concurrent with intravenous infusion of 0.5 mol/L sodium lactate and then three post-infusion scans. PEPSI slabs were coregistered to the corresponding T2 image set for the each subject and then the PEPSI spectra were inverse Fourier transformed and were peak-aligned and fit with the LCModel software package (Provencher, 1993). Low quality spectra were identified and excluded systematically using SD and FWHM values output from the initial processing with LCModel. For both the water and metabolite data, the LCModel-phased and peak-aligned spectra were averaged in the time domain across the entire slab. An example of the individual and averaged spectra is shown in Figure 1. The average spectrum was then fitted with LCModel to yield metabolite concentration values. For comparison, the chemical concentrations produced by this approach (referred to here as Average Spectrum Analysis, or ASA) were compared to those obtained by simply averaging individual voxel metabolite concentrations from the initial run through LCModel (referred to here as Individual Spectrum Analysis, or ISA). Chemical concentrations were corrected for acquisition parameters and CSF partial volume effects.

Results: The quantified chemical concentrations for all time points averaged across all 19 subjects is shown in Figure 2. Both methods demonstrate a gradual rise in lactate concentration with time, consistent with the timing of the infusion. Average Spectrum-based Analysis, however, results in a lactate concentration that is approximately 50% of that computed with Individual Spectrum-based analysis. Both methods generate NAA concentrations that are both stable over time, and are relatively equivalent. The SD values from the LCModel fits are significantly reduced for Average Spectrum-based analysis compared to Individual Spectrum-based Analysis. Whereas the NAA SD values do not change significantly over time, lactate SD values are decreased at times of increased lactate concentration.

Conclusion: This dynamic lactate infusion study provided an opportunity to demonstrate advantages of using the Average Spectrum Analysis method to measurement of cerebral lactate, which is present in the adult brain at relatively low concentrations and difficult to measure. The results demonstrate that when combining information provided by multiple spectra in MRSI, the methodology used can have a substantial effect on the calculated chemical concentrations for brain chemicals at low abundance, and significant consequences of the interpretation of findings. While this study has focused on analysis from average voxels across the entire PEPSI slab, the ASA approach also can be applied to individual brain regions to retain the information on regional specificity that is contained in the MRSI data. Further work will explore additional benefits of ASA for other applications.
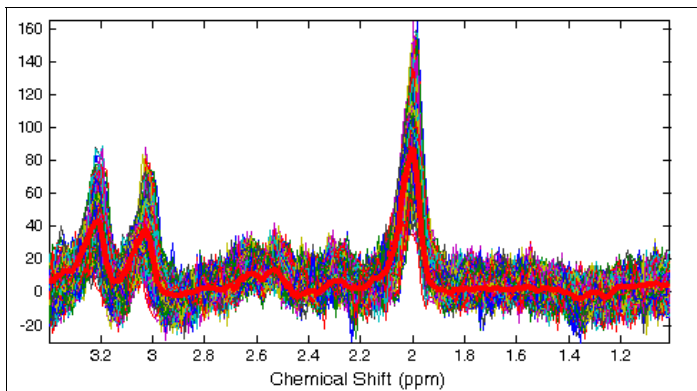

Figure 1. Individual voxel spectra from entire slab after initial processing with LCModel superimposed. The average spectrum for all of the voxels is shown in red.
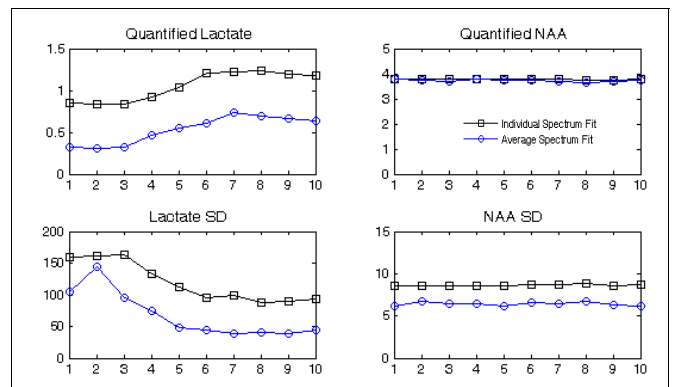

Figure 2. Lactate and NAA concentrations and Cramer-Rao bounds (SD values) for the two methodologies.