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APPLICATION OF GENETIC ALGORITHM TO MEASUREMENT SYSTEM CALIBRATION INTENDED FOR DYNAMIC MEASUREMENT

The paper presents an application of the genetic algorithm method for calibration of measurement systems intended for the measurement of dynamic signals. The process of calibration is based on the determination of the maximum value of a chosen error criterion.

The solutions presented in the paper refer to the integral-square error if the magnitude and rate of change constraints are imposed simultaneously on the calibrating signal. The practical application of the presented algorithm has been illustrated on the example of sixth order low-pass system calibration.

Keywords: maximum dynamic error, genetic algorithm

1. INTRODUCTION

The calibration process depends on the determination of the maximum error which can be generated by a calibrated system in reference to its standard. For a measurement system intended for static measurements the problem of calibration was worked out a long time ago. For a measurement system intended for the measurement of dynamic signals, usually undetermined, the question of calibration is considerably complicated owing to the fact that the determination of the maximum error requires knowledge of the input calibrating signal, which maximizes the chosen error criterion. In the literature [1, 2, 3] it was proved that the signals maximizing the integral square error always achieve one of the constraints imposed on it. If only magnitude A of the calibrating signal is constrained, the signal maximizing integral square error is always of the 'bang-bang' type, while in the case of two constraints relating to the magnitude A and the rate of change \mathcal{G} , the signal maximizing this criterion can be only of triangular or trapezoid shape with slopes resulting from the values of \mathcal{G} and A .

For the integral square error and for the above constraints the analytic solution referring to the shape of the signal maximizing this criterion has not been found so far, because the space of possible solutions is infinite and of infinite dimension.

The solution of the problem of maximum integral square error determination proposed in this paper is based on the application of the genetic algorithm method. This method guarantees that the result will be obtained in minimized calculation time which depends only on the assumed number of population as well as on the stop condition.

The practical application of the genetic algorithm worked out is illustrated on an example of calibration of a low-pass sixth order system if two constraints are simultaneously imposed on the input signal.

2. CALIBRATION OF A MEASUREMENT SYSTEM INTENDED FOR DYNAMIC MEASUREMENT

Calibration of a measurement system based on determination of the maximum error implies that the following tasks are to be solved [1]:

- Synthesis of the mathematical model of the calibrated system and its standard.
- Choice of an error criterion.
- Analysis of the constraints imposed on the calibration signal.
- Analysis of the attainability of the signal maximizing the chosen error criterion.
- Writing a computer program for determination of the maximum value of error.

For linear systems the magnitude constraint of the input signal maximizing the output is obvious, irrespective of the assumed error criterion. For this constraint the signal maximizing criterion (1) is always of the ‘bang-bang’ type [1, 2, 3]. However the ‘bang-bang’ signals are not matched to the dynamics of low-pass systems, since they can only transmit signals with a limited value of the rate of change. Therefore it is necessary to impose the second constraint, related to the signal rate of change \mathcal{G} . Proper matching is obtained if the maximum rate of the input signal change is less or at most equal to the maximum rate of the step response of the system.

Figure 1 presents the diagram of measurement system calibration by means of genetic algorithms if the magnitude and rate of change constraints are imposed simultaneously on the input signal $u_0(t)$, and the error criterion is:

$$I(u_0) = \max_{t \in [0, T]} \int_0^T \varepsilon^2(t) dt; \quad u_0 \in U, \quad (1)$$

where the set U is assumed to contain signals being measurable in the meaning of Lebesgue.

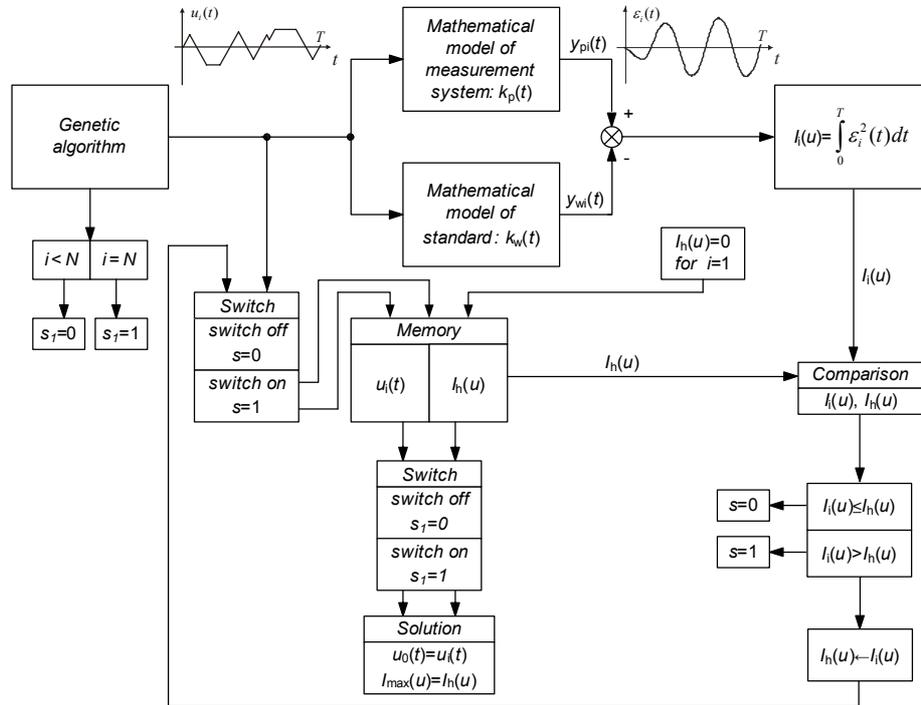


Fig. 1. Diagram of measurement system calibration by means of genetic algorithms.

$$i = 1 \dots N, \quad N = nch \cdot np, \quad (2)$$

where: nch - number of chromosomes in population, np - number of generated populations for which the stop condition is carried out.

The mathematical model of the calibrated measurement system is obtained as a result of parametric identification, however the mathematical model of its standard is usually attained in the context of realization of no-distortion transformation [12, 14].

A genetic algorithm generates one by one the switching vectors describing the $u_i(t)$ signal, for which outputs (3), error (4) and functional (1) are determined.

$$y_{pi}(t) = \int_0^t k_{pi}(t-\tau)u_i(\tau)d\tau, \quad (3)$$

$$y_{wi}(t) = \int_0^t k_{wi}(t-\tau)u_i(\tau)d\tau, \quad (4)$$

$$\varepsilon_i(t) = y_{pi}(t) - y_{wi}(t). \quad (5)$$

In every iterative cycle, the $I_i(u)$ value is compared with the $I_h(u)$ value stored in memory, which for $i = 1$ has the initial value equal zero. If $I_i(u) > I_h(u)$, then $I_i(u)$ is ascribed to $I_h(u)$ and then stored. Simultaneously with this operation the vector of signal $u_i(t)$ values is saved in memory.

For $i = N$ stored in memory the values $u_i(t)$ and $I_h(u)$ are ascribed to the pair of $u_0(t)$ and $I_{max}(u)$. In this manner the solution for $i = N$ consists of two data: the vector of data which describes signal $u_0(t)$ and the corresponding signal value of functional $I_{max}(u) = I(u_0)$.

3. APPLICATION OF GENETIC ALGORITHM TO CALIBRATION OF A MEASUREMENT SYSTEM

In order to determine signal $u_0(t)$ it is necessary to search a set of permissible input signals $u_i(t)$ [1, 2, 5]. If we give up the requirement of solution optimality and its approximate value yields a satisfying result, then the genetic algorithm technique can be applied as a searching method.

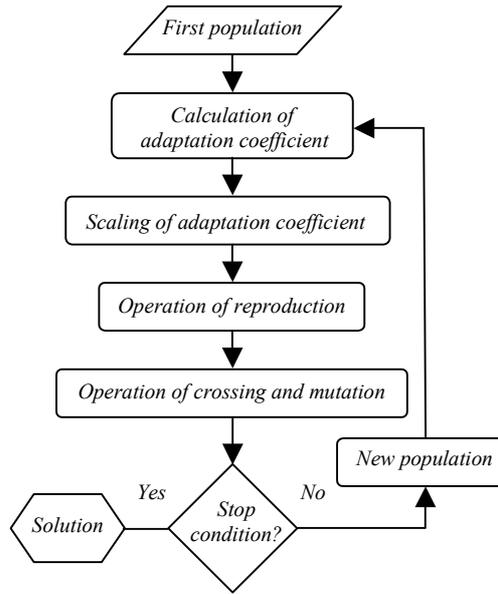


Fig. 2. Genetic algorithm block diagram.

Figure 2 presents a genetic algorithm block diagram. According to genetic algorithm specificity [7, 8, 9], the determination of the unknown $u_0(t)$ signal is performed in three steps:

- operation of reproduction,
- operation of crossing,
- operation of mutation.

In the first step, the initial population composed of an even chromosome number is selected at random. Each chromosome consists of detectors the number of which corresponds to the interval between switching times of $u_i(t)$ [5]. For each chromosome the value of functional (1) is determined (Table 1), and then on the basis of the obtained results, following formulae (6) and (7), an adaptation coefficient is calculated.

This coefficient presents each chromosome percentage share in the total error [5]:

Table 1. Chromosomes population and adaptation index for each chromosome.

Chromosome:	detectors				Adaptation coefficient
	1	2	...	m	
p_1	t_{11}	t_{12}	...	t_{1m}	I_{21}
p_2	t_{21}	t_{22}	...	t_{2m}	I_{22}
...
p_n	t_{n1}	t_{n2}	...	t_{nm}	I_{2n}

$$I_{2s} = I_{21} + I_{22} + I_{23} + \dots + I_{2n}, \quad (6)$$

$$I_{21}' = \frac{I_{21}}{I_{2s}} 100 [\%],$$

.....

$$I_{2n}' = \frac{I_{2n}}{I_{2s}} 100 [\%], \quad (7)$$

where: I_{2s} is the total error, and $I_{21}' \dots I_{2n}'$ present the share of individual adaptation coefficients in the total error.

Knowledge of adaptation coefficients is necessary for each chromosome in order to estimate their usefulness in population. In the case when the difference between the obtained values of adaptation coefficients is too small it is necessary to carry out the operation of adaptation coefficient scaling, because the next steps of genetic algorithm would not give desirable effects [8, 9].

In the next step the operation of reproduction is carried out, and according to the probability calculated on the basis on (2) from the initial population the chromosomes are selected at random. Depending on the value of the adaptation coefficient a particular chromosome has a larger or smaller chance to be found in the next generation. There are several ways of calculating the chances for each chromosome [8, 10].

The most common way is represented by the roulette wheel method, where the process of random selection is carried out as many times as the number of chromosomes in the population, and the results of random selection are rewritten to the new descendant population.

All chromosomes have different random selection probability, proportional to the value of the adaptation coefficient. As a result of the reproduction operation a new population composed of chromosomes: $p_1' \dots p_n'$ is obtained.

The next step is the crossing process. Chromosomes of $p_1' \dots p_n'$ are joined in pairs in a random way and for the given crossing probability P_k a number from the range [0,1] is selected at random. If the selected number is in the range $[0, P_k]$, then the crossing process is performed.

Otherwise the equivalent detectors of joined chromosomes are not crossed. The crossing probability P_k is usually established on a high level, which is about 0.9.

The crossing process is carried out according to the formula [7, 11, 13]:

1. In the case of crossing detectors t_{11} from the first chromosome and t_{21} from the second chromosome we have:

$$t_{11}' = (1-\alpha) t_{11} + t_{21}, \quad (8)$$

$$t_{21}' = \alpha t_{11} + (1-\alpha) t_{21},$$

where: t_{11}' is a descendant detector of the first chromosome, and t_{21}' is a descendant detector of the second chromosome.

Coefficient α is selected according to the following procedure.

In the first step:

$$\alpha_1 = \frac{-t_{11}}{t_{21} - t_{11}}, \quad \alpha_2 = \frac{t_{12} - t_{11}}{t_{21} - t_{11}}, \quad (9)$$

$$\alpha_3 = \frac{-t_{21}}{t_{11} - t_{21}}, \quad \alpha_4 = \frac{t_{22} - t_{21}}{t_{11} - t_{21}},$$

are calculated

where: α_1 and α_2 present the minimum and maximum limit of α coefficient changeability for the detector from the first chromosome, and α_3 , α_4 present the minimum and maximum limit of α coefficient changeability for the detector from the second chromosome. The changeability range of α is contained in the range between zero and the third value of α_{max-1} coefficient (9) minus α_{max-1} multiplied by the changeability step of t from interval $[0, T]$.

In the next step the α value is selected at random from the above range and then this value is substituted into formula (8).

2. In the case of crossing detectors: t_{1m} from the first chromosome and t_{2m} from the second chromosome we have:

$$t_{1m}' = (1-\alpha)t_{1m} + \alpha t_{2m}, \quad t_{2m}' = \alpha t_{1m} + (1-\alpha)t_{2m}, \quad (10)$$

where: $m = 2 \dots n$, t_{1m}' is the first chromosome descendant m detector and t_{2m}' is the second chromosome descendant m detector. Coefficient α is selected following the procedure.

First:

$$\alpha_1 = \frac{t_{1m-1} - t_{1m}}{t_{2m} - t_{1m}}, \quad \alpha_2 = \frac{t_{1m+1} - t_{1m}}{t_{2m} - t_{1m}},$$

$$\alpha_3 = \frac{t_{2m-1} - t_{2m}}{t_{1m} - t_{2m}}, \quad \alpha_4 = \frac{t_{2m+1} - t_{2m}}{t_{1m} - t_{2m}}, \quad (11)$$

are calculated, where: α_1 and α_2 present the minimum and maximum limit of α coefficient changeability for the detector from the first chromosome, and α_3 , α_4 present the minimum and maximum limit of α coefficient changeability for the detector from the second chromosome. The changeability range of α is contained in the range between zero and the third value of $\alpha_{\max-1}$ coefficient (11) minus $\alpha_{\max-1}$ multiplied by the changeability step of t from interval $[0, T]$.

In the next step the α value is selected at random from the range determined above and then this value is substituted to (10) formula.

The operation of crossing is presented in Fig. 3.

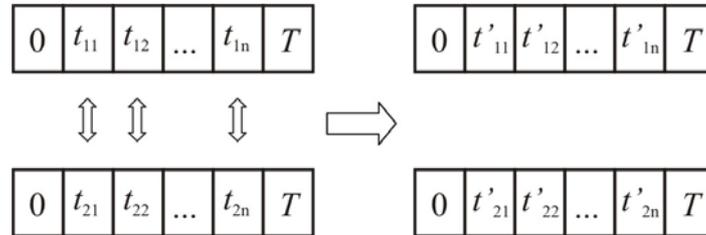


Fig.3. Operation of crossing.

The crossing procedure described by formulae (8-11) assures that in the descendant chromosomes the subsequent detectors will possess a value larger than the value of the detectors situated immediately before them. This requirement must be met, because individual detectors included in the chromosome contain the interval of switching times of the signal $u_i(t)$.

The operation of mutation is the last step of the genetic algorithm. In case of each detector included in the descendant chromosomes, we ask whether the mutation operation will be carried out or not. This process usually is carried out at small probability ($P_m < 0.1$). Mutation is a sort of supplement to the operation of crossing. There are many varieties of mutation and the choice of a relevant mutation depends on the algorithm application. The linear mutation described by formula (12) is often applied [7, 8, 11, 13]:

$$d_{1m}'' = (d_{1m+1}' - d_{1m-1}') \alpha + d_{1m-1}', \quad \alpha \in \langle 0, 1 \rangle, \quad m \in 1 \dots n. \quad (12)$$

The operation of mutation is presented in Fig. 4.

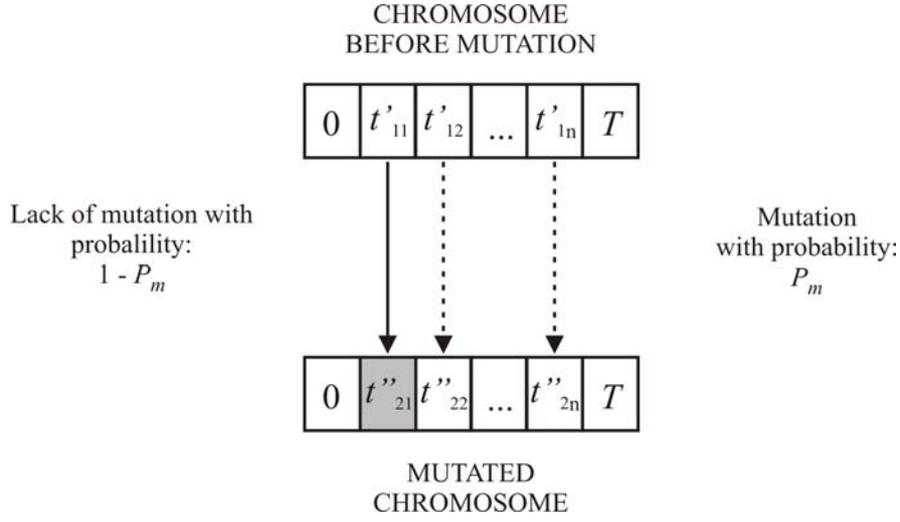


Fig. 4. Operation of mutation.

After the operation of mutation, the genetic algorithm process starts to recur. The populations number of the genetic algorithm searching the $u(t)$ signals space of possible solutions should be as large as possible. It must be taken into consideration that the increasing number of population increases the time of genetic algorithm calculation. This time might be reduced many times, if the stop condition is applied [7, 8, 9]. This condition stops the algorithm if the value of $I_h(u)$ stored in memory does not change.

4. RESULTS OF RESEARCH

As an example let us consider a low-pass system, described by the following equation:

$$K_p(s) = \frac{1}{(s^2 + 1.65 \cdot s + 1)(s^2 + 1.35s + 1)(s^2 + 1.55s + 1)} \quad (13)$$

and let its standard be:

$$K_w(s) = \frac{1}{(s^2 + 1.92s + 1)(s^2 + 1.41s + 1)(s^2 + 0.01s + 1)}. \quad (14)$$

Equation (14) represents a model of the standard, which was determined on the basis of the optimized procedure presented in [12], in the context of realization of no-distortion transformation.

In order to determine signal $u_0(t)$ maximizing functional (1), if two constraints are imposed on this signal, the procedure described in Points 2 and 3 was applied. The magnitude $A = 1$ was assumed and the rate of change $\mathcal{G} = 0.418$ was calculated as a maximum of the impulse response $k(t)$ of the system (13).

Figure 5 presents the impulse response $k(t)$ as well as $u_0(t)$ and the error $\varepsilon(t)$ corresponding to it.

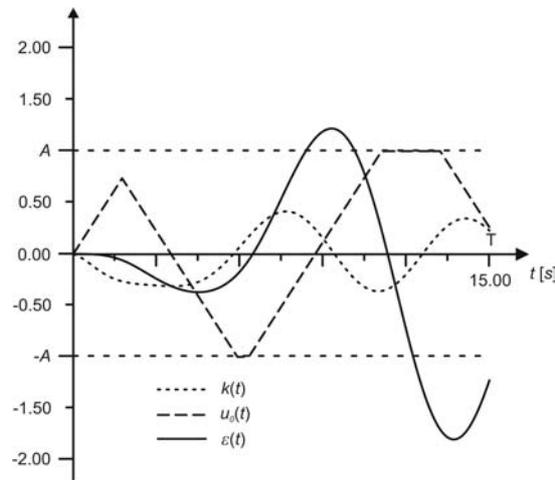


Fig. 5. Impulse response of $k(t)$ and signals $u_0(t)$ and $\varepsilon(t)$.

The signal $u_0(t)$ is in the form (15) and it generates the maximum value of the error equal $I(u) = 10.91 \text{ V}\cdot\text{s}$.

$$u_0 \Rightarrow \mathcal{G}_+[0.0, 1.76\text{s.}], \mathcal{G}_-[1.76, 5.92\text{s.}], -1[5.92, 6.32\text{s.}], \quad (15)$$

$$\mathcal{G}_+[6.32, 11.12\text{s.}], +1[11.12, 13.22\text{s.}], \mathcal{G}_-[13.22, 15.0\text{s.}].$$

In (15) the following notation is used [2, 3]: \mathcal{G}_+ signal increasing in the interval, \mathcal{G}_- signal decreasing in the interval, ± 1 a constant signal in the interval.

5. CONCLUSION

The paper presents an application of a genetic algorithm for the calibration of a measurement system intended for dynamic measurements. In the process of calibration the maximum error (1) has been determined.

The research was conducted by means of a computer program implemented in C language, with reference to a low-pass sixth order system. The mathematical model of the sixth order system was applied as standard.

The shape of the signal with two constraints imposed on it, maximizing error (1), was determined by means of the genetic algorithm technique.

The following parameters of the genetic algorithm have been assumed: number of population = 1000, stop condition = 100, number of chromosome included in each population = 32, crossing probability: $P_k = 0.9$, mutation probability: $P_m = 0.07$, step of calculation = 0.01s.

The best result was obtained for 712 population, computing time was: 6 hrs, 32mins. Research was conducted by means of a 1 GHz PC.

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ZASTOSOWANIE ALGORYTMU GENETYCZNEGO DO WZORCOWANIA SYSTEMÓW POMIAROWYCH PRZEZNACZONYCH DO POMIARÓW DYNAMICZNYCH

Streszczenie

Artykuł przedstawia zastosowanie algorytmu genetycznego do wzorcowania aparatury pomiarowej przeznaczonej do pomiarów dynamicznych, w oparciu o wartości maksymalne błędów, jakie może generować rozpatrywana aparatura pomiarowa w odniesieniu do jej wzorca.

Badania przeprowadzono w odniesieniu do całkowo-kwadratowego funkcjonału błędu, rozpatrując sygnały wejściowe ograniczone zarówno w amplitudzie jak i prędkości narastania, gdyż jedynie dla takich sygnałów można uzyskać wartości maksymalne rozpatrywanego funkcjonału. Z uwagi na fakt, iż dla całkowo-kwadratowego kryterium błędu nie można w sposób analityczny określić kształtu sygnału maksymalizującego to kryterium, uzasadnione jest zastosowanie techniki algorytmu genetycznego jako narzędzia przeszukującego przestrzeń możliwych rozwiązań sygnałów wejściowych.

Badania przeprowadzono w oparciu o program komputerowy zaimplementowany w języku C, w odniesieniu do dolnoprzepustowej aparatury szóstego rzędu. Jako wzorzec zastosowano matematyczny model układu szóstego rzędu, który został wyznaczony w oparciu o procedurę optymalizacyjną przedstawioną w [12], w kontekście realizacji przez ten model transformacji nieznieskształcającej.

Działanie algorytmu genetycznego oparto o metodę koła ruletki, z klasycznym sposobem budowania chromosomów, przy zastosowaniu kodowania opartego na liczbach rzeczywistych dodatnich. W procesie generowania kolejnych populacji wykorzystano operacje: reprodukcji, krzyżowania oraz mutacji. Przyjęto następujące parametry algorytmu genetycznego: liczba założonych do przeszukania populacji 1000, wartość warunku stopu = 100, liczebność chromosomów wchodzących w skład każdej populacji 32, prawdopodobieństwo krzyżowania: $P_k = 0.9$, prawdopodobieństwo mutacji: $P_m = 0.07$, krok dyskretyzacji obliczeń 0.01s.