LPSVD ALGORITHM FOR PARAMETER ESTIMATION OF DAMPED SINUSOIDS

Ing. Miroslav ŠTĚPÁN, Doctoral Degree Programme (1) Dept. of Telecommunications, FEEC, BUT E-mail: stepan@feec.vutbr.cz

Supervised by: Dr. Karel Bartušek

ABSTRACT

This article is focused on estimation of initial amplitude, frequency, initial phase and damping factor of sinusoids contained in signal of nuclear magnetic resonance (NMR). It describes algorithm called LPSVD, based on singular value decomposition signal matrix and linear prediction. In Practical results appendix observations are issued and possibility of noise suppression is outlined.

1 INTRODUCTION

LPSVD (Linear Predictive Singular Value Decomposition) is one of the most commonly used algorithm in biomedicine signal processing applications [1] [2] for parameter estimation of damped sinusoids. It is based on two major principles – singular value decomposition and estimation of linear prediction coefficients. Algorithm was introduced first by Kumaresan & Tufts in 1982 [3] and adjusted by Porat & Friedland. This contribution was issued to explain detailed theory to make clear and unify partial information available on the net.

2 LPSVD MAIN STEPS

Following six main steps to determine signal parameters:

- Choice of model fitting data
- Creation of Hankel signal matrix
- Estimation of prediction coefficients
- Singular value decomposition of Hankel matrix
- Estimation of frequencies and dampings of signal components in NMR.
- Estimation of amplitudes and initial phases of signal components in NMR

2.1 CHOICE OF MODEL FITTING DATA

Algorithm uses model to fitting data – this model attempts to approximate original noisy data and minimizes the difference between data and nonlinear model in least squares sense. Main types [5] of models used in NMR signal processing are:

Lorentzian model:

$$y_{n} = \overline{y_{n}} + e_{n} = \sum_{k=1}^{K} a_{k} e^{j\phi_{k}} e^{(-d_{k} + j2\pi f_{k})t_{n}} + e_{n}$$
(1)

Voight model:

$$y_{n} = \overline{y_{n}} + e_{n} = \sum_{k=1}^{K} a_{k} e^{j\phi_{k}} e^{(-d_{k} - g_{k}t_{n} + j2\pi f_{k})t_{n}} + e_{n}$$
(2)

Equations (1),(2) describing complex signals. It is also possible to define real value model using sin function, for example:

$$y_{n} = \sum_{k=1}^{K} a_{k} e^{-d_{k} n T_{vz}} \sin(\omega_{k} n T_{vz} - \varphi_{k})$$
(3)

The most commonly used is the Lorentzian model, which is also used in this contribution.

2.2 CREATING OF HANKEL SIGNAL MATRIX

Considering the vector x of input noisy data, we create the Hankel signal matrix X using next equation:

$$X = \begin{pmatrix} x_1 & x_2 & \cdots & x_M \\ x_2 & x_3 & \cdots & x_{M+1} \\ \vdots & \vdots & \ddots & \vdots \\ x_{N-M+1} & x_{N-M+2} & \cdots & x_N \end{pmatrix}$$
(4)

Size of Hankel matrix is LxM, where rows of matrix are parts from input vector x with length M and offset of each part is equal to row index -1 (starting with index 1).Number of rows is equal to N-M+1, N is the number of samples in input vector. M value is based on number of sinusoids contained in input vector, called FIDs (Free induction decay signals). M is optional and is determined from N in interval (1/3N - 2/3N). In theory for noise free signal compounded from K FIDs it is enough to choose M two times more K. Main problem is, we do not know number of FIDs in signal and input signal is always noisy, it makes difficult estimation of parameters.

2.3 ESTIMATION OF PREDICTION COEFFICIENTS

Next step is the estimation of prediction coefficients q_j from input noisy signal using backward (5) or forward (6) linear prediction definition:

$$x_{i}^{bpred} = \sum_{j=1}^{M} x_{i+j} q_{j}$$
 (5)

$$x_{i}^{fpred} = \sum_{j=1}^{M} x_{i-j} q_{j}$$
 (6)

Order of prediction depends on M and determine number of prediction coefficients. Here is the backward prediction used (5). It is important to realise that backward prediction is not workable in the real time processing – we do not have next samples in time domain yet. Equation (5) may be re-written using Hankel matrix (4):

$$\overline{x^T} = H * \overline{q^T} \tag{7}$$

From equation (7) we see that infinite number solutions for q available. We want to find solution q which produces estimation of x minimized the sum of square differences between original and estimation. This request is satisfying using singular value decomposition of Hankel matrix and Cadzow filtration [4].

2.4 SINGULAR VALUE DECOMPOSITION OF HANKEL MATRIX

Singular value decomposition (SVD) produces three matrixes, such as:

$$H_{L,M} = U_{L,L} * S_{L,M} * V_{M,M}^{\dagger}$$
(8)

Where L is the row index and M is the column index of *H*. Matrix *S* is diagonal, elements represent harmonic components in input signal (FID signals). Components are in order from dominant to negligible. Last diagonal numbers represent noise. SVD is implemented in Matlab software for example, using function svd.

In next we apply Cadzow filtration to modify matrix S (8). It is based on cutting off rows and columns of matrix S, this way it is possible to create square matrix S. We retain only first F rows and columns of S -main goal is to eliminate noise from diagonal and to make square matrix. In addition we cut off columns of U and V (8) too, retain only first F columns. Now it is possible to create Hankel matrix inversion:

$$inv(H) = V_{M,F} * S_{F,F} * U'_{L,F}$$
(9)

From equations (7) and (9) we compute prediction coefficients q:

$$\overline{q} = V_{M,F} * S_{F,F} * U_{L,F}' * \overline{x}$$
(10)

If we reconstructed signal using these coefficients q, the prediction error will be minimized in least squares sense, as has been already written.

2.5 ESTIMATION OF FREQUENCIES AND DAMPINGS OF SIGNAL COMPONENTS IN NMR.

This problem is focused on searching roots of polynomial using prediction coefficients from (10):

$$z^{M} - q_{1} z^{M-1} - q_{2} z^{M-2} - \dots - q_{M} z^{0} = 0$$
(11)

It is possible to use Matlab software function roots to find solution. As a result we obtain M complex roots z_j , from which is straightforward to determine angular frequencies (12) and damping factors (13):

$$\omega_j = \frac{-\arg(z_j)}{T_{yz}} \tag{12}$$

$$\alpha_j = \frac{1}{abs(z_j)T_{vz}} \tag{13}$$

 $T_{\rm vz}$ is sampling interval of input signal. Now we have first two sets of parameters.

2.6 ESTIMATION OF AMPLITUDES AND INITIAL PHASES OF SIGNAL COMPONENTS IN NMR

Using the roots from polynomial (11) it is possible to recover input signal:

$$x_{i}^{sig} = \sum_{j=1}^{M} z_{j}^{0} \left(\frac{1}{z_{j}}\right)^{t-1}$$
(14)

Where z_{j}^{0} is initial amplitude and phase – the second two sets of parameters we are looking for. It is similar problem as in eq.(5) and to compute it we applying additional SVD of matrix Z(15) and searching the best solution for z_{j}^{0} :

$$Z = \begin{pmatrix} \left(\frac{1}{z_1}\right)^0 & \cdots & \left(\frac{1}{z_M}\right)^0 \\ \vdots & \ddots & \vdots \\ \left(\frac{1}{z_1}\right)^{N-1} & \cdots & \left(\frac{1}{z_M}\right)^{N-1} \end{pmatrix}$$
(15)

From z_{j}^{0} we obtain last sets - initial amplitude (16) and phase (17):

$$A_j = abs(z_j^0) \tag{16}$$

$$\phi_j = \arg\left(z_j^0\right) \tag{17}$$

3 PRACTICAL RESULTS

LPSDV algorithm was tested in MRUI software [7]. Parameters of FIDs was opted to approach adjacent peaks to each other to worsen estimation in Fourier spectra. Input noisy signal is shown in Fig.1, contain three harmonic compounds with parameters shown in Tab.1. Noisy level was opted to SNR=13,9 dB. To this signal LPSVD was applied, estimation of parameters is shown in Tab.2.

On figure 2. is spectra of noisy original signal shown (left) and noise free estimation (right) reconstructed from Tab.2.:



Fig. 2: Spectra of original signal (left) and estimation using LPSVD (right)

Input noisy signal	1.FID	2.FID	3.FID
A [-]	0,50	4,98	4,03
α [Hz]	3,00	2,00	4,10
f [Hz]	90,00	100,00	103,00
φ [deg]	0,70	-0,10	0,10

 Tab. 1:
 Parameters of FIDs in input signal from Fig.1

Estimation of signal	1.FID	2.FID	3.FID
A [-]	0,56	4,58	4,10
α [Hz]	3,80	1,60	4,10
f [Hz]	89,00	100,00	103,00
φ [deg]	28,50	0,10	-1,40

Tab. 2:Estimation of parameters using LPSVD

Algorithm is capable to obtain parameters even in noisy environment, especially estimation of frequency parameters proved distinguished.

4 CONCLUSIONS

Algorithm is often used in biomedical signal processing applications to obtain unknown parameters of signals, but it's not binded only on this group of signals. Main disadvantage is computational burden compared to classic FIR filtering and next, prior knowledge of some FIDs cannot be included. But the main goal is a minimum user involvement and cooperation during process, algorithm is almost autonomous.

There are many applications where algorithm has been implemented already, for example MRUI software package [7] or NMRLab toolbox [8] [9] for Matlab software. Software MRUI is the powerfull tool for biomedical signal processing, also including another algorithms based on different principles – non linear approach such as VARPRO and AMARES.

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