Influence of the background-handling strategy on the metabolite concentration estimates

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Introduction

Localized proton Magnetic Resonance Spectroscopy (MRS) brain signals acquired at short echo-time contain contributions from metabolites, water and a 'background' which mainly originates from macromolecules and lipids. The purpose of the present study was to compare the influence of the background-accommodation strategy on the metabolite concentration estimates. The investigated strategies were: 1) the measured background signal was incorporated in the metabolite basis set; and 2) the background signal was estimated and subtracted from the *in vivo* signal using 'Subtract'-QUEST [1].

Method

Experimental conditions: The experiments were performed on a horizontal 7T Biospec BRUKER system. Healthy adult rats (Sprague-Dawley, 6 animals) were anesthetized by a gas mixture with isofluorane. Acquisitions were performed using a short–echo time PRESS sequence (TE=20ms, bandwidth of 4kHz, 4096 data-points). All first- and second- order shim terms were adjusted using FASTMAP for each volume of interest centered in the hippocampus (left size of the brain, 3.2x2x3.2mm3). The background signals (the metabolite-nulled signal) were measured using an Inversion-Recovery module included prior to the PRESS sequence (Figure 1). The inversion time after the inversion pulse was set to 675ms.

Monte Carlo studies: The influence of the background-accommodation strategy on the metabolite concentration estimates was addressed with the aid of Monte-Carlo studies. A signal mimicking an *in vivo* rat brain signal acquired at 7 Tesla was created. It consists of a weighted sum of eleven *in vitro* measured metabolite signals according to the *in vivo* intensity ratios. A measured *in vivo* background signal was added too. Two different linewidths were chosen (35Hz and 40Hz). A total of 270 realizations of a white Gaussian distributed noise were added to the low-noise signal. Two noise levels were chosen corresponding to signal to noise ratio (SNRs) of 60:1 and 24:1 compared to the Cr amplitude.

Quantifications: The Monte Carlo and *in vivo* signals were processed in the time-domain using the jMRUI software [2]. Removal of residual water components was performed using HLSVD. The metabolite concentrations were estimated with QUEST combined with an *in vitro* metabolite basis-set [3] and with the two mentioned approaches to accommodate the background. When the Subtract-QUEST method was invoked, the background signal was estimated from the first 24 data-points of the signal.

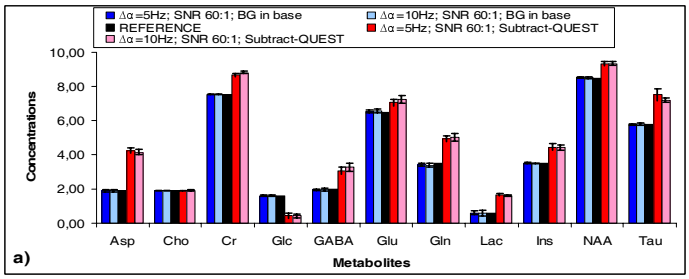

Figure 1: Monte Carlo quantification results. Quantifications were performed with QUEST combined with two approaches to accommodate the background, 1) the measured background signal was incorporated in the metabolite basis set (dark and light blue bars); and 2) the background signal was estimated and subtracted from the *in vivo* signal using 'Subtract'-QUEST (dark and light red bars), for SNR 60:1. The black bars referred to the true metabolite concentration values.

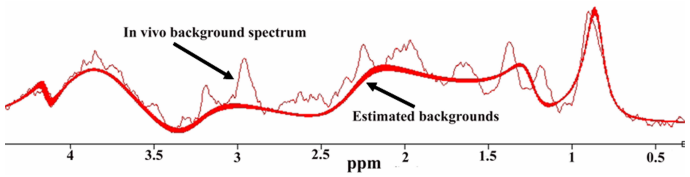

Figure 2: Measured *in vivo* background spectrum superimposed on the estimated background signals for 270 realizations of added noise, obtained using QUEST and the 'Subtract' approach.

Results

For the Monte Carlo studies, the mean of the relevant estimates and the corresponding error bars (±2SD) were computed (Figure 1).

The metabolites were successfully estimated using QUEST combined with the basis set that included the measured *in vivo* background signal, even for low SNRs and large damping factors. Note that the structure of the *Monte Carlo* signal favors the quantification with the first approach over the quantification with Subtract-QUEST because the background signal used in the Monte Carlo signal was the same as the one included in the basis-set.

In Figure 2, the measured *in vivo* background spectrum is superimposed on all the 270 estimated background spectra. The main resonances of the background were well identified. However, all the estimated background spectra were underestimated around 2, 3 and 3.2 ppm.

For the *in vivo* study, nine metabolites were well identified using the two approaches. The concentration estimates were consistent with the values from the literature. The concentration estimates with the first approach were below those obtained with Subtract-QUEST. Indeed, the presence of residual contribution of metabolite signals with short T_1 in the measured background led to an underestimation of metabolite concentration estimates. The observed underestimation of the background component using Subtract-QUEST led to an overestimation of the metabolite estimates.

Conclusions

In conclusion, the two approaches considered in this study to accommodate the background present advantages and drawbacks:

1) The measured *in vivo* background provides strong prior knowledge to the fitting algorithm. This strategy needs a longer acquisition time.
2) The background estimates using Subtract-QUEST depends on the chosen number of truncated data-points. An automatic and robust way to select the number of truncated data-points and spectral components used for background modelling is in progress [4]. Also we point out that the main advantage of the 'Subtract' approach is that it obviates repeating experimental work needed for acquiring the *in vivo* background signal.

References

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