An Affinity Based Lateral Fuzzy Artificial Immune Network and Its Applications

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Summary
Inspired by the natural immune system, the artificial immune system has been attracting more and more attentions. In our previous works, an artificial immune network (AIN) based on the immune principles and a lateral interaction artificial immune network (LAIN) which considers the relationship between different antibodies were proposed. However, there are still some problems such as input and memory are all binary representation and it does not consider the antigen diversity of immune system. In order to solve these problems, in this paper we propose a fuzzy artificial lateral immune network (FLAIN) model by considering the antigen diversity which is the most important property to be exhibited in the immune system. Simulations based on the noisy pattern recognition and clustering show that the proposed model outperforms the traditional ones in terms of noisy tolerance and precision.

Key words:
Artificial Immune System, Pattern Recognition, Clustering

1. Introduction

In biology, immunity is the ability of an organism to resist attacks by invasive foreign substances. Such a foreign substance is called a pathogen and is recognized by the Immune System (IS) as an antigen (Ag). Biological immune system has several excellent abilities such as self/nonself discrimination, reinforcement learning, memory and etc. These abilities have made immune system a useful tool for solving engineering problems. Since initiated by Jerne, who constructed a differential equation to describe the dynamics of a set of identical lymphocytes [2], the artificial immune system (AIS) has been developed largely. A clonal selection theory inspired algorithm, named CLONALG was proposed in [3] to perform pattern recognition. And it has been adapted to solve multi-objectives optimization tasks. At the beginning of 1990s, some efforts have been paid to the research of seeking correspondence between GA and the immune system [4].

In our previous works, we have proposed a binary immune network based on the biological immune system [5]. After that, multi-valued system and clonal selection theory based network have been proposed in [6] and [7], respectively. In these papers, immune network was treated as a competition process using WTA (winner-take-all) rule. Considering the immune behavior of biological immune system, an affinity based lateral interaction AIS was proposed by the authors of [1]. However, the models of those immune networks were only used for the pattern recognition with an input of either 0 or 1.That is to say, they were all binary-value networks.

According to Inman's research [8], in order to distinguish self cells and molecules from foreign cells and molecules, the biological immune system can recognize at least 10^{16} foreign molecules. Therefore, immune system has to be designed to be capable of being applied to arbitrary sequences of analog antigen inputs. However, because our earlier models were all binary representations, the number and complexities of antigen inputs that they can manage are limited. In order to solve more sophisticated problems, a more precise simulation of biological immune system is needed. On the other hand, as a correspondence of human logic, fuzzy logic has been widely used in recent years. In fuzzy logic, individual elements can be members of a set to only a certain degree, that is, they can belong in different degrees to different sets simultaneously. This character makes fuzzy logic a good approximate of biological immune system.

In this paper, we propose a fuzzy lateral artificial immune network (FLAIN) by considering the antigen diversity and apply it to noisy pattern recognition and clustering. Simulation results show that the proposed model is less sensitive to random noises than earlier models and it also clusters input patterns into their corresponding categories with a high precision.

2. Natural Immune System

To perform the self/nonself discrimination process, the immune cells have several special properties. The most important one is that they have many receptor molecules on their surfaces. These molecules have a very powerful function: they can recognize an almost limitless range of antigenic patterns. There are two major kinds of immune cells. One kind is B cells, and the other is called T cells. They are so called because they mature within the bone (B) marrow and the thymus (T) respectively. The main differences between these two kinds of immune cells are

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the way they recognize antigens and their function roles on antigens. The B cells are responsible for producing single specificity receptors to bind to antigens, known as antibodies, and indicating for the invading cells to be destroyed. They have receptors highly specific for a given antigenic determinant. Other main functions of B cells include the production and secretion of antibodies as a response to exogenous proteins like bacteria, viruses and tumor cells. Each B cell is programmed to produce a specific antibody. The production and binding of antibodies is usually a way of signaling other cells to kill, ingest or remove the bound substance. The T cells are subdivided into three major subclasses: T helper cells (T_H), cytotoxic (killer) cells and suppressor T cells (T_S). The T helper cells are essential to the activation of the B cells and other T cells. The killer T cells are capable of eliminating microbial invaders, viruses and cancerous cells. The suppressor T cells are responsible for the maintenance of the immune response. They function by inhibiting actions of other immune cells.

Figure 1 illustrates the basic immune response mechanism. Firstly, when an antigen is detected by antigen presenting cells (APC), such as macrophages, it is ingested by the APC and then digested into antigenic peptides. These peptide pieces are joined to major histocompatibility complex (MHC) molecules and are displayed on the surface of the cell. Then the antigen is recognized by T cell's receptors. The T cell is activated to secret interleukin, which is second signal to B cells. The B cells are stimulated by the interleukin. Then the stimulated B cells break up and divide into antigen synthetic cells (plasma cells). In plasma cells, antibody molecules are synthesized in great volume and secreted. The immune is effected when a sufficient quantity of antibody and lymphocytes have been composed. If the antigen is excluded, the interleukin which suppresses the generation of the antibody is secreted by suppressor T cells, and the immune response process is finished. A part of the divided B cells are preserved as immune memory cells, whose responsibility is to boost the second immune response. If the same antigen invades once again, the memory cells divide into plasma cells rapidly, and a large amount of antibodies are generated in a short period.

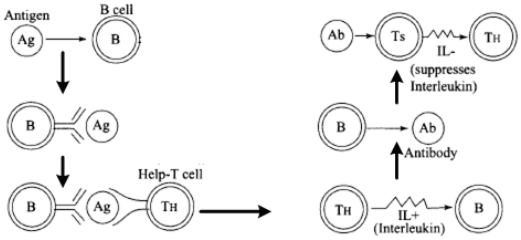

Figure 1. The Immune Response Mechanism

3. Affinity Based Lateral Fuzzy Immune Network and Its Learning Algorithm

3.1 Antigen Presentation

In natural immune system, antigens are cut into smaller pieces by antigen present cells (APC) before they are presented to immune cell. In this model, the input layer is corresponding to APC. After input patterns reached the input layer, they are normalized and then presented to Th cell layer. The normalization is done according to Eq. (1).

$$Ag' = \frac{Ag}{\|Ag\|} = \frac{Ag}{\sqrt{ag_1^2 + ag_2^2 + ... + ag_M^2}} \quad (1)$$

where ag_i (i=1,2,…,M) is the ith element of antigen Ag.

3.2 Competition in Th cell layer

The normalized antigen is presented to Th cell layer through a weight path W according to Eq. (2).

$$u_j = \frac{\left|\mu(\vec{A}g') \wedge \mu(\vec{W}_j)\right|}{e + \left|\mu(\vec{W}_j)\right|}, \quad j=1, 2, \ldots, M \quad (2)$$

where M is the number of Th cells and e is a small positive constant to prevent a float point overflow when $\left|\mu(\vec{W}_j)\right|$ is too small. Size of a vector is determined by L1-norm according to Eq. (3).

Fuzzy operator $\wedge$ is defined as: $(\vec{x} \wedge \vec{y})_i \equiv \min(x_i, y_i)$. $\mu(\cdot)$ is a membership function. In our simulation, the generalized bell function which is defined in Eq. (4) is used.

$$\mu(x, \alpha, \beta, \varsigma) = \left[1 + \left|\frac{x - \varsigma}{\alpha}\right|^{2\beta}\right]^{-1} \quad (4)$$

where α, β and ς are user defined parameters. α and β vary the width of the curve and ς locates the center of the curve. In this simulation, they adopt the value of 0.5, 1.0 and 1.0 respectively.

3.3 Activation of Th cells

Different from early artificial immune system models, WTA rule is not used in this model. Instead, affinity based neighborhood is used to determine which Th cells are to be activated. Affinity is defined as the combine strength between the binding sites of immune cells and the invading antigen. Because the binding is done based on shape complement, affinity is computed as the similarity between

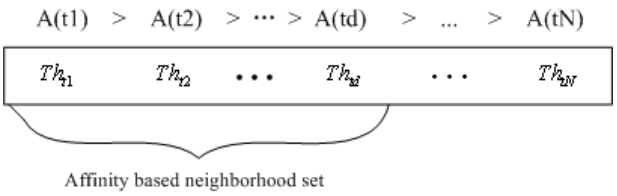

Figure 2. Affinity based neighborhood set

antigen and weight vector W between APC layer and B cell layer. In this fuzzy model, affinity is defined as the degree of Ag' being a subset of $\vec{W}$. That is to say, u_j computed by Eq. (2) is the affinity between input antigen and Th_j. So the affinity based neighborhood set is defined as the first *d* Th cells in a descending affinity sequence, as depicted in Figure 2.

$A(t_j)$ is the affinity between the antigen and the t_j th Th cell in the descending affinity sequence. Parameter *d* is defined as the response depth. The Th cells located in this neighborhood set are activated and the others remain silent. Activation function of Th cells is defined as follows: $O(Th_{t_j}) = 1$, when *j*=1,2,…,*d* and $O(Th_{t_j}) = 0$ otherwise.

3.4 Activation of B cells

B cells in competition and cooperation layer receive two signals: stimulation signal from Th cells and information from antigen.

Excitatory interleukin (IL+) secreted by the activated Th cells are sent to B cell layer through a weighted path V.

$$V = (v_{ji}),\ \text{j=1, 2, … , N; i=1, 2… M.} \qquad (5)$$

Stimulation for B cell b_i for Th cell layer can be computed as:

$$b_i = \sum_{j=1}^{d} O(Th_{tj}) v_{t_j i} \quad i=1, 2, \dots, M \qquad (6)$$

The second signal to B cells is the normalized antigen Ag'.

3.5 System Update

In natural immune system, an organism would be expected to encounter a given antigen repeatedly during its life time. The initial exposure to an antigen is handled by a spectrum of small clones of B cell, each producing antibodies of different affinities. The secondary response to the same or related antigen is achieved by storing some high affinity antibody producing cells from the first infection [9].

In this model, weight between input layer (APC layer) and Th cell layer serves to classify the input antigens, whereas, weight between Th cell and B cell layer remember the information of encountering antigens. Weights W and V are adjusted according to Eq. (7) and Eq. (8) respectively.

$$\vec{W}_j^{(new)} = \beta(\vec{A}g \wedge \vec{W}_j^{(old)})Ts(t)\frac{\vec{U}_j}{\vec{U}_{best}} + (1-\beta)\vec{W}_j^{(old)}$$
$$j=1, 2,\dots, d \qquad (7)$$

$$\vec{V}_j^{(new)} = \beta(\vec{A}g \wedge \vec{V}_j^{(old)})Ts(t)\frac{\vec{U}_j}{\vec{U}_{best}} + (1-\beta)\vec{V}_j^{(old)}$$
$$j=1, 2,\dots, d \qquad (8)$$

where β is learning rate; $Ts(t) = 1 - \frac{t}{T_{\max}}$ reflects Ts cells' regulating effect and $T_{\max}$ is predefined response period; $\vec{U}_j$ is the affinity between Th_j and the invading antigen and U_{best} is the best affinity.

4. Application to Noisy Pattern Recognition

Firstly, the proposed model was used to do pattern recognition. A set of binary patterns which consists of ten Arabic numerals are presented to the model as input antigens. Each pattern is composed of 19 × 19 pixels, as illustrated in Figure 3.

4.1 Learning and Memory Ability

The primary response can be regarded as a training process. The objective of training is to adjust weights so that a set of inputs can produce desired outputs. Due to the length of input antigen is 19×19=361 and there are ten input antigens, numbers of B cells and Th cells are 361 and 10 respectively. That is to say: M=361 and N=10. Weight W between APC layer and Th cell layer and weight V between Th cell layer and B cell layer have to be initialized before the training begins. In this simulation, weights W are initialized to $\frac{1}{M}$, and weights V are initialized to 1. Immune response period TT is set to 100 and learning rate β is given a value of 0.5.

In this process, Arabic numbers 0 to 9 are presented to the network randomly for ten times.

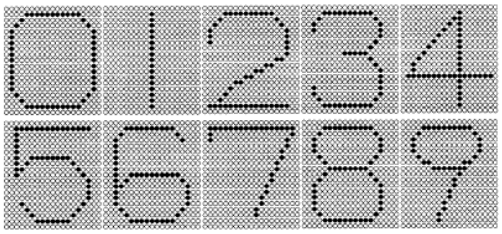

Figure 3. Binary Input Patterns

Because weights from APC layer and Th cell layer are all initialized to 1, affinities for number "3" when it is presented to the newly initialized system are same: 0.996211. Then weights are adjusted according to their affinities (*d*=3). Affinities for the next number "2" are shown in Table 1.

During the learning process, the memory patterns are adjusted towards their corresponding input patterns so that affinities between the input patterns and the memory patterns increase. At the end of this process, affinity between each input pattern and its corresponding memory pattern is very high, that is, the input patterns have been memorized in the memory patterns.

4.2 Noisy Pattern Recognition

The network is said to be trained correctly if it can recognize input patterns which have noise data with a high probability. In this simulation, noise patterns are generated by assign noise to the original patterns. Input patterns can be regarded as vectors. Noise is inserted into these original patterns by randomly changing a vector element from 1 to 0, or vice-verse. The correct recognition rate CRR is defined as: $CRR = N_{CR} / NN$. N_{CR} is the number of noise patterns be correctly recognized and NN is the number of noisy patterns be presented to the network.

In order to show how the training processes influence the noisy pattern recognition, network underwent different training processes are used to noisy patterns generated in the same way (but they are not guaranteed to be the same ones for noises are added randomly). Noisy pattern recognition rate with different ds are shown in Figure 4 (These data are recorded after the network converges).

From Figure 4, we can see that a larger *d* does not affirm a better performance in noisy pattern recognition. This is possibly because that a larger response depth will lead to changes in Th cells' weights whose similarities with the input pattern are very low, thus information of earlier presented input patterns are destroyed. So the response

Table 1 Affinities for number "2"

	A(1)	A(2)	A(3)	A(4)	A(5)	A(6)	A(7)	A(8)	A(9)	A(10)
Input Pattern"2"	0.964	0.997	0.997	0.976	0.976	0.976	0.976	0.976	0.976	0.976
Response Sequence	Th_9	Th_0	Th_1	Th_2	Th_3	Th_4	Th_5	Th_6	Th_7	Th_8

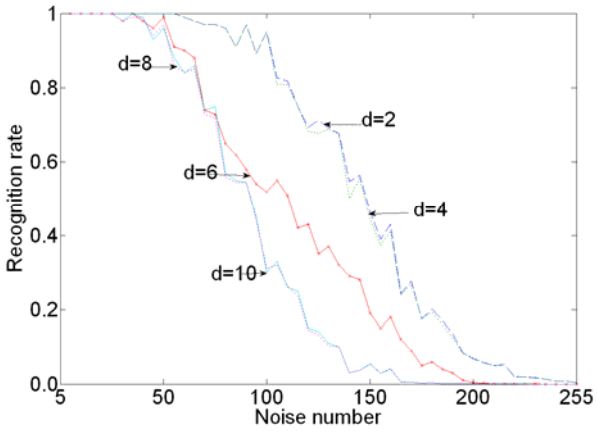

Figure 4. Pattern Recognition Results with Different Response Depth

depth parameter is critical in this model. An appreciate response depth needs to be selected in order to make the Th cells located in the neighborhood set have their weights updated effectively. But because there is no guideline to direct choose of response depth, it should be chosen experimentally.

Finally, noisy pattern recognition ability of the proposed model is compared with the affinity-based immune network proposed in [1]. Figure 5 shows the results. It can be found that the proposed model has a better performance than the model in [1].

5. Application to Clustering

The immune system can learn the structures of pathogens and group them according to their same characters so that the secondary responses to the same pathogens are faster and stronger [10]. To test the proposed model's grouping ability, clustering of analog input patterns is performed.

5.1 Input Patterns

A pattern set, consisting of 100 different patterns is used. Pattern values are taken from the interval [0.1, 1.0] evenly.

Before presented to the network, input patterns are put through a normalization procedure which is called

complement coding. This is done to represent input patterns in an on-response/off-response manner. In this

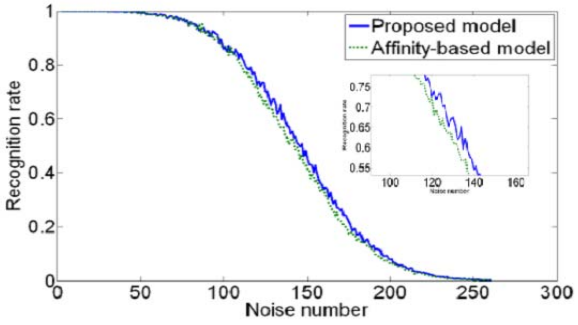

Figure 5. Pattern recognition results of proposed model and Affinity-based model

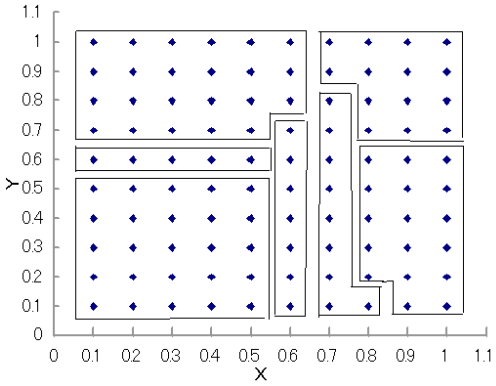

Figure 6. Clustering Results

simulation, input antigens are vectors of each dots' x- and y-coordinates. Complement coding is done according to Eq. (9).

$$\vec{A}g = (\vec{a}, \vec{a}^{c}) = (a_1, a_2, 1-a_1, 1-a_2) \quad (9)$$

5.2 Simulation and Result Analysis

Weights between APC layer and Th cell layer and weights between Th cell layer and B cell layer are all initialized to 1.0. Learning rate β is set to 0.1. That is to say, the network is in a slow learning model. Network vigilance parameter ρ is set as 0.5 and response depth *d* is given value of 3. The network reaches a stable state after 37 iterations. The result is illustrated in Figure 6. 100 input patterns are sorted into 7 clusters. Response depth *d* is set from 1 to 10 and numbers of iterations needed to reach stable states are listed in Figure 7 (a). Form this figure, an increasing tendency can be seen. This is because a larger *d* leads to adjustments of weights associated with more Th cells and each adjustment makes the weights closer to the current input pattern. Because there will be more weights similar to the input pattern, this will add difficulty to the assignment of an input pattern to a certain category; but this assures the input pattern be clustered to a category which is more suitable. As a result, number of result clusters also increases as d becomes larger.

But there are also exceptions. For example, when *d* is 4, number of iterations is smaller than when *d* is 3 by a large extent. The network converges faster if input patterns are assigned to their fated clusters during early iterations. That is to say, input patterns that seldom change their clusters contribute to the convergent of the system. This means that some Th cells' weights are always the most similar with these input patterns among all of the Th cells. So adjustments of weights have important effects in the speed of convergence. When *d* is 4, Th cells which win competition always have similarities larger than the vigilance parameter, so their weights can be adjusted towards the input pattern by the largest extent. And other weights are only adjusted rarely. So they lost basics to compete with the winner and the winner can always be the winner.

The increase in number of result clusters can also be explained in a similar way. Larger *d* makes more weights be adjusted. This reduces differences between these weights and gives chance to more Th cells to win the competition. This brings uncertainty to the network, so more clusters would appear.

Different vigilance parameters are also considered. Figure 7 (b) gives the simulation results. From this figure, we can see that both number of iterations and number of result clusters increase largely as the vigilance parameter increases. To explain this phenomenon, meaning of vigilance parameter ρ needs to be made clear.

ρ represents the degree of mismatch which is to be accepted between the memory pattern and input pattern. With a high value of ρ, the network makes fine distinctions; on the other hand, a low value causes input patterns which are only slightly similar be sorted to a same cluster. So a larger ρ leads to more clusters. In practical problems, this parameter should be defined according to the precision requirements. Experiments with 0.9 and 1.0 values of ρ are not done because their corresponding systems need too many steps to convergent. But considering ρ's meaning, it is not difficult to get this conclusion: when ρ is set to 1.0, the 100 input patterns will be sorted to 100 different clusters.

6. Conclusions

In this paper, we proposed a new artificial immune network model by introducing affinity and fuzziness. In this model, both input and memory are represented in the

fuzzy manner. And there are several B cells respond to one antigen by secreting antibodies with strengths according to their affinities. The model was used to do noisy pattern recognition and clustering. Simulation results showed that the proposed model outperformed our earlier models. In this model, the response depth is critical. An appreciate response depth makes the Th cells located in neighborhood set have their weights updated effectively. In the application of clustering, it classified 100 input patterns into appreciate clusters according to the given vigilance parameters. This showed that it extractives characters of input patterns properly.

In the future, a more comprehended understanding of existing AIS models is aimed. As AIS is inspired by natural immune system, attentions on developments of immunology will also be paid. For example, apoptosis which is a form of programmed cell death has attracted much attention. An inclusion of it to AIS may give some inspiration

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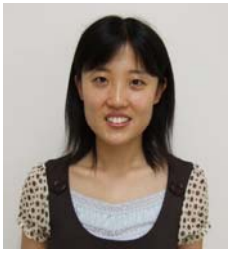

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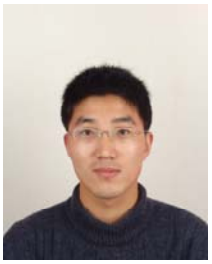

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