Sampling strategy effects on in vivo 2D J-Resolved spectroscopy quantification

T. Roussel[1], S. Cavassila[1], and H. Ratiney[1]
[1]CREATIS, CNRS UMR 5220, Inserm U630, INSA-Lyon, Université de Lyon 1, Université de Lyon, Villeurbanne, France

Introduction

Two-dimensional (2D) spectroscopy has great potential to unambiguously distinguish metabolites [1,2]. J-Resolved magnetic resonance spectroscopy allows the indirect dimension to be encoded following a various number of echo times. Till now, *in vivo* 2D MRS related studies did not investigate sampling strategies of the indirect dimension as a way of improving the quantification of metabolite concentrations. This paper presents a statistical study carried out on simulated J-PRESS data containing macromolecular contamination. 2D J-Resolved spectroscopy quantification accuracy was evaluated for several sampling strategies and compared to the one obtained in 1D MRS designed with the same acquisition time. *In vivo* 2D quantification following these strategies is shown.

Method

A 2D global fitting procedure employing a non-linear optimization algorithm has been developed [4]. It relies on a strong prior-knowledge consisting of a set of 2D metabolite signals simulated with GAMMA [5]. Unlike the metabolite signals, no a priori knowledge is available for 2D macromolecular signal. Thus, in order to reduce the detrimental macromolecular influence in the fitting procedure, the first data-points were truncated according to an exponential function applied along the echo-time (TE) dimension. Consequently the first 35 data-points (corresponding to 9 ms) were removed at short TE (TE=20ms) while no truncation was applied at long TE (TE>60ms). Furthermore, to alleviate the sensitivity of the optimization procedure to the starting values, multiple random starting values were used.

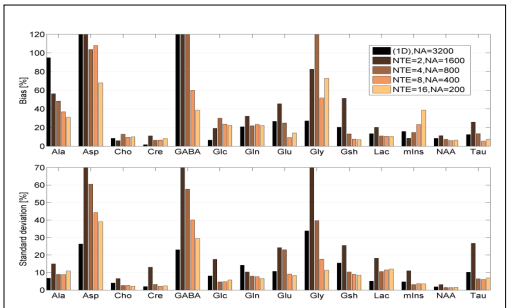

Fig. 1: Monte Carlo study results: Normalized biases and standard deviations of all the estimated metabolite concentrations.

Monte Carlo simulations

The 1D and 2D simulated 7T MRS signals consisted of a sum of 14 metabolite signals with typical *in vivo* amplitudes, linewidths and transverse relaxation times [6,7]. Several realizations of simulated signals were generated using several TE values (equally distributed within 20 to 150ms) and numbers of accumulation (NA). In order to preserve acquisition time and perform a realistic comparison between 1D and 2D quantification, each TE/NA combination was selected in order to maintain a constant acquisition time. A 1D macromolecular signal was acquired *in vivo*, then modelled using an expectation-maximization algorithm [8] and added to the simulated signals with a T2 relaxation time of 25ms. The Monte Carlo study consisted of quantification of the above simulated data added to 200 realizations of Gaussian-distributed noise. For each estimated metabolite concentration, biases and standard deviations were computed and normalized to the actual values (Fig. 1).

In vivo 2D MRS study

The experiment was performed on a horizontal 7T Biospec BRUKER system. The mice were anesthetized by inhalation of isoflurane. The body temperature was maintained at 37°C by warm water circulation. A pressure probe was used to monitor the respiratory cycle. Localized *in vivo* 2D spectroscopy was performed using a J-PRESS sequence (TE Є [20ms;150ms], TR=3s, VAPOR water suppression). A volume transmit coil and a surface coil were used to collect the signal from a 64 µL voxel within the brain of a 3 month old female swiss mouse. Several acquisitions were achieved using different TE/NA combinations and keeping the total scan time fixed to 1h40min. The experiments were conducted according to the procedures approved by the Institutional Animal Care and Ethical Committee of our University.

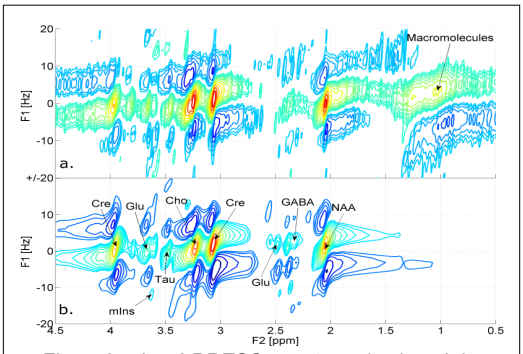

Fig. 2: In vivo J-PRESS spectrum (top) and the corresponding estimated spectrum (bottom).

Results

Biases and standard deviations were generally lower for 2D quantification than for 1D (Fig. 1), especially for coupled metabolites. Accurate and reliable amplitude quantifications were reached for Aspartate, GABA (SD<30%) and Glutamate (SD<10%). The values of standard deviations are in accordance with the Cramér-Rao bounds. Moreover, the increased reliability of the estimation using 2D quantification can mainly be attributed to reduction of biases. *In vivo* 2D MRS signal were quantified with an algorithm execution time less than one minute (Fig. 2).

Discussion/Conclusion

A new fitting algorithm has been developed allowing various studies related to the quantification of *in vivo* 2D J-Resolved acquisitions starting at short echo times. Different precision and accuracy were obtained according to the considered metabolite and the echo times used. By handling macromolecular contribution by simple truncation strategy, a 2D MR spectroscopy experiment leads to a more accurate quantification compared to 1D MRS time equivalent experiment, as demonstrated by a general reduction of bias and standard deviation.

References

[1] Braakman N et al., Magn Reson Med 2008;60:449–456
[2] Méric P et al., MAGMA 2004;17:317-338
[3] Schulte RF and Boesiger P, NMR Biomed 2006;19:255–263
[4] Roussel T, Ratiney H and Cavassila S, ISMRM 2009;2398
[5] Smith SA et al., J Magn Reson 1994;A106:75–105
[6] Cubaldu C et al, CR Chimie 2008;11:442-447
[7] Mlynárik V et al., J Magn Reson 2008;194:163-168
[8] Ratiney H, Bucur A, Cudalbu C, and Cavassila S. ISMRM. 2008;1625