Time-Domain Fitting of ^{1}H-MR Spectra of the Human Brain: A Model-Free Integration of the Macromolecular Baseline

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Quantification of short-TE ^{1}H-MR spectra requires accounting for strong baseline contributions, which originate from residual water, macromolecules and lipids. In this study, we present a novel time-domain estimate for broad background signals, which parameterises the baseline as a model-free signal of finite duration. Our approach can easily be integrated into time-domain linear combination model fitting, which therefore benefits from all advantages of modelling in this domain such as handling of truncation points, easy model parameterisation, and no computational burden for FFT. Quantification of simulated and short-TE in-vivo data demonstrates reliable modelling of metabolites and macromolecules.

INTRODUCTION

Various baseline representations have been incorporated into linear combination model fitting to quantify spectra with broad background contributions. Typically, respective contributions are modelled with the help of splines, wavelets, Voigt lines, or experimentally-defined model spectra [1-3]. In the present study, we describe the baseline as a time signal of finite duration.

METHODS

Macromolecules have T_1 and T_2 values significantly shorter than metabolites [4]. To account for the fast signal decay of such components, we use a finite baseline model of length t_B. In this model, the baseline is parameterised in the time-domain with the help of an extra set of complex parameters, where each parameter describes a time-domain point of the baseline. No further restrictions are imposed.

Unlike reference [1], we model the signal in the time-domain as a sum of Gaussian metabolite signals and the baseline estimate. Thus, the proposed method benefits from all advantages of modelling in this domain such as handling of truncation points, easy model parameterisation, and no computational burden for FFT. The metabolites are represented as simulated signals [5], using a priori knowledge of the metabolites [6]. A least square fit-procedure optimises all fit parameters simultaneously.

The maximal frequency-domain curvature, which can be modelled with our baseline estimate, is limited by the time-constraint. The corresponding maximal spectral full width at half maximum, $FWHM_{max}$, is determined over the associated spectral sinc-function, i.e. $FWHM_{max} \sim (2\ t_B)^{-1}$. Based on published T_2 values [4], we use a baseline length t_B of 30 ms, corresponding to a $FWHM_{max}$ of 17 Hz.

DATA

Simulated data were generated by modelling Gaussian signals representing singlet resonances of NAA, creatine (Cr) and choline (Cho), with the addition of a large baseline, which consisted mainly of lipids. Measured data of brain regions were acquired on commercial Siemens 1.5 T scanners, using CSI and SVS sequences (SE, TR/TE = 1500/30 ms). The basis set for quantification of the in-vivo data comprised: alanine (Ala), aspartate (Asp), Cho, phosphocholine (PCho), Cr, phosphocreatine (PCr), GABA, glucose (Glc), glutamate (Glu), glutamine (Gln), myo-inositol (μIns), scyllo-inositol (sIns), NAA, NAAG, taurine (Tau) and water.

RESULTS & DISCUSSION

Fig. 1 indicates excellent agreement between the simulated data and the fit results. Correct separation between the metabolite resonances and the underlying baseline is obtained. Stronger varying background signals may be modelled incorrectly if the baseline representation is not sufficiently extensive as discussed above.

Similarly, the quantification of in-vivo data yields realistic and accurate results (Fig. 2). The fitted baseline displays the specific distribution of measured macromolecular baselines [4]. However, it should be noted that in CSI-data, the baseline model must cope with water residuals of the order of the metabolite concentrations and the algorithm occasionally computes inadequate spectral baseline rolls. As the absorption spectra of such baseline estimates reveal negative values in the metabolite range, such results can be identified and discarded. In addition, these situations can be circumvented with the implementation of optimised water suppression during the acquisition, dedicated water removal as a preprocessing step, or a refined modelling procedure.

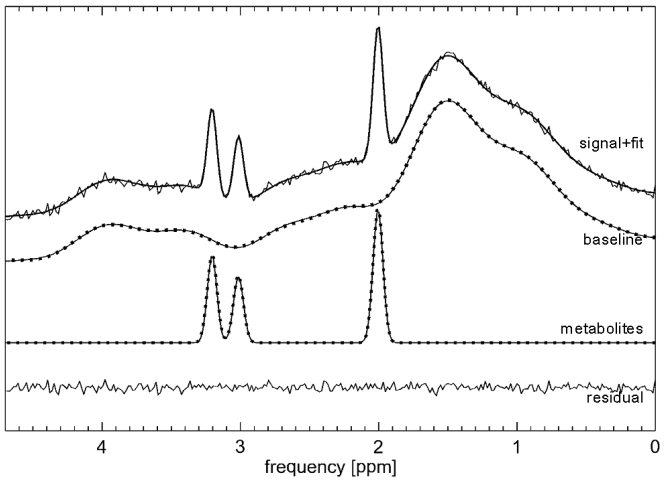

Fig. 1: Results for simulated data (top to bottom): the simulated spectrum overlaid by the fit result (thicker line); the simulated (dashed line), and the fitted baseline (solid line); the simulated (dashed line), and the fitted metabolite signal (solid line); and the residual of the fit. (t_B = 30 ms)

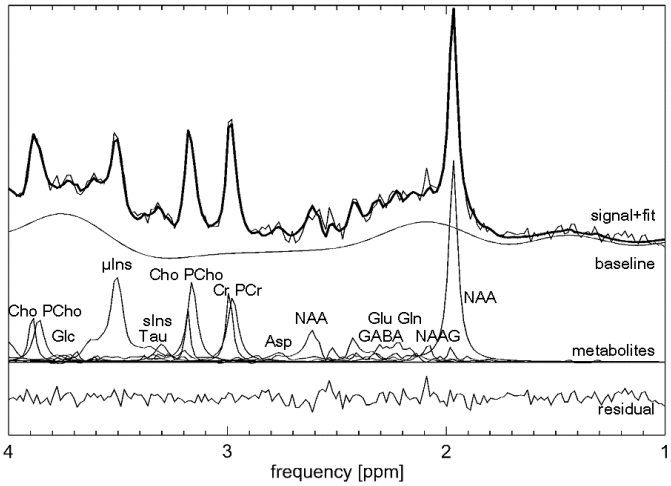

Fig. 2: Results of a human brain SVS spectrum (TR/TE = 1500/30 ms, voxel-size = 8 cm^3), from top to bottom: the acquired spectrum overlaid by the fit result (thicker line); the fitted baseline; the fitted individual metabolite signals; and the residual of the fit. (t_B = 30 ms)

CONCLUSIONS

Incorporation of a time-finite baseline estimate into a parameterised metabolite fit yields robust time-domain quantification of short-TE in-vivo data. As the baseline estimate can handle various broad resonances, it can easily be extended to analyse spectra from other tissues, e.g. prostate data. With respect to higher fields, the concept of time-finite baseline is very promising, as the decay function of the macromolecular signals is further shortened due to reduced T_2 values.

LITERATURE

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