Subspace-based MRS Data Quantitation of Multiplets using Prior Knowledge

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Introduction

Automatic and accurate quantitation of MRS signals is an essential step before converting the estimated signal parameters into biochemical quantities (concentration, pH). Many time-domain algorithms for parameter estimation have been developed, in which the MRS signals are modeled as the sum of exponentially damped complex sinusoids. We focus on subspace-based methods. They directly estimate the model parameters by means of robust linear algebra tools, such as QR decomposition and Singular Value Decomposition (SVD), and can be fully automated, therefore requiring minimal user interaction. However, they suffer from a serious drawback: they allow little inclusion of biochemical prior knowledge about the model parameters, which is important for resolution and accuracy.

A well known subspace-based method is HTLS [1], in which the noisy signal is arranged into a Hankel matrix. By truncating the SVD of the Hankel matrix appropriately, a "signal" subspace and a "noise" subspace are computed and the parameter information is extracted from the "signal" subspace. More efficient and accurate subspace-based methods have been developed by incorporating different types of prior knowledge (PK) into HTLS: known frequency and damping of some exponentials, resulting in HTLSPK(fd) [2]; known frequency and phase of some exponentials, resulting in HTLSPK(fp) [3]; known frequency difference between doublet components and equal damping factors, resulting in HTLSPK(Δfd_{eq}) [4]. Here a new subspace-based method for parameter estimation is presented: KNOB-SVD (Knowledge Based SVD) and its improved variant KNOB-TLS [5, 6]. Extensive simulation and in vivo studies show that KNOB-SVD/TLS outperforms the aforementioned HTLS-based methods in terms of robustness and accuracy.

Method

KNOB-SVD/TLS allows the inclusion of significantly more prior knowledge in MRS data quantitation than the HTLS-based methods. More precisely, we assume as prior knowledge that the parameters of the components within a multiplet (e.g. the ATP complex in ^{31}P MRS or the lactate doublet in ^{1}H MRS) satisfy the following relations: the amplitudes are equal and unknown, the phases are equal and unknown, the damping factors are equal and unknown and the frequency difference between the individual resonances is known.

Results and conclusion

The proposed method was applied to simulated as well as in vivo ^{31}P signals measured in the brain and calf muscle, respectively, of healthy humans. The simulation results show that KNOB-SVD/TLS is much more robust than HTLS and HTLSPK(Δfd_{eq}), see Fig.1. The robustness is evaluated by computing the success rate, i.e. the number of times, out of the total number of simulation runs, each method is able to resolve the signal peaks within specific frequency intervals lying symmetrically around the true frequencies of the peaks. Moreover, the simulation and in vivo studies show that KNOB-SVD/TLS outperforms the above mentioned HTLS-based methods in terms of accuracy, as shown in Fig. 2.

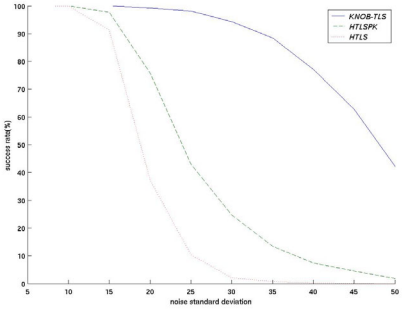

Fig. 1 Success rate as a function of the noise standard deviation.

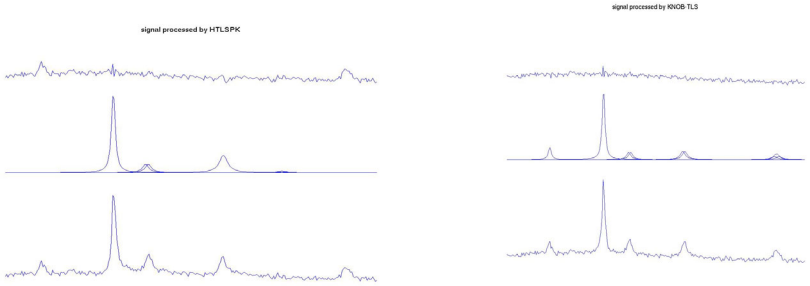

Fig. 2 Bottom: real part of the original in vivo ^{31}P signal; middle: real part of the spectrum of the the individual peaks estimated by HTLSPK(Δfd_{eq}) (left) and KNOB-TLS (right); top: real part of the residual signal spectrum after estimation with HTLSPK(Δfd_{eq}) (left) and KNOB-TLS (right).

References

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