# Automated Model Fitting of *in vivo* $^1$H-MR Spectroscopic Imaging data of the Human Prostate

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## Introduction

Clinical prostate data has been primarily quantified by simple integration or line fitting [1, 2]. However, prostate data contains citrate, a strongly coupled spin system, which pattern cannot always be accounted for by simple integration. Model fitting provides the possibility to describe the citrate pattern appropriately, but has been mainly used for brain data. In this study, we transfer model fitting to clinical prostate data and integrate it into an automated and robust quantification procedure of 3D MR spectroscopic imaging (MRSI) data.

## Materials and methods

Model fitting is based on using concise model patterns for the metabolite signals. In this study, model signals are generated by simulation [3], using a priori knowledge of MR specific properties as chemical shifts and coupling constants of the metabolites [4, 5]. This allows for the flexible and precise representation of the citrate signal, which pattern varies significantly with respect to field strength and sequence timing. Based on the simulated model signals, the metabolite signals of the prostate are modelled in the time-domain as a linear combination of Gaussian signals. Additional broad background signals are accounted for by a baseline estimate, which involves truncation of the first data points of the time signal.

Prostate data is furthermore characterized by a low signal to noise ratio and relatively broad line widths due to shimming difficulties in this part of the body. It also may contain spurious interfering lipid and water signals and $B_0$ shifts, which all hamper its automated quantification. To allow for its robust and automatic quantification, an assumption-free identification of the prominent peaks in the spectrum is realized, from which precise initial starting values of the fit parameters are derived automatically. Therefore no pre-processing or user interaction is required and a fully automated processing is guarantied. Our quantification procedure is denoted as PRISMA (prior knowledge based modelling for spectroscopic magnetic resonance applications).

*In vivo* data of patients, covering the whole prostate gland, were acquired on Siemens 1.5 T and 3.0 T scanners, using 3D-MRSI PRESS sequences [6]. For 1.5 T the typical echo time of 120 ms was used, at 3 T we chose an echo time of 145 ms. Both result in a mainly upright citrate spectrum. The basis set for quantification of the *in vivo* data comprised: phosphocholine (Cho), creatine (Cr) and citrate (Ci). Cho and Cr were modelled with a common line width.

## Results and discussion

Fig. 1 shows PRISMA quantification results of *in vivo* prostate data, measured under different experimental settings at 1.5 and 3 T. With the help of the model signals the citrate signal can be described satisfactory in the fit, as can be seen at the low residual around 2.6 ppm. Nevertheless, small deviations still exist which might be due to simplification made in the simulation. The signals of Cho and Cr partly overlap (b.), but are modelled appropriately by the common line width. The fact, that all voxels of the 3D data set, which contain substantial signal intensities, are successfully processed by PRISMA, demonstrates the robustness of the overall fitting procedure. This holds also for data with minor lipid contamination (upper row in a.). Only voxels, which comprise major lipid signal contamination, i.e. large overlap between lipid and citrate signals, cannot be handled correctly by the described procedure. This limitation might be overcome by integration of a HLSVD filter to suppress the lipid signals.

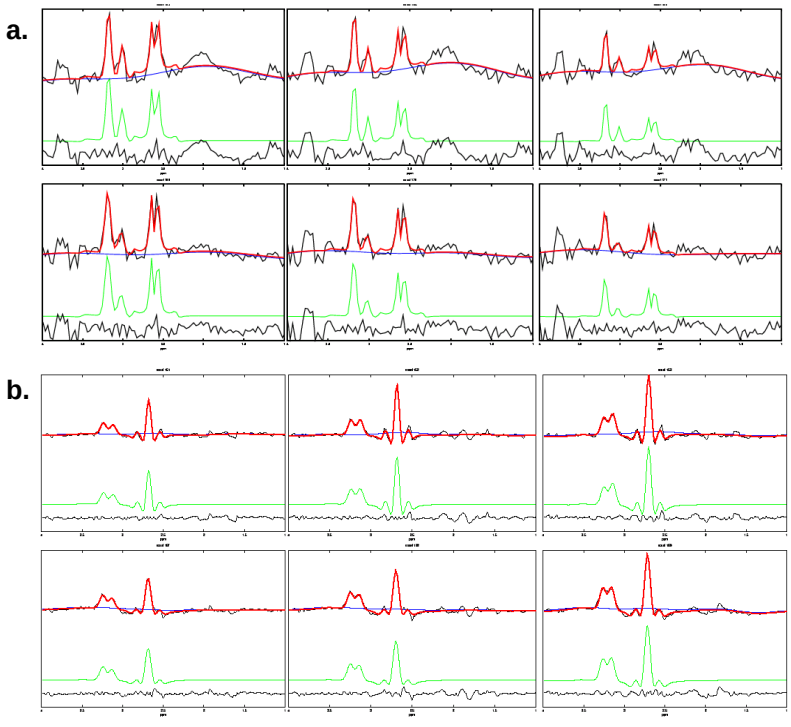


Fig. 1: PRISMA fit of prostate data at different field strengths. Sections of 3D MRSI data sets are displayed: a) 1.5 T, TE 120 ms, b) 3 T, TE 145 ms. For each voxel are shown, from top to bottom: measured spectrum (black) overlaid with the fit (red) and baseline (blue), metabolite fit (green), residual between data and fit (black).

## Conclusions

*In vivo* 3D-MRSI data of the prostate can be quantified robustly and reliably by automated model fitting. The use of simulated model signals enables the easy and flexible adaptation to quantify data from various sequence timings and field strengths. Hence the presented fitting procedure provides a promising tool in quantifying prostate spectroscopy data and helps to facilitate the development of new sequence timings to optimize the MRS examination of the prostate at higher fields.

## Literature

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