Evolutionary Biomedical Signal Processing Techniques

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Abstract. *Digital Signal Processing techniques constitute the basic scientific approach used in most of the current advances in medicine. In particular, the development of algorithms in order to extract, predict and model raw biomedical data series has revolutionized many routine, but data-intensive, areas of current medical practice. In this contribution, we present an evolutionary technique for modelling and analysing Non-linear Time Series (NLTS). The proposed methodology has been already used in two cases with great biomedical importance and we therefore explore its effectiveness on other biomedical signals.*

1. Introduction

The central issue in all system identification problems, including non-linear signal processing, consists of identifying the optimal model order and computing its parameters, taking real observation data as input signals. Going from linear to non-linear system identification makes the problem much harder since the set of non-linear models is larger and more complicated than the linear one. Therefore, it is important to take into consideration the attributes and constraints of each signal, in order to design reliable, accurate and cost effective (real-time) applications.

The subject of Non-linear Time Series modelling has attracted considerable attention during the last years. So it has been studied extensively from different points of view including statistics and identification theory, approximation theory, signal processing, information theory, physics and optimisation theory among others and a large number of numerous approximate non-linear estimation algorithms, have been proposed for certain data models in the relative literature [1-5].

2. Materials and methods

In our approach, we initially reformulate the problem in the standard state space form and implement a bank of extended Kalman filters, each one fitting a different model. In order to select the best model, of the bank of candidate models, we use a Genetic Algorithm to give optimum estimations of the noise sequences, the variances and the initial conditions of the filters [6]. The final selection of the model is based on the maximum a posteriori probability criterion, using the Multi-model Partitioning theory [7]. The sequential flow of the proposed methodology is shown in the following figure (Figure 1).

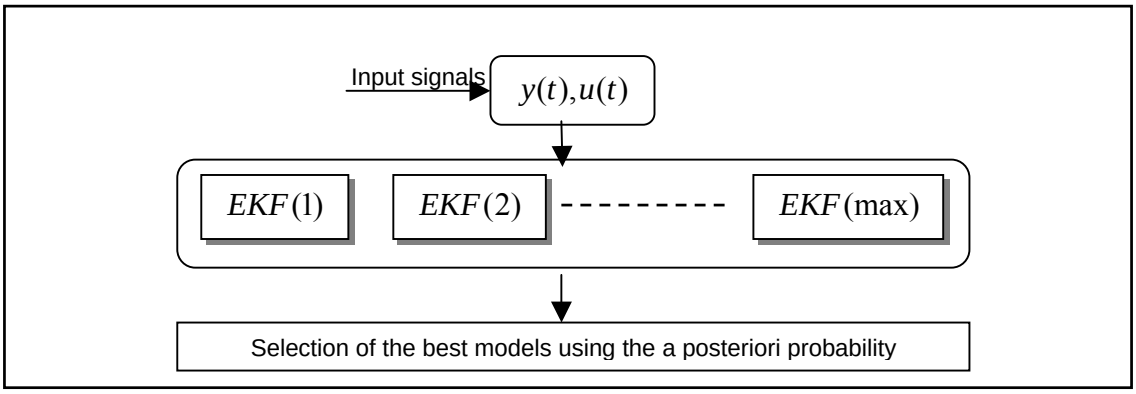

Figure 1. Sequential flow of the proposed methodology. The Extended Kalman Filter (EKF), Genetic Algorithms and the Multi Model Partitioning (MPP) theory are well known signal-processing techniques.

Taking an observation signal sequence $y(t)$ and a noise sequence $u(t)$ from a $NLTS(n)$ process, as input, where $0 \le t \le N$ (N is the number of observations), we firstly implement a Genetic Algorithm in order to estimate the unknown values of the noise sequence, the variances and the initial conditions. After that, we select the order of the predictor and compute the signal $x(t)$ and the predictor coefficients. The population of the Genetic Algorithm consists of Extended Kalman Filters, (numbered from EKF(*1)* (first individual) to EKF(*max)* (last individual) as shown in the above figure). The best model is selected using as fitness function for the GA the a posteriori probability, according to the Multi-Model Partitioning theory.

Specifically, the variables used in the model identification procedure are divided in three categories:

a. The previous values of the dependent variable which lead to autoregressive (AR) terms;
b. Sequences of independent random processes (white noise not necessarily Gaussian) which lead to moving average (MA) terms;
c. Input variables, which are called external inputs and lead to exogenous (X) terms.

Therefore, the non-linear autoregressive moving average with exogenous input (NARMAX) model can be written as:

$$x(t+1) = f_t\left(h^T(t), \vartheta(t)\right) + e(t), \quad (1)$$

$$y(t) = g_t(x(t)) + v(t), \quad (2)$$

where $x(t)$ is the signal produced by the pure dynamics of the system, $e(t)$ is the ambient dynamical noise of the system, $y(t)$ is the observation data and $v(t)$ is the external (observation) noise. Furthermore,

$$h^T(t) = \left[x(t),...,x(t-n_x+1), u(t-1),...,u(t-n_u), e(t-1),...e(t-n_e)\right], \quad (3)$$

$$\vartheta = \left[a_1,...,a_{nx}, b_1,...,b_{nu}, c_1,...,c_{n_e}\right]^T \quad (4)$$

In addition, f_t and g_t are known matrix-valued non-linear functions and $n = (n_x, n_u, n_e)$ is the order of the NARMAX model. In the general case, $e(t)$ and $v(t)$ are uncorrelated zero

mean white noise processes, not necessarily Gaussian, with variances R and V respectively; $a_i : i = 1,...,n_x$, $b_j : j = 1,...,n_u$, $c_k : k = 1,...,n_e$ are the predictor coefficients. The coefficients a_i, b_j and c_k can been replaced by $a_i(t), b_j(t)$ and $c_k(t)$ to reflect the possibility that the coefficients are subject to random perturbations. This fact can be modelled by assuming that:

$$\vartheta(t+1) = \vartheta(t) + w(t) \tag{5}$$

where $w(t)$ is also a $n \times 1$ zero mean white noise process not necessarily Gaussian with variance W (we assume that processes $e(t)$, $v(t)$ and $w(t)$ are independent).
The NLTS model identification problem is translated to the determination of the unknown parameter vector:

$$v = [x(t), e(t), \vartheta(t), n, R, V, W] \tag{6}$$

3. Results and discussion

Simulations have shown that the proposed methodology selects the correct model order and computes the model parameters in real time. In [8] the same methodology was used for the modelling and analysis of the Magneto Cardiogram (f-MCG) while in [9] the methodology was applied on the Magneto Encephalogram (MEG) of epileptic patients. In the first application, the f-MCG signals were generated from the ionic microcurrents of the fetal heart recorded with the use of specific Superconductive Quantum Interference Devices (SQUIDs). SQUIDs are very sensitive superconductive magnetometers with the ability to detect and measure very weak magnetic fields, of the order of fT (= 10^{-15}T) and they can be used ideally for the recording of f-MCG, since they do not emit any radiation and they are totally non invasive [10]. On the other hand SQUIDs are extremely sensitive and they provide high spatial and temporal resolution and therefore they can account as a promising diagnostic technique in gynaecology and obstetrics [11]. The derived model can be used for the monitoring of pregnancy.

In the second application, the addressed problem involved the choice of the model structure and computation of the coefficients of the system, namely brain structures, which generate epileptic behaviour. The observation data consisted of the Magneto Encephalogram (MEG) of epileptic patients also recorded with the use of specific totally non-invasive Superconductive Quantum Interference Devices (SQUIDs). SQUIDs are considered as a promising diagnostic technique for the investigation of neurological diseases and the exploration on normal brain function [12], [13], complementary to the EEG method and other brain functioning techniques [14], [15]. In general the MEG signals are generated from the ionic micro-currents of the brain, originated at the cellular level [16], [17]. The MEG analysis can provide information of vital importance for the monitoring of brain dynamics in both normal and pathological conditions of the Central Nervous System [18]. Our methodology was used for the analysis and classification of the epileptic MEG signals. Using the resulted model, neurologists are considerably assisted in order to interpret the information provided, detecting correlation with the clinical status of the epileptic patients.

4. Conclusion

The proposed method selects the correct model structure, identifies the model parameters, in a sufficiently small number of iterations, and tracks successfully changes in the signal, in real

time. Moreover, the algorithm is able to model the ambient as well as the extraneous noise that is incorporated in the pure dynamics of the system. Also, it would be of great interest to apply the proposed methodology on other biomedical signals. Results of these investigations will be presented in the future. Finally, the algorithm can be parallel implemented and also a VLSI implementation is feasible which raises its value in practical applications.

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