

바이러스-진화 유전 알고리즘을 이용한 비선형 시스템의 피지모델링

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Fuzzy Modeling for Nonlinear Systems Using Virus-Evolutionary Genetic Algorithm

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Abstract - This paper addresses the systematic approach to the fuzzy modeling of the class of complex and uncertain nonlinear systems. While the conventional genetic algorithm (GA) only searches the global solution, Virus-Evolutionary Genetic Algorithm(VEGA) can search the global and local optimal solution simultaneously. In the proposed method the parameter and the structure of the fuzzy model are automatically identified at the same time by using VEGA. To show the effectiveness and the feasibility of the proposed method, a numerical example is provided. The performance of the proposed method is compared with that of conventional GA.

1. Introduction

When modeling complex and/or uncertain nonlinear systems, it is difficult to obtain satisfactory result even by using high-order model or model approximation. In order to cope with this problem, fuzzy modeling method has been widely studied [1-6].

The main purpose of fuzzy modeling is to depict the given system with fuzzy linguistic rules and fuzzy sets. The conventional fuzzy model is constructed based on the knowledge from human experts. However, the design of the fuzzy model is tedious and time-consuming. To solve this problem, many automatic identification methods have been studied [7]. Recently many researchers are interested in the identification of fuzzy model by GA for its powerful global optimization ability. For example, Joo identified the parameter and the structure of fuzzy model using GA and clustering method [8].

The GA is the primary unifying principle of modern biological thought. GA is an optimization process that simulates the biological evolution using computer. The interest in such simulations has increased drastically in recent years and applications of this technology have been developed to supplant conventional technologies in many fields such as power systems, pattern recognition and control systems.

Though the GA makes it possible to search global optimum effectively, it also has the problem of a premature local convergence that occurs when a genetic diversity is lacking in a population. The VEGA simulates coevolution based on both a horizontal propagation between host and virus individuals and a vertical inheritance of genetic information from ancestors to offspring. In this paper, the VEGA is applied to the parameter and

structure identification of fuzzy model. To show the effectiveness and the feasibility of the proposed method, a numerical example is provided and the performance of the proposed method is compared with that of the conventional GA.

2. Fuzzy model

Fuzzy rules typically appear in the form :

Rule i : If x_1 is A_{i1} , ..., x_n is A_{in} , ($i=1, \dots, c$)
then y_i is w_i

(1)

where *Rule i* are the *i*th rules, x_j , the *j*th input variables, y_i , the *i*th output variables, and A_{ij} , membership functions of the *i*th rule for the *j*th input.

In this paper, the numerical output of fuzzy model is calculated through the following three basic steps.

Fuzzification : a mapping from the observed input to the fuzzy sets in the corresponding universes of discourse. That is, $U \subset R^n$ to $[0, 1]$.

Inference Process : a decision making logic which determines fuzzy outputs corresponding to the fuzzified inputs, with respect to the fuzzy rules.

$$\mu_i = A_{i1}(x_1) \times A_{i2}(x_2) \times \dots \times A_{in}(x_n) \quad (2)$$

Defuzzification : a producing procedure a nonfuzzy output.

$$y_i^* = \frac{\sum_{i=1}^c \mu_i w_i}{\sum_{i=1}^c \mu_i} \quad (3)$$

Then, The evaluation of fuzzy model can be obtained from follows.

$$E = \frac{1}{N} \sum_{i=1}^N (y_i - y_i^*)^2 \quad (4)$$

where, *N* is the number of data, y_i , the real output data, y_i^* , reasoned value from fuzzy model.

3 Genetic design of Fuzzy system

3.1 Simple GA

Genetic algorithms are probabilistic search techniques that emulate the mechanics of evolution. GA explores the optimal space in parallel. Each solution in the population is encoded as a chromosome, and a collection of chromosomes forms a generation. A new generation evolves by performing genetic operators, such as reproduction, crossover and mutation operators, on the individuals in the current population and then replacing the old generation with new generation[9]. Reproduction is a process in which individuals are copied according to their fitness. After the members of the newly reproduced strings in the gene pool are mated at random, offsprings are constructed by copying the portion of parent strings designated by random crossover points with a crossover probability. While each gene is copied from parents to offspring, its value may be changed with the mutation rate.

3.2 Virus-evolutionary GA

Virus have the potential to reduce the fitness of its host. Consequently, the importance of virus as a ecological force has often been underestimated. As evidenced by recent ecology texts[10], it is becoming clear that virus may have significant effects on both ecological and evolutionary time-scale.

Because the GA is the optimization technique that emulate ecological evolution, VEGA under virus theory has been having great effect on evolution is presented. While GA deals with schemata indirectly, VEGA does directly. The population of GA is evolved vertically and the population of VEGA is evolved horizontally as well as vertically in virtue of reverse transcription operator and transduction operator. In general, The local information is important to find optimal solution. Virus infection gradually increases effective schemata. The VEGA generates a substring like a schema as a virus individual[11]. Fig.1 shows the structure of infected individuals.

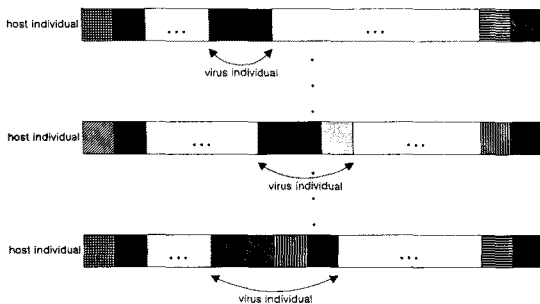


Fig 1. Infected host individuals

The additional operators in VEGA are as follows.

Reverse transcription operator : a virus individual transcribes a substring of a host individual.

Transduction operator : according to the fitness of host, a virus individual transduces a substring from a host individual additionally or reductively. A virus has parameters such as infection rate, fitvirus and life.

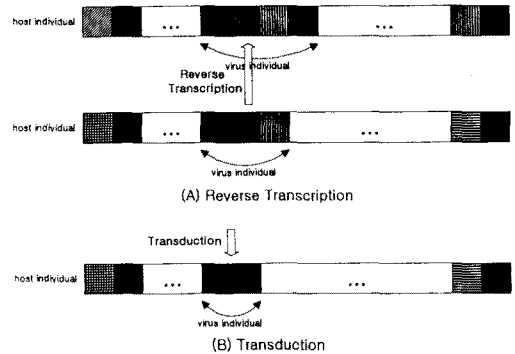


Fig. 2 The mechanism of reverse transcription and transduction

$$\text{Fitvirus} : \text{fitvirus}_{ij} = \text{fithost}'_j - \text{fithost}_j \quad (5)$$

$$\text{fitvirus}_i = \sum_{j \in S} \text{fitvirus}_{ij} \quad (6)$$

where, $\text{fithost}'_j$ and fithost_j are fitness before and after the infection to the j th host individual, respectively. Therefore, fitvirus_{ij} means the difference of fitness between before and after the fitness of the i th virus infects the j th host, and fitvirus_i means the fitness of the i th virus.

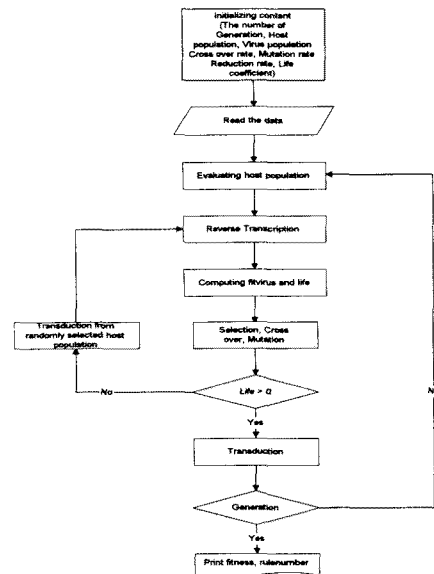


Fig. 3 The procedure of VEGA

Infection rate : The rate of infection to host population. If fitvirus has positive value, the infection rate decreases. Otherwise, increases.

$$\text{Life} : \text{life}_{i,t+1} = r \times \text{life}_{i,t} + a \times \text{fitvirus}_i \quad (7)$$

where, $\text{life}_{i,t+1}$ is the survival rate in $t+1$

generation, $life_{i,t}$, t generation, r , reduction rate, a , life coefficient. If life takes positive value, the virus will survive. Otherwise, the virus will transduce the new substring.

Fig. 3 shows the mechanisms of VEGA

4. Simulation

$$y = (1 + x_1^{-2} + x_2^{-1.5})^2, \quad 1 \leq x_1, x_2 \leq 5 \quad (8)$$

This system was applied to fuzzy inference system and parameter identification.[12] Sugeno's 50 input and output data is used to demonstrate the effectiveness of VEGA.

Fig. 4 shows that VEGA guarantees the diversity, preserves the effective schemata and prevent early convergence. Therefore, the fitness increases continuously.

Though the number of rules in VEGA is more than GA, mean square error in VEGA is much less than GA.

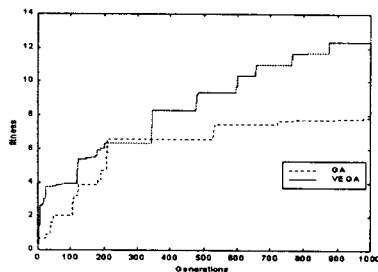


Fig. 4 The changes of fitness

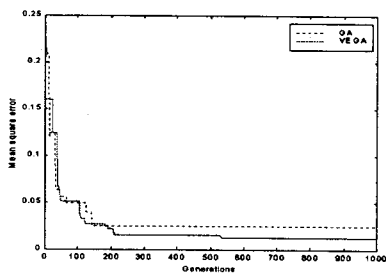


Fig. 5 The changes of mean square error

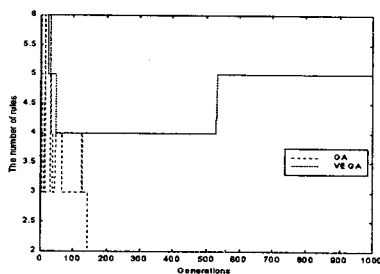


Fig. 6 The number of rules

5. Conclusion

In this paper, the systematic fuzzy modeling method of nonlinear system, which may scarcely be modeled mathematically, was proposed. The proposed method identifies the parameter and the structure of the fuzzy model by VEGA, which avoids the premature convergence of solutions. Finally, we show the effectiveness and the feasibility of the proposed method by the fuzzy modeling of a numerical example.

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