MRS data quantification through the KBDM: reducing the effect of noise by using multiple signal truncations

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TARGET AUDIENCE: MR physicists, MR spectroscopists and clinicians.

PURPOSE: To describe and evaluate a magnetic resonance spectroscopy (MRS) deconvolution method that can be used for quantification of clinical MRS data.

INTRODUCTION: The Fourier transform (FT) formalism is a powerful mathematical tool for a wide range of applications, including the spectral analysis of MRS signals. The quantification can be done by employing fitting algorithms using an adequate basis composed of model functions, such as, in the frequency domain, Lorentzian, Gaussian or Voigt functions. However, the quantification process of MRS data can be tricky, especially when overlapping peaks are found. This is particularly critical in *in vivo* MRS and is a well-known confounder for proper quantification of selected spectral peaks. As an alternative to FT-based spectral analysis, the solution of harmonic inversion problemusing Lorentzian model functions through the Krylov Basis Diagonalization Method (KBDM) has already shown its potential in the MR field[1-4]. This method is a promising tool that can provide complimentary information to the well-established FT techniques, especially when overlapping peaks are present, and is being studied in our group with the purpose of establishing an alternative approach for processing clinical MRS data[4,5]. A major concern related to the feasibility of clinical MRS data processing using KBDM is the noise level commonly present in *in vivo* data since the method accuracy appears to be correlated to the signal-to-noise ratio (SNR). Thus, the main goal of this work is to develop a strategy to reduce noise impact to enable the method to be used in clinical MRS data processing.

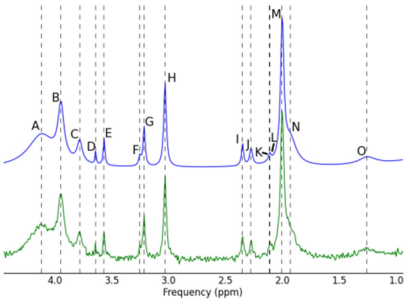

Figure 1: Simulated spectrum based on experimental clinical MRS. Top row shows a noiseless spectrum while bottom row presents noisier data.

METHODS: KBDM is a parametric non-linear method that allows fitting and spectral analysis of experimentally measured transient time signals[1-3]. In summary, a typical MRS signal can be represented by the sum of exponentially damped sinusoids, $c(t)$, sampled with a dwell time t, as follows: $c_n = c(t_n) = \sum_{k=0}^{K-1} |A_k| e^{i\phi_k} e^{i2\pi f_k t_n} e^{-\gamma_k t_n}$; $t_n = n\tau$; $n = 0, \dots, N-1$.The magnitude and phase of the complex amplitude A_k are, respectively, $|A_k|$ and ϕ_k, while the frequency and the transversal relaxation rate of the k[th] component are given by f_k and γ_k, respectively. In order to apply the KBDM, we need to generate two MxM complex matrices defined in the Krylov space, where $4K \leq M \leq N/2$, given by: $U^p_{i,j} = c_{i+j+p}$, $p = 0, 1$. These two matrices lead to a generalized eigenvalue problem: $U_1 B_k = \mu_k U_0 B_k$. This problem will provide eigenvalues and eigenvectors that may be used for determining all the parameters needed to describe all signal components: $e^{i2\pi f_k - \gamma_k} = \mu_k$ *and* ${A_k}^{1/2} = {B_k}^T \cdot c_n$, $n = 0, \dots, M-1$. To evaluate the performance of the KBDM we employed numerically simulated data, generated to mimic typical experimental clinical spectra, as can be seen in Fig. 1 (top).Gaussian noise was added to the free induction decay signal before subsequent analysis, as shown in Fig. 1 (bottom). All spectra were simulated with 2048 points, dwell time of 500 us and 15 components (peaks) representing most of the common brain metabolites. The KBDM algorithm was implemented in Python using the NumPy, SciPy and MatplotLib libraries. To minimize the impact of the noise in the KBDM quantification, we implemented a modified version that produced a set of estimations of the parameters for multiple subsets of the signal. To do this, we exploited the fact that signals can be truncated appropriately to generate less noisy representations[6]. Thus, we created multiple U^p matrices for the same signal using different numbers of points. After applying the KBDM for each truncation, we removed the outliers by eliminating the upper and lower 25% of the obtained estimations of each known component and averaged the remaining points, which lead to the final KBDM-estimated values.

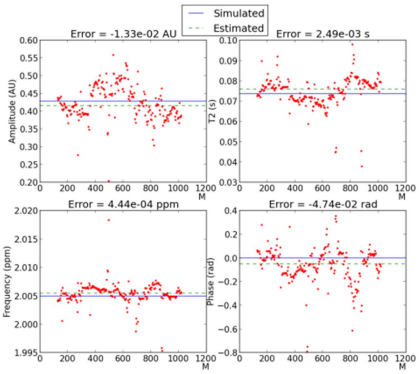

Figure 2: Multipoint analysis using KBDM-estimated parameters of peak 'M' (Figure 1).

RESULTS: In the absence of noise, the KBDM is capable of estimating all simulated spectral components within computer arithmetic precision (results not shown). However, when noise is added, fluctuations in the spectral estimation can be observed which impair the proper quantification of spectral components. Fig. 2 shows the estimated parameters of a selected peak (peak M) using the multipoint analysis proposed in this work for a signal generated with SNR similar to that obtained in typical brain 1.5T clinical spectra. The signal was analyzed by applying the KBDM multiple times varying the number of points from the original signal used for data processing (M = 128 to 1024 in steps of 4). Even though a large dispersion is present for each truncation for all parameters, the KBDM-estimated value (green dashed line) is consistent with the simulated values (blue line). The obtained errors are shown on top of the panels in Fig. 2 and decrease with the reduced noise levels. Similar analysis was done for all peaks of interest and the obtained values are shown in Fig. 3. Note that even peaks with low SNR can be properly estimated.

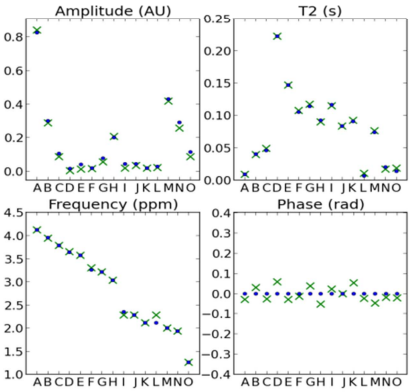

Figure 3: KBDM-estimated parameters using the proposed analysis. Blue points are simulated and green 'X' represent the estimated values.

DISCUSSION AND CONCLUSIONS: We have shown that KDBM can lead to accurate spectral analysis for simulated MRS data. It has been previously shown that noise can impose a serious limitation for the KBDM analysis[5] and our proposed approach intends to circumvent this limitation. Instead of using the conventional approach where signal is processed once using a selected number of points, we implemented a protocol where data is processed multiple times using different numbers of points. Our results show that our method is robust to noise levels that are typical in clinical MRS at 1.5T. We were able to recover the simulated value for all analyzed peaks with very high accuracy. Further studies are in progress to validate the proposed method for *in vivo* data processing. We suggest for future investigation using this KBDM implementation not only for spectral quantification, but in signal pre-processing. For instance, the prominent water peak or components with very broad linewidth could be identified and eliminated from the signal to improve spectra quantification and thus extend the applicability of KBDM.

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