On-Line Parameters Estimation Using Fast Genetic Algorithm

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Abstract- The requirements for on-line identification of system parameters have a critical need for engineering applications, such as fault diagnosis and process detection. The classical identification methods, such as least-square method, are calculus-based search method. These methods are suffered from many problems, such as a proper initial values of the identified parameters; the objective function requires an exact definition of the gradient or higher-order derivatives; also a possibility to fall into a local minimum. In this paper we develop on-line, robust, efficient, and global optimization method for parameters estimation based on fast genetic algorithms with special reserve elite population. The simulation results show that the proposed algorithm is very fast to find and adapt the estimated parameters.

Keywords- Parameters Identification; Reserve Elite Population; Fast Genetic Algorithm for Real Time Applications

I. INTRODUCTION

System identification is the process of manipulating measured data to construct mathematical models of dynamical systems. 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). When a good model is obtained, then it can be used for the analysis or designing of many system applications, such as analysis; prediction or controller design. The system identification problem can be manipulated simply as an optimization problem, where the goal is to find a suitable model and a set of accurate parameters that minimize the prediction error between actual system output y(t) (the measured data), and model output ŷ(t, ê) at each measure time-step t [1].

The use of genetic algorithms for process identification is beginning to attract interest. Genetic algorithms search from a population of points and have a random component, quantified as a mutation rate, that helps drive the model parameters towards values corresponding to the global minimum of a possibly multimodal cost function; such cost functions often arise in the identification of delayed processes [2]. Genetic algorithms trade off large computation time, and poor accuracy of the global minimum, with reliability in calculating the global minimum [3]. Yang et al. [4] use a genetic algorithm to estimate the denominator parameters and delay of a reduced order process model, while using the less computationally intensive least squares algorithm to subsequently determine the numerator model parameters (which is a linear problem). Similar approaches are also described [5, 6].

Genetic algorithm (GA) is a heuristic search that simulates the process of natural selection. This heuristic is used to generate useful solutions to optimization and search problems [7]. Genetic algorithms generate solutions to optimization problems using techniques inspired by natural evolution, such as inheritance, selection, crossover, and mutation.

A simple genetic algorithm consists of a population of random chromosomes. Then evaluates these chromosomes and allocates reproductive opportunities in such a way that those chromosomes which represent a better solution to the target problem are given more chances to reproduce than those chromosomes which are poorer solutions. The goodness of a solution is typically defined with respect to the current population [8].

In basic genetic algorithms, it is possible for the next generation to have a best individual with a lower fitness than the best individual encountered in a preceding generation. This loss of the best individual occurs due to the probabilistic nature of the GA selection, crossover and mutation, and hence helps to improve the overall performance of the algorithm. To overcome this problem, elitism technique is used [9-14]. It is an effective tool to improve the performance capability of GAs, because it prevents losing the best found solutions by conserving the best solutions obtained in the optimization process.

Thus elitism in GA is a mechanism to ensure that the traits of the fittest individuals are transferred to the next generation. This is achieved by selecting some of the fittest individuals and keeping them as part of the next generation. These chromosomes are not affected by mutation and crossover. In many cases, the employment of elitism can produce better search results.

Meskine et al [9] used elitism genetic algorithms based image registration. Where, the best 5 percent of individuals in the population are preserved and copied in the next generation. The remaining are from the top ranked individuals after all the GA operations are performed.

Kalyanmoy et al [10] proposed a fast elitist multiobjective GA. In his work, the offspring population is
combined with the current generation population and selection is performed to set the individuals of the next generation. Since all the previous and current best individuals are added in the population, elitism is ensured. Population is now sorted based on non-domination. The new generation is filled by each front subsequently until the population size exceeds the current population size. If by adding all the individuals in front \( F_1 \) the population exceeds \( N \) then individuals in front \( F_1 \) are selected based on their crowding distance in the descending order until the population size is \( N \). And hence the process repeats to generate the subsequent generations.

Morales [11] described a GA which departs from canonical GAs (CGA) and achieves most of the characteristics of what, in the literature, has been called an Idealized GA (IGA). This GA is designed to approach the IGA and they have it called an Eclectic Genetic Algorithm (EGA). They describe the application of an EGA to the solution of a set of six constrained nonlinear problems.

Franck et al. [12] presented the elitism GA, in which they analyzed the behavior of an evolutionary algorithm designed to estimate the parameters of a complex organ behavior model. Yang [13] introduced an elitism-based immigrants scheme and investigated for GAs in dynamic environments. In this scheme, the elite from previous generation is used as the base to create immigrants via mutation to replace the worst individuals in the current population. Chakraborty and Chaudhuri [14] used GA with elitism to provide a general formulation for the problems that arise in the computation of many robust and nonparametric estimates in terms of a combinatorial optimization problem.

In this paper, we introduce a fast genetic algorithm based on some modification of classical GA, and due to presence of special reserve elite population can significantly reduce the search for acceptable solutions for individuals through the measurement steps. The reserve elite population used in the proposed work differs from the known elitism mechanism, in which it is not used in the GA routine loop at all, as we will describe it later.

The paper is organized follows: section II describes the statement of the problem. Section III describes the proposed real-time parameters identification procedure based genetic algorithm. Section IV describes the simulation and results.

II. STATEMENT OF THE PROBLEM

Consider the general time-invariant recursive system described by ARMA model:

\[
y(k) = - \sum_{i=2}^{p} a_i y(k-i) + \sum_{j=0}^{q} b_j x(k-j)
\]  

where \( y(k) \) is the output signal, \( x(k) \) is the input signal, \( a_i \) and \( b_j \) are the parameters of the ARMA model, \( p \) is the order of the autoregressive part and \( q \) is the order of the moving average part. System model (1) can be written as a rational transfer function in z-domain:

\[
W(z) = \frac{Y(z)}{X(z)} = \frac{b_1 + b_2 z^{-1} + \cdots + b_q z^{-q}}{1 + a_1 z^{-1} + \cdots + a_p z^{-p}}.
\]  

The output data signal is usually observed with an additive white Gaussian noise, \( v(k) \), given by

\[
y_m(k) = y(k) + v(k)
\]  

Parameters estimation have significant engineering applications, because of in many real-world problems the physical values of the system are not known a priori, which is made it difficult for use in tasks such as control, monitoring, or fault diagnosis [1, 15]. Beyond adaptive control, one of the main applications of parameter estimation is the detection of faults and the monitoring of system condition [16]. By detecting estimated parameter drifts and/or abrupt changes in system parameters, the onset of a fault can be detected in a timely manner [17, 18].

The classical identification methods are calculus-based search method. These methods are suffered from many problems, such as a difficulties to define a proper initial values of the identified parameters; the objective function requires an exact definition of the gradient or higher-order derivatives; also a possibility to fall into a local minimum [1, 19].

The least-squares (LS) method is a basic technique often used for parameters estimation. It has been successfully used to estimate the parameters in the static and dynamical systems. Mathematically the LS method appears very good. It does however have difficulty when dealing with real data as noise and in adequacy of system models can cause the results to deviate significantly. Though the derivation of the method assumes noise on the output, it does not allow for noise in the regressors, which is unavoidable in a real situation.

The aim of this paper is to identify the unknown parameters of the system (1) or (2) with measurements (3), using the same model for the unknown parameters identification by fast GA, as shown in figure 1.

![Identification procedure](image)

Fig. 1 Identification procedure

The objective function for parameter identification (i.e. the fitness function for GA) is to minimize the normalized square error of the output predicts (the residual or innovation):

\[
e(k) = (y(k)-\hat{y}(k))^2.
\]  

III. PROPOSED REAL TIME PARAMETER IDENTIFICATION BASED 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 [19]. 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 [20]. GAs work on a population of individuals represents solutions to the optimization problem. These individuals consist of strings (called chromosomes) of genes. 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) [19].

GAs have been shown to be an effective strategy in the off-line design of many fields. The GAs are not too demanding, as could be natural to expect, in terms of their needs of computational power.

However, in this paper we present some modifications on the conventional genetic algorithm, which made it applicable in the real time optimization. The basic principle of this fast genetic algorithm is by creating an array called reserve elite population. This population contains the best fitted chromosomes from the previous optimizations cycles.

The following steps describe the parameters identification procedure using fast genetic algorithm, which are described in details at [21] (figure 2):

1- Defines and initialize the variables and the known parameters of system and GA:

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:

$$B_k^l \leq \theta_k \leq B_k^u,$$

where $k=1,2,...,M$; $\theta$ - 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.

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 (4).

5- Adding the best individuals in the reserve elite population:

During operation of the classical genetic algorithm, reserve elite population is constantly formed from the individuals with the best fitness function. Further, if the reserve 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 reserve elite population, then this individual replaces the individual having the worst fitness of the current function in the reserve elite population.

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elite population has at least one such individual has a fitness function better than the specified precision optimization error ($\epsilon$).

7- Classical genetic algorithm (Figure 2 inner loop):

The classical or conventional genetic algorithm has following major components [22]: 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 one of the individuals and changes its characteristics in a random way. 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 ($\epsilon$), i.e. convergence of GA population [7]; 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 reserve 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 reserve 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 real-time algorithm.

Firstly, the fast genetic algorithm (figure 1) generates a random chromosome (which represents parameters of model) with a NIND sets. These chromosomes (parameters) are selected randomly from the range limits defined in equation (5). The reserve elite population is filled by checking the objective function (4) by choosing the best chromosomes that produced minimum objective function less or equal than $\epsilon$. If there is no chromosomes produced this minimum objective function, then proceeds to the classical GA loop to find the best chromosomes. These chromosomes produced by classical GA will be saved in the reserve elite population.

Further, for each measuring step, the algorithm checks the objective function with the reserve elite population chromosomes, if there is good chromosomes that produced an objective functions less or equal than $\epsilon$, then take the next measurement. If the reserve elite population had not chromosomes that produced objective functions less or equal than $\epsilon$, then proceed to operate the classical GA to generate the best chromosome in which objective functions less or equal than $\epsilon$, this chromosome is saved in the reserve elite population until it reach its maximum size MAXELIT; otherwise replace this chromosome by the worst chromosome saved in the reserve elite population. This procedure is repeated for every new measurement.

The proposed fast genetic algorithm for parameters identification at each step of measurement is able to provide some acceptable results, which, most often, will satisfy a predetermined requirement for accuracy ($\epsilon$), and only in relatively rare cases where the reserve elite population, and in all population (MAGEN) generations of classical GA fail to find the right individual, this requirement will be violated. In addition, from the scheme of the algorithm (Fig. 2) shows that in those cases when it is possible to find an acceptable solution in the elite population, the procedure is not performed classical GA, and this leads to the release of a significant amount of time between consecutive measurements for other concurrent real-time task.

IV. SIMULATION RESULTS

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

$$W(s) = \frac{K}{(T^2s^2 + 2\xi Ts + 1)},$$

where: $s$ - Laplace operator, $K$ is the system gain, $\xi$ 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: $K=0.9$, $T=0.02$ sec, and $\xi=0.1$, and the initial values are all zero.

Let $T_0$ is the sampling time. Then, the identification process by the fast genetic algorithm is to find the best chromosomes that represent the unknown parameters such that $y(k) \rightarrow y(k)$, where; $k=0,1,2,...$ discrete time space; $x(k)=\sin(2\pi f) \text{ known input signal; } f=5 \text{ Hertz; }$ sampling time $T_0=0.001 \text{ sec; } n=KT_0; y(k) \text{ - measuring output signal; } \tilde{y}(k) \text{ - estimating output signal. The noise v(k) is assumed to be random, white, Gaussian noise sequence with zero means and covariance 0.1.}$

The GA has the following parameters: $\text{NIND}=20; \text{MAXELIT}=20; \text{MAXGEN}=100; \epsilon=10^{-5}; P_s=0.9; P_m=0.04$, genes are selected randomly in the range $[0 \div 1]$. 

Figure 3 shows the number of generations required by the proposed algorithm compared with classical GA. As indication for total number of generation, following table shows the statistics performance for both methods:

<table>
<thead>
<tr>
<th>Statistics measure</th>
<th>Proposed algorithm</th>
<th>Classical GA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Min. value</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>Max. Value</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Mean</td>
<td>13.01</td>
<td>20.59</td>
</tr>
</tbody>
</table>

Fig. 3 Number of generations required by the proposed algorithm and the classical GA.
Figure 4 shows the identification process of the unknown parameters.

As seen from figures above that the proposed algorithm gave good results for parameters identification. As noticed in figure 3 and table 1, that the number of generations required to optimization by the proposed GA is about 60% of the generations required by the classical GA. Also as seen from figure 4, that the proposed algorithm has a fast convergence of identification procedure, which it need approximately less than 10 measuring steps. As shown in figure 4-a, the identification error is very small and bias is absent. In figure 4-b and 4-c, there are an accepted error and small bias. Finally note, the amount of error may be reduced according to the required accuracy of the algorithm (c).

V. CONCLUSIONS

As mentioned earlier, the classical identification methods are suffered from many problems, such as a proper initial values of the identified parameters; the objective function required an exact definition of the gradient or higher-order derivatives; also a possibility to fall into a local minimum. In this paper we developed the algorithm for parameters estimation of the system transfer function. The adaptive stage to optimize the parameters values is by using a fast genetic algorithm. A modification was made to the classical genetic algorithm by introducing a reserve elite population, which makes the search for an acceptable solution for most steps of measurement takes a minimum time. As seen from the simulation results that the adapted GA try to correct the estimated parameters at very fast time.

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