A hybrid method to construct Fuzzy Cognitive Map

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Abstract: - This paper presents a hybrid methodology of automatically constructing fuzzy cognitive map (FCM). The proposed method is based on immune algorithm to learn the connection matrix of FCM. In the algorithm, the DNA coding method is used, and in order to utilize the experts' knowledge and the feature of system, they are used as "vaccine". Finally, an illustrative example is provided. The results suggest that the method is capable of automatically generating FCM model.

Key-Words: - fuzzy cognitive map, immune algorithm, system modeling

1 Introduction

Fuzzy cognitive maps (FCM) are a soft computing method for simulation and analysis of complex system, which combines the fuzzy logic and theories of neural networks. Kosko introduced them as an extension of cognitive map in 1986[1]. It has several desirable properties, such as: it is relative simple to use for representing structured knowledge [2], and the inference can be computed by numeric matrix operation instead of explicit IF/THEN rules [3]. Most importantly they are the flexibility in system design, model and control, the comprehensive operation and the abstractive representation of behavior for complex systems [4]. These advantageous modeling features of FCM encourage us to study and broaden the functionality and applicability of FCM in more problems and systems.

However, the development of FCM models always relies on human experts; experience and knowledge. Due to the subjectivity and limitation, human experts can only handle relatively simple problems. In addition, it still exhibits weaknesses in the learning method of FCM. These problems lead to the development of methods for learning FCM: In 1992, Kosko has initially proposed the Differential Hebbian Learning (DHL), but without any mathematical formulation and applications in real problems [5]. In 2002, the Balanced Differential Learning Algorithm [6] for FCM training was proposed. This new algorithm is an extension of DHL and is based on weight updating formula, for which the updated value depends on values of all concepts that are acting at the same time as a cause of change for the concept, but this method was applied only with binary concept to FCM. In 2003, another unsupervised learning algorithm—Nonlinear Hebbian Learning (NHL)[8] was developed, so as to learn connection matrix of FCM. The NHL algorithm is based on the nonlinear Hebbian learning rule and updates only the initially suggested (non-zero) weights of the FCM. These weights are updated synchronously at each iteration step till the termination of the algorithm. The algorithm requires human intervention before the learning process starts, which is a disadvantage. In 2003, Particle Swarm Optimization (PSO) method, one of the swarm intelligence algorithms [9,10] was proposed, so as to learn FCM connection matrix, the algorithm applied to find the connection matrix in a search space that is restricted to certain FCM concepts values, and imposes constraints on the connection matrix, all of which are specified by domain experts.

Based on above analysis, in this paper, we propose a new method for the automatic generation of FCM model, which is based on immune learning algorithm. It aims to provide a means for modeling complex system.

The organization of this paper is as follows. Section 2 gives an introduction to FCM. This is followed in section 3 introduces natural immune system. Section 4 introduces learning method of FCM. Section 5 applies the algorithm to train the FCM model of a stock short-team prediction. Section 6 is the conclusion and suggestions for future works.

2 Fuzzy Cognitive Map

A FCM consists of nodes-concepts, each node-concept represents one of the key-factors of the system, and it is characterized by a value $C \in (0,1)$, and a causal relationship between two concepts is represented as an edge w_{ij}. The sign of w_{ij} indicates

whether the relation between the two concepts is direct or inverse.

A fuzzy cognitive map F is a 4-tuple (V, E, C, f) where

--$V=\{v_1, v_2, \dots, v_n\}$ is the set of n concepts forming the nodes of a graph.

--$E:(v_i, v_j) \rightarrow w_{ij}$ is a function $w_{ij} \in E$, $v_i, v_j \in V$, with w_{ij} denoting a weight of directed edge from v_i to v_j. Thus $E (V \times V)=(w_{ij})$ is a connection matrix.

--$C: v_i \rightarrow C_i$ is a function that at each concept vi associates the sequence of its activation degrees, such as $C_i(t)$ given its activation degree at the moment t. C(0) indicates the initial vector and specifies initial values of all concept nodes and C(t) is a state vector at certain iteration t.

--f is a transformation function, which includes recurring relationship between C(t+1) and C(t).

$$C_i(t+1) = f\left(\sum_{\substack{i=1 \\ j \neq i}}^{n} w_{ij} C_j(t)\right) \quad (1)$$

Eq. (1) describes a functional model of FCM. It describes that the value of each concept is calculated by the computation of the influence of other concepts to the specific concept; the transformation function is used to confine the weighted sum to a certain range, which is usually set to [0, 1].

$$o_i(t+1) = \frac{1}{1 + e^{-C(t)}} \quad (2)$$

3 Natural Immune system

The natural immune system is a complex adaptive pattern-recognition system that defends the body from foreign pathogens. The main purpose of the immune system is to recognize all cells within the body and categorize those cells as self or non-self. It has dramatic and complex mechanisms that recombine the gene to cope with the invading antigens, produce the antibodies and exclude the antigens. A two-tier line of defense is in the system including the innate immune system and adaptive immune system, its basic components are lymphocytes and antibodies [11]. The cells of the innate immune system are immediately available to combat against a wide variety of antigen without previous exposure to them. The antibody production in response to a determined infectious antigen is the adaptive immune response mediated by lymphocytes, which are responsible for recognition and elimination of the pathogenic antigens [12]. The lymphocyte is the main type of immune cell participating in the immune response that possesses the attributes of specificity, diversity, memory, and adaptability, there are two subclasses of the lymphocyte; T and B. each of these has its own function. The B-lymphocytes are the cells produced by the bone marrow, where each exhibits a distinct chemical structure. A B-lymphocyte can be programmed to make only one antibody that is placed on the outer surface of the lymphocyte to act as a receptor. The antigens will only bind to these receptors with which it makes a good fit [13]. In contrast, the T-lymphocytes are the cells produced by the thymus. By use of these T-lymphocytes, they help regulate (suppression or promotion) the production of antibodies. These receptor molecules are able to recognize disease causing pathogens. When antigens and receptor molecules have complementary shapes, they can bind together. Once the binding ensures the recognition of the antigen, the immune response proceeds. After an antigen is recognized by immune cell receptors, the antigen stimulates the B-cell to proliferate (divide) and mature into terminal (non-dividing) antibody secreting cells (plasma cells) [14]

Based on above facts, for solving the optimization problems, the antibody and antigen can be looked as the solution and objection function, respectively.

4 Learning of Fuzzy Cognitive Map

4.1 The Proposed Approach

The presented algorithm simulating the principles of natural immune system is called immune algorithm. In this algorithm, In order to increase encoding efficiency and use gene level operator, we use DNA coding method. In other hand, in order to utilize characteristics of system and the experts' knowledge, we use for reference the object immune of natural immune system, characteristics of system and the experts' knowledge are abstracted to be a schema; then, the schema is made the basis for the immune operator to generate new individuals (vaccine).

The immune algorithm is a 9-tuple (C, I, E, P, M, S, R, U, T), where C—DNA coding; I—vaccination, E—fitness function; P—initialize antibody population; M—population size; S—immune selection; R—crossover; U-mutation; T—stopping condition

The main steps of this algorithm are as follows:

1) An initial individuals (antibodies) population are randomly formed;
2) Calculate the objective function and the affinity between antigen and antibodies and normalize the vector of the objective function;

3) The set of the cloned will suffer the crossover and mutation operation process;
4) The set of the cloned are vaccinated;
5) Select the best n individuals (antibodies) with highest fitness values;
6) Clone the best n individuals (antibodies) ;
7) The fitness values of these new individuals (antibodies) are calculated.
8) Check the stopping criterion. If a termination condition is satisfied, stop the algorithm. Otherwise, go to step 2..

The essential elements of algorithm are explained as follows:

4.1.1 Antibody structure and DNA coding

We know that the fundamental unit of information in living systems is the gene. In general, a gene is defined as a portion of a individual that determines or affects a single character or phenotype. This genetic information is capable of producing a functional biological product, which is most often a protein. The basic elements of DNA are nucleotides. Due to their chemical structure, nucleotides can be classified as four different bases [15], Adenine (A), Guanine (G), Cytosine (C), and Thymine (T), A and G are purines while C and T are pyrimidines. A triplet code of nucleotide bases specifies the codon, which in turn contains a specific anticodon on transfer RNA and assists subsequent transmission of genetic information in the formation of a specific amino acid. There are 64 possible triplet codes, 20 amino acids are interpreted by codons. There exist three major processes in the cellular utilization of genetic information, replication, transcription and translation. They are illustrated as follows: (Fig. 1.)

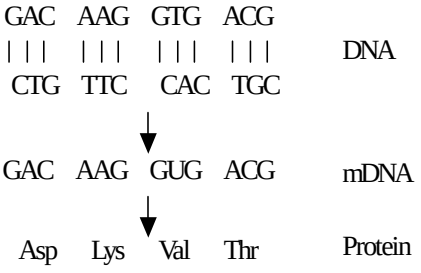

Fig.1. From DNA to protein

In the proposed algorithm, we mimic biological DNA genetic encoding and translation process. Each individual is defined as a vector; each individual consists of $n \times n$ weight variables.

Definition: $C = [w_{11}w_{12}\ldots w_{1n}\ldots w_{nn}]$

Each weight variable is encoded with 6 characters, which consist of A, G, C, T, i.e. corresponding to 2 codons. Each individual consists of $n \times n \times 6$ genes. Fig.2 shows our design of DNA code framework

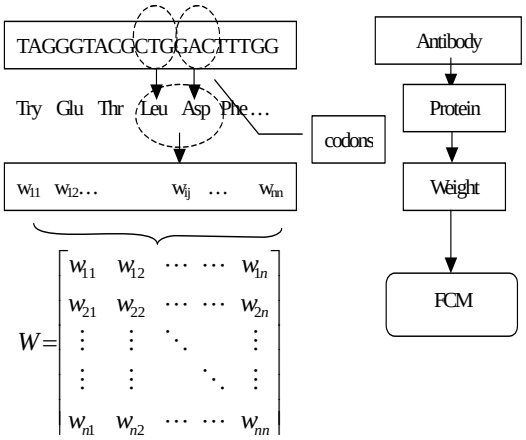

Fig. 2. The DNA coding framework of FCM

When calculating fitness value, the DNA code must be decoded to its phenotypic values. The translation process is: each amino acid corresponds to a value within [-9,9] as tabulated in Table 1[15].

Table 1 From codon to amino acid

1	2				3
	T	C	A	G	
T	Phe(-9)	Ser(-7)	Tyr(-6)	Cys(-5)	T
	Phe(-9)	Ser(-7)	Tyr(-6)	Cys(-5)	C
	Leu(-8)	Ser(-7)	Stop(0)	Stop(0)	A
	Leu(-8)	Ser(-7)	Stop(0)	Try(0)	G
C	Leu(-8)	Pro(-4)	His(-3)	Arg(-1)	T
	Leu(-8)	Pro(-4)	His(-3)	Arg(-1)	C
	Leu(-8)	Pro(-4)	Gln(-2)	Arg(-1)	A
	Leu(-8)	Pro(-4)	Gln(-2)	Arg(-1)	G
A	Lle(1)	Thr(2)	Asn(3)	Ser(-7)	T
	Lle(1)	Thr(2)	Asn(3)	Ser(-7)	C
	Met(0)	Thr(2)	Lys(4)	Arg(-1)	A
	Met(0)	Thr(2)	Lys(4)	Arg(-1)	G
G	Val(5)	Ala(6)	Asp(7)	Gly(9)	T
	Val(5)	Ala(6)	Asp(7)	Gly(9)	C
	Val(5)	Ala(6)	Glu(8)	Gly(9)	A
	Val(5)	Ala(6)	Glu(8)	Gly(9)	G

According to the specific need of the problem, the weight is transformed to interval [0,1] via formula (3).

$$w=0.5+x/198 \quad x \in [-99, 99] \qquad (3)$$

Where w specifies the value of weight.

4.1.2 Fitness function

According to the related knowledge of neural networks. We define the following objective function, it is shown below::

$$E(w) = \frac{1}{2}\sum_{t=1}^{k-1}\sum_{i=1}^{n}(d_i(t) - o_i(t))^2 \quad (4)$$

Where, d_i (t) denotes the known system response for di (t-1) initial vector, $o_i(t)$ is the system response of he candidate FCM for d_i (t-1) initial vector.

The objective function can be used as the core of fitness function

$$F(x)=g(E(x))$$

Where g is an auxiliary function.

The following function g is used:

$$g(x) = \frac{1}{x+1} \quad (5)$$

4.1.3 Antibody selection

In order to guarantee diversity of antibody, we use consistency-adjusting factor based on fitness selection.

Define p is selection probability of antibody, p_f is selection probability based on fitness, p_d is selection probability based on consistency antibody.

$$p_i = \alpha p_{fi} + (1-\alpha)p_{di} = \alpha\frac{f(i)}{\sum_{i=1}^{n} f(j)} + (1-\alpha)\frac{1}{n}e^{-\mu C_i} \quad (6)$$

Where α, μ are adjusting constant, n is antibody number, C_i is the consistency of antibody, its is calculated as given below..

The antibody pool is seen composed of N antibodies having M genes. For those cells marked with S={k_1, k_2, …, k_s}, they are alleles that come from the jth gene. From the information theory, the entropy H_j (N) of the jth gene in the immune system can be computed as given below:

$$H_j(N) = \sum_{i=1}^{S} - p_{ij}\log p_{ij} \quad (7)$$

Where P_{ij} is the probability that the ith allele comes out of the jth gene. By this entropy calculation, it assigns a measure of uncertainty to the occurrence or non-occurrence not of a single allele of genes, but of the whole set of alleles of genes. Note that if all alleles at jth genes are the same, then the entropy of that gene becomes zero.

The similar degreed between antibody u and antibody v:

$$ac_{uv} = \frac{1}{1+H(2)} \quad (8)$$

the consistency of antibody v:

$$C_v = \frac{1}{n}\sum_{i=1}^{n} c_{vj} \quad (9)$$

$$c_{ij} = \begin{cases} 1 & ac_{ij} > T_{ac} \\ 0 & other \end{cases}$$

Where: ac_{ij} is the similar degreed between antibody i and antibody j, T_{ac} is threshold.

4.1.4 Genetic operators

There are many different crossover operators. In our experiments, we consider uniform crossover. Since strong relativities between weights of FCM, there is a small effect to evolution of FCM if we only change one of them. Uniform crossover generalizes this scheme to make every locus a potential crossover point. A crossover mask, the same length as the individual structures is created at random and the parity of the bits in the mask indicates which parent will supply the offspring with which bits. Consider the following two parents, crossover mask and resulting offspring:

P_1 … TAGGGTACGCTGGACTTTGG…
P_2 … ACGGTAATCTCTGTAGGACT…
Mask …0 1 1 0 0 1 1 1 0 0 1 0 1 0 0 0 1 0 1 1…
O_1 … TCGGGAATGCCGAACTGTCT…
O_2 … AAGGTTACCTTTGTAGTAGG…

Fig 3 uniform crossover

In the algorithm, we use transition mutation, in a transition, purines are replaced by purines, and pyrimidines by pyrimidinesl i.e. T-A goes to C-G or vice versa. The effect of mutation is illustrated in Fig 4

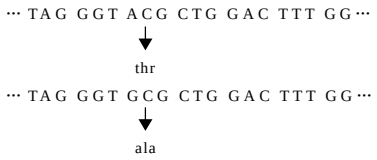

Fig 4 transition mutation

4.1.5 Vaccine and vaccination

A vaccine can be regarded as estimation on some genes of the optimal individual [16]. In application, the vaccine is made from a deep analysis of the characteristics s of system and experts' knowledge. Firstly, a detailed analysis is carried out on the pending problem, and at the same time, as many basic characteristics of the problem as possible ought to be found. Then, the characteristics are abstracted to be a schema. Finally, the schema is made the basis for the immune operator to generate new individual, the vaccine structure is the same as the chromosome structure. In this algorithm, each gene uses integer value 0 or 1. For example, experts provide the following knowledge: (Fig. 5)

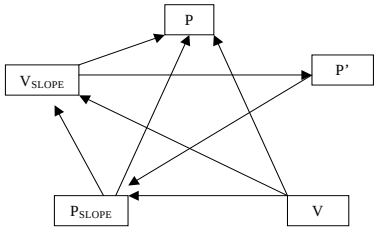

Fig. 5. The expert knowledge

The vaccine is extracted according to the experts' knowledge (Fig.5.) Which is shown below:
Y={0 0 0 0 0 0 0 0 1 0 1 0 0 1 1 1 0 0 0 1 1 1 0 0 0}

Vaccination is a process of modifying the genes on some bits in accordance with expert knowledge so as to gain higher fitness with greater probability. The aim of vaccination is to increase individual quality. Vaccination operation must satisfy the following two conditions. Give an individual x, vaccine (optimal individual) y, if the information on gene bit of the vaccine is 0， then the information on corresponding gene bit of the individual x transforms to 0, if the information on gene bit of the vaccine is 1, then the information on corresponding gene bit of the individual x is changed. The process of vaccination is illustrated as follows:

Example:

Define A as an individual, B as vaccine, C as a new individual. A is vaccinated by B.

A={0.60684 0.30276 0.51551 0.027185 0.31422}

B={0 1 0 0 1}

C={0 0.30276 0 0 0.31422}

5 Application

To demonstrate feasibility of the proposed method, we tried the method on modeling short-term stock prediction. The data come from Shanghai Securities Exchange, dating from 2002-02-27 to 2002-06-20, 52 days of them are used for training and the rest are used for testing.

According to relation theory of finance market, we select 5 variables for modeling. They are:

P—present stock index

P' — yesterday's stock index

V— yesterday's volume

P_{slope} — the slope of stock index in the past four days.

V_{slope} —the slope of volume in the past four days

The training data are normalized to [0,1] by pretreatment (owing to the size of the data, they are not exhibited in the present paper.).

The experts provide the following knowledge:

Y={0 0 0 0 0 0 0 0 1 0 1 0 0 1 1 1 0 0 0 1 1 1 0 0 0}

The example is conducted via simulation based on Matlab with the Genetic Toolbox.

The parameters of the algorithm are reported below: Population_ size: 50, Probability of crossover: 0.7, Probability of mutation: 0.0175, the maximum number of generations: 2000.

The learning result as follows:

$$W = \begin{bmatrix} 0.82141 & 0 & 0 & 0 & 0 \\ 0 & 0.75052 & 0 & 0.014669 & 0.70185 \\ 0.24403 & 0.7218 & 0 & 0.51361 & 0 \\ 0.44865 & 0.89951 & 0 & 0.22333 & 0.67098 \\ 0.74298 & 0.85779 & 0 & 0.75046 & 0.70675 \end{bmatrix}$$

The map can be conveniently drawn according to connection matrix, see Fig. 6.

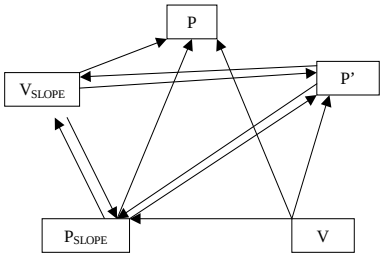

Fig. 6. The FCM of stock market

The variation of optimal and the average fitness among individuals in offspring with generations is shown in Fig.7.

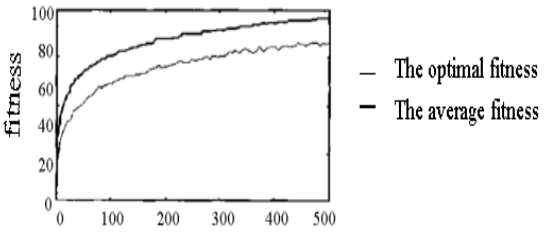

Fig.7. Immune algorithm calculating curve

The prediction curves for Shanghai stock data see Fig. 8

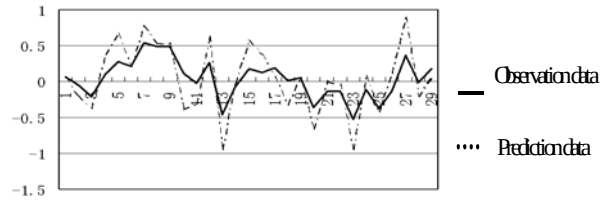

Fig. 8. Prediction curves

The test results show that the method is capable of automatically generating FCM model.

6 Conclusion

We have developed a learning algorithm for automatically generating FCM and have discussed how immune optimization helps construct FCM from input data that consist of a single sequence of state vector values. We illustrated the feasibility and effectiveness of the learning method. Consummating the proposed learning method and exploring the applying area are the direction of our future work.

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