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Genetic Algorithm-Based Estimation of Nonlinear Transducer

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Abstract: This paper describes an innovative, genetic algorithm-based inverse model of nonlinear transducer. In the inverse modeling, using a genetic algorithm, the unknown coefficients of the model are estimated accurately. The simulation results indicate that this technique provides greater flexibility and suitability than the existing methods. It is very easy to modify the nonlinear transducer on line. Thus the method improves the transducer's accuracy. With the help of genetic algorithm (GA), the model coefficients' training are less likely to be trapped in local minima than traditional gradient-based search algorithms.

Key words: nonlinear transducer, genetic algorithm, inverse model

Nonlinear transducers find extensive applications in various systems such as instrumentation, medicine, and process control. These applications demand that the transducer be of low cost, high sensitivity and resolution and be easy mass production. Further, to have an easy digital interface for direct readout, the response characteristics of the transducer should be linear and independent of variations in the environmental conditions such as temperature, humidity, etc. But the nonlinearly associated with these transducers gives rise to several difficulties for on-chip interface, direct digital readout, etc. To convert the nonlinear output change into linear digital output, two techniques have been proposed with satisfactory result[1]. In the first technique a ROM-based look-up table is employed. In the second method, a nonlinear coding scheme is utilized with the help of a D/A converter, and the input is linearly encoded by a nonlinear decoding function. Using the above techniques, it is shown that good linearity and error within ± 1% can be achieved[2]. For obtaining direct digital output the above two methods employ some approximation techniques for converting the nonlinear characteristics into linear ones. These two methods have the following limitations. First, in the case of extreme change of environmental conditions, such as temperature, humidity, etc. the look-up table or the nonlinear encoding function needs modification to adapt to the new nonlinear transducer output. Secondly, in the case of replacement and aging of the transducer, the data stored in the ROM requires updating. Further, in spite of the advanced manufacturing technology, the response characteristics of transducer of the same manufacturer differ from sample to sample. As a result, in the case of replacement, aging or extreme change in environmental conditions, frequent calibration of the transducer is required. In this paper, we propose a different method that circumvents the problems associated with existing methods. The inverse modeling of the transducer by which the applied input is estimated for calibration and direct digital readout have been studied. The problems have been solved by adaptive techniques using a genetic algorithm. GA is less likely to be trapped in local minima traditional gradient-based search algorithms. It does not depend on gradient information. Thus these features make it much more robust than many other search algorithms.

1 Inverse Modeling of Transducer Characteristics

The nonlinear response characteristics of a transducer for the entire dynamic range of measurement are modeled based on a power series expansion[2]. The response of the transducer may be expressed as follows:

$$y = a_0 + a_1 x + a_2 x^2 + \cdots \quad (1)$$

where y is the normalized change in transducer output and x is the normalized applied input. The unknown coefficients represent the characteristic parameters of the transducer.

The inverse model can be also represented as follows:

$$x = b_0 + b_1 y + b_2 y^2 + \cdots \quad (2)$$

The inverse modeling of transducer characteristics is required for direct digital readout and for calibration purpose. Since the transducer's characteristics are

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nonlinear in nature, we employ an adaptive technique by using genetic algorithm to obtain an inverse model of the transducer.

Consider P input patterns, $\{x_P\}$, each with a single element applied to a pressure sensor producing an output pattern $\{y_p\}$, $p = 1,2,\cdots,P$. The weighting factor along the link is denoted by $\boldsymbol{W}$. The output corresponding to P patterns may be expressed in a matrix form as follows:

$$\boldsymbol{X}_{p\times 1} \cdot \boldsymbol{W}_{1\times 1} = \boldsymbol{Y}_{p\times 1} \tag{3}$$

From (3) it is evident that the weight $\boldsymbol{W}$ may be found by solving a system of linear simultaneous equations. Let the functional link be used so that the columns of $\boldsymbol{X}$ are increased from 1 to N_{FL}. Under this situation, $\boldsymbol{X}$ and $\boldsymbol{W}$ are changed to $\boldsymbol{X}_{FL}$ and $\boldsymbol{W}_{FL}$, respectively. Thus, the modified equation is given by (4).

$$\boldsymbol{X}_{FL} \cdot \boldsymbol{W}_{FL} = \boldsymbol{Y} \tag{4}$$

where $\boldsymbol{X}_{FL} \in \boldsymbol{R}^{p\times N_{FL}}$, $\boldsymbol{W}_{FL} \in \boldsymbol{R}^{N_{FL}\times 1}$, $\boldsymbol{Y} \in \boldsymbol{R}^{p\times 1}$.

If $N_{FL} = P$ and det $(\boldsymbol{X}_{FL}) \neq 0$, then we have

$$\boldsymbol{W}_{FL} = \boldsymbol{X}_{FL}^{-1} \cdot \boldsymbol{Y} \tag{5}$$

If $N_{FL} > P$, let $Q = N_{FL} - P$, we can partition $\boldsymbol{X}_{FL}$ to $[\boldsymbol{X}_{Fl}^{(1)}\ \boldsymbol{X}_{FL}^{(2)}]$, $\boldsymbol{X}_{FL}^{(1)}: P \times P$, $\boldsymbol{X}_{FL}^{(2)}: P \times Q$, and $\boldsymbol{W}_{FL}$ to $[\boldsymbol{W}_{FL}^{(1)}\ \boldsymbol{W}_{FL}^{(2)}]^{\mathrm{T}}$, $\boldsymbol{W}_{FL}^{(1)}: P \times 1$, $\boldsymbol{W}_{FL}^{(2)}: Q \times 1$. Thus

$$[\boldsymbol{X}_{FL}^{(1)}\ \boldsymbol{X}_{FL}^{(2)}] \cdot [\boldsymbol{W}_{FL}^{(1)}\ \boldsymbol{W}_{FL}^{(1)}]^{T} = \boldsymbol{Y}$$

Let $\boldsymbol{X}_F = \boldsymbol{X}_{FL}^{(1)}$, $\boldsymbol{W}_F = \boldsymbol{W}_{FL}^{(1)}$, and set the weights $w_p = 0$ for $p \geqslant P + 1$, thus $\boldsymbol{W}_{FL}^{(2)} = \boldsymbol{0}$, then we have

$$\boldsymbol{X}_F \cdot \boldsymbol{W}_F = \boldsymbol{Y}$$

and then, we obtain the solution given by

$$\boldsymbol{W}_F = \boldsymbol{X}_F^{-1} \cdot \boldsymbol{Y} \tag{6}$$

If $N_{FL} < P$, the solution is obtained by using the conventional pseudo inversion technique given by

$$\boldsymbol{W}_{FL} = (\boldsymbol{X}_{FL}^{\mathrm{T}} \cdot \boldsymbol{X}_{FL})^{-1} \boldsymbol{X}_{FL}^{\mathrm{T}} \cdot \boldsymbol{Y} \tag{7}$$

where $(.)^{\mathrm{T}}$ denotes the transpose of $(.)$.

Thus, it may be observed that the functional expansion technique always yields a flat net solution. This is achieved by the use of a GA together with an adaptive supervised learning algorithm.

Referring to Fig.1, x and y represent the applied normalized input and measured output, respectively.

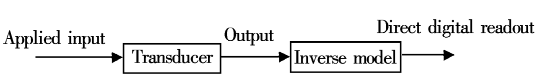

Fig. 1 The scheme of inverse model

The task of the inverse modeling is now changed to the problem of estimating the coefficients b_0, b_1 and b_2 approximately. The structure of parameter identification using genetic algorithm shown in Fig.2 is used to estimate these coefficients.

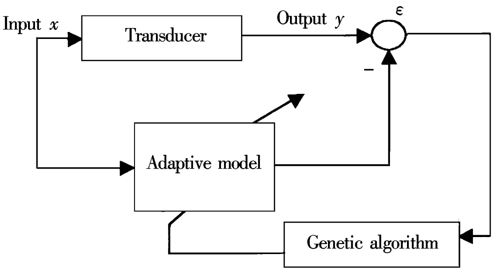

Fig. 2 Parameter identification using GA

The objective is to minimize the error between the transducer output and the output of the estimation model. Hence, the objective function may be defined as the windowed mean square error

$$\varepsilon = \frac{1}{N}\sum_{i=1}^{N}(y(k) - x(k)H(z))^2 \tag{8}$$

where $x(k)$ and $y(k)$ are the digitized input and output values of the transducer, respectively; N is the windows size.

2 Genetic Algorithm

The genetic algorithm is a search algorithm based on the mechanics of natural selection and natural genetics. It combines survival of the fittest among string structures with a structured yet randomized information exchange to form a search algorithm with some of the innovative flair of human search. In genetic algorithms, each parameter is represented by a string structure that is similar to the chromosome structure in natural genes. A group of string is called a population. Strings in a given population, when it is mutated and/or crossed over, produce a new generation of strings. For each generation, all the populations are evaluated based on fitness. The individual with higher fitness, or survival probability, will have more chances of survival. The general concept of a genetic algorithm can be illustrated as Fig.3.

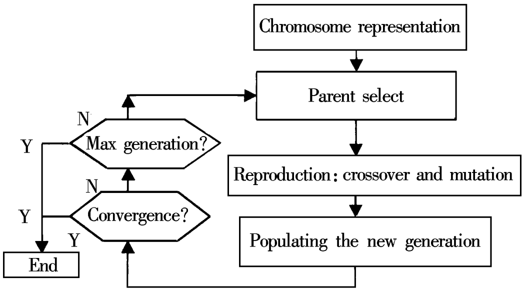

Fig. 3 Flow diagram of genetic algorithm

1) Chromosome representation

To directly estimate the coefficients of the model and avoid restriction of the initialization, a GA can be introduced. Each phenotype is a value-decoded from a chromosome, and each chromosome can be represented as a binary string[3].

For example, a 24-digit binary string is chosen to represent a chromosome. The coefficients in this case, directly represented by a binary string. The chromosome is defined in (9)

$$f = (\mathrm{bit}_0, \mathrm{bit}_1, \cdots, \mathrm{bit}_{23}) \tag{9}$$

and its structure is depicted in Fig.4.

8-bit	8-bit	8-bit
b_0	b_1	b_2

Fig.4 Chromosome structure

2) Parent selection

In keeping with the ideas of natural selection, the individuals with a higher fitness are more likely to mate than individuals with a lower fitness. The method used in this paper in parent selection is called the roulette-wheel method[4]. In principle, a roulette wheel is constructed where each member of the population is given a sector whose size is proportional to the fitness of that individual. Then the wheel is spun and whichever individual comes up becomes a parent.

3) Crossover

Crossover is a random process of recombination in which each parent contributes part of its genetic structure to offspring. The crossover method employed in this paper is called the multi-point crossover[5].

4) Mutation

Mutation is the occasional random alteration of the value of a string. With the binary string representation, this simple means flipping the state of a bit from 1 to 0 or vice versa[3].

5) Populating the new generation

An approach called the generational replacement technique, which mates enough parents so that enough children are produced to completely replace their parents is utilized in building a new generation.

3 Results and Discussion

In this paper, a capacitive pressure transducer is applied to give an example. These pressure transducers find extensive application in various systems such as instrumentation, medicine, automobiles, etc. The implementation of the inverse modeling for estimation may be done in two stages. In the first stage, the learning process is carried out off-line as shown in Fig.2. This yields the coefficients b_0, b_1 and b_2. In the second stage, the computer is applied on-line as shown in Fig.1.

The parameter setting of the GA used in the simulations are tabulated in Tab.1.

Tab.1 Parameter settings of GA

Representation	8-bit per variable (total 24 bit)
Population size	50
Generation gap	0.7
Fitness assignment	ranking
Selection	roulette wheel selection
Crossover	multi-point crossover
Crossover rate	0.6
Mutation	bit mutation
Mutation rate	0.001

Another problem we must take into consideration is the terminating condition of the GA optimization process. Generally speaking, the required maximum number of generations of GA optimization is problem-dependent. It may take too long to obtain the best result. From the engineering point of view, a convergence decision is needed to terminate the GA operations when the result is good enough. For this consideration, the following termination decisions are introduced: ① If the considered fitness function does not change much (less than $T = 0.005$) in a certain number of generations ($G = 50$ generations). We assume that the optimization has converged and the process is terminated; and ② Otherwise, the process shall be terminated at the maximum number of generation ($G = 200$ generations). Obviously, the selection of the above numbers is not unique. Generally speaking, smaller T or larger G will lead to better optimization results but need longer optimization time. The introduction of the above convergence decision may cause the problem of local minimum, but it is more realistic in practice.

Assumption of the first three terms in the power series expansion of the inverse model has led to a maximum error of 2.3% between the measured and estimated values. Considering more terms in the series expansion can further minimize the error. However, this will increase the complexity. The overall simulation results of transducer inverse model indicate that this GA approach is a useful alternative to the existing ones.

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基于遗传算法的非线性传感器模型辨识

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摘　要　提出了一种新的、基于遗传算法的非线性传感器逆模型建模方法. 利用遗传算法建模, 可以方便、准确地辨识未知非线性模型的系数. 仿真实验表明该方法较传统方法, 具有更好的灵活性与适应性, 可以方便地实现在线修正模型系数, 因此提高了传感器的测量精度. 由于遗传算法可以实现模型系数空间的全局搜索, 因此可以避免在模型系数训练过程中陷入局部极小点.

关键词　非线性传感器, 遗传算法, 逆模型

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