Enhancing quantitation precision in multiecho spectroscopic imaging

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Introduction

Magnetic Resonance Spectroscopy Imaging (MRSI) is a useful tool for non-invasive evaluation of *in vivo* tissue. Multi-echo MRSI provides the advantage of simultaneously obtaining information from both the short T2 and long T2 metabolites in a single acquisition.[1] In addition to the intrinsic advantages offered by each data set [higher signal-to-noise ratio (SNR) and measurement of short T2 metabolites for short TE acquisitions; reduced lipid and macromolecular contamination for long TE acquisitions], this multiecho approach to spectroscopic imaging (SI) is useful for measuring the relaxation time T2 of metabolites in various spatial locations of in vivo tissue. Nonetheless, the need for clinically feasible acquisition times as well as T2-imposed SNR limitations at extremely long echo times will require that one or more of the echoes are sampled at a higher rate, ultimately resulting in poorer spectral resolution, lower SNR and truncation artifacts in the spectra. In a previous study from our research lab, we described a novel dual echo (DE) MRSI acquisition in which the short TE (TE=30) data set was sampled with an acquisition bandwidth (BW) that was 5 times the standard acquisition, yet still capable of detecting traumatic brain injury (TBI) induced neurometabolic changes.[2] The aim of the current study is to optimize the precision with which low SNR metabolites in short TE SI data (as measured by DE-MRSI) are quantified. Specifically, the glutamate/glutamine (Glx) Cramer-Rao Lower Bound (CRLB) value generated by LCModel,[3] is minimized using an optimized Lorentz-Gaussian (LG) filter function (Equation 1). Herein, we propose a processing technique that allows the use of the most appropriate filter for the local condition from which the spectra is obtained by optimizing the Lorentz-Gaussian function in a manner that minimizes the CRLB. We compare the results of applying this optimized method to short TE DE-MRSI (high bandwidth, low spectral resolution) data obtained from a human brain to the same data set processed without the optimization scheme. Also, the result of this optimization is compared to an identical data set acquired using a standard single echo (SE) acquisition to show that the linear relationship between both acquisitions is preserved in other metabolites.

$$F_{filter}(t) = e^{+t\nu_L} e^{-t^2\nu_G^2}$$

Equation 1: Lorentz-Gaussian filter function. F_{filter} is the value of the filter function to be multiplied by the time domain signal at the time (t) of the FID; ν_L(Hz) and ν_G(Hz) are the Lorentzian line narrowing and Gaussian line broadening parameters respectively. The filter is optimized on a voxel-wise basis to yield the minimum CRLB for Glx quantitation.

Methods

The DE-MRSI sequence was developed by modification of a vendor supplied standard MRSI sequence. In order to accommodate for the dual acquisition scheme, the short TE echo was sampled with an acquisition BW that is 5 times the standard acquisition. All scans were implemented on a Siemens Tim-Trio 3T MRI scanner using a 12-channel receive only head coil. The DE-MRSI sequence is implemented with scan parameters as follows: TE1 30ms, TE2 270ms, TR 1320ms, BW1 5kHz, BW2 1kHz, FOV = 160 x 160 x106mm, VOI = 106 x 106 x 48mm, interpolated resolution 16x16x8, total acquisition time 7min 40 secs. The full width at half maximum (FWHM) of the water signal within the VOI was 22.6Hz.The standard SE acquisition was implemented with identical parameters but with an acquisition BW of 1kHz. Metabolite quantitation was performed using LCModel[3]. We carried out a voxel-wise minimization of the CRLB by filtering the time domain data using an optimized LG filter function (Equation 1) prior to signal quantitation by LCModel. The optimum ν_L and ν_G parameters for each voxel were determined by applying the filter with every combination of ν_L and ν_G in a step-wise fashion, within the range of 1.2774Hz - 12.774 Hz for both ν_L and ν_G, at intervals of 1.2774Hz. The combination of ν_L and ν_G yielding the lowest Glx CRLB were determined to be the optimum values for any particular voxel.

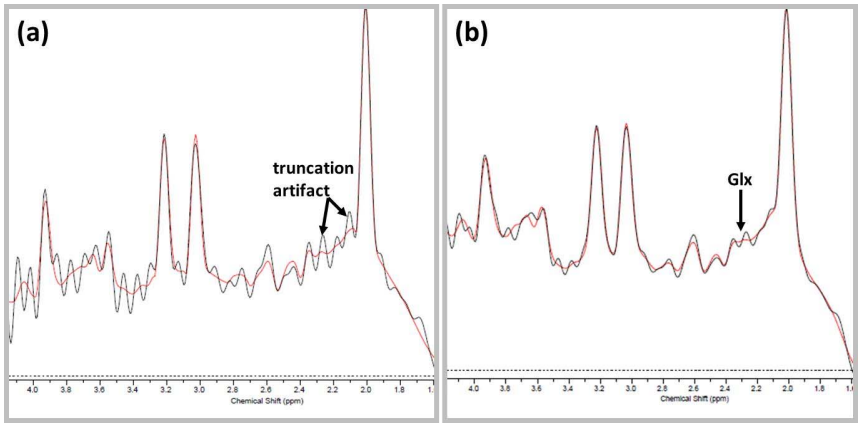

Figure 1: ^{1}H-MRSI spectra from a voxel in human brain. The spectra was acquired from short TE DE-MRSI data processed with- (b) and without (a) the optimized LG filtering method. Processing with the optimized method allows truncation artifacts to be suppressed ultimately leading to more precise quantitation of metabolite signals. In this example, the Glx CRLB was reduced from 35% to 16% after the optimized filter function was applied.

Results

Figure 1 shows the result of applying an optimized LG filter to a single voxel in short TE DE-MRSI data. Truncation artifacts are substantially suppressed allowing more robust quantitation of all metabolites. In particular, the quantitation of the Glx signal went from unreliable (CRLB>20%) to reliable (CRLB<20%) deeming it suitable for spectroscopic analysis. In the overall data, voxel-wise optimization of the CRLB led to an increase in the total number of voxels with reliable Glx quantitation (from 41% of the voxels in the data set before application of the optimized LG filters to 72% of the voxels after filters were applied). Even though the Glx CRLB was used to determine the optimum filter parameters, application of the optimization method either led to a decrease in the CRLB for all metabolites, or left the CRLB unchanged. More so, the linear relationship expected between a standard acquisition and the optimized high BW data is still preserved as shown for NAA/Cre in Figure 2.

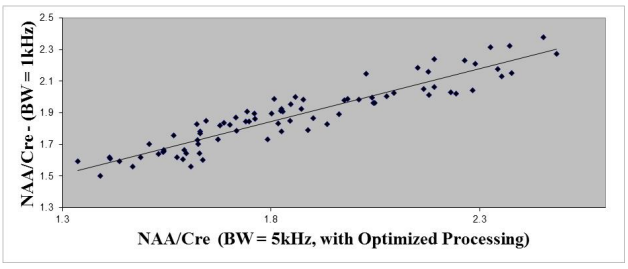

Figure 2. Linear correlation of NAA/Cre values in different voxels of a human brain measured by a standard-MRSI method (BW =1kHz) with NAA/Cre values in the corresponding voxels from optimized low spectral resolution (BW=5kHz) MRSI measurements. r = 0.935, p<<<0.001

Conclusion

We have demonstrated the utility of voxel specific processing of data for accurate quantification of metabolites through adaptive filter methods on a voxel basis in large scale spectroscopic data sets. Future work will include incorporating derivative-free global optimization methods in determining optimum filter parameters.

References: [1] Dreher W. et al., Magn Reson Imaging. 1995;13(5):753-61. **[2]** George E. et al., Proceedings of 21st Annual Meeting of ISMRM (Abstract), Salt Lake City, Utah 2013. Program Number : 2383 **[3]** Provencher SW. NMR Biomed. 2001 Jun;14(4):260-4.

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