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Linear Prediction Matrix segmentation for Matrix Pencil Method in backscattering signal scenarios

A. Gallego
Department of Electrical and Electronic Engineering
Universidad Nacional de Colombia,
Bogot´a, Colombia
ajgallegog@unal.edu.co

F. Roman
Department of Electrical and Electronic Engineering
Universidad Nacional de Colombia,
Bogot´a, Colombia
fjromanc@unal.edu.co

E. Neira
Technology Innovation Institute
Directed Energy Research Center Abu
Dhabi, United Arab Emirates e-mail:
ernesto.neira@tii.ae

F. Vega
Technology Innovation Institute
Directed Energy Research Center Abu
Dhabi, United Arab Emirates e-mail:
felix.vega@tii.ae

C. Kasmi
Technology Innovat ion Institute
Directed Energy Research Center Abu
Dhabi, United Arab Emirates e-mail:
chaouki.kasmi@tii.ae

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***Abstract*—Here we propose and evaluate a method for segmenting the Linear Prediction Matrix used during the Matrix Pencil Method. This proposal considers the division of a time domain signal in W frequency segments that can be processed individually and whose results can be put together in the final stage. The evaluation of the suggested approach is presented here in terms of the coefficient of determination R^2 for the reconstructed signal, and focuses on either reducing the hardware requirements for back-scattering signal processing, its parallelisation or reduced execution time for portable GPR operations.**

I. INTRODUCTION

The Singularity Expansion Method (SEM), and more specifically the Matrix Pencil Method (MPM) calculates the poles and complex amplitudes of a time signal [1] [2]. This method starts with the back-guard Linear Predictor data Matrix resulting in, for a function with N samples, a matrix size $N/3 \times N/3$ or bigger which is decomposed and transformed through expensive Hardware consuming methods like several Singular Value Decompositions (SVD). Either processing algorithms focused on reducing the size of the matrix or increasing the core math functions capabilities are the alternatives for portable signal processing devices.

Here, we propose and validate a process for the division of the input signal in smaller segments, each one processed individually through MPM. Every calculated set of poles and residues is then combined with other segments results to form the original set of resonances, validated through the reconstruction of the time-domain signal.

II. BACKGROUND

A. Matrix pencil method

SEM models a signal $y(t)$ in terms of complex poles s_i and residues R_i associated as in Eq. (1) [1], [3]. The method begins with N samples of a signal $y(t)$ and, in order to calculate its principal components. A Hankel matrix $[Y]$ is constructed and then decomposed several times through SVD in order to calculate the CNRs of the signal.

$$y'(t) = \sum_{i=0}^{M} R_i e^{s_i t}, \tag{1}$$

MPM details and its implementation can be consulted in [4].

B. Signal Alias and Sub-sampling

Let $y[n]$ be the input signal with N samples, and $y_d[m]$ the down-sampled signal with M samples such that $M = N/d$ with d as the down-sampling factor. Solving the discrete Fourier Transform of the down-sampled signal leads to

$$Y_d[k] = \frac{1}{d} \sum_{i=0}^{d-1} Y \left[k + i\frac{N}{d} \right] \tag{2}$$

which indicates that the down-sampled spectrum is a decimated version of the original one and several shifted versions of itself.

Frequency Folding or Alias Frequency shifting, which is used in high frequency band-pass signals to sample at a lower rate deals with the minimum frequency at which the input signal can be sampled [5], [6]. Classic sampling theorem would define the minimum sampling frequency f_s as twice f_u, but the aliasing phenomenon occurring when $f_s < 2f_u$ allows lower sample rates in signal analysis using the band-pass sampling theorem for uniform and instantaneous sampling.

Also, a signal can be recovered if:

$$f_s \geq \frac{2f_u}{m} \tag{3}$$

where m is defined as the largest integer of $f_u/(f_u - f_l)$.

Figure 1 shows an example of the sub-sampling effect, with $f_c = 20$,$f_u = 22$ and $f_l = 18$ (showed in green).

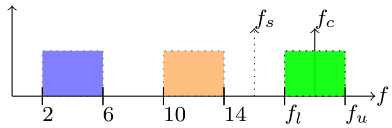


Fig. 1. Bandpass signal folding. The middle one comes from the periodicity of the alias located at a negative part of the frequency spectrum.

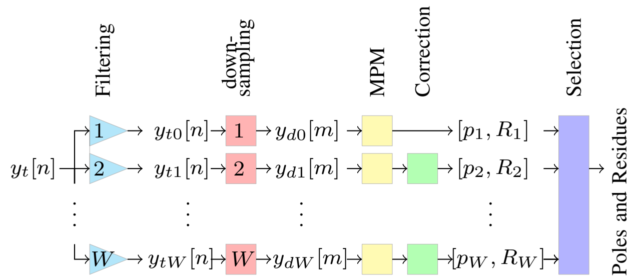


Fig. 2. Foldel Matrix Pencil Method schematic

The integer $m = 5$ establishes $f_s \geq 8.8$ needed to recover the signal, so we chose the $f_s = 16$ case in figure 1. Notice the alias spectrum that falls into base-band, because there is a copy of the original one at ± 4 (blue), ± 12 (orange) and ± 20 (green). Filtering at $f_{lowpass} = 6$ will result in the original signal centred at f_c shifted to base-band. The frequency for every alias N of a signal f_o can be defined using Eq. (4):

$$f_N(f) = f_o(f - \frac{N f_s}{2}) \tag{4}$$

III. FOLDED MATRIX PENCIL METHOD

The idea is to filter a time domain signal and divide it into multiple frequency bands W and after sub-sampling it in order to apply MPM to each band independently. Fig. 2 shows this approach, and the algorithm is as follows:

1) *Filtering* the input signal $y_t[n]$ gives $y_{t0}[n]$, $y_{t1}[n]$, $\cdots$ $y_{tW}[n]$ signals, with W as the number of desired phase zero pass-band filters .
2) *Down-sampling* for each $y_{ti}[n]$ where $i = 0, 1, \ldots, W$, the number of samples N is still the same as in $y_t[n]$. As the objective here is to reduce input N so a limited hardware can process the input data, signals $y_{ti}[n]$ are down-sampled according to the number of filters or windows W, resulting in $y_{d0}[m]$, $y_{d1}[m]$,$\cdots$ $y_{dW}[m]$(see Section II-B)
3) *MPM:* Now, for each filtered and down-sampled signal y_{di}, MPM is applied obtaining poles p_{di} and residues R_{di}.
4) *Correction:* this alias signal is a frequency-scaled one, and this means that a correction in frequency must be applied to shift the frequency of the poles obtained back according to the relationship between the alias y_{di} and the original filtered signal y_{ti}. Then, if $p_{di} = \alpha_{di} + j\omega_{di}$, the new set of poles is $p_i = \alpha_{di} + j\left[\omega_{di} + \frac{N}{2i}\right]$, for $i = 2, 3, \cdots, W$. The whole set of poles is the collection of p_i.
5) *Selection* is the last step. Here, irrelevant poles are discarded by comparing against the biggest one. Rule applied in this paper was discarded if the residue magnitude is 1000 time less than the biggest one.

As an example, a sine benchmark signal with frequencies at 16, 48, 96, 160 and 226 Hz is used and then filtered as in Fig. 3.

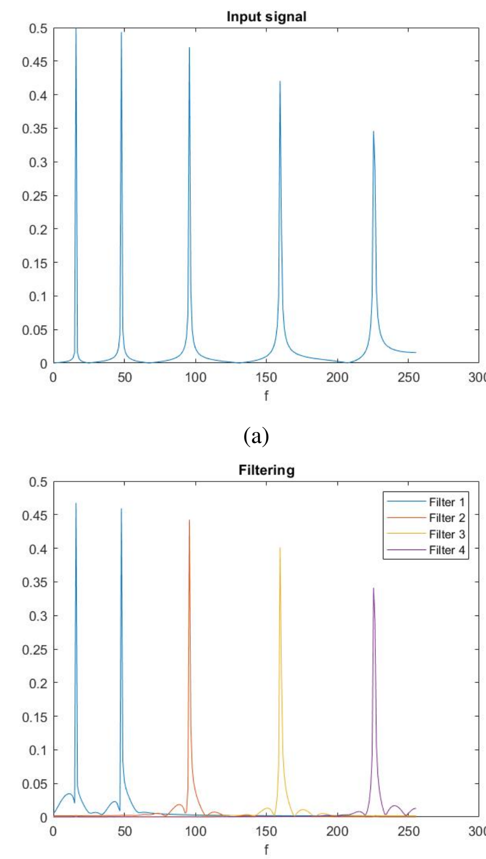
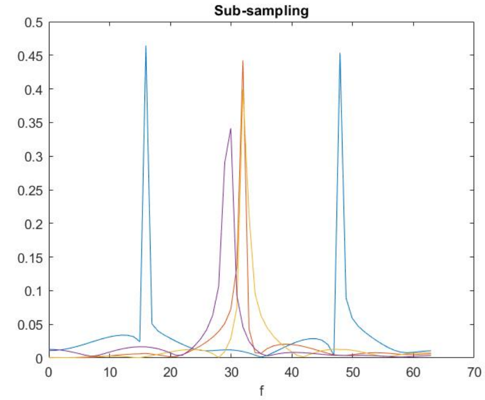
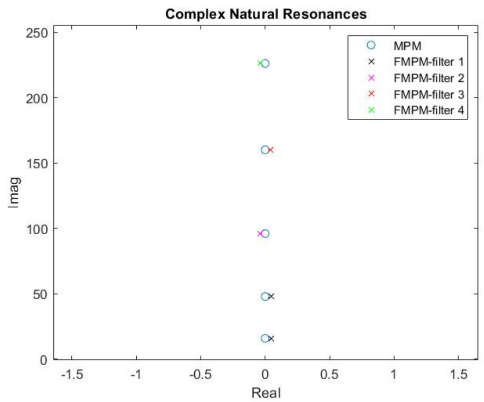


Fig. 3. benchmark signal (a) frequency domain plot and (b) filtered

The subsampling process and the CNRs of each filtered signal are then calculated through MPM, and these are shifted according to the corresponding sub-sampling before being displayed in Fig.4. This process allows the processing of every sub-sampled signal to be treated independently without losing reconstruction fidelity.



(a)



(b)

Fig. 4. Benchmark signal (a) sub-sampled and (b) CNRs.

IV. Results

The accuracy of this method depends highly on W. Here, five back-scattering signals (1 experimental and 4 simulated) of 512 samples were processed comparing the coefficient of determination R^2 of the reconstructed signal. Results are presented in Fig. 5. As MPM uses SVD with complexity of $O(N^3)$ [7], notice how this approach reduces complexity to $O(N^3/W^2)$. i.e., for the experimental signal (blue bars, fig 5), with $W = 8$, complexity seems to be reduced 64 times remaining almost the same accuracy of the original MPM (See Fig 5 bottom). However, that accuracy is not the same for $W = 8$ in all the processed signal.

V. Analysis and conclusions

This is a initial report of a research in progress, however, next stages of the study will be focused on identifying the origin of some of the accuracy errors and its variability according to the signal. Currently, optimal W has not been identified yet. Future works with more input signals will address this task. However, excepting the back-scattering signal resulting from the sphere, $W = 8$ presented a good accuracy.

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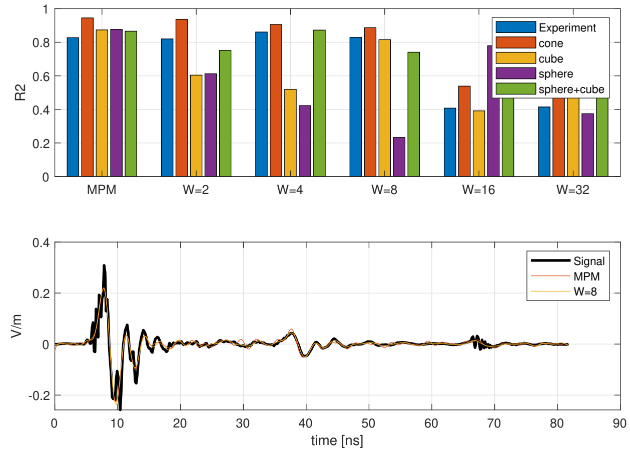

Fig. 5. Coefficient of determination R2 for 5 back-scattering signal reconstructed for $W = 2, 4, 8, 16, 32$ and comparison between one original signal, reconstructed with original MPM and the Folded MPM proposed here.

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