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. 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 both metabolites, even though 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. 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, 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.

\[ F_{\text{filter}}(t) = e^{-i\nu_L t} e^{-\frac{t^2}{2\nu_G^2}} \]

Equation 1: Lorentz-Gaussian filter function. \(F_{\text{filter}}\) is the value of the filter function to be multiplied by the time domain signal at the time \(t\) of the FID; \(\nu_L(\text{Hz})\) and \(\nu_G(\text{Hz})\) 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 Gnx 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 x 106mm, VOI = 106 x 106 x 48mm, total acquisition time 7min 40 secs. The full width at half maximum (FWHM) of the water signal within the VOI was 22.6Hz.

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