

AN EVOLUTIONARY ALGORITHM FOR LINEAR SYSTEMS IDENTIFICATION

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Abstract— This paper presents a systems identification method, for discrete time linear systems, based on an evolutionary approach, which allows achieving the selection of a suitable structure and the parameters estimation, using non conventional objective functions. This algorithm incorporates parametric crossover and parametric mutation along a weighted gradient direction [1]. The performance of the proposed method is illustrated with computer simulations using ARX model structures, where parameters, model dynamical order and input-output delay values are estimated.

Key-Words: - System identification, Discrete time systems, Regression models, Evolutionary computation.

1 Introduction

System parametric identification is usually achieved in two steps: the first step is selecting a model family from which a candidate model is produced by minimizing some error criterion. The second step is validating the identified candidate model in terms of verifying some performance indicators, such as noise independence, error auto-correlation, input/error correlation and real response following among others. If results do not satisfy some of the performance indicators, an alternative model must be produced over an efficient model family. Least square methods have been traditionally used, for achieving parametric estimation, in systems identification due to their computational efficiency. Least square methods properties have been well analyzed by many authors, [2]. On the other hand, evolutionary approaches for system identification have been used in recent years, for making error criteria more flexible and for improving performance of system identification process in parameters estimation. The efficiency of a new evolutionary algorithm for discrete time, linear system identification is illustrated in this work by computer simulation results.

2 Evolutionary computation

Evolutionary Computation methods are associated to computational models which use some mechanism related to the Evolution Theory and intended to the design and implementation of a variety of systems applications [3], [4], [5], [6], [7], [8], [9], [10]. The most important evolutionary computation contribution to problems solving methodology, has been the use of selection mechanisms of potential solutions and the construction of new candidates using characteristics from the recombination of existent individuals, similar to the organisms in natural evolution [11], [12], [13], [14], [15], [16], [17], [18], [19]. The main objective associated to these techniques is to take advantage from some generic ideas behind evolutionary processes, in order to solve search and learning complex problems.

The generic purpose of these algorithms is to guide a stochastic search, making evolve a set of structures and selecting iteratively the fittest of them. All these algorithms are characterized by their simplicity from the computational viewpoint, even though they are complex enough to provide robust and powerful search mechanisms [20].

In Evolutionary Computation it is possible to distinguish five paradigms: [5], [6], [7], [8], [9], [10] a)

Genetic Algorithms: A population of binary numbers or character strings evolve using a set of unitary and binary transformations and a selection process, b) Evolutionary Programs: A population of data structure evolve through a set of specific transformations and a process selection, c) Evolutionary Strategies: A population of real numbers is made evolve to find possible solutions of a numerical problem, d) Evolutionary Programming: The population is constituted by finite state machines which are subjected to unitary transformations, e) Genetic Programming: The population consists of programs which solve a specific problem. The objective is to make evolve the population in order to find the best program that solves the problem under study. The algorithm proposed in this paper may be considered as an evolutionary strategy, since it is designed to solve parametric optimization problems, and it is based on some ideas presented in [1], [21], [22].

3 A system identification method for discrete time linear systems.

The ARX model structure may represent a wide variety of linear systems. For single input and single output (SISO) systems, the ARX model is represented by:

$$A(q^{-1})y(k) = B(q^{-1})q^d u(k) + e(k) \tag{1}$$

where

$$A(q^{-1}) = 1 + \sum_{i=1}^n (a_i q^{-i}) \tag{2}$$

$$B(q^{-1}) = \sum_{j=1}^m (a_j q^{-j})$$

The variables $y(k)$, $u(k)$ and $e(k)$ represent output, input and noise at time k , respectively. The system order is $n \geq m$ and d is the dynamical system time delay.

3.1 Chromosome coding for parameters estimation

The chromosome coding for a fixed ARX structure is defined as a real values string containing the polynomials coefficients and the time delay corresponding to the ARX model. The chromosome structure, where each polynomial coefficient represents a gem, is illustrated in figure 1.

The proposed chromosome coding facilitates the calculation of model parameters for different system orders n and time delay d . Chromosomes lengths mainly depend on n . System order n , time delay d and the order of polynomial $B(q^{-1})$, m , are chosen taking into account their contribution to the fitness function

associated to each set of chromosomes with fixed structure.

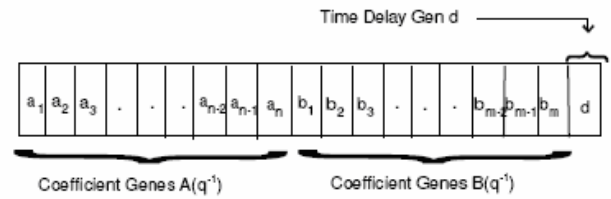


Figure 1. Chromosome structure for parameters estimation

Some parameters are required to create different sets of chromosomes: maximum system order n_{max} and maximum time delay d_{max} . All possible combinations will be considered to generate the sets of chromosomes with fixed structure, for example if $n_{max} = 2$ and $d_{max} = 2$, the different sets of chromosomes with fixed structure are illustrated in figure 2.

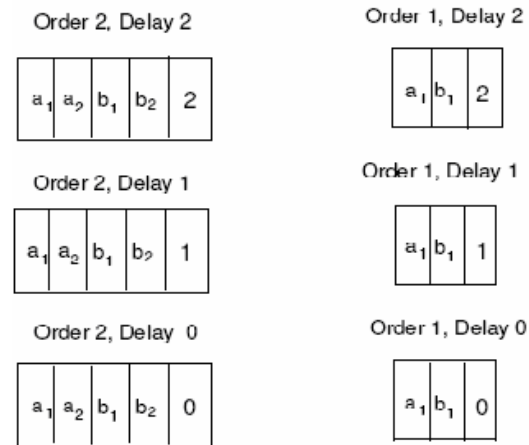


Figure 2. Sets of fixed structure chromosomes

Without loss of generality, m has been considered to be, at most equal to n in order to generate the chromosomes lengths. Solutions associated to $m < n$ are included in these sets of chromosomes and solutions for which $a_n = 0$ are discarded.

4 An Evolutionary algorithm for parameters and structure estimation.

In this section an evolutionary algorithm for Linear Systems Identification is proposed. This approach allows finding a suitable ARX model structure and performing parameter estimation. The algorithm uses parametric crossover and parametric mutation according to results presented in [1], [21], [22]. Consider the following non conventional index which may be used as fitness function for the proposed algorithm.

$$h(a_i, b_i, d) = \exp\left(-\sum_{l=k-p+1}^k \frac{(e_l)^2}{2} - \sum_{i=k-p+1}^k \frac{abs(de_l)}{p}\right) \tag{3}$$

where p is the number of data patterns, taken from the process under study over a time window $[k-p+1, k]$, which is long enough to be able to obtain crucial dynamic characteristics from the input/output system data. This data is used to perform the offline system identification procedure; where e_l is the error and de_l is the error derivative, corresponding to the 1st data pattern. Notice that the following equation holds true

$$A(q^{-1})y(k) - B(q^{-1})q^{-d}u(k) = e(k) \tag{4}$$

Notice also that such fitness function h is affected by a_i , b_j and d . According to the fitness function definition, $h(a_i; b_i; d)$ must be maximized in order to minimize the estimation error. Therefore it is required to solve the following optimization problem

$$Max_{a_i, b_j} h(a_i, b_i, d) \in D_1; d \in D_2(h(a_i, b_i, d)) \tag{5}$$

where $D_1 \subset \mathbb{R}$, and $D_2 \subset \mathbb{Z}^+$ (polynomial coefficients are represented with finite real values and the time delay is represented by a finite positive integer). Taking into account equations 4 and 5, the proposed algorithm may be written as follows:

Reproduction: Given the maximum system time delay and maximum dynamical system order, begin generating all possible sets of fixed structure for chromosomes. Then, start with an initial population of N individuals or chromosomes for each type of structure. Let $x_s(r)$ be the chromosome corresponding to the r^{th} generation associated to the s^{th} structure

$$x_s(r) = [a_{1s}(r), \dots, a_{ns}(r), b_{1s}(r), \dots, b_{ms}(r), d_s] \tag{6}$$

for reproduction stage $r = 1$ and

$$x_s(1) = \zeta_s(1) \tag{7}$$

where $\zeta_s(1)$ is an array and the first $n+m$ elements constitute a random array with each element in $(-1, 1)$, selected to guarantee appropriate initial population values which improve the algorithm convergence. The last element value of $x_s(1)$, as well as the length of the chromosomes are given by the s^{th} generated structure.

Fitness Function Evaluation: The fitness function is evaluated for every population of individuals corresponding to each structure. The individuals are sorted in a list, from the greatest fitness function value to the lowest. There will be one list for each structure.

Parametric Crossover: Let $x_s^i(r)$ be the chromosome corresponding to the i^{th} position in the list associated to the structure s^{th} , during the r^{th} generation; $i = 1 \dots N$, the n_1 fitter individuals participate in the crossover operation. Let $x_s^i(r)$ and $x_s^j(r)$ be two individuals, then the parametric crossover results in:

$$\begin{aligned} \tilde{x}_s^i(r) &= x_s^i(r) + \sigma(x_s^i(r) - x_s^j(r)) \\ \tilde{x}_s^j(r) &= x_s^j(r) + \sigma(x_s^j(r) - x_s^i(r)) \end{aligned} \tag{8}$$

σ must be a very small positive number as compared to the magnitude order associated to individual elements. This operation is only achieved for the first $n + m$ chromosome elements. The element corresponding to the time delay d is generated with the chromosome fixed structure in the reproduction stage. Next these operation parents and new individuals are sorted according to their fitness function from the greatest value to the lowest value.

Parametric Mutation: The parametric mutation is achieved along a fitness function weighted gradient direction, based on the parametric mutation algorithm proposed in [1]. This is the most important operator for the convergence of the proposed evolutionary algorithm. Additionally, it uses a penalty function for evaluating the solutions which violate the optimization problem constraints. According to the parametric algorithm proposed in [1], constraints of type $g_j(x) \leq 0, j = 1 \dots J$, may be imposed on the optimization problem. For this case, one constraint associated to the error tolerance ET_{max} , may be imposed in order to accelerate the algorithm convergence $J = 1$.

$$g_1 = \sum_{l=k-p+1}^k \frac{(e_l)^2}{2} - \sum_{i=k-p+1}^k \frac{abs((de_l))}{p} - ET_{max} \leq 0 \tag{9}$$

All of N individuals are subjected to parametric mutation, according to the weighted gradient direction method which may be written as follows:

$$d(x) = \Delta h(x) - \sum_{j=1}^J ((\rho_j \Delta g_j)) \tag{10}$$

ρ_j corresponds to a penalty multiplier associated to each constraint. For this case $J=1$, then

$$d(x) = \Delta h(x) - (\rho_1 \Delta g_1) \tag{11}$$

In general these multipliers may be defined as

$$\rho_j = \begin{cases} 0, & g_j \leq 0 \\ \delta_j, & g_j \geq 0 \end{cases} \tag{12}$$

$$\delta_i = \frac{1}{g_{\max} - g_i(x) + \delta} \tag{13}$$

$$g_{\max}(x) = \max(g_j(x)), i = 1..J \tag{14}$$

where δ is a very small positive number. Let $x_s^i(r)$ corresponds to the i^{th} position in the list associated to the structure s^{th} , during the r^{th} generation; $i = 1..N$ then the parametric mutation operator may be expressed in the following way

$$\hat{x}_s^i(r) = x_s^i(r) + \beta d(x) \tag{15}$$

β must be a small positive number. A convergence proof, related to an evolutionary algorithm which uses only the parametric mutation method, may be found in [1]. This operation is only achieved for the first $n + m$ chromosome elements; the time delay d is generated with the fixed structure in the reproduction stage.

Replacement: The least suitable individuals are replaced, with individuals that result from parametric crossover and/or parametric mutation processes, in order to keep constant the number N of population individuals.

Selection: The fittest individual, corresponding to each fixed structure, is selected and the chosen ones are sorted according their fitness function from the greatest to the lowest value. The first individual in the final list corresponds to the best solution for the identification problem using ARX structures.

5 Simulation results

The results presented in this section are associated to data from a Data Base for Systems Identification (DAISY), developed by SISTA: Signals, Identification, Systems Theory and Automation, which may be accessed from <http://www.esat.kuleuven.ac.be/sista/daisy/>. This Data Base provides data from different kind of

processes. It has been selected an Industrial Process (Ethane-Ethylene Distillation Column), to illustrate the potentials of the proposed evolutionary algorithm. The output-input data used to perform the simulation corresponds to: Bottom Ethylene Composition, Bottom-Top Differential Pressure and Ratio between Reflux and Feed Flow. The results are presented with linearized data.

Simulation

Maximum delay 10, maximum order: 4. Input: ratio between reflux and feed flow, output: bottom ethylene composition. The ARX model polynomials are the following:

$$\begin{aligned} A(q^{-1}) &= 1 - 1.3578q^{-1} + 0.3767q^{-2} \\ B(q^{-1}) &= -0.1263 + 0.0092q^{-1} + 0.06q^{-2} \\ d &= 2 \end{aligned} \tag{16}$$

Figures 3, 4 and 5 illustrate the real output vs. estimated output, residual analysis and zero-pole map respectively for the ARX model, calculated with the evolutionary algorithm.

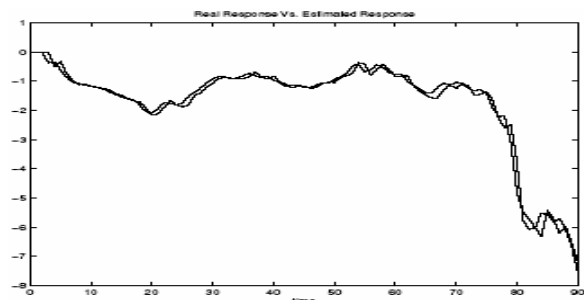


Figure 3. Real Output Vs. Estimated Output (Bottom Ethylene Composition)

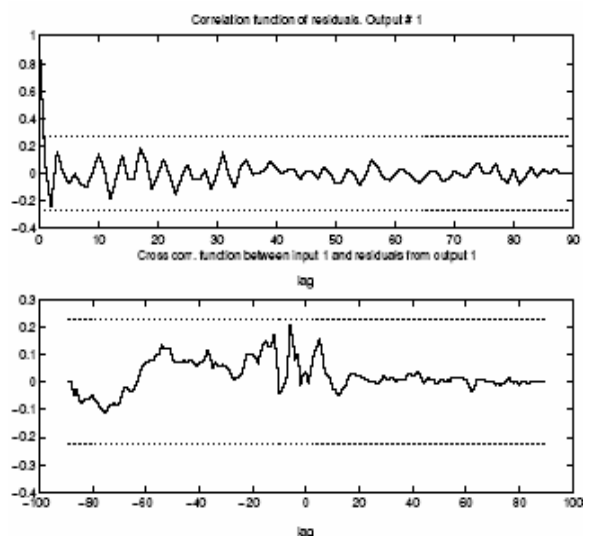


Figure 4. Residuals Analysis

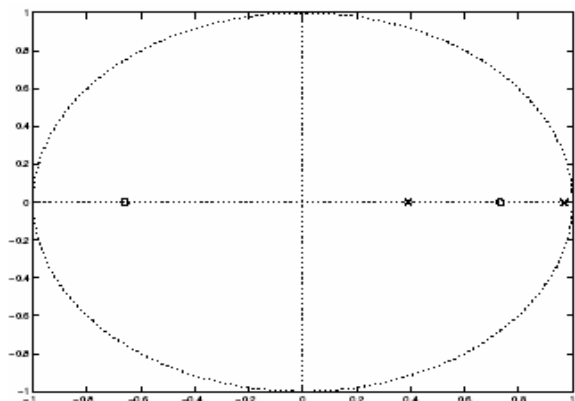


Figure 5. Zero Pole Map

6 Conclusions

A new evolutionary algorithm for linear systems identification has been presented. The algorithm incorporates parametric crossover and parametric mutation along a weighted gradient direction. The evolutionary method proposed in this paper not only allows the parametric estimation process for a fixed model structure, with non conventional objective functions but additionally, calculates a system structure while minimizing the time involved in the identification process validation step. The efficiency of the proposed evolutionary method is illustrated by computer simulation results.

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