INTERNATIONAL JOURNAL OF COMPUTERS
Issue 3, Volume 1, 2007

Application Study in Decision Support with Fuzzy Cognitive Map

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***Abstract*—**Fuzzy cognitive map is an approach to knowledge representation and inference; it emphasizes the connections of concepts as basic units for storing knowledge, and the structure that represents the significance of system. One of the most useful aspects of the FCM is its prediction capability as a prediction tool. Little research has been done on the goal-oriented analysis with FCM. In this paper, we propose a methodology for decision support, the method uses immune algorithm to find the initial state of system in given goal state. The proposed algorithm takes the error objective function and constraints as antigen, through genetic evolution, an antibody that most fits the antigen becomes the solution. Finally, an illustrative example is provided, and its results suggest that the method is capable of goal-oriented decision support.

***Keywords*—**Fuzzy cognitive map, Immune algorithm, Knowledge representation, Decision support

I. Introduction

FCM is a soft computing method for simulation and analysis of complex system, which combines the fuzzy logic and theories of neural networks. It offers a more flexible and powerful framework for representing human knowledge [1, 2] and reasoning. FCM have been used for representing knowledge and artificial inference, and have found many applications, for instance, geographic information systems [3, 4], fault detection [5], policy analysis [6], etc. One of the most useful aspects of the FCM is its prediction capability as a prediction tool. Little research has been done on the goal-oriented analysis with FCM. In this paper, we propose a methodology for decision support, the method uses immune algorithm to find the initial state of system in given goal state. The proposed algorithm takes the error objective function and constraints as antigen, through genetic evolution, an antibody that most fits the antigen becomes the solution. It aims to provide a means for goal-oriented decision support.

The paper is organized as follows. Section 2 presents the formalization and the inference process of FCM. Section 3 presents a brief overview of the immune algorithm. Section 4 presents how to use FCM for goal-oriented decision support. Section 5 applies the proposed methodology to goal-oriented analysis. Section 6 is the conclusion and suggestions for future works.

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II. 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 [7]. 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. In contrast, the T-lymphocytes are the cells produced by the thymus. kes a good fit [8]. 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 and mature into terminal (non-dividing) antibody secreting cells (plasma cells) [9].

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

III. Fuzzy Cognitive Map

A. Formalization of Fuzzy Cognitive Map

The graphical illustration of FCM is a signed directed graph with feedback, which is consisted of nodes and weighted arcs. Nodes of the graph stand for the concepts that are used to describe the behavior of the system and they are connecte3d by

signed and weighted interconnections representing the causal relationships. A FCM is a method to draw a graphical representation of a system, and 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 wij. wij indicates whether the relation between the two concepts is direct or inverse. The direction of causality indicates whether the concept Ci causes the concept Cj.

A FCM is a 4-tuple (***V, E, C, f***) where --$V=\{v_1, v_2, \ldots, v_n\}$ 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: vi $\rightarrow$ Ci is a function that at each concept vi associates the sequence of its activation degrees, such as Ci(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 iteration t.

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

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

The transformation function is used to confine the weighted um to a certain range, which is usually set to [0, 1].

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

Eq. (1) describes a functional model of FCM. An FCM represents a dynamic system that evolves over time, it describes that the value of each concept is calculated by the computation of the influence of other concepts to the specific concept.

B. Inference in Fuzzy Cognitive Map

Considering it as a discrete dynamic system and calculating its final state numerically can carry out the inference process of the FCM. It is by numeric matrix operation instead of explicit IF/THEN rules [10], this is one of the main advantages of FCM.

The inference of FCM includes forward-evolved inference and backward-evolved Inference. The forward-chains of FCM to derive future states of the system it represents.. The backward-evolved inference uses the transpose of E, our FCM matrix, Et. Backward-evolved inference yields a specific concept node value that should be accompanied with a given consequence.

The forward inference process of FCM starts with a stimulus event vector. Inputting the event into the FCM. Multiplying the stimulus vector to the FCM matrix is the first in a series of such multiplications that eventually yields one of the following:

A fixed point: if the FCM equilibrium state of a dynamical system is a unique state vector, the state vector remains unchanged for successive iterations, then it is called the fixed point.

A limit cycle: if the FCM settles down with a state vector repeating in the form

$A_1 \rightarrow A_2 \rightarrow \ldots \rightarrow A_i \ldots \rightarrow A_1$

Then this equilibrium is called a limit cycle.

A chaotic attractor: the FCM state vector keeps changing with each iteration repeating states are never found.

We Infer with FCM we pass state vectors X repeatedly through the FCM connection matrix W, thresholding or non-linearly transforming the result after each pass.

$$X(t+1)=\begin{bmatrix} x_1(t+1) \\ x_2(t+1) \\ \vdots \\ x_n(t+1) \end{bmatrix} = f(WX^T(t)) = f\left(\begin{bmatrix} w_{11} & w_{12} & \cdots & w_{1n} \\ w_{21} & w_{22} & \cdots & w_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ w_{n1} & w_{n2} & \cdots & w_{nn} \end{bmatrix} \begin{bmatrix} x_1(t) \\ x_2(t) \\ \vdots \\ x_n(t) \end{bmatrix}\right)$$

We illustrate this by the following example:

The first concept node vector be:**X**1 = (1 0 0 0 0), the connection matrix W

$X_1W=[0,0,-1,0,1]$ $X_2=f(X1W)$ $(1,0,0,0,1)=X_2$

$$W = \begin{bmatrix} 0 & 0 & -1 & 0 & 1 \\ 0 & 0 & 0 & -1 & 0 \\ 0 & -1 & 0 & 0 & -1 \\ -1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \end{bmatrix}$$

$X_2W=[0,0,-1,1,1]$ $X_3=f(X3W)$ $(1,0,0,1,1)$ $=X_3$

$X_3W=[-1,1,-1,1,1]$ $X_4=f(X3W)$ $(1,1,0,1,1)$ $=X_4$

$X_4W=[-1,1,-1,0,1]$ $X_5=f(X4W)$ $(1,1,0,0,1)$ $=X_5$

$X_5W=[0,0,-1,0,1]$ $X_6=f(X5W)$ $(1,0,0,0,1)=X_6=X_2$

So X_2 is a fixed point of the FCM dynamic system. This example illustrates that we can apply this kind of FCM-based forward-evolved inference approach to decision-making problems.

We can also compute backward-evolved inference by using the transpose of W, our FCM matrix, Wt. Backward-evolved inference yields a specific concept node value that should be accompanied with a given consequence, it does the opposite with forward-evolved inference.

IV. IMMUNE ALGORITHM

The proposed algorithm takes the error objective function and constraints as antigen, through genetic evolution, an antibody that most fits the antigen becomes the solution.

The immune algorithm (IA) is a heuristic search and optimization technique inspired by simulating the principles of natural immune system to guide their trek through a search space.

The computation procedures of the proposed immune algorithm-based approach illustrated in Fig.2.

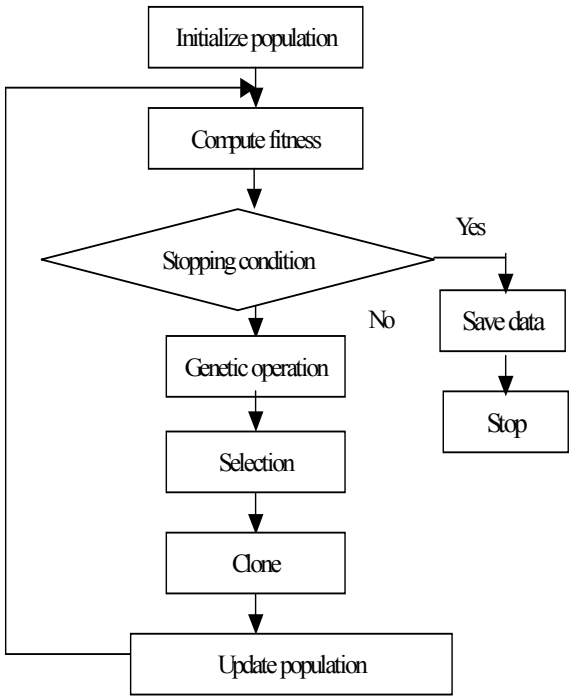

Fig .1. Flowchart of the algorithm

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. Select the best n individuals (antibodies) with highest fitness values;
5. Clone the best n individuals (antibodies)
6. The fitness values of these new individuals (antibodies) are calculated.
7. Check the stopping criterion. If a termination condition is satisfied, stop the algorithm. Otherwise, go to step 2.

V. Goal-Oriented Analysis

Many decision support systems ask the user to identify a goal and then proceed directly to the process of finding recommendations for achieving the selected goal. The goal –oriented decision analysis starts with an expectation goal that can cause an FCM to converge to a given fixed or limit cycle attractor. The objective of finding the appropriate initial state from among a large number of possible states that an FCM can represent is essentially a search problem, which can be optimized. This turns out to be an NP hard problem in FCM's.

A. *The Proposed Approach*

The forward-evolved inference uses a series of vector matrix multiplication to find attractors for a given stimulus vector, while the backward-evolved inference aims to find what initial state, it does the opposite with forward-evolved inference.

The presented methodology for backward-evolved inference proposed by following four steps:

Define the goal state vector F;

Define a diagonal matrix D for calculate error. The ith diagonal value, di□[0,1],of matrix D;

Use IA to Optimize the objective function in Eq(3)

$$E(a,g)=(a-g)D(a-g)T \qquad (3)$$

Where E(a,g) defines the error between the target state G and the attractor A. a denotes the attractor the FCM converges to, g denotes the target state. The essential elements of algorithm are explained as follows.

B. *Explanation of The Algorithm*

1. Antibody Encoding

In the proposed algorithm, individuals (antibodies) population is the binary coded. Each antibody is defined as a vector and consists of n variables.

Definition: $\boldsymbol{B}=[x_1 \boldsymbol{x_2 \ldots x_i \ldots x_n}]$

Each antibodies can be decoded back into a candidate initial state.

2. Fitness Function

The search initial state from among a large number of possible states requires the definition and calculation of an objective examining function (usually an error function) when the objective function reaches a minimum that corresponds to a set of weights. When the objective function is very small, a steady state is reached.

We define the following objective function.

$$\mathbf{E}(\boldsymbol{A},\boldsymbol{G})=\min(\mathbf{E})$$
$$e(a,g)=(a-g)D(a-g)^T \qquad (4)$$

where, *A* denotes the candidate initial state vector, is G denotes the target state D is a n×n diagonal matrix.

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

$$F(x)=I(E(x))$$

where I is an auxiliary function.

The following function $\boldsymbol{g}$ is used:

$$I(x)=\frac{1}{x+1} \qquad (5)$$

The fitness function is normalized to (0, 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, pf is selection probability based on fitness, pd is selection probability based on consistency antibody.

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

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={k1, k2, …, ks}, they are alleles that come from the jth gene. From the information

theory, the entropy Hj (N) of the jth gene in the immune system can be computed as given below:

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

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:

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

The consistency of antibody v:

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

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

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

4. Genetic Operators

The implementation of genetic operations is same as in genetic algorithms. It including the crossover operator and mutation operator requires the selection of the crossover point(s0 and mutation point(s) for each antibody under a predetermined crossover probability and mutation probability. The crossover operator provides search of the sample space to produce good solutions. The mutation operator performs random perturbations to selected solutions to avoid the local optimum.

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.

In natural evolution, mutation is a random process which one allele of a gene is replaced by another to produce a new individual structure. In the algorithm, also, random mutation and roulette wheel selection are applied.

VI. Application

To demonstrate the feasibility of the proposed method, we applied the method to Goal-Oriented Analysis. We adopted following example.

The structure of system is shown in Fig.2.[11]

Where

MP—market position;

CP—competitive position;

PROF—profitability;

FIN—Financing position;

PROD—Productivity position;

INV—Investments

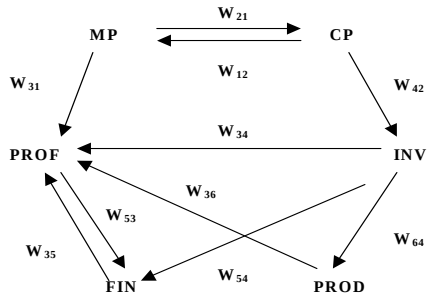

Fig .2. FCM modeling

The connection matrix of decision system is follows

$$W = \begin{bmatrix} 0 & 0.65 & 0 & 0 & 0 & 0 \\ 0.46 & 0 & 0 & 0 & 0 & 0 \\ 0.54 & 0 & 0 & 0.33 & 0.14 & -0.05 \\ 0 & 0.23 & 0 & 0 & 0 & 0 \\ 0 & 0 & -0.18 & 0.31 & 0 & 0 \\ 0 & 0 & 0 & 0.27 & 0 & 0 \end{bmatrix}$$

We set the goal state vector F:

F=[0.6,0.55,0.7,0.5, 0.5,0.6]

Define diagonal matrix D:

$$D = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}$$

Using Immune algorithm optimize the search for the initial state from among a large number of possible states. We set the population (antibodies) size at 50, and probability of crossover: 0.7, probability of mutation: 0.015, the maximum number of generations: 500.

The search result is follows:

[0.5514, 0.6103, 0.7012, 0.6237, 0.5403, 0.5223]

The average fitness among individuals in offspring with generations is shown in Fig.3.

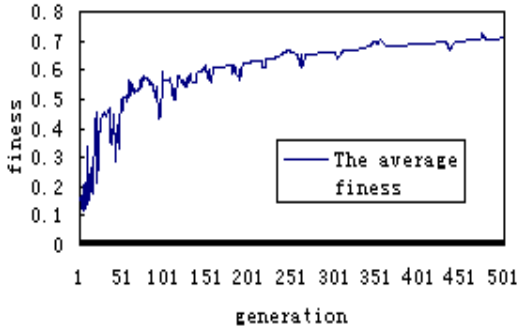

Fig .3. The average fitness

The test results show that the method is capable of Goal-Oriented Analysis.

VII. CONCLUSION

We have developed a method for goal-oriented analysis and have discussed how immune optimization finds the appropriate initial state from among a large number of possible states. The feasibility and effectiveness of the method were illustrated. Consummating the proposed method and exploring the applying area are the direction of our future work.

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