Comparision of Metabolite Correlations in 1D and 2D Quantitative Spectroscopy

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Introduction

In vivo proton spectroscopy is a valuable tool that provides additional knowledge about basic metabolic processes for example in the human brain or important diagnostic information for various diseases. A topic of particular interest is the detection and quantification of neurotransmitters and their precursors such as Glutamine, Glutamate and GABA as well as antioxidants such as GSH and ascorbic acid, whose important role in the pathophysiology of psychiatric and neurological disorders is still not fully understood. Accurate quantification is essential if any conclusion should be drawn from the calculated concentrations of these metabolites. Unfortunately in a commonly used short-echo one-dimensional single voxel spectrum the independent quantification of these strongly coupled and often low concentrated resonances is hampered by the heavy overlap of the individual signals. Two-dimensional spectroscopic sequences like JRESS [1] or L-COSY [2] can be used spread out the multiplet structure of J-coupled spin systems into a second frequency dimension and therefore increase the separation of the different signal contributions. In this work the correlation matrices of different spectroscopic sequences are compared for typical in vivo line widths and spectral separation at 3T. It is shown that 2D spectroscopy experiments lead to better orthogonality of the basis set's components and result in an increased possibility to obtain accurate fits of all the metabolite signals independently.

Materials & Methods

A basis set containing 18 metabolites was simulated using the density matrix formalism [3] for a field strength of 3T. The spectra of all metabolites were calculated for a standard PRESS sequence TE=25ms, a maximum echo sampled JPRESS sequence with a minimum echo time of 25ms and a L-COSY sequence with minimum TE=25ms. The time increment to encode the second dimension of the JPRESS spectra was set to 2ms leading to a bandwidth of 500Hz in the indirect dimension. The F1 encoding step for L-COSY was set to 1ms. All FIDs were apodized with an estimated T_2 time of about 210ms which corresponds to an exponential line broadening of 1.5Hz in both dimensions. Additional Gaussian line broadening of 6Hz was used in the direct dimension to model inhomogeneous line broadening. After LC-Model and ProFit based quantification of simulated spectra that were adjusted to in vivo line width and noise levels, the Fisher information matrices and the corresponding correlation coefficients between the individual components of the basis set were calculated.

Results & Discussion

In the one-dimensional spectrum the correlation between Glutamate and Glutamine resulted in about 75% [Fig. 1] whereas in the jPRESS or L-COSY simulation it decreased to about 20%-30% [Fig. 2, 3]. Furthermore the correlation between Glutamine (Gln) and GABA dropped from 31% to 1% and between Glutamate (Glu) and GABA the correlation was also highly reduced from about 52% to about 20% for the two-dimensional experiments. Even Glycine (Gly) which is usually strongly overlapped by myo-Inositol (mI) might be quantified more accurately in a JPRESS experiment as the correlation between these two metabolites decreased from about 83% to only 23%.

Although there is only a slight difference between both 2D experiments it can easily be seen from the correlation matrices in Fig. 1–3, that using two-dimensional spectroscopic experiments like JPRESS or L-COSY can drastically increase the orthogonality of the basis metabolites when compared to commonly used SV PRESS. As a consequence the possibility of getting reliable, independent concentration estimates also for strongly overlapping metabolite signals like Glutamate, Glutamine and GABA or even Glycine is highly improved.

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[2] M. Albert Thomas et. al., Magnetic Resonance in Medicine 46:58–67, 2001
[3] S. A. Smith et. al., Journal of Magnetic Resonance Series A 106:75–105, 1994

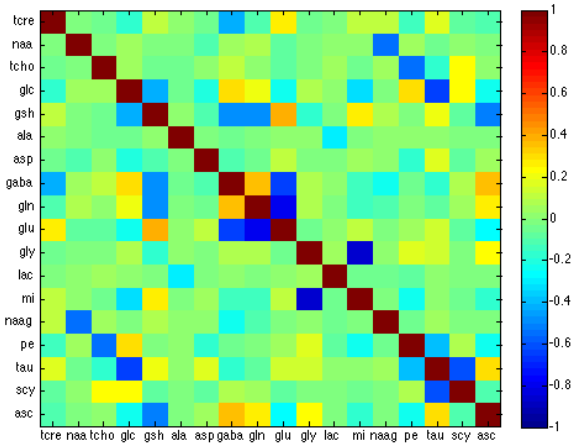

Fig. 1: Metabolite correlation matrix of a commonly used SV PRESS experiment

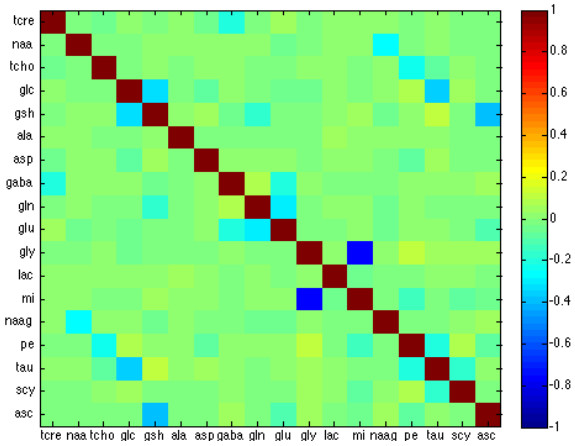

Fig. 2: Metabolite correlation matrix of an L-COSY experiment

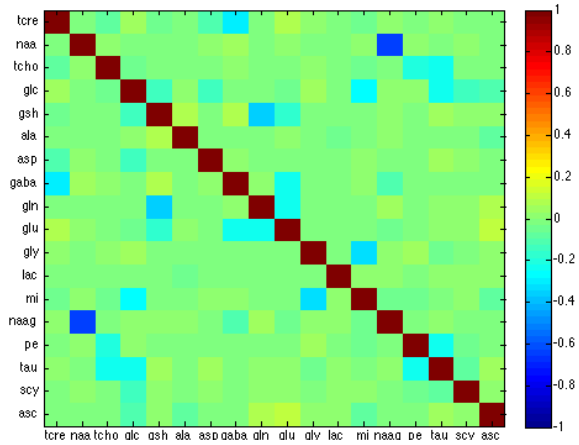

Fig. 3: Metabolite correlation matrix of standard JPRESS experiment