DNA 코딩 기반 카오스 시스템의 퍼지 모델링

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DNA coding-Based Fuzzy System Modeling for Chaotic Systems

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Abstract – In the construction of successful fuzzy models and/or controllers for nonlinear systems, the identification of a good fuzzy inference system is an important yet difficult problem, which is traditionally accomplished by a time-consuming trial-and-error process. In this paper, we propose a systematic identification procedure for complex multi-input single-output nonlinear systems with DNA coding method. A DNA coding method is optimization algorithm based on biological DNA as conventional genetic algorithms(GAs) are. The strings in the DNA coding method are variable-length strings, while standard GAs work with a fixed-length coding scheme. the DNA coding method is well suited to learning because it allows a flexible representation of a fuzzy inference system. We also propose a new coding method for applying the DNA coding method to the identification of fuzzy models. This coding scheme can effectively represent the zero-order Takagi-Sugeno (TS) fuzzy model. To acquire optimal TS fuzzy model with higher accuracy and economical size, we use the DNA coding method to optimize the parameters and the number of fuzzy inference system. In order to demonstrate the superiority and efficiency of the proposed scheme, we finally show its application to a Duffing-forced oscillation system

1. INTRODUCTION

Fuzzy logic theory has been successfully applied to a wide spectrum of applications such as the identification and control of complex, uncertain, and ill-defined nonlinear systems. Since fuzzy logic controllers and identifiers are implemented by fuzzy inference systems, it is crucial to design good fuzzy inference systems with the minimum number of rules and optimized parameters. Conventional fuzzy modeling procedure is based on tedious trial-and-error procedures, which leads to the study of automatic fuzzy modeling methods, and many researchers have worked on this fruitful field.

On the other hand, genetic algorithms (GAs), which are based on the mechanism of biological genetics and natural selection, are developed as an alternative method for the identification of fuzzy inference systems. Since GAs have global convergence property, they can outperform the conventional fuzzy modeling methods using fuzzy neural networks. Recently, A DNA coding method is proposed in [1]. In this method, the genes are coded by four bases, namely, Adenine (A), Guanine (G) Cytosine (C), and Thymine (T), while traditional GAs use simplified coding such as binary coding, real number coding etc.. DNA coding is more realistic emulation of natural genetics than traditional GAs. Furthermore, the optimization performance is improved with DNA coding method since its inherent features such as

overlapping and redundancy give more extended search space and give less possibility of early convergence of solution.

In this paper, we propose an automatic algorithm for identification of fuzzy inference systems based on DNA coding method, which processes variable length string , redundant and overlapping genes in contrast to the conventional GAs that work with the fixed length string. The proposed identification schem is able to optimize the structure and parameters of fuzzy inference system effectively.

This paper is organized as follows: Section 2 describes the fuzzy model used for identification. In Section 3, the DNA coding method is briefly introduced, and shows how the fuzzy rule base is represented using the DNA coding method. Section 4 shows the simulation results on a Duffing-forced oscillation system. Conclusions are summarized in the last section.

2. FUZZY MODEL AND REASONING

A typical format for a fuzzy rule based consists of a collection of fuzzy IF-THEN rules in the following form:

$$\text{Rule } i: \text{ if } x_1 \text{ is } A_{11} \cdots x_n \text{ is } A_{in}, \text{ then } y \text{ is } w_i \qquad (1)$$

where Rule i is ith rule x_j ($j=1,2,\cdots,$)are input variables and y is an output. A_{ij} is the fuzzy variable defined as in (2) and w_i is the real number of the consequent part.

$$A_{ij}(x_i\,a_y, b_y) = \max(\min(\frac{2x_j-2a_{ij}+b_{ij}}{b_y}, \frac{2a_{ij}+b_{ij}-2x_j}{b_{ij}}), 0) \quad (2)$$

where a_{ij} and b_{ij} are the center point and the width of an isosceles triangle. Given the l th input/output data $\{x_{l1}, x_{l2}, \cdots, x_{ln}, y_l\}$ the numerical output of the fuzzy inference system with center average defuzzifier, product inference rule, and singleton fuzzifier is of the following form:

$$y_i^* = \frac{\sum_{i=1}^{c} w_i \prod_{j=1}^{n} A_{ij}(x_j)}{\sum_{i=1}^{c} \prod_{j=1}^{n} A_{ij}(x_j)} \qquad (3)$$

where c is the number of fuzzy rules and n is the number of inputs. This simplified fuzzy inference system can approximate any real continuous function to any desired degree of accuracy, if sufficiently many fuzzy logical rules are available[2].

3. DNA CODING METHOD

In this section, we briefly review the basic mechanism of DNA coding method, and present a DNA coding method for identification of fuzzy inference system[1].

The biological DNA consists of nucleotides which have four bases, Adenine(A), Guanine(G), Cytosine(C), Thymine(T) [3]. The biological DNA have mRNA. and mRNA have the unused

parts. Then the unused parts are cut out. This poeration is a splicing. After this splicing occurred, the mRNA is completed. Three successive bases called codons are allocated sequentially in the mRNA. These codons are the codes for amino acids. 64 kinds of codons correspond to 20 kinds of amino acids. The details of translation into amino acid from codons are omitted here. Amino acid makes proteins, and The proteins make up cells.
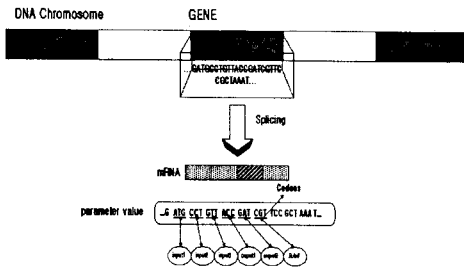

Fig. 1 Biological DNA coding method

In the DNA coding method, a codon is regarded as a gene value in conventional GAs. For example, a codon (A,G,C) may represent real value 24. Figure 2 shows an example of the DNA chromosome and its translation

Fig. 1 shows the diagram of DNA coding method The GA usually used a coding method specifically devised for each problem and it had no redundant parts. In this paper, A, G, C and T are represented by integer number 1, 2, 3, and 4 for simplicity. In the DNA coding method, the overlapping of genes is a crucial feature, which makes DNA coding more effective. Figure 2 shows the overlapping of genes. As shown in the Figure 2, many genes can be constructed from a single DNA. For this reason, One may ask how to select end-codon for a start-codon. This problem can solved by *first-come-first-serve* rule.
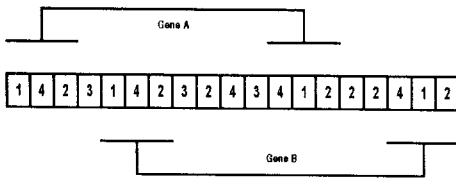

Figure 2 Overlapping of genes

In DNA coding method the crossover is simply replaced the parts of DNA on the crossover points as in conventional GAs and the mutation is change the a randomly selected base to its complement. Figure 3 (a) shows an example of crossover and (b) shows an example of mutation

parent1 = 413244|2142
parent2 = 344312|4424
offspring1 = 413244|4424
offspring2 = 344312|2142

(a)

parent = 4132444142
parent = 4132442142

(b)

Figure 3 (a) Crossover (b) Mutation

The next step is to construct the proper structure of DNA code. In this paper we use n input - 1 output fuzzy inference system. If the number of required parameter to represent the membership function is p, and the number of fuzzy rules is r, then the number of parameters to represent the fuzzy inference system is given by
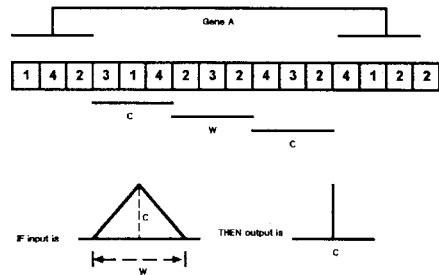
$$N_p = r(np + 1) \qquad (4)$$

Figure 4 Coding example of DNA coding method

Fig. 4 shows the of parameter input membership function by the DNA coding method.

4. SIMULATION RESULT

The Duffing forced oscillation system has the dynamic equations as follows:

$$\dot{x}_1 = x_2 \qquad (4)$$

$$\dot{x}_2 = -0.1x_2 - x_1^3 + 12\cos(t) + u(t) \qquad (5)$$

where
The above system is chaotic without control. The trajectory of the system with $u(t) = 0$ is shown in the phase plane in Fig.5 for the initial condition $x(0) = [2\ 2]^T$ over the time period form $t_0 = 0$ to $t_f = 20$. We use the proposed controller to control the system state x_1 to track the reference trajectory $y_m(t) = \sin(t)$. The fuzzy model for this chaotic system can be obtained by liberalizing the nonlinear equations over a number of operating points in the phase plane of (x_1, x_2)
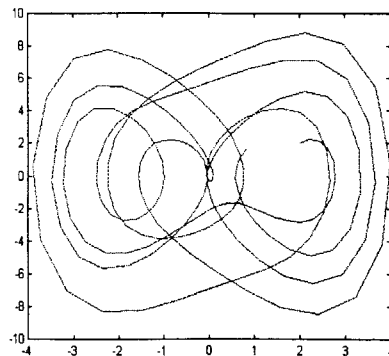

Figure 5 Trajectory of the chaotic Duffing system in the phase plane, with $u(t) = 0$ and $x(0) = [2\ 2]^T$

Training data for the optimization of TS fuzzy model is obtained through the simulation with the controller in [1].

The parameters of DNA coding method are as follows: The length of each initial DNA chromosome was 600. The probability of the mutation rate was 0.5 and crossover rate was 0.8.
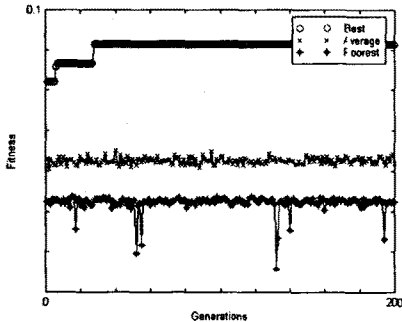

Figure 6 Fitness value

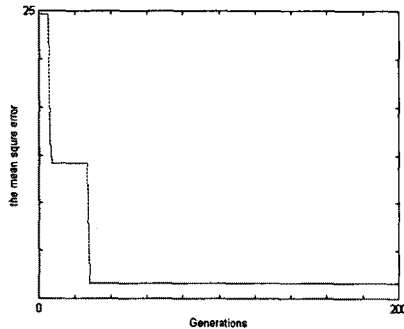Figure 6 show fitness value and represented to increase fitness value.

Figure 7 Performance error

Figure 7 show the between train data and output of fuzzy model by DNA coding method. Generation was 100.

5. CONCLUSION

In this paper, A systematic fuzzy modeling procedure for complex multi-input single-output nonlinear systems with DNA coding method is presented. DNA coding method is optimization algorithm based on biological DNA as conventional genetic algorithms (GAs) are. The strings in DNA coding method are variable-length strings, while standard GAs work with a fixed-length coding scheme. DNA coding method is well suited to learning because it allows a flexible representation of a fuzzy inference system. We also propose a new coding method for applying the DNA coding method to the identification of fuzzy models. This coding scheme can effectively represent the zero-order Takagi-Sugeno (TS) fuzzy model. To acquire optimal TS fuzzy model with higher accuracy and economical size, we use the DNA coding method to optimize the parameters and the number of fuzzy inference system. The effectiveness and feasibility of the proposed method is verified through a numerical simulation on a Duffing-forced oscillation system

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