Quantitative assessment of sensitivity enhancement in short echo time ^{1}H MRSI of the Human Brain at 3T using a spin locking pulse sequence

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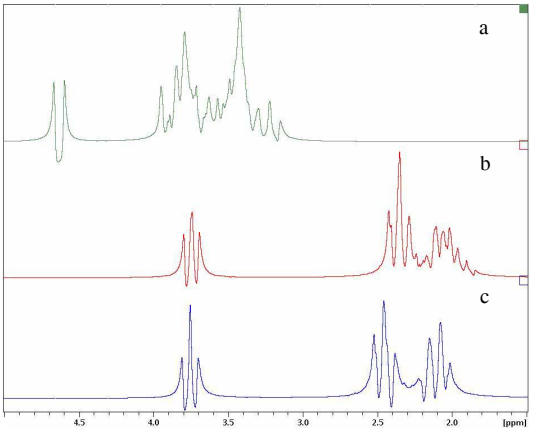
Introduction
Reliable and efficient analysis of MR Spectroscopic Imaging (MRSI) data, especially of ^{1}H MRSI at short echo time, is still challenging. The LCModel method, often used to analyse ^{1}H MR spectra [1], requires the separate measurement of spectra of individual compounds under the specific 'in vivo' experimental conditions. In principle, this can also be achieved by simulation of the spectra of individual compounds (e.g. [2]). Not only avoid these simulations the extensive time for phantom production and measurement, they can also be used to efficiently compare or optimize different sequences for best sensitivity. This work presents a procedure to analyse short echo time ^{1}H MR spectra with simulated model spectra of a number of metabolites, and demonstrates its usefulness in the comparison of human brain data obtained by a conventional PRESS sequence and a semi LASER sequence [3] at 3T. Here we demonstrate that the latter sequence favorably suppresses J modulation of strongly coupled spin systems in a number of metabolites in the brain, such as glutamate, glutamine and glucose, resulting in a more absorptive spectral profile with increased intensity.

Methods
Short echo time MRSI spectra of a healthy volunteer and a phantom have been acquired at 3 Tesla, by a semi LASER spectroscopic imaging pulse sequence that uses a non-adiabatic optimized slice-selective excitation pulse in combination with two couples of adiabatic refocusing pulses to produce a spin echo at an echo time of 30 ms [3]. The spectra are analyzed by LCModel [1]. The basis set is simulated by NMRSIM [4]. Spectral profiles of glycerophosphocholine (GPC), choline (Cho), phosphoryl choline (PC), creatine (Cr), phosphocreatine (PCr), glutamate (Glu), glutamine (Gln), taurine (Tau), myo-inositol (mI), glucose (Glc), n-acetyl-aspartate(glutamate) (NAA(G)), alanine (Ala), GABA, aspartate (Asp), glutatione (GSH) and lactate (Lac) are simulated using the Louiville equation [4,5]. The spectral lines are simulated with 4Hz widths. Both the semi LASER sequence and the PRESS sequence, including shaped RF pulses, are applied to the metabolites in the simulation procedure using an echo-time of 30ms. The spectral profiles of some coupled spin systems like glucose, glutamate and glutamine are compared for sensitivity. A phantom with 100mM glutamine and 50mM glutamate is measured at 37^o Celcius using the semi LASER sequence (TE=30 ms, TR=10s, 8x8 matrix) to validate the simulation of these spins systems. Finally, we show that these simulated basis sets can be used for robust analyses of in vivo MRSI spectra obtained by complex sequences.



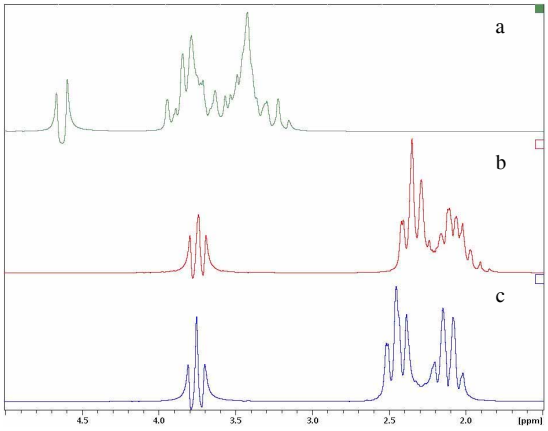


Figure 1: simulated MR spectra of glucose (a), glutamate (b) and glutamine (c) using a conventional PRESS sequence (left) and the semi LASER sequence (right). Note the more absorptive spectral profiles using the semi LASER sequence.

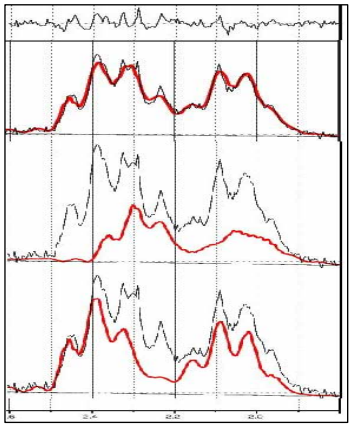


Figure 2: LCModel fit of MRSI results obtained with the semi LASER on a phantom with glutamate and glutamine

Results
The integrals under the simulated curves of glucose, glutamate and glutamine appear 22%, 40% and 33% larger by the semi LASER sequence (figure 1, right) compared to the PRESS sequence (figure 1, left), using the same echo time of 30ms. The LCModel analysis of the Glx phantom shows minimal residual signal (figure 2). The result of the LCModel analysis of the MRSI spectra of the human brain at a typical spatial resolution of 8mm x 8mm x 10mm nominally, show accurate line fitting as the residual signal (fitted spectra subtracted from original signal) consists of noise only (figure 3).

Discussion
The increased intensity of the glucose, glutamate and glutamine signals reveal a 'spin locking' property of the semi LASER pulse sequence. Usage of this sequence significantly increases the sensitivity in the measurement of strongly coupled spin systems. This is of great advantage for the investigation of metabolic diseases, in which metabolites such as glutamate glutamine and glucose, play important roles. The additional signal to noise gain may also be of advantage for the discrimination between glutamate and glutamine. The metabolite concentrations of all brain metabolites are estimated very well and are in agreement with values reported in literature [4]. T1 and T2 relaxation times are not known for all metabolites and therefore are not included in the simulation process, however, extended knowledge about relaxation times may improve the accuracy of the method.

Conclusion
The semi LASER sequence shows a spin locking property that favorably influences SNR of metabolites containing strongly coupled spin systems compared to a PRESS sequence. A relatively simple generation of basis sets of this sequence, including shaped pulses, can improve and stimulate the use of fully automated absolute quantification methods for MRSI at 3T in clinical practice.

References
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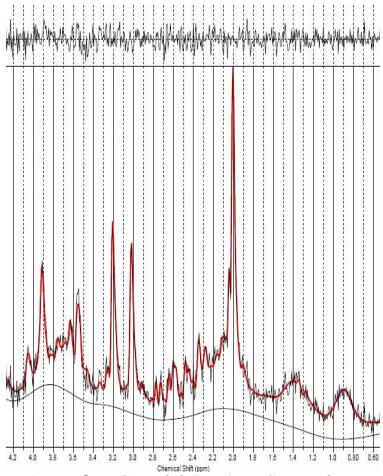

Figure 3: LCModel fit of MRSI results obtained with the semi LASER on a volunteer. Note the absence of signal residues fitted spectra subtracted from original signal (top)