

State Space Parameters Estimation Using Online Genetic Algorithms †

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Abstract – **A**ccurate on-line estimates of critical system states and parameters are needed in a variety of engineering applications, such as condition monitoring, fault diagnosis, and process control. In these and many other applications it is required to estimate a system variable which is not easily accessible for measurement, using only measured system inputs and outputs.

The classical identification methods, such as least-square method, are calculus-based search method. They have many drawbacks such as requiring a good initial guess of the parameter and gradient or higher-order derivatives of the objective function are generally required also there is always a possibility to fall into a local minimum. In this paper we develop on-line, robust, efficient, and global optimization identification for parameters estimation based on genetic algorithms. The simulation results show that the proposed algorithm is very fast to find and adapt the estimated parameters.

Keywords – State space parameters estimation, online genetic algorithm.

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1. Introduction

Modern estimation theory [1] – [14] can be found at the heart of many electronic signal processing systems designed to extract information. These systems include: - radar, sonar, speech, image analysis, biomedical, communications, and control, etc., and all share a common problem of needing to estimate the values of states and/or a group of parameters. State estimation plays an important role in process industries. It is the mean to estimate the unmeasured information and parameters and filter noisy measurements.

According to Gelb [1], Estimation is the process of extracting information from data; which can be used to infer the desired information and might contain errors. Modern estimation methods use known relationships to compute the desired information from measurements, taking account of measurement errors, the effects of disturbances and control actions, on the system, and prior knowledge of the information. Diverse measurements can be blended to form best estimates, and information which is unavailable for measurement can be approximated in optimal fashion. The quantity of interest in an estimation problem can be a parameter - a time-invariant quantity (parameter estimation), or the state of a dynamic system (state estimation) [15]. Estimation theory is concerned with inferring the value of a quantity of interest from indirect, inaccurate and uncertain observations. It consists of four components [16]:- parameter space, observation space, probabilistic relation between the parameter space and the observation space, and estimation criteria. The probabilistic relation between parameter space and observation space determines the formulation of the

problem. The parameter is estimated from the observations based on the probabilistic relation, most often, through the optimization procedure with objective function defined by estimation criterion [17].

Genetic algorithms (GAs) are a family of general stochastic search methods, which can be viewed as computational models of Darwinian evolution theory. They use the analogs of evolutionary operators on a population of states in a search space to find those states that optimize a fitness function. The search space consists of character strings of fixed or variable length (chromosomes or genotypes) composed of the elements of a given alphabet (alleles). The genotype space is mapped onto another (phenotype) search space. The fitness function is defined as a function of a state in the phenotype space [18] – [20].

An implementation of a genetic algorithm begins with a population of typically random chromosomes. One then evaluates these structures 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 [21].

In this paper, we introduce an on-line genetic algorithm based on some modification of classical GA, and due to presence of special elite-population can significantly reduce the search for acceptable solutions for individuals through the measurement steps.

The paper is organized as follows: section 2 describes statement of the problem. Section 3 describes the estimation of parameters using real-time

genetic algorithm. Simulation and results are given in section 4.

2. Statement of the Problem

Consider the classical discrete-time state space problems in case of linear model of the form:-

$$x(k+1) = Fx(k) + Gu(k) + w(k) \quad (1)$$

where $x(k)$ is the discrete-time state. The matrix F referred to as state transition matrix, G is input matrix. The vector $u(k)$ is the inputs and assumed to be known at perspective times. The state noise process $w(k)$ is a Gaussian random variable with zero mean and known covariance Q . The state noise at different times are assumed to be mutually uncorrelated, that is,

$$\text{cov}(w(k), w(j)) = E[w(k)w(j)^T] = Q\delta(k, j) \quad (2)$$

where $\delta(k, j)$ is the Kronecker delta.

The linear observation equation is of the form:-

$$y(k+1) = Hx(k+1) + v(k+1) \quad (3)$$

where $y(k)$ is a vector including the measurements at time k , and H is the associated observation matrix. The observation noise $v(k)$ is a Gaussian random variable with zero mean and known covariance R . For the observation noise, it is also assumed that:

$$\text{cov}(v(k), v(j)) = E[v(k)v(j)^T] = R\delta(k, j) \quad (4)$$

and $\text{cov}(w(k), v(j)) = 0 \forall k, j$.

Parameter estimation aims to estimate some parameters of the state-space system, in addition to the state variable. Such parameters can be for example the variance of the observation noise, state noise, or parameter related to transition properties of the state evolution operator. Parameter estimation is also of significant

engineering importance, because in many real-world problems accurate values of physical system parameters are not known a priori for use in tasks such as control, monitoring, or fault diagnosis. Parameter estimation can be formulated as a state estimation problem, by considering the parameters of interest as additional states. Beyond adaptive control, one of the main applications of parameter estimation is the detection of faults and the monitoring of system condition. By detecting estimated parameter drifts and/or abrupt changes in system parameters, the onset of a fault can be detected in a timely manner [22] – [23].

The classical identification methods are calculus-based search method. They have many drawbacks such as requiring a good initial guess of the parameter and gradient or higher-order derivatives of the objective function are generally required. There is always a possibility to fall into a local minimum (see Fig. 1).

Depending upon the choice of the initial parameter values, the algorithm could prematurely stop and return a sub-optimal set of parameter values. This is called the local minima problem. Note that although the starting parameter value at point a_2 will lead to the optimal point B called the global minimum, the starting parameter value at point a_1 will lead to point A , which is a sub-optimal solution.

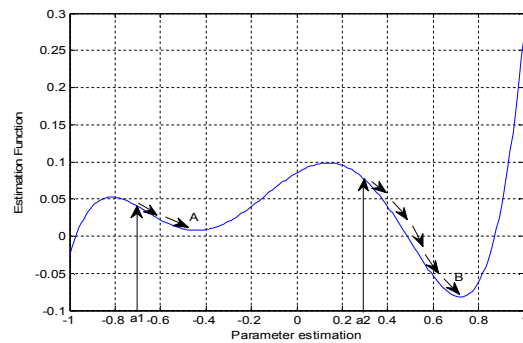


Figure 1 A schematic plot of the function for a fictitious one-parameter model. Point B is the global minimum whereas point A is local minima.

The least-squares method (LS) is a basic technique often used for parameters estimation. It has been successfully used to estimate the parameters in the static and dynamical systems, respectively. But, the least-squares method is only suitable for the model structure of system having the property of being linear in the parameters. Once the form of model structure is not linear in the parameters, this approach may be invalid. 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 regressor, which is unavoidable in a real situation.

3. Proposed Parameter Identification Based on Real Time 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. 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 [24]. 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 fittest, selection, reproduction, crossover (recombining), and mutation on these individuals to get, hopefully, a new better individuals (new solutions).

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 in state space 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 pool called elite-population, this population contains the best fitted chromosomes from the previous optimizations cycles. The elite-population used here differs from elitism chromosomes that described in many literatures, in that; the chromosomes saved in it do not reinsert in the GA routine. 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 produce 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. 2 shows the proposed algorithm flowchart.

The following steps describe the state space parameters identification using real time genetic algorithm [26]:-

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

$$B_k^l \leq \theta_k \leq B_k^u \quad (5)$$

where $k=1,2,\dots,M$, 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 [20]–[25].

- 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. 2 inner loop):

The classical or conventional genetic algorithm has the following major components [25]: 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 [16]; 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 real-time algorithm.

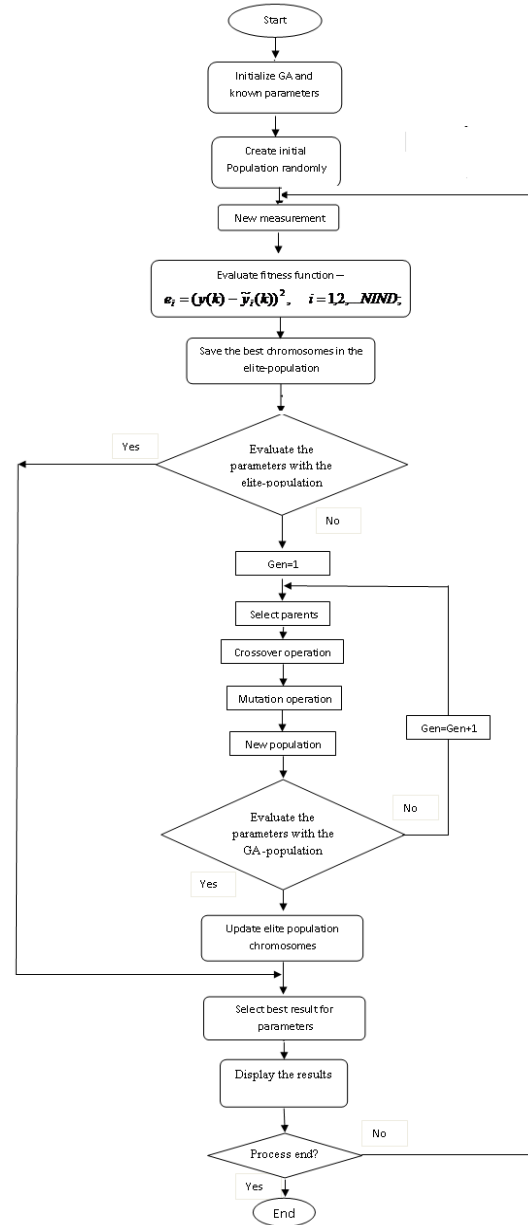


Figure 2. Proposed on-line GA

4. Simulation Results

Let $\theta \in \Omega \subset R^q$ unknown vector (estimation parameters). Then let the system to be identified by the proposed fast genetic algorithm:

$$\hat{x}(k+1) = F(\hat{\theta})\hat{x}(k) + G(\hat{\theta})u(k) \quad (6)$$

$$\hat{y}(k+1) = H\hat{x}(k+1) \quad (7)$$

The identification process by the on-line genetic algorithm is to find the best chromosomes that represent the unknown parameters such that $\hat{y}(k+1) \rightarrow y(k+1)$.

To show how the proposed algorithm works, let us consider the following second order state space system, which has five known parameters and three unknown parameters as following:

$$\begin{bmatrix} x_1(k+1) \\ x_2(k+1) \end{bmatrix} = \begin{bmatrix} \theta_1 & 1 \\ \theta_2 & 0 \end{bmatrix} \begin{bmatrix} x_1(k) \\ x_2(k) \end{bmatrix} + \begin{bmatrix} \theta_3 \\ 0 \end{bmatrix} u(k) + w(k) \quad (8)$$

$$y(k+1) = [1 \quad 0] \begin{bmatrix} x_1(k+1) \\ x_2(k+1) \end{bmatrix} + v(k) \quad (9)$$

where; $k=0,1,2,\dots$ discrete time; $u(k)=\sin(2\pi nf)$ known input signal; $f=5$ Hertz; sampling time $T=0.001s$; total time is 1 seconds which corresponds to 1000 sampling space; $y(k)$ – measuring output signal; $\hat{y}(k+1)$ – estimated output signal; θ – coefficients to be identified.

The unknown parameters have the following values as shown in table 1:

Table1. Real Values of the Unknown Parameters.

Identified coeff.	Parameter representation	Real value
θ_1	F(1,1)	1.988
θ_2	F(2,1)	-0.99
θ_3	G(1)	2.24

The initial values are: $x_1(0)=0$, $x_2(0)=0$, and $u(0)=0$. Noise vectors $v(k)$ and $w(k)$ with zero mean and co-variances

$$\begin{aligned} E(v(k)v^T(j)) &= \delta(k,j)Q; & Q &= 10; \\ E(w(i)w^T(j)) &= \delta(k,j)R; & E(w(i)w^T(j)) &= \\ \delta_{ij}R(i); & R = \begin{bmatrix} 100 & 0 \\ 0 & 100 \end{bmatrix}; \end{aligned}$$

δ – is the Kronecker delta, $E[v(k)w^T(j)]=0$.

The GA has the following parameters:
NIND=20; MAXELIT=20;
MAXGEN=100; $\epsilon=10^{-5}$; $P_c=0.9$;

$P_m=0.04$.

θ – (coefficients to be identified) are selected randomly in the range $[-10,10]$.

The fitness function used to evaluate each chromosome is minimizing the square error:

$$ObjFun = \min(e_i) = \min((y(k) - \hat{y}_i(k))^2) \quad (10)$$

where $i=1,2,\dots, NIND$; i – is the chromosome number in the population.

Figure 3 shows the identification time of the first parameter (F(1,1)), Fig. 4 shows the identification time of the second parameter (F(1,2)), and Fig. 5 shows the third parameter (G(1)). Fig. 6 shows the number of generations for each measure ($y(k)$).

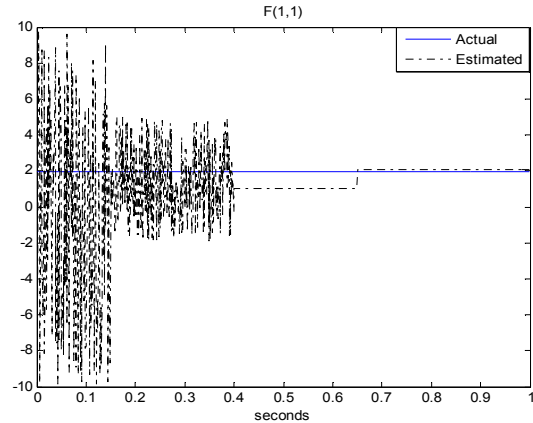


Figure 3. Simulation result of identification of the parameter F(1,1).

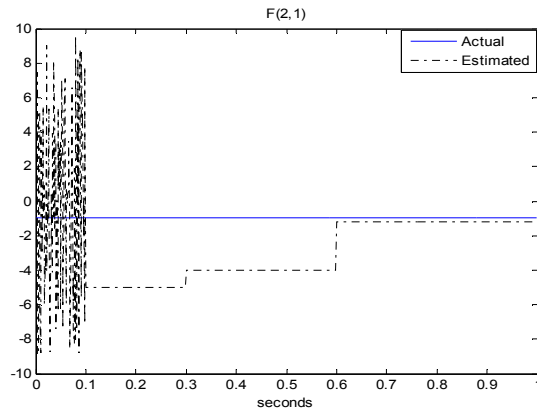


Figure 4. Simulation result of identification of the parameter F(2,1)

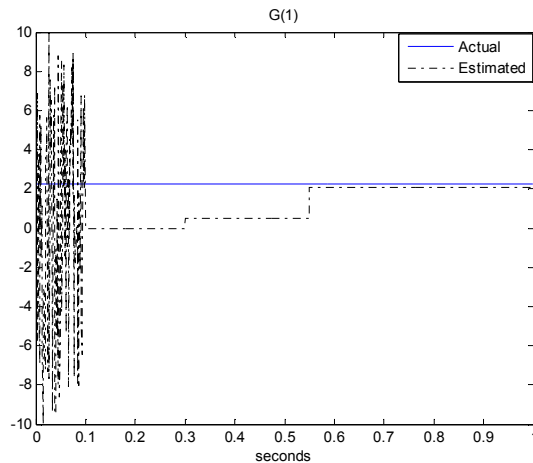


Figure 5. Simulation result of identification of the parameter $G(1)$.

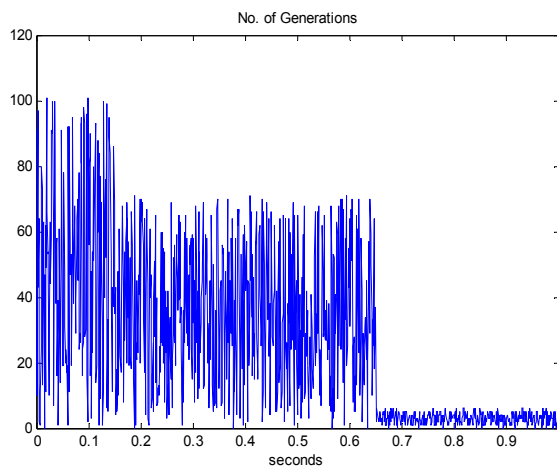


Figure 6. Number of generations for each sampling space (or measure).

5. Conclusions

The classical identification methods are calculus-based search method. They have many drawbacks such as requiring a good initial guess of the parameter and gradient or higher-order derivatives of the objective function are nearly required. There is always a possibility to fall into a local minimum. In this paper we developed the algorithm for parameters estimation of the state space system. 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 an elite-population, which makes the search for an acceptable solution for most steps of measurement takes a minimum time. As seen from the figures that the adapted GA try to correct the estimated parameters at very fast time. Another advantage of using this method, in that is, correcting the parameters in each sample time.

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