Postprocessing of Spectroscopic Imaging Data with Incomplete k-Space Sampling Using a Maximum Entropy Method

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Introduction: Minimum data acquisition techniques are of crucial interest for fast MRI as well as for fast spectroscopic imaging (SI) [1]. They may help to further reduce the minimum total measurement time T_{min}, to avoid truncation artifacts, and to enable non-uniform k-space sampling. Specific improvements can be expected for UFLARE [2], RARE [3] and SSFP based fast ^{1}H SI [4]. A reduced k_ω-interval allows shorter t_e times for spectroscopic U-FLARE or RARE, which can help to increase the SNR and to optimize t_e with respect to J-coupled resonances. Shorter acquisition times in SSFP based fast SI will shorten TR values resulting in higher SNR_t. values. Recently, the number of k_ω steps in spectroscopic U-FLARE was minimized by extensive use of a priori knowledge in the adjusted phase encoding (APE) method. [5] The matrix pencil method assuming exponentially decaying signals in the time domain (TD) was applied to incomplete data measured by spectroscopic RARE or SSFP based fast SI [6,7]. In this study, we used a maximum entropy method (MEM) [8-10] because it requires no a priori knowledge on the measured data. MEM was used to reconstruct or extrapolate simulated and measured fast SI data detected as echo-like signals in k_ω.

Method: Although MEM has been employed in various fields of image or spectrum reconstruction including in NMR spectroscopy (e.g., [8-10]), it almost disappeared from in vivo NMR, mainly because its potential was unrealistically overestimated e. g. claiming simultaneous improvements of resolution and sensitivity. Furthermore, the limited use for MRI and inherent nonlinear amplitude errors were put forward [11,12]. However, MEM can be advantageous for processing incomplete spectroscopic data. If a reduced number of data points along k_ω is acquired either the spectra can be reconstructed or the missing TD data can be are extrapolated by MEM, both with reduced truncation artifacts. In the used MEM version, the entropy $S = - \Sigma_{J=1,N} f_j \log(f_j/m_j)$ of a spectrum f is maximized under the constraint C_1: $\chi^2 = \Sigma_{keK} (F_k-D_k)^2/\sigma^2 < M + a_1 M^{1/2}$ where K denotes the set of M measured data points, F_k the elements of the inverse FT of f, D_k the (used) measured data along k_ω (transformed from complex- to real-valued data) and σ the standard deviation of noise. The parameter a_1 represents a chosen confidence level. As no a priori knowledge was used, m_j was constant. Optionally, another constraint was applied which ensures that F_k-D_k is within statistically reasonable limits: C_2: $|F_k-D_k| < a_2 \sigma$, $\forall$ keK. Thus, MEM determines one spectrum out of all spectra which are statistically compatible with the measured data. Since maximum entropy corresponds to minimum information content, not only noise is suppressed in MEM spectra but also truncation artifacts are reduced. However, MEM also tends to suppress small signals. Therefore, a correction procedure [13] was applied before using the MEM data for extrapolating the measured TD data.

Experimental: The MEM algorithm was implemented using FORTRAN95 (g95). It was tested on simulated echo-like TD data superimposed by Gaussian noise. Then it was applied to spectroscopic RARE data measured on a rat brain in vivo. Typically 96 k_ω steps are used in spectroscopic RARE. Therefore, it was evaluated how MEM reconstruction or extrapolation may improve the data reconstruction if only 32-64 k_ω steps (symmetric around k_ω=0) are performed. All measurements were acquired on a 4.7T Biospec system (Bruker, Germany) using standard parameters [3], in particular a nominal voxel size of $3.0*1.5^2$ mm^3, TR=1.9 s, one accumulation per k_ω step and t_e=136 ms.

Results and Discussion: Fig.1 shows an example for simulated data (7 signals (frequency in ppm, relative amplitude): (4.7, 2.0), (3.62, 1.0), (3.44, 1.0), (3.2, 2.5), (3.0, 3.0), (2.36, 1.5), (2.0, 5.0) with only 64 k_ω values (SW=899 Hz). The spectra were reconstructed with 1K data points by (a) FT without apodization, (b) FT with cosine apodization, (c) MEM, (d) FT of the measured data extrapolated by MEM TD data. It is obvious that truncation error (leading to sinc-wiggles and linebroadening, cf. Fig.1a) can be reduced by using MEM for spectrum reconstruction or data extrapolation of the TD data, while apodization leads to considerable linebroadening (cf. Fig1b). Fig.2 shows similar results for measured in vivo data of one voxel taken from an SI matrix. The number of k_ω-steps was reduced to 40. The separation between the total choline and the total creatine signal is improved by use of MEM, while noise (cf. Fig.2c) and/or sinc-wiggles (cf. Fig.2c,d) are suppressed. By this means, minimum data reconstruction improved the spectrum quality for SI data acquired with a reduced number of k_ω steps. This may be used to further reduce T_{min} or to perform more accumulation for the central part of k-space which will improve the SNR.

Conclusion: MEM is a robust tool to improve the reconstruction of SI data with incomplete sampling along k_ω requiring neither prior knowledge nor user interaction.

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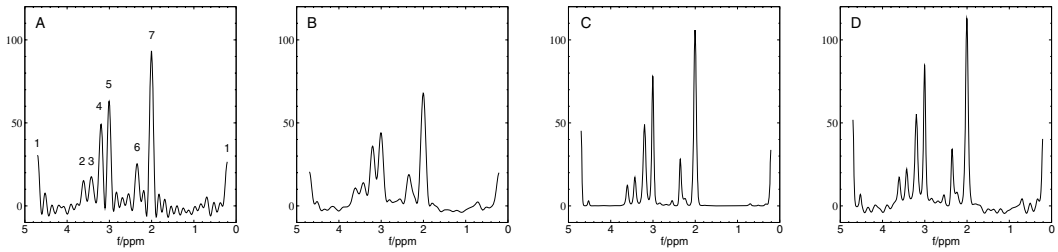

Fig.1: Spectra from simulated data: (a) FT without apodization, (b) FT with cosine apodization, (c) MEM spectrum, (d) FT of measured + MEM extrapolated TD data.

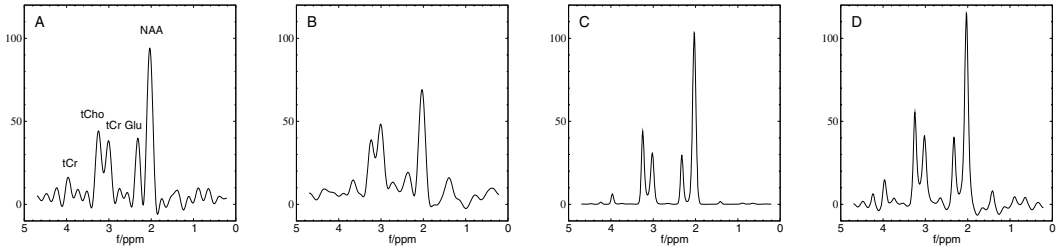

Fig.2: In vivo spectr. RARE spectra: (a) FT without apodization, (b) FT with cosine apodization, (c) MEM spectrum, (d) FT of measured + MEM extrapolated TD data.