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Structure and parameter identification based on Raybman method and genetic algorithms

Ali Hussein Hasan

University of Sumer – Iraq - Al-Rifaie

ABSTRACT

Correlation identification methods have a significant interest in control and system identification engineering; one of these methods is Raybman model-table identification method. This method based on Wiener–Hopf integral equation and allows to make an approximate for structural and parametric identification of stable linear dynamic control objects up to the third order. In this paper we made an improvement to the Raybman model-table identification method; where we used the basic algorithm for structural identification while we used GA for parameters estimation.

Keywords: system identification; correlation identification; Raybman model-table method; GA.

1. INTRODUCTION

Dynamic systems are encountered almost everywhere in reality, e.g., in target tracking, chemical reaction, satellite guidance and navigation, power transmission and distribution, orbit determination, weather and financial forecasting, optimal control, fault diagnosis, etc. A continuous increase in the complexity, efficiency, and reliability of modern industrial systems necessitates a continuous development in the control and fault diagnosis theory and practice. An early detection and maintenance of faults can help avoid system shutdown, breakdowns and even catastrophes involving human fatalities and material damage.

The temporal behavior of technical systems from the areas of electrical engineering, mechanical engineering, and process engineering, as well as non-technical systems from areas as diverse as biology, medicine, chemistry, physics, economics, can uniformly be described by mathematical models. This is covered by systems theory. However, the application of systems theory requires that the mathematical models for the static and dynamic behavior of the systems and their elements are known. The derivation of mathematical system and process models and the representation of their temporal behavior based on measured signals is termed system identification.

Despite the fact that the theoretical analysis can in principle deliver more information about the system, provided that the internal behavior is known and can be described mathematically, system identification has found ever increasing attention. The main reasons that make system identification is preferred over theoretical analysis are a) theoretical analysis can become quite complex even for simple systems. Also some systems are very complex, making the theoretical analysis too time-consuming. b) mostly, model coefficients derived from the theoretical considerations are not precise enough. c) not all actions taking place inside the system are known. And sometimes, the actions taking place cannot be described mathematically with the required accuracy. and d) identified models can be obtained in shorter time with less effort compared to theoretical modeling.

System identification deals with constructing mathematical models of dynamical systems from measured data. Such models have important applications in many technical and nontechnical areas. System Identification is the process of finding a model that best produces a data, obtained by a system with a known input. Obtaining a model of a system is quite useful in studying its behaviour. This model can be obtained by either the use of physical laws that govern the system or by identification procedures (which can be performed by processing input/output data obtained by performing various experiments). Once a good model is obtained, it can be used for the analysis of the system properties, prediction and controller design. Mathematical models of dynamical systems are of rapidly increasing importance in engineering and today all designs are more or less based on mathematical models. Models are also extensively used in other, nontechnical

areas such as biology, ecology, and economy. If the physical laws governing the behavior of the system are known we can use these to construct so called white-box models of the system. In a white-box model, all parameters and variables can be interpreted in terms of physical entities and all constants are known a priori. At the other end of the modeling scale we have so called black-box modeling or identification. Black-box models are constructed from data using no physical insight whatsoever and the model parameters are simply knobs that can be turned to optimize the model fit. Ljung [1] stated a basic rule in estimation, that is, one should not estimates what is already known. In other words, one should utilize prior knowledge and physical insight about the system when selecting the model structure and type to be used. There are three types of models based on the prior knowledge [2] :-

White Box Models: This is the case when a model is perfectly known and has been possible to construct it from prior knowledge and physical insight by taking into account the connection between the components of the system.

Grey Box Models: This is the case when some physical insight is available, but several parameters remain to be determined from observed data. It is useful to consider two sub-cases:

Physical Modeling: A model structure can be built on physical grounds, which has a certain number of parameters to be estimated from data. This could for example be a state space model of given order and structure.

Semi-Physical Modeling: Physical insight is used to suggest certain non-linear combinations of measured data signal. These new signals are then subjected to structures of black box character.

Black Box Models: No physical insight is available or used, but the chosen model structure belongs to families that are known to have good flexibility and have been successful in the past. The only chance to get the model is to collect data and use them to guess the links between inputs and outputs.

Despite the quite simplistic nature of many black-box models, they are frequently very efficient for modeling dynamical systems, require less engineering time to construct, and also useful to deal with very complex systems than white-box models [3].

According to the modelling approach, dynamical systems models are generally of two types, parametric non-parametric models. In parametric model, model parameters have meaningful values in the real process (i.e. theoretical model). While in non-parametric model, model parameters have no meaningful values for the process (empirical model, neural network model, etc.). According to this there are two types of identification categories− parametric and non−parametric approaches.

1- Parametric approach− suppose a set of candidate models has been selected (such as transfer function or impulse response), and it is parameterized as a model structure using a parameter vector ɵ. The parametric methods determine or estimate the best values of the vector ɵ. These methods are sometimes referred as parameter estimation methods [1]. Example of the parametric approaches: least square, recursive least square, generalized least square, maximum likelihood and instrumental variables. The parametric approach can take a known model structure or a limited number of unknown parameters.

2- Non−Parametric approach− these methods aim to determine the system model without first selecting a confirmed set of possible models. These methods are often called nonparametric since they do not employ a finite-dimensional parameter vector in the search for a best description [1]. They can be divided into nonparametric time-domain modelling and nonparametric frequency-domain modelling. Example of this approach includes transient analysis, frequency analysis, correlation analysis, spectrum analysis, genetic algorithms (GA) and Neural Networks (NNs). Nonparametric approach may be no definite model structure or described in many points (frequency characteristics, impulse response

In general non-parametric methods are easy to use but they give moderately accurate models. According to that, system identification problem consists of two subtasks:-

a) Structural identification of the equations in the model,
b) Parameter identification of the model's parameters $\tilde{\theta}$.

In this paper we used Raybman model-table identification method for structure identification while the genetic algorithm is used for parameter estimation. The paper is organized as following, in section 2 describe the Raybman model-table identification method. Section 3 Raybman model-table identification method algorithm. Section 4 described the statement of the correlation problem. Section 5 described the proposed genetic algorithm. Section 6 illustrative example.

2. Raybman Model-Table Identification Method

Consider a linear stationary dynamic system with one input and one output, described by the convolution integral over the impulse response function based on noise measurement output

$$y(t) = \int_0^{\infty} w(\tau)u(t-\tau)d\tau + \eta(t) \quad (1)$$

The problem of identification is to build the impulse response function estimation w(t) according to the observations of y(t) and u(t) at a certain time interval [0,T] as shown in figure 1. The average quadratic loss function is:

$$Q = \frac{1}{T}\int_0^T [y(t) - y_M(t)]^2 dt = \frac{1}{T}\int_0^T [y(t) - \int_0^{\infty} w(\tau)u(t-\tau)d\tau]^2 dt \quad (2)$$

In numerous studies [4,5, 6,7, 8, 9, 11, 12] for the identification of linear dynamic systems shows that the evaluation of the impulse response function linear stationary system obtained by the criterion of minimum mean squared error, defined as the solution of the integral equations of Wiener-Hopf:

$$R_{yu}(t) = \int_0^{\infty} w(\tau)R_{uu}(t-\tau)d\tau \quad (3)$$

where $R_{uu}(t)$ is the autocorrelation function of a stationary ergodic process u(t); $R_{yu}(t)$ - The cross-correlation function of a stationary ergodic process u(t) and y(t), calculated on the interval [0, T] for $T\to\infty$. Unfortunately, the problem of finding the impulse response function w(t) of integral Wiener-Hopf equation (3), except for the special case when the input is absolutely random signal such as white noise, belongs to a class of so-called incorrect or incomplete problems [4, 6, 7, 10] . In practical terms, the incorrectness of the problem means that even small errors in input data can lead to large errors in the solution of the problem or in general to the inability to obtain any decision. Thus, for the solution of (3) it is necessary to provide the correlation functions in analytical form, which is not always possible, because in practice these functions are determined by numerical methods, the experimentally removed implementations of input-output signals in normal operation of the facility. Furthermore, it is theoretically required to determine the correlation functions for infinite samples, in practice it is possible their estimation methods of mathematical statistics only for a finite time interval [0, T]. All this leads to random errors in the estimates of correlation functions, which makes the task of solving the Wiener-Hopf equation (3) incorrect problem. Under the guidance of the Russian professor Raybman [7] developed a method called the model table of identification of linear dynamic control object, which avoids many of the problems associated with the decision incorrect problems when used for the identification of Wiener-Hopf equation (3).

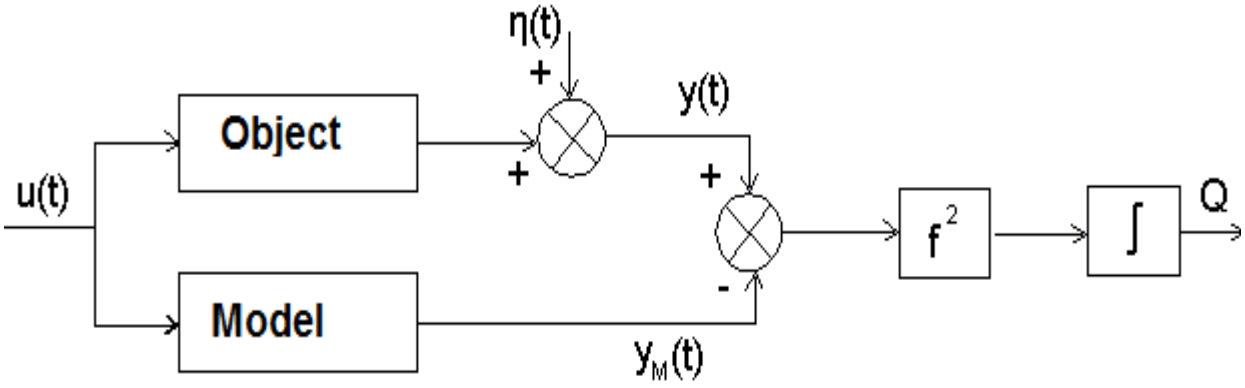


Fig. 1: correlation identification model

3. Raybman model-table identification algorithm

The basic idea of this method in identification the impulse transfer function is by calculation the experimental correlation functions $R_{yu}(t)$ and $R_{uu}(t)$ and special prepared table [7]. This table contains three columns:- the first one contains the graphic and analytical characteristics of the input action, namely the autocorrelation function $R_{uu}(t)$. The second one contains the graphic and analytical characteristics of the output action, namely, cross-correlation function $R_{yu}(t)$. The third one contains differential equation objects with these parameters that convert $R_{uu}(t)$ into $R_{yu}(t)$. Identification is produced by the visual selection of the corresponding tabular and experimental autocorrelation and cross-correlation functions , followed by recalculation of the parameters of the resulting differential equations using graphs found on scaling factor of the correlation functions. This method allows the operator to determine the approximate object with a very low cost of work and time of implementations of input-output signals control object received in its normal mode of operation. However, because of its proximity, it can only be used as a rapid method for the preliminary analysis and solution of problems of identification that do not require very high precision or when the designed control system will be quite rough (insensitive) to the parameters of control object. In addition, this method is completely manual, as required by the experimenter's visual selection of the most similar to the experimental table of auto and cross-correlation function of a sufficiently large number of functions listed in the tables of the book [7]. This method allows to get a model of differential equations up to third order:-

$$y'''(t) + a_1 y''(t) + a_2 y'(t) + a_3 y(t) = b_0 u''(t) + b_1 u'(t) + b_2 u(t)$$

4. Statement of the Problem

Consider the wide class of dynamic objects described by linear discrete difference equations of the form

$$y(k) = -\sum_{i=1}^{p} a_i y(k-i) + \sum_{j=0}^{q} b_j u(k-j) \quad (5)$$

where $y(k)$ object output signal; $u(k)$ object input signal; a_i and b_j parameters of the differential equation; p and q parameters of the structure model. The discrete form of model (5) can be described by z-transfer function:

$$W(z) = \frac{Y(z)}{U(z)} = \frac{b_0 + b_1 z^{-1} + \cdots + b_q z^{-q}}{1 + a_1 z^{-1} + \cdots + a_p z^{-p}} \quad (6)$$

Suppose that the measured output signal of object (5) is affected by additive white noise $v(k)$ with zero mean and bounded variance:

$$y_m(k) = y(k) + v(k) \quad (7)$$

then the problem of correlation parameter identification of model equation (4) and measurement signal output by equation (7) could be formulated as minimization quadratic loss function of the form:

$$Q = \sqrt{\frac{\sum_{k=0}^{n} (R_{yu}^{M}(k) - \hat{R}_{yu}(k))^2}{n-1}} \quad (8)$$

where $R_{yu}^{M}(k)$ is the cross-correlation function between the input signal and output signal of the model; n is the number of samples or correlation window.

Note that preliminary problem to be solved is structural identification, i.e. found the order and form of the operator model (5) or (6). Recall that this problem can be solved, for example, using a table model identification table [3, 5]. Thus, the method of sample identification table [3, 5] can also determine the initial parameter estimates, and hence define the actual range of variation. Thus; structure identification and initial parameters estimation could be solved using Raybman method; while the accurate parameters values will be estimated using genetic algorithm; as shown in figure 2.

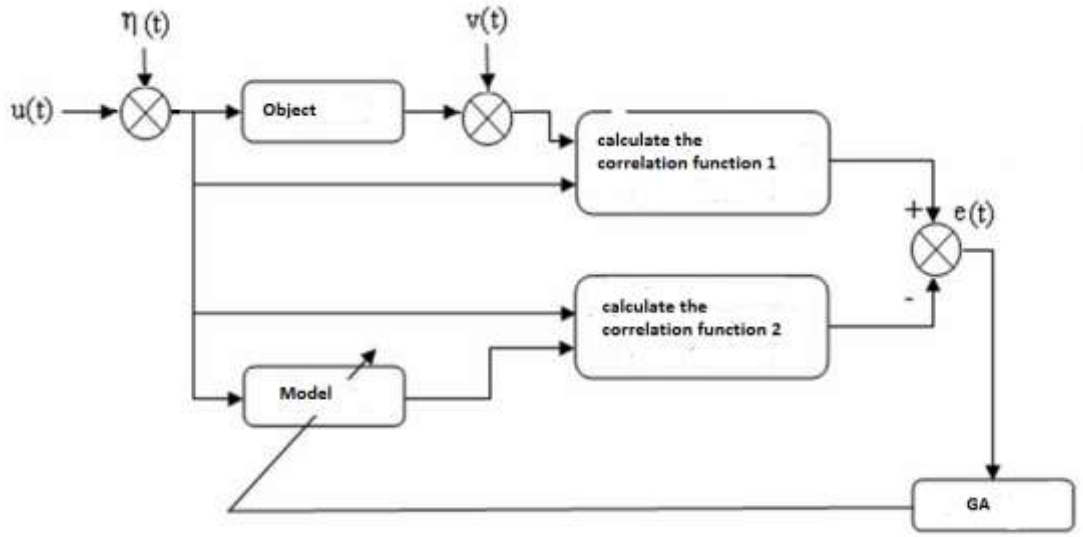


Figure 2:- structure correlation identification and parameter estimation by GA

5. Genetic algorithm

Genetic algorithms (GAs) are powerful and widely applicable stochastic search and optimization methods based on the concepts of natural selection and natural evaluation. GAs are applied to those problems which either cannot be formulated in exact and accurate mathematical forms and may contain noisy or irregular data or it takes so much time to solve or it is simply impossible to solve by the traditional computational methods [13]. Genetic algorithms were first invented by John Holland in 1960s and were developed by Holland and his students and colleagues at the university of Michigan in the 1960s and the 1970s [14]. GA shows great promise in complex domains because it operates in an iterative improvement fashion. The search performed by it is probabilistically concentrated towards regions of the given data set that have been found to produce a good classification behavior. GAs work on a population of individuals represents candidate solutions to the optimization problem. These individuals consist of strings (called chromosomes) of genes. The genes are a practical allele (gene could be a bit, an integer number, a real value or an alphabet character, etc. depending on the nature of the problem). GAs apply the principles of survival of the fitness, selection, reproduction, crossover (recombining), and mutation on these individuals to get, hopefully, a new butter individuals (new solutions) [13].

GA has been shown to be an effective strategy in the off-line design of many fields. In this paper, GA has been used to provide an adaptive decision algorithm for determining the optimum parameters for system identification form. We present some modifications on the conventional genetic algorithm, which made it applicable in the real time optimization. The basic principle of the real-time genetic algorithm is by creating a population called elite-population, this population contains the best fitted chromosomes from the previous optimizations cycles. The identification procedure starts with random predefined values. When prediction error r (the residual or innovation) is greater than an acceptable value (desired error), which indicates that the identification starts diverge from desired output, then the genetic algorithm begin to find the parameters values (optimization procedure). The best values of the parameters will be saved in the elite-population. In the next measurements, when the prediction error r greater than an acceptable value, we check the elite-population pool. If elite-population pool results produced an error greater than the desired error, we start the genetic algorithm optimization to find other parameters values, which they are saved in the elite-population. This procedure is repeated for every prediction error. Fig.3 shows the proposed algorithm flowchart.

The following steps describe the parameters identification using the proposed genetic algorithm [15]:-

1- Defines and initialize the variables and the known parameters of system and GA (the most important of them are):

NIND: number of individuals or chromosomes in the population. MAXELIT: maximum number of individuals in the elite-population. MAXGEN: the maximum number of generation for each optimization cycle. ε : desired error value.

2- First generation initialization:

First generation is initialized by a random real numbers. Each real number corresponds to gene in the individual (or chromosome). Number of individuals is equal to NIND, while the number of genes equals to number of variables to be optimized. The genes are randomly generated from predefined limits as follows:

$$B_k^l \le \theta_k \le B_k^u \qquad 9$$

where $k = 1,2,....,M$, θ is representing a gene. M is the number of genes in the chromosome. B_k^l and B_k^u are lower and upper limits of the gens respectively. The real value encoding scheme saves memory and improves processing speed.

3- Read the new measurements:

The new measurements are made to clarify the current values of the objective function (fitness function) in real-time tasks.

4- Fitness evaluation of each individual in a generation:

For each individual in the current generation, calculate the fitness function using a predefined formula or procedure. For example, in the problems of identification of dynamic objects, this may be the square prediction error output at the current time.

5- Adding the best individuals in the elite population:

Elite population, which has a maximum size equal to MAXELIT, during operation of the genetic algorithm, it is constantly formed from the individuals with the best fitness function. Further, if the elite population has MAXELIT individuals and we get an individual from the current population, which has a best fitness function value better than the current fitness function of one or more individuals from the elite population, then this individual replaces the individual having the worst fitness of the current function in the elite population.

6- Checking the termination criterion optimization of elite population:

Decision to complete the procedure of searching an acceptable solution at the current step of the algorithm and output measurement results shall be accepted if the elite population has at least one such individual has a fitness function better than the specified precision optimization error (ε). If such individuals are more than one, of course, select the individual which has the best fitness function. Otherwise, the decision will be on the implementation of the main stages of the classical GA.

7- Classical genetic algorithm (Fig.3 inner loop):

The classical or conventional genetic algorithm has following major components [16]: selection of the parents - the most appropriate individuals to participate in the creation of a new generation (recombination); crossover: genes are exchanged or combined during recombination; mutation: selects probabilistically one of the fittest individuals and changes a number of its characteristics in a random way. The formation of a new generation and evaluation for its constituent is species of the fitness function. Finally, for each new generation a verifiable criterion formed at the end of the optimization process. This criterion is met in two ways: if at least one of the individuals of the current generation of fitness function is better than the specified precision optimization (ε), i.e. convergence of GA population; or turn out of maximum generation (MAGEN). With this approach, in principle, complete the loop of optimization procedure, and then quit the GA.

8- Choosing the best individuals from the current genetic population or the elite population, then output of the result:

In this step, the current chromosome is selected from either the classical genetic algorithm population or from the elite-population individuals, which has the best fitness function. This chromosome is taken as the result of solving the problem at the current step measuring algorithm.

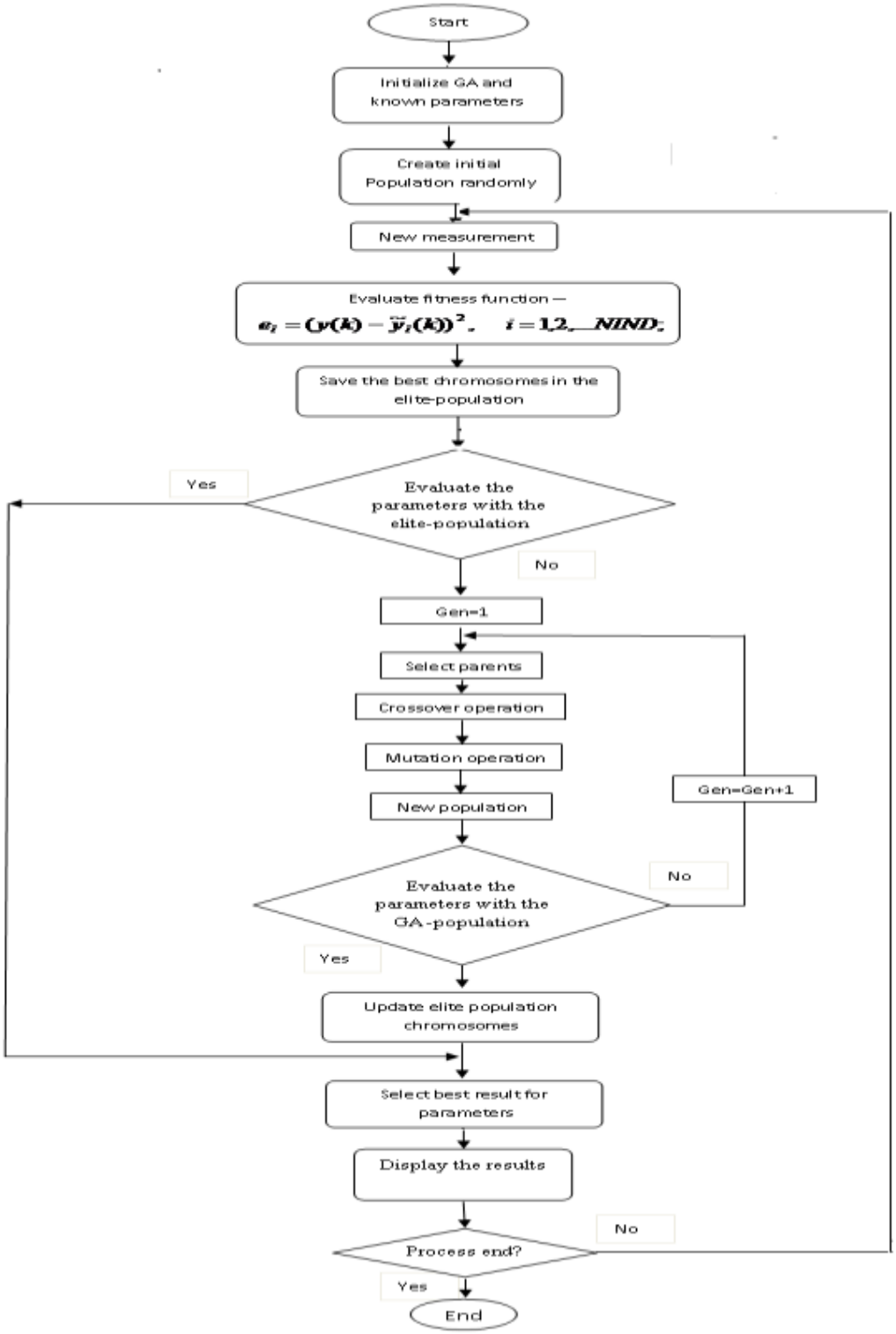


Figure 3: Proposed GA

6. SIMULATION RESULTS

Consider as an example the linear system described it transfer function of the form:

$$W(s) = K/(T2s2+2\xi Ts+1) \quad 10)$$

where; s – Laplace operator, K is the system gain, ξ is called the damping ratio of the system, and T is called the natural frequency of the system (or time constant).

The actual parameters have the following values: K=0.9, T=0.025 sec, and ξ=0.25, and the initial values are all zero. Consider we have the following responses corresponding to the input auto-correlation graph R_{xx}; cross-correlation graph between the input and output signals R_{yx}; as shown in figures 4 and 5 respectively.
Let T_0 is the sampling time. Then, the identification process takes the following steps:- 1) Find system transfer function: search the tables listed in the book and check the response like the given in figures 4 and 5. After that we have the following system equation:-

$$W(s)=K/(T^2s^2+2\xi Ts+1) \quad 11)$$

2) Parameters estimation: equation number (10) is used in genetic algorithm for validation of parameters identification algorithm as shown in figure 6. The fast genetic algorithm is used to find the best chromosomes that represent the unknown parameters such that $\tilde{y}(k)\rightarrow y(k)$, where; k=0,1,2,… discrete time space. The GA has the following parameters: NIND=20; MAXELIT=20; MAXGEN=100; ε=10−5; Pc=0.9; Pm=0.04, genes are selected randomly in the range [0 ÷ 1].

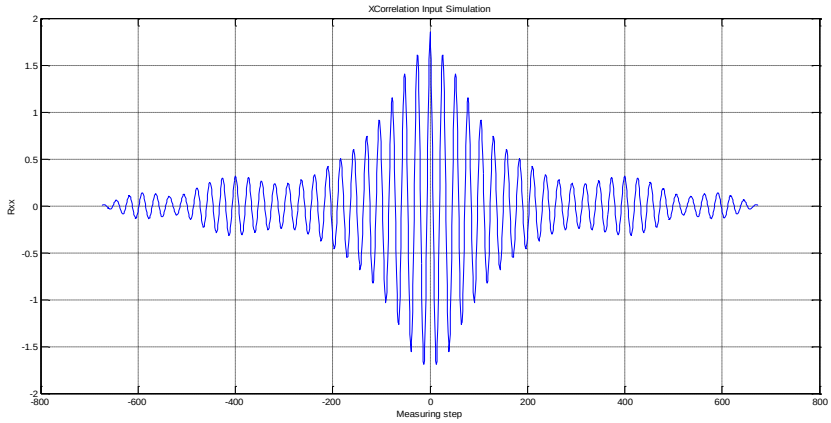


Figure 4: Autocorrelation of the input signal

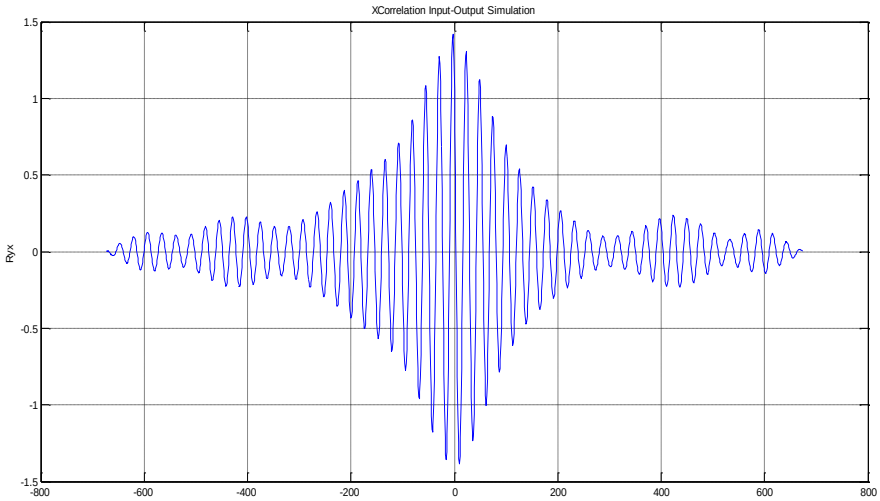
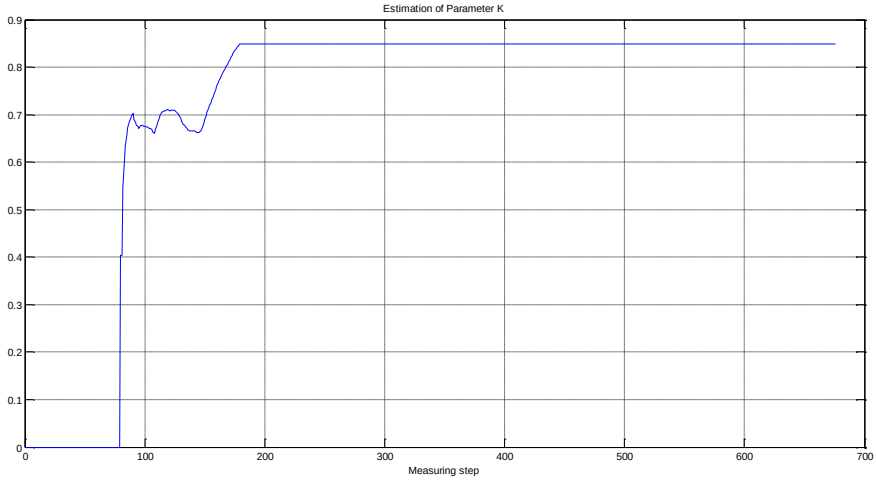
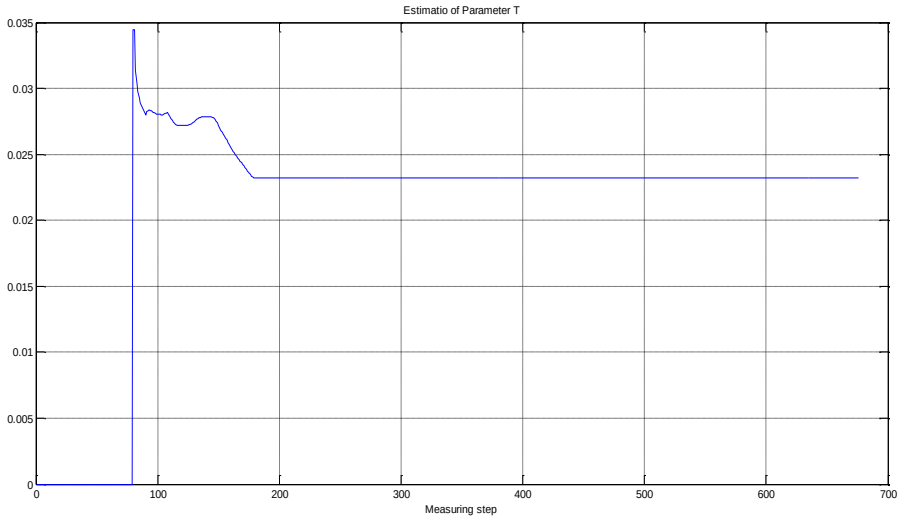


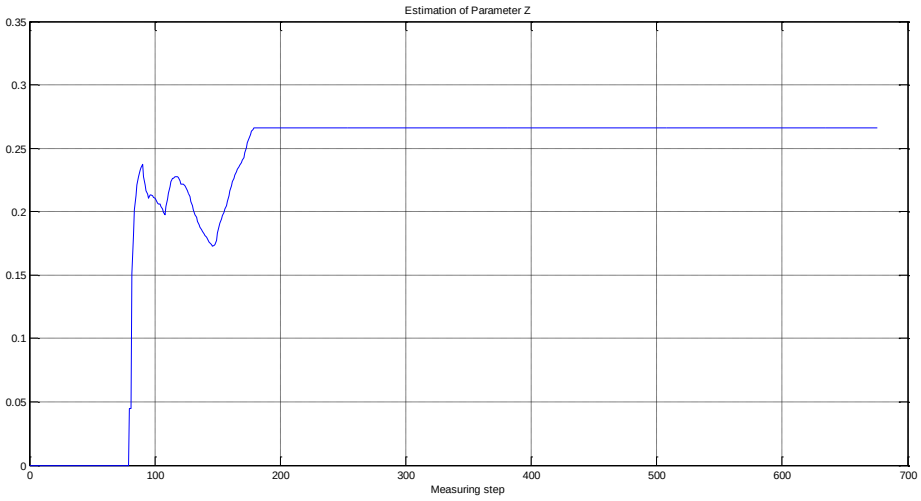
Figure 5: Cross correlation between the input and output signal



(a)



(b)



(c)

Fig. 6: Simulation result of identification of the parameters. (a) - Estimation of the gain K, (b) - estimation of time constant T, and (c) - estimation of damping ratio ξ.

CONCLUSIONS

Raybman model-table identification method is very simple, easy and practical method for structure and parameters system identification problem. This method is based on correlation information got for input and output signals and database of related correlation graphs. The main drawback of this method is low accuracy, very slow; which is completely depending on searching the graphs. In this paper we maintained the drawback of this method, where we used the main Raybman method only to find the structure or the model equation of the system, while we proposed the fast genetic algorithm to estimate the system parameters. As shown from simulation; the proposed work has good and fast identification process.

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