

Time Domain Analysis of SSFP based Proton SI Data using the Matrix Pencil Method

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Introduction

Various pulse sequences for proton spectroscopic imaging (SI) based on the condition of steady-state free precession (SSFP) have been proposed and implemented on a 4.7T animal scanner [1] and are currently transferred onto a 3T head scanner. While their high signal-to-noise ratio (SNR) per unit measurement time and their short minimum measurement time enables examinations with high spatial and temporal resolution, the achievable spectral resolution is intrinsically limited with conventional Fourier transform (FT) because of the rather short acquisition time. Different to well-established approaches such as LC-Model [2] or AMARES [3] a standard model for the analysis of SSFP based proton SI data is yet unknown. Therefore, this work examines the improvement on spectral resolution when a time domain fitting procedure based on the Matrix Pencil Method (MPM) is used instead of conventional FT.

Conventional spectral estimation of NMR data is based on the Fourier transform, which decomposes the time series into a sum of undamped sinusoidal oscillations. However, Fourier transformation of signals that are truncated leads to well-known spectral distortions. Besides, there is no built-in mechanism for noise suppression. The linear nature of FT implies that reducing these problems respectively improving apparent resolution (e.g. by apodization) can only be done at the expense of spectral resolution and/or sensitivity. In general, the goal of spectral estimation is to obtain an estimate of the frequency response function of the originating spin system from the measured signal. The quality of spectral estimation is often improved by incorporating further information into the signal model. This is conventionally done by assuming that the signal can be decomposed into a set of exponentially damped oscillations. The so-called matrix pencil method (MPM, [4-6]) locates the signal poles directly by solving a generalized eigenvalue problem. A potential difficulty applying the matrix pencil in practice is the ambiguity to assess the precise number of signal components. Here, the number of signal components is determined based on information theory (IT) for model order selection [7] by means of calculating the so-called minimum description length (MDL, [8,9]).

Materials and Methods

A number of pulse sequences for proton SI using the condition of steady-state free precession exist already on a 4.7T NMR imaging system (Bruker, Ettlingen, Germany) [1]. In contrast to the well-known TRUE-FISP [10] sequence, which aims at the coherent superposition of the FID-like signal S1 and the echo-like signal S2, the proposed sequences acquire either the S1- or the S2-signal to avoid off-resonance effects. In this work data acquired with the S2-variant (termed spectroscopic CE-FAST [11]) are reconstructed using the standard FT with optimized apodization functions and compared to the MPM-based reconstruction scheme.

Phantom measurements were carried out on spheres (38mm i.d.) filled with an aqueous solution of creatine (tCr, 20mM) and choline (Cho, 80mM). In vivo measurements were recorded on healthy female Wistar rats. 4D data sets (three spatial and one spectral dimension) are reconstructed using the Interactive Data Language IDL (Research Systems, Inc., Boulder, USA). The spatial information is retrieved by FT of the spatial components of k-space. Thereafter, the spectral dimension is reconstructed by optimized FT (apodization and zero-filling) and compared to the parameter estimation result based on the MPM algorithm (written in C).

Results and Discussion

Fig.1 compares the spectral resolution of the FT based spectral reconstruction and the MPM reconstruction as a function of the length of the acquisition window for various SNR (data are simulated with a typical spectral width of 5kHz). The spectral resolution for FT reconstruction is determined as the sum of the inverse of the acquisition length and the natural linewidth (10Hz) of the resonances. The spectral resolution obtained with the MPM algorithm is determined by the minimum difference of two separated spectral lines with a linewidth of 10Hz. Due to the advanced signal model used in the Matrix Pencil approach the spectral resolution is higher than in the FT based reconstruction, especially if time domain data with high SNR are reconstructed, since MPM is a non-linear technique in contrast to FT.

Fig.2 compares in vivo SI data from a healthy rat brain obtained by spectral decomposition of the time domain signal via the MPM and FT processing. MPM allows identification and separation of resonances with higher accuracy than the FT approach (see separation of Cr/Cho resonances, denoted **c** and **d** in Figure 2).

Conclusion

By use of the proposed Matrix Pencil Method the limited spectral resolution of SSFP based proton SI measurements due to the length of the acquisition window can be improved at the expense of reasonable computational complexity. This will be a prerequisite for a completely automated signal processing and quantification algorithm for SSFP based proton SI.

References

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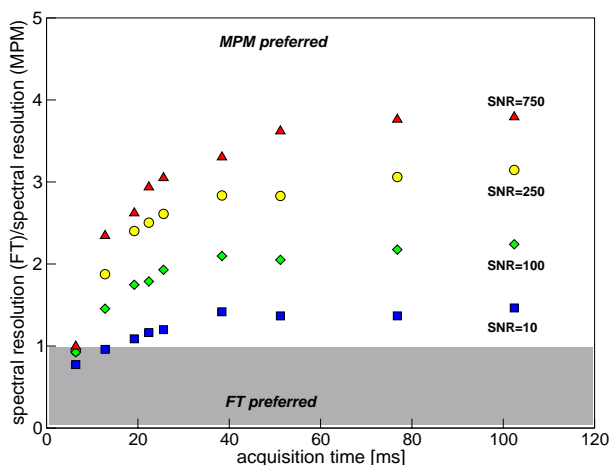


Figure 1: Theoretical evaluation of accessible spectral resolution with MPM compared to FT for typical acquisition times in SSFP based proton SI (based on synthesized data with a sampling rate of 5kHz)

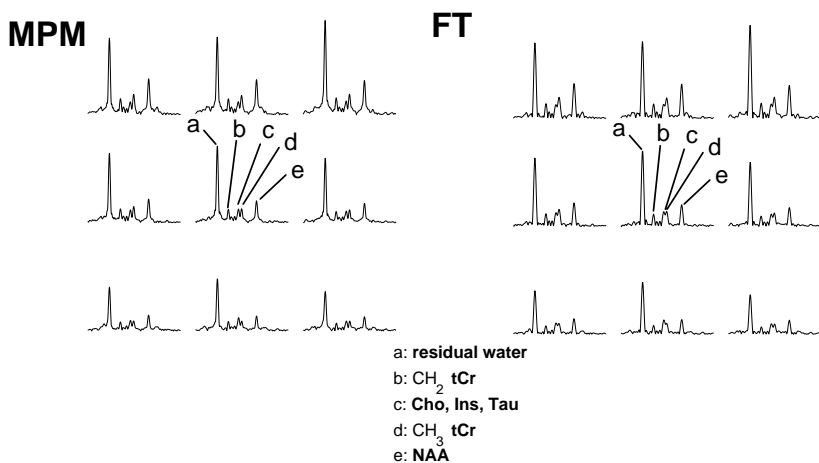


Figure 2: in vivo SI spectra (healthy rat brain) processed via MPM and FT (spectral range 6.3-0.0ppm, $t_{ACQ}=51.2ms$)