

# Pattern Classification Using A Fuzzy Immune Network Model

Weidong SUN (Toyama University, sonkaitou@hotmail.com)  
Zheng TANG (Toyama University, tang@iis.toyama-u.ac.jp)  
Hiroki TAMURA (Toyama University, tamura@iis.toyama-u.ac.jp)  
Masahiro ISHII (Toyama University, ishii@iis.toyama-u.ac.jp)

**Abstract:** It is generally believed that one major function of immune system is helping to protect multicellular organisms from foreign pathogens, especially replicating pathogens such as viruses, bacteria and parasites. The relevant events in the immune system are not only the molecules, but also their interactions. The immune cells can respond either positively or negatively to the recognition signal. A positive response would result in cell proliferation, activation and antibody secretion, while a negative response would lead to tolerance and suppression. Depending upon these immune mechanisms, an immune network model (here, we call it the binary model) based on biological immune response network was proposed in our previous work. However, there are some problems like input and memory in the binary model. In order to improve the binary model, in this paper we propose a fuzzy immune network model. In the proposed fuzzy immune model, we add a normalization B cell layer for normalizing the large-scale antigen information on the base of the binary model. Meanwhile, a fuzzy AND operator ( $\wedge$ ) and a normalization procedure called complement coding were employed in the proposed fuzzy immune model. Compute simulations illustrate that the proposed fuzzy model not only can improve the problems existing in the binary model but also is capable of clustering arbitrary sequences of large-scale analog input patterns into stable recognition categories.

**Keywords:** Immune Response, Fuzzy immune theory, Immune Network, Pattern Classification

## 1 Introduction

The biological immune system is highly complicated and appears touned to the problem of detecting and eliminating infections; it provides a compelling example of a massively parallel adaptive information processing system [1]. The immune discipline has attracted biologists who are interested in modeling biological immune networks and physicists who envisage analogies between immune network models and the nonlinear dynamical systems. The theoretical development of immune networks was initiated by Jerne, who constructed a differential equation to describe the dynamics of a set of identical lymphocytes [2]; After that, several theoretical investigations and modeling of the immune system have taken the approach of mapping into coupled nonlinear dynamical systems and solving differential equations of motion of corresponding parameters [3]-[6]; Three examples of application about an immune system in an engineering system were given while Fujita et al. described the immune system [6]; there are several efforts seeking correspondence between GA and the immune system [8]-[12]. However, in these researches the details how an immune response was concretely applied on an engineering system were not seen.

In our previous work, an immune network model (here, we call it the binary model)based on biological immune response network was proposed [13]. A class of immune networks has since been characterized as a system of

recognition to binary or multiple-valued input patterns [14]-[18]. However, the models of those immune networks were only used for the pattern recognition with an input either 0 or 1 in many cases although the application has been performed with the former various networks. Furthermore, they have the problem that they cannot be applied to the large-scale analog pattern classification because not only the consumption of memory becomes remarkably large, but also it is a problem that long time is required for the processing of pattern classification.

On the other hand, to perform its tasks the immune system must be capable of distinguishing self cells and molecules, which it should not destroy, from foreign cells and molecules (antigens), which it should destroy. The enormity of this task has not been fully quantified, but Inman [19] has calculated that the immune system appears to be able to recognize at least  $10^{16}$  foreign molecules. Therefore, it is necessary to consider the recognition system to apply to the large-scale antigen inputs.

Therefore, in order to improve the binary model, in this research we propose a fuzzy immune network model and apply it to pattern classification. The results of simulations illustrate that the proposed fuzzy model not only can improve the problems existing in binary model but also is capable of clustering arbitrary large-scale input patterns into stable categories corresponding to large-scale antigen in immune system.

## 2 Fuzzy Immune Network Model

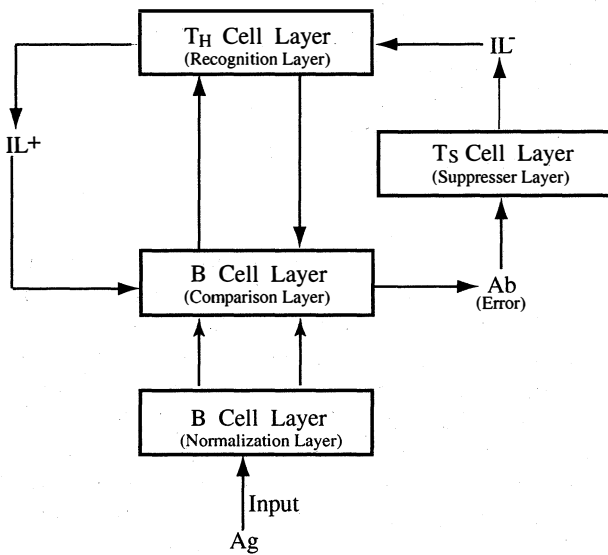


Figure 1: The Model of Fuzzy Immune Network

In our previous binary model, we restrict our discussion on the interaction between B cells and T cells only, although various cells participate in the immunity mechanism. The principle cells related to this action are B cells (B), T cells (T), help T cells ( $T_H$ ), suppressor T cells ( $T_s$ ), antigen (Ag) and antibody (Ab).

At this time, a normalization layer of B cell is employed in the proposed fuzzy immune model. Fig.1 illustrates the proposed fuzzy immune network model. Here, B cell layer not only involves comparison layer but also involves normalization layer.

In the following simple scheme, we describe the information-processing flow about one cell within immune system.

(1) Ag(input)  $\rightarrow$  B cell (normalization layer  $\rightarrow$  comparison layer)  $\rightarrow$  Output

When antigen (Ag) invades living bodies, it can be regarded as an input to the immune network and taken in by B cell. Firstly, the information about antigen is normalized in the normalization layer of B cell.

An alternative normalization rule, called complement coding, achieves normalization while preserving amplitude information. Complement coding represents both the on-cell and the off-cell to  $a$  (see Fig.2, here we let  $a$  present the antigen Ag). To define this operation in its simplest form, let  $a$  itself represent the on-response. The complement of  $a$ , denoted by  $a^c$ , represents the off-response, where

$$a_i^c \equiv 1 - a_i \quad (1)$$

The complement coded input Ag to the recognition system is the  $2N$ -dementsional vectors:

$$Ag = (a, a^c) \equiv (a_1, \dots, a_N, a_1^c, \dots, a_N^c) \quad (2)$$

When normalized information about input Ag is received at the recognition layer of B cell, it is transformed

into a pattern of activation across the B cells and transferred to the next stage of  $T_H$  cell layer.

(2) Output  $\rightarrow T_H$  cell  $\rightarrow IL+$

$T_H$  cell can recognizes the antigen information from B cell and secretes the interleukin ( $IL+$ ) that activates the immune response.

(3)  $IL+ \rightarrow B$  cell  $\rightarrow$  Antibody (Ab)

The interleukin ( $IL+$ ) becomes the second signal to the B cell. Once B cell recognizes this signal, it divides into antigen synthetic cells (plasma cells), and then synthesizes and secretes the antibody finally. Here, B represents both the B cell and plasma cell.

(4) Antibody  $\rightarrow T_s \rightarrow IL-$

If the antibody excludes the antigen, we can say that the immune of living body is effective. At this time, the suppressor  $T_s$  cell will be stimulated to secrete suppressing interleukin ( $IL-$ ) to suppress the immune response. The immune response is finished as long as the generation of the antibody stops.

According to the immune response process mentioned above we can obtain an important features about the proposed fuzzy model: the normalization layer plays an important role on the antigen information processing in the system. This makes the proposed fuzzy model to be possible for applying to large-scale antigen inputs.

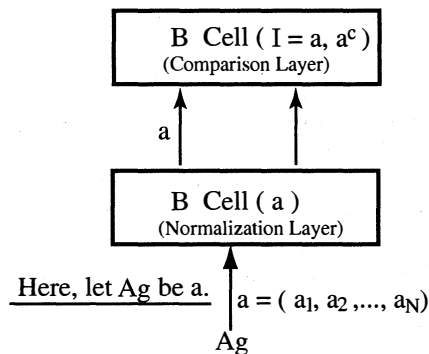
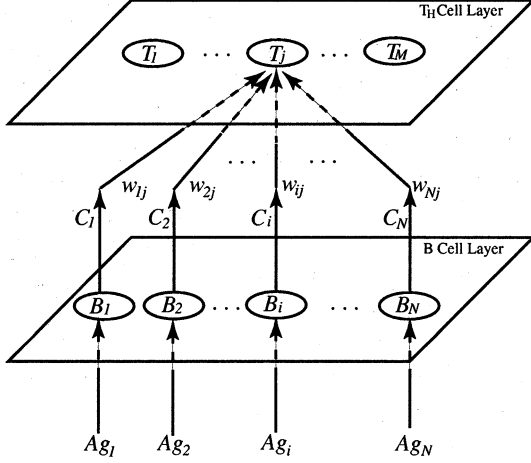


Figure 2: Complement Coding Uses On-Cell and Off-Cell Pairs to Normalize Input Vectors

## 3 Algorithm

We resume that the number of B cell in B cell layer is  $N$  and the number of T cell in  $T_H$  cell layer is  $M$ . In the proposed fuzzy model, the antigen corresponds to input; B cell corresponds to attention subsystem as a feature representation field;  $T_H$  cell corresponds to orienting subsystem as a category representation field;  $T_s$  cell corresponds to suppressing layer and antibody (Ab) to the error between the input pattern and the memory pattern. The network is connected by connection circuits between B cell layer and  $T_H$  cell layer:  $w_j (j = 1, 2 \dots M)$  (weight vector). It is worth noting that the weight vector in this fuzzy model subsumes both the weight vectors from B cell layer to  $T_H$  cell layer and the weight vectors


 Figure 3: Weight Connections From B Cells To  $T_H$  Cells.

from  $T_H$  cell layer to B cell layer. The initial values for these weights are chosen to be equal to 1, so for all  $j$ :

$$w_1 = \dots = w_j = \dots = w_N = 1 \quad (3)$$

The value is also critical; if it is too small there will be no matches at the B cell layer and no training.

When antigen ( $Ag$ ) is received at the stage B cell layer, it can be regarded as input of our model. This is called antigen presentation. Each input  $Ag$  is an  $N$ -dimensional vector  $(Ag_1, Ag_2, \dots, Ag_N)$ , where each component  $Ag_i (i = 1, 2, \dots, N)$  is in the interval  $[0, 1]$ . The information about antigen is normalized according to equations (1)(2).

When normalized information is received at the recognition layer of B cell, each B cell whose activity is sufficiently large generates excitatory signals along pathways to target cells at the next processing stage  $T_H$  cell layer (see Fig.4). When a signal from a B cell in B cell layer is carried along a pathway to  $T_H$  cell layer, the signal is multiplied, or gated, by the pathway's Trace  $w_j$ . The gated signal, we let it  $u$ , reaches the target:  $T_H$  cells. Namely, for  $j = 1, 2, \dots, M$ :

$$u_j = \frac{|Ag \wedge w_j|}{\alpha + |w_j|} \quad (4)$$

where  $\alpha$  is a choice parameter  $\alpha > 0$ , the fuzzy AND operator  $\wedge$  is defined by

$$(z \wedge y)_i \equiv \min(z_i, y_i) \quad (5)$$

and where the norm  $|\square|$  is defined by

$$|Z| \equiv \sum_{i=1}^N |z_i| \quad (6)$$

In the following process  $T_H$  cell will choose the cell, which receives the largest input by competition interaction. That is to say, the  $T_H$  cell that received the largest stimulus can be chosen and we let it  $u_{jmax}$ .

$$u_{jmax} = \max\{u_j : j = 1, 2, \dots, M\} \quad (7)$$

At this time  $T_H$  cell which has the value of  $u_{jmax}$  can secrete interleukin ( $IL+$ ). The interleukin ( $IL+$ ) is then weighted and sent back to B cells once again by the pathway of  $w_j$  (see Fig.5). We call it memory pattern.

The interleukin ( $IL+$ ) becomes the second signal to the B cell. Once B cell recognizes this signal, it divides into antigen synthetic cells (plasma cells), and then synthesizes and secretes the antibody finally. Here, antibody is regarded as the error between the input pattern and memory pattern. We use the fuzzy AND operator to compute the error as follow.

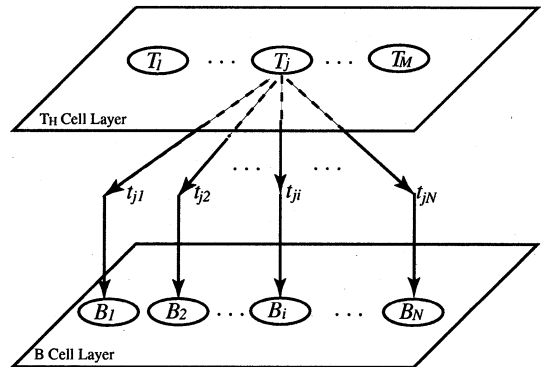
$$Ab(error) = \frac{|Ag \wedge w_{jmax}|}{|Ag|} < \rho \quad (8)$$

where,  $\rho$ , which is called vigilance parameter, is set in the range of 0 to 1, depending upon the degree of mismatch that is to be accepted between the memory vector and the input vector. The input pattern mismatch occurs if the inequality (equation (8)) is true.

If the error is less than the vigilance parameter, a reset signal is sent to disable the firing unit in the  $T_H$  cell layer. The effect of the reset is to force the output of the  $T_H$  cell layer back to zero, disabling it for the duration of the current classification in order to search for a better match. Namely, in this case inhibitory interleukin ( $IL-$ ) is secreted from the  $T_H$  cells. The inhibitory interleukin ( $IL-$ ) tends to suppress the  $T_H$  cells that secrete the excitatory interleukin. Thus, a new competition in  $T_H$  cell layer occurs. The same process will be repeated while the error is decreased below the vigilance parameter.

If the error is bigger than the vigilance level, the memory pattern must be searched, seeking one that matches the input vector more closely, or failing that, terminating on an uncommitted cell that will then be trained. That is to say, the winner  $jmax$  is accepted and it represents the category of this kind of antigen, i.e., the recognition for this kind of antigen of immune network is successful. And then the network enters a training cycle that modifies the weight  $w_j$ .

Training is the process in which a set of input vectors are presented sequentially to the input of the network, and the network weights are so adjusted that similar vec-


 Figure 4: Weight Connections From  $T_H$  Cells To B Cells.

tors activate the same  $T_H$  cell. If the same antigens invade once again, the immune response can be activated by the network recognition rapidly; a large quantity of antibodies is generated in a very short period (the secondary immune response). The adjusting weight equations can be given

$$w_{jmax}^{(new)} = \beta(Ag \wedge w_{jmax}^{(old)}) + (1 - \beta)w_{jmax}^{(old)} \quad (9)$$

where,  $\beta$  is a learning rate parameter,  $\beta \in [0, 1]$ , it defines how quickly prototypes converge to the common minimum of all input patterns assigned to the same cluster.

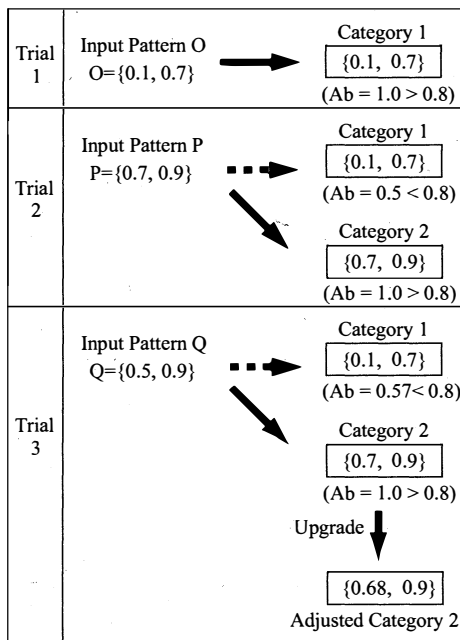


Figure 5: The Matching Process of Input Patterns.

## 4 Simulations

Simulations on the proposed fuzzy immune network are described in this section. Antigen is regarded as an input in our simulations.

### 4.1 Matching process

Firstly, in Fig.5 we give the matching process of patterns O, P and Q in detail to illustrate the effectiveness of the proposed fuzzy immune network model. It consists of two columns: input pattern on the left column and category on the right column. On the left column, the top equations show the original input pattern O, P and Q. On the right column, memory pattern in the middle, category number on the top and the Ab (error) computed by the equation (8) on the bottom are presented respectively. In addition, system vigilance  $\rho$  is set to 0.8.

The first row on trial 1 shows that pattern O establishes the category 1 when there is no any other pattern

in the system and the computed error is bigger than system vigilance. The second row on matching 2 shows the response of memory pattern O (category 1) to the input pattern P. The input pattern and memory pattern are matched and the value of error between them is computed to be 0.5. Because the system vigilance is 0.8, the error (0.5) is less than vigilance (0.8). It suggests that the input pattern P is not belong to category 1. Therefore, category 1 is suppressed, namely IL- is secreted. Then pattern P establishes its new category 2. In the third row on matching 3, category 1 and category 2 response to the stimulus of input pattern Q. When the error is computed to be 0.57, category 1 is suppressed. In category 2, the error is computed to be 0.9 which is bigger than the system vigilance (0.8). Thus, the input pattern Q is classified into this category 2. And then the memory pattern in category 2 is adjusted.

### 4.2 The Difference Between Two Immune Network Models

In the proposed fuzzy immune network model, a fuzzy AND operator is employed, while in the binary immune network this kind of operator is not used. In the binary immune network [13], the input pattern for learning is restricted in either 0 or 1. When we employ the fuzzy AND operator, it becomes to be possible for the proposed fuzzy immune network model to learn and cluster the arbitrary sequences of large-scale analog input patterns as well as binary patterns.

In this simulation we compare the system action between the binary immune network and the fuzzy immune network. System vigilance is set to 0.8 in each model. Parameter  $e$  is set to 0.001 in the fuzzy immune network. The values of input vectors are either 0 or 1 in the binary immune network, but in the fuzzy immune network the values of input vectors are varieties in the interval [0.0, 1.0].

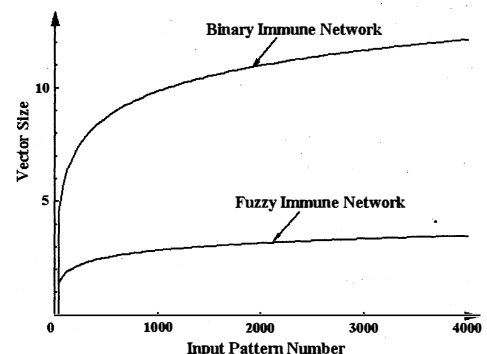


Figure 6: The Change Situation of Vector Size.

Fig.6 shows the change of vector size with the input pattern number. When input patterns increase, the vector sizes also increase in both the binary immune network and fuzzy immune network. But under the same input

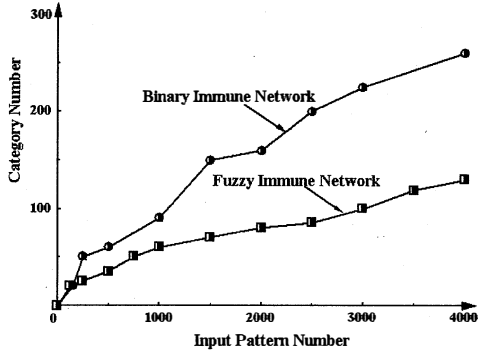


Figure 7: The Relation Between Input Pattern Number And The Category Number.

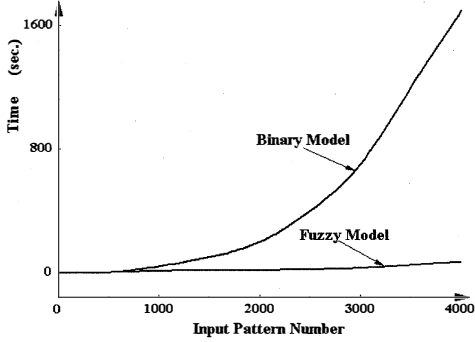


Figure 8: The Change Situation of Clustering Speed.

pattern number, the vector size of the binary immune network is larger than that of fuzzy immune network. This is because the input value of variety dimension is only 0 or 1 and if there is no larger size then it cannot work for the input pattern in the binary immune network. In contrast, in the fuzzy immune network the input value of variety dimension is variety in the interval  $[0.0, 1.0]$ , it can work for the input pattern even if there is smaller size only.

Fig.7 shows the relation between input pattern number and category number. It illustrates that under the same input pattern number, the category number in the fuzzy immune network is less than that in the binary immune network.

In Fig.8, the Y-axis presents the clustering time until the classification finishes; the X-axis presents the input pattern number. It represents the change of clustering speed with the increase of category number. When the input pattern number is around 500, the difference of speed between two immune networks is almost zero. But, when the input pattern number is over 500, the remarkable difference can be seen between two immune networks. It suggests that the clustering time is shortened in the fuzzy immune network. It can be considered as

that the size of used memory in the simulation is remarkable smaller because both category number and vector size are smaller in the fuzzy immune network than that in the binary immune network.

### 4.3 The clustering performance of fuzzy model

This section presents clustering examples for the proposed fuzzy model discussed in the previous section. A pattern set, consisting of 100 different patterns, is used to analyze and compare clustering performances. Pattern values are taken from the interval  $[0.1, 1.0]$  to fit the input restriction. Patterns are presented in different random orders. For definiteness, let the input  $I$  consist of two-dimensional vectors  $a$  preprocessed into the four-dimensional complement coding form. Thus, a formula of the concrete normalized input pattern can be given as following:

$$I = (a, a^c) = (a_1, a_2, 1 - a_1, 1 - a_2) \quad (10)$$

Thereby, the size of weight vector becomes doubles. Among these normalized input patterns the portion (portion of  $a$ ) of the first half is performing fuzzy AND operation and the portion (portion of  $a^c$ ) of the second half is performing fuzzy OR ( $X \vee Y = \max(x_i, y_i)$ ) operation in the operation with a weight vector. In this case, as shown in Fig.6, each category  $j$  has a geometric representation as a rectangle  $R_j$ . The weight vector can be written in complement coding form:

$$w_j = (u_j, v_j^c) \quad (11)$$

where  $u_j$  and  $v_j$  are two-dimensional vectors. Let vector  $u_j$  define one corner of a rectangle  $R_j$  and let  $v_j$  define another corner of  $R_j$ . The size of  $R_j$  is defined to be

$$|R_j| = |v_j - u_j| \quad (12)$$

which is equal to the height plus the width of  $R_j$  in Fig.9.

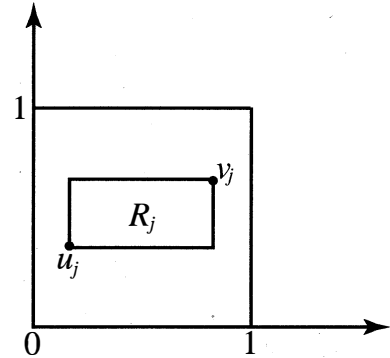


Figure 9: Each Weight Vector  $w_j$  Has A Geometric Interpretation As A Rectangle  $R_j$  with Corners  $(u_j, v_j)$ .

In our simulations, portion of  $a$  is presented in X-axis and portion of  $a^c$  is presented in Y-axis. Thus, the simulation results can be presented in two-dimensional graph (see Fig.10).

$$\begin{aligned} w_1 &= (0.1, 0.4, 0.4, 0.2) \\ &= ((0.1, 0.4), (0.6, 0.8))^c \\ w_2 &= ((0.7, 0.2), (0.9, 0.9))^c \\ w_3 &= ((0.3, 0.1), (1.0, 0.3))^c \\ w_4 &= ((0.3, 0.9), (1.0, 1.0))^c \\ w_5 &= ((0.1, 0.1), (0.2, 0.3))^c \\ w_6 &= ((1.0, 0.4), (1.0, 0.8))^c \\ w_7 &= ((0.1, 0.9), (0.2, 1.0))^c \end{aligned}$$

With higher learning rate  $\beta = 1.0$ , the first adaptation of a category toward an input pattern not yet lying within its area, stretch the according rectangle to the minimum area, covering all patterns assigned to the same category for at least one time. With  $\beta = 1.0$ , a stable system network state is reached as soon as all training patterns have been presented just one time.

Second, we let the learning rate  $\beta = 0.1$ , namely, the system is in the slow-learning rate mode. In this case, the category rectangles do not tend to overlap that often. Fig.10(c) shows the clusters with same vigilance, but lower learning rate than in Fig.10(a), after adaptation to the same random training sequence. Because training stopped when each pattern was presented at least one time, category is in a non-stable state. Fig.10(d) shows the clusters when pattern presentation is continued until each pattern is processed at least ten times. Categories now reached their stable values. The number of categories increases from four to seven. This illustrates that with learning rate  $\beta < 1.0$  the number of categories, as well as the distribution of patterns to clusters, might vary through out pattern presentation as long as categories have not yet reached their stable equilibrium. In Fig.10(e), system vigilance parameter  $\rho$  is raised to 0.6 and the other parameters are the same with those used in Fig.10(d). The number of categories increases from 7 in Fig.10(d) to 10 in Fig.10(e). This illustrates that at a high value of  $\rho$  the network makes fine distinctions; on the other hand, a low value causes the grouping of input patterns that may be only slightly similar. Fig.10(f) uses the same values for parameters  $\beta$  and  $\rho$  as Fig.10(e). Each pattern is again presented at least ten times, but in a different order. The example demonstrates that even lower vigilance do not necessarily prevent category from overlapping. The number of resulting clusters depends not only on vigilance parameter  $\rho$  but also on the order of pattern presentation.

Continuously, we gave the trials of clustering performance for higher dimensional data with the proposed immune algorithms. Here, the task is to discover the biological immune system states by analyzing the shapes of specific time dependent variety signals. Input patterns in

this case do not cover the whole multidimensional input space, but tend to form groups in geometrically separated areas.

We focus whether our algorithm based on the proposed fuzzy immune model has the ability or not to either discover stable categories of patterns with a minimum required similarity or to set up recognition maps of an input space. In the meantime, we also observed the effects of noise to the clustering performance, since input patterns will always vary, even when representing exactly the system state.

As shown in Fig.11 as an example for a more general signal shape, we examined the clustering capabilities of our network by using step response of second-order systems. The response function is normalized so that the resulting converges around a value of  $f(t) = 0.5$ .

$$f(t) = 0.5[1 - e^{-\zeta\omega_0 t}(\cos g(t) + c \sin g(t))] \quad (13)$$

$$g(t) = \omega_0 t \sqrt{1 - \zeta^2} \quad (14)$$

$$c = \frac{\zeta}{\sqrt{1 - \zeta^2}} \quad (15)$$

Input vectors are formed out of 100 consecutive values of  $f(t)$  with  $t = 1, 2, \dots, 100$ . A useful property of the step response is the fact that it is completely defined by two physical parameters, eigenfrequency  $f_0 = \omega_0/2\pi$  and damping  $\zeta$ . Therefore, input patterns as shown in Fig.11, as well as clusters, can be depicted in a two-dimensional PT2-parameter plane to illustrate the influence of different network-parameter variations. The period length of the step responses in terms of inverse eigenfrequency is varied from 10 to 100 time intervals in steps of ten. The damping is varied from 0.1 to 0.9. Step responses of the training-pattern set are equally distributed over this physical parameter plane, but represent points in discrete subareas of a 100-dimensional pattern space. So in contrast to the two-dimensional pattern set of the previously, there are geometrical preferences for clustering, which should be discovered independently of the random order in pattern presentation. Since exclusively damping and eigenfrequency determine the shape of the trained step responses, networks are expected to set up clusters, including shapes referenced by neighboring points in the parameter plane. The training set is presented in random orders, as with the two-dimensional pattern set.

Generalization capabilities of our network are tested by classifying the pattern set with previously trained networks and learning rate  $\beta = 0$ , after any pattern has been corrupted with a random white noise (see Fig.13). The more noisy patterns are assigned to the clusters of their undisturbed origins, the higher is the quality of generalization.

Fig.13 shows clustering examples of step responses in fast-learning mode, learning rate  $\beta = 1.0$ , and slow-learning mode,  $\beta = 0.01$ . The random pattern sequences

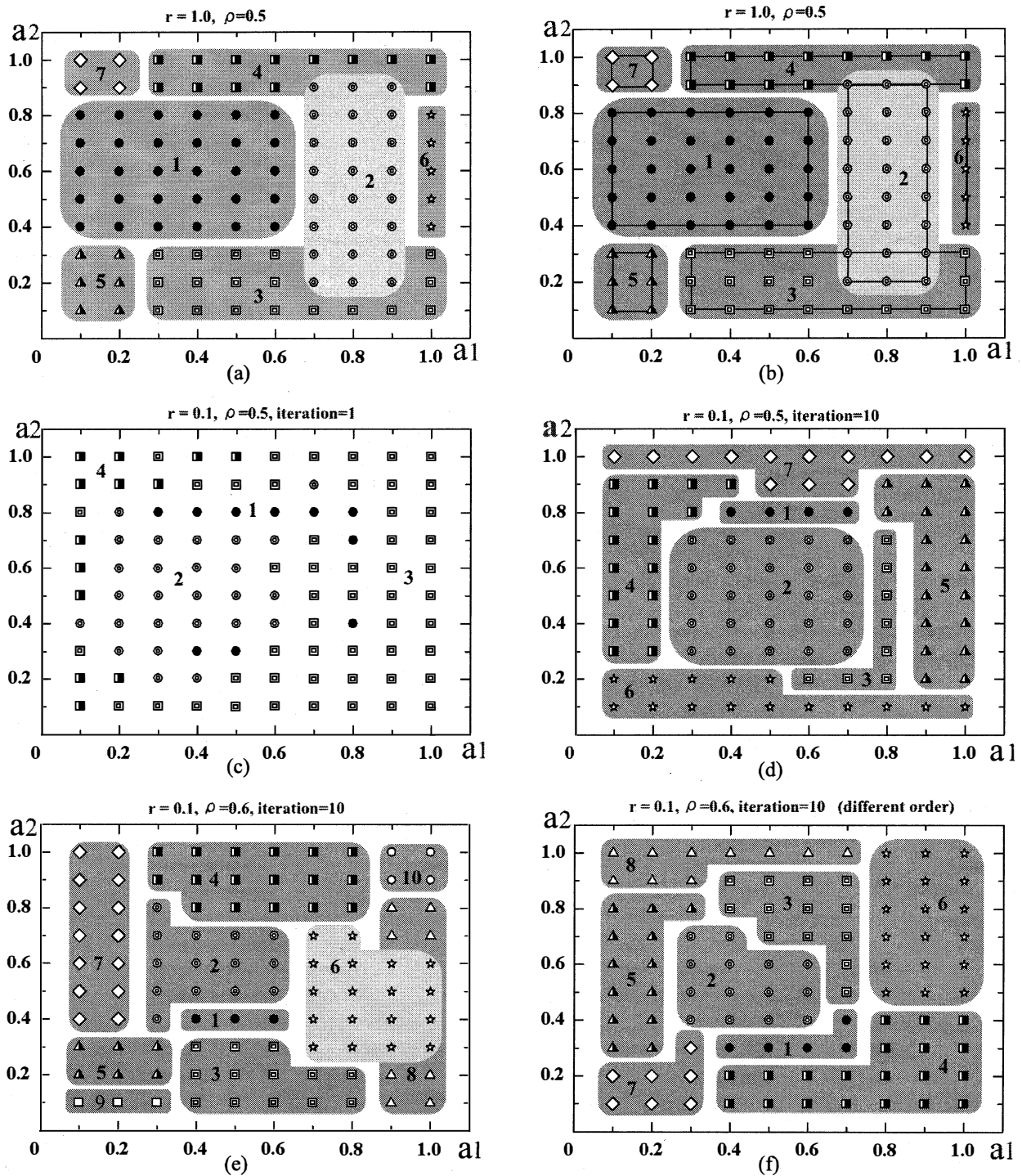


Figure 10: The Two-Dimensional Clustering Performance of 100 Random Input Patterns for Our Fuzzy Immune Model. Variety of Marks Present The Spatial Positions of Input Patterns. Patterns Assign to A Common Cluster Are Marked With An Underlying Gray Shade.

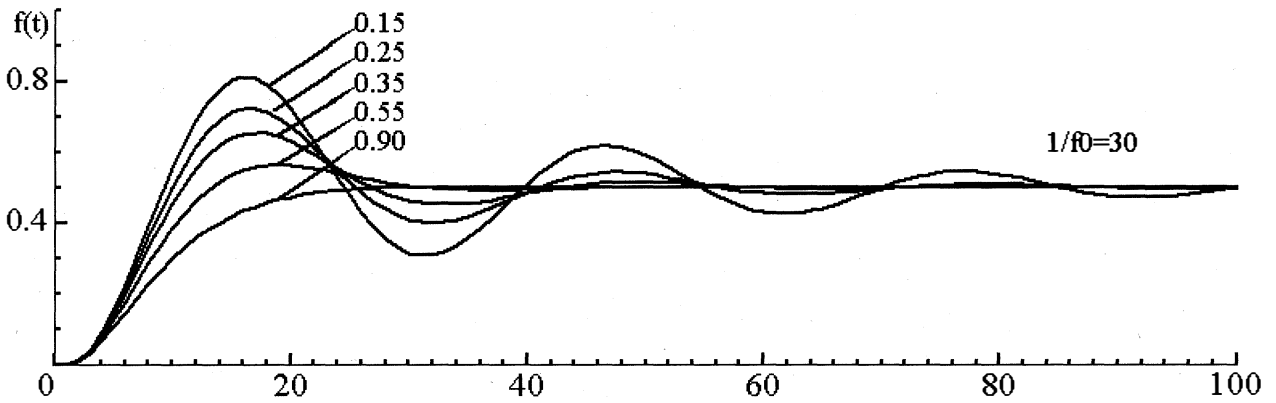
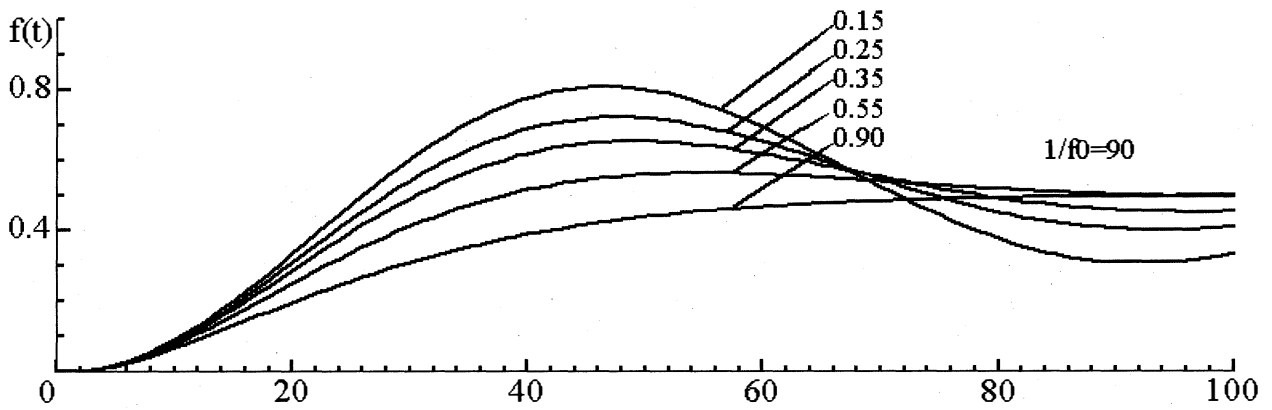


Figure 11: Step Response of Second-order System (PT2) With Different Eigenfrequencies And Dampings. Input Patterns Consists of 100 Samples Taken At Equidistant Time.

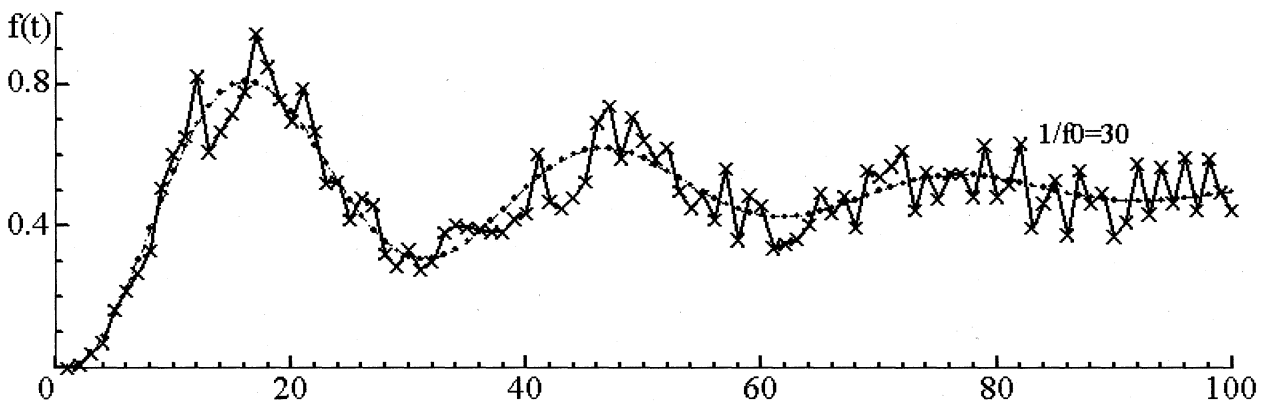


Figure 12: PT2 Step Response With Period Length  $1/f_0 = 30$  And Damping  $\zeta = 0.15$ . The Original Signal (Dotted Line) Is Corrupted by A Random White Noise with Maximum Amplitude 0.25.



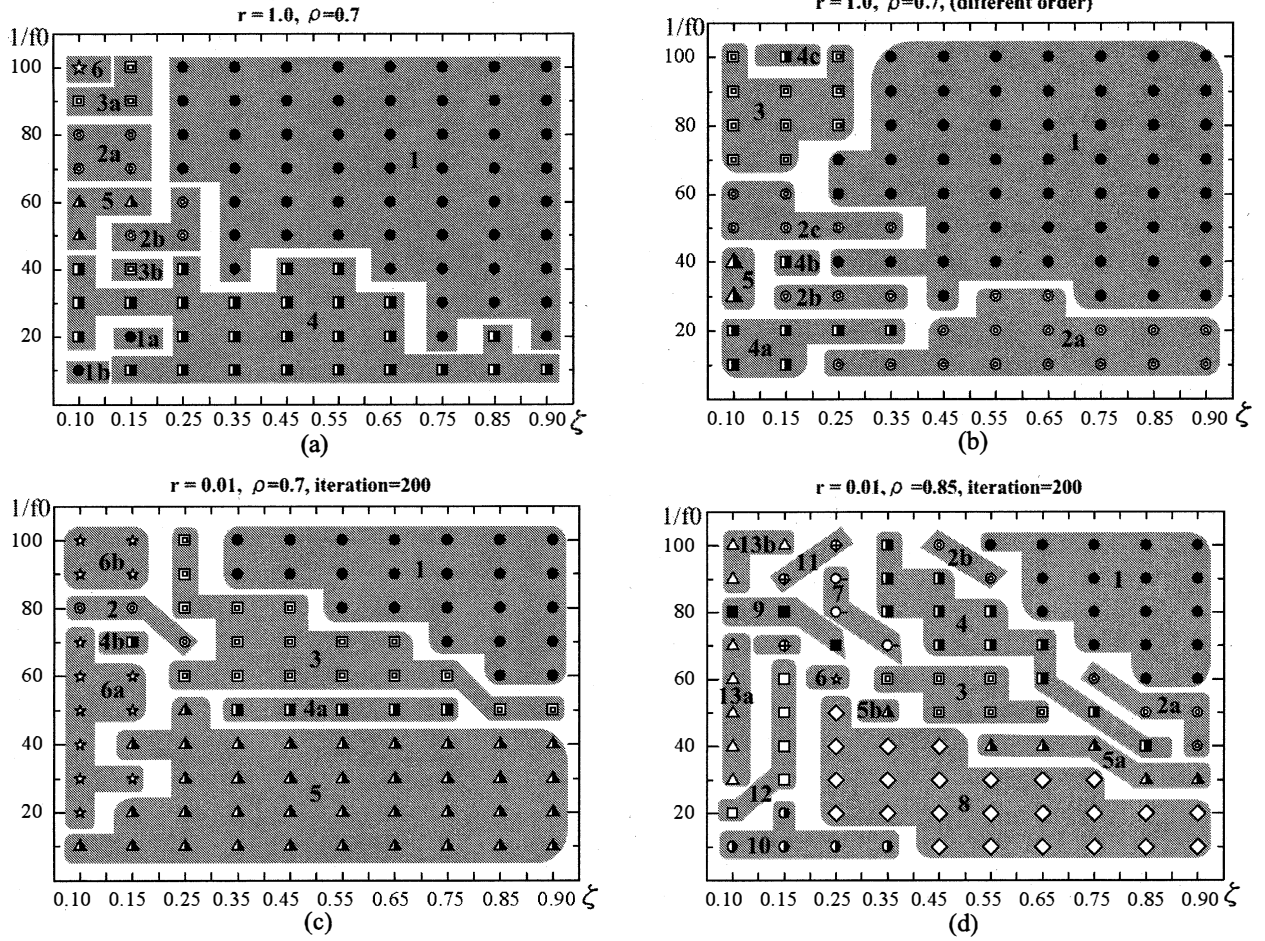


Figure 13: High-dimensional Clustering Performance of Our Fuzzy Immune Network. Step Response of Second-order System Are Defined by The Eigenfrequency and Damping  $\zeta$ , Marked On The Parameter Plane. Gray Shades Group Neighboring Patterns in The Parameter Plane, Assigned To The Same Category.

were presented with a minimum of one presentation per pattern with  $\beta = 1.0$ , and 200 presentations per pattern with  $\beta = 0.01$ . Fig.13 (a) shows an example of fast-learning with vigilance set to  $\rho = 0.70$ . The network set up six categories on the pattern set. The patterns of category 4 are distributed over up to three separate coherent areas on the parameter plane. The category numbers represent the temporal order during training in which prototypes were accessed for the first time. Categories in Fig.13 (b) are set up with the same network-parameters but a different random order in pattern representation. The scene is again dominated by a huge category 1 and several additional categories, dividing the PT2-parameter plane in distinctly different categories. Categories 1, 2 and 3 are split in up to several separate areas. This illustrates that the clustering of our network remains incoherent in the physical parameter-plane and highly dependent on the order of pattern presentation. In Fig.13(c) slow-learning mode, six categories were set up, showing the same characteristics as with Fig.(a) and Fig.(b) in fast-learning mode. Except this property, in

Fig.13(d) the category number was raised to 13 when using high vigilance, showing the same functions of vigilance as with two-dimensional pattern data.

## 5 Conclusion

In this paper, we proposed the fuzzy immune network model for improving the binary model proposed in our previous work. In the fuzzy model we introduced the B cell normalization layer and employed the fuzzy AND operator  $\wedge$  in the algorithm. Computer simulation tested the dynamic of the fuzzy network model and illustrated that the proposed fuzzy model was able to solve the problems like input and memory that exist in the binary model.

By establishing the fuzzy immune network to which the analog input pattern between 0 and 1.0 correspond from the simulation results, it changed so that application to large-scale pattern recognition could be performed and the proposed fuzzy immune model turns out to be an effective, transparent clustering algorithm.

Properties of our networks depend on two main parameters,  $\rho$  and  $\beta$ . Higher vigilances increase the total number of categories set up on a static pattern set. Learning rate  $\beta$  regulates adaptation of stored categories toward input patterns. If no geometric preferences are given for a specific pattern set, the number of categories is also slightly dependent on the order of pattern presentation.

Two-dimensional pattern sets illustrated the geometric nature of clustering. The proposed fuzzy model uses the degree of an input pattern being fuzzy subset of a stored prototype to measure the similarity between two patterns. When using complement encoded input patterns, prototypes converge toward the common MIN- and MAX-values of all patterns assigned to the according category. Categories separate the pattern space along the pattern space axes.

The example of sampled PT2-step responses in our simulation illustrated that the clustering of the proposed fuzzy model can even be incoherent in the physical parameter space. When all training patterns are enclosed by the MIN- and MAX- bounds defined by the prototypes, all network weights are fixed. The extension of prototypes is limited by the vigilance parameter  $\rho$ . Once the maximum extension of a prototype has been reached, no further patterns are assigned to the according category not lying completely within the MIN- and MAX-borders. This makes our network highly sensitive to additional noise on trained input patterns and its output unpredictable. Even if the geometric distribution of input patterns in pattern space gives preferences for the distribution of these patterns to categories. The clustering of our network remains highly dependent on the random order of pattern presentation and tends to be incoherent in pattern space.

## References

- [1] S. A. Hofmeyr, S. Forrest, "Architecture for an Artificial Immune System", *Evolutionary Computation*, 7(1):45-68, by the Massachusetts Institute of Technology, 1999.
- [2] N.K. Jerne, "Towards a network theory of the immune system," *Ann. Immunol*, vol.125c, pp.373-389, 1974.
- [3] *Theoretical Immunology, Parts I and II*, Edited by A. S. Perelson, Addison-Wesley, Redwood City, CA, 1988.
- [4] A. S. Perelson, "Immune Network Theory", *Immunology Review*, 110, 5-36, 1989.
- [5] *Theories of Immune Networks*, H. Atlan and I.R.Cohen, Eds., Springer-Verlag, Berlin, 1989.
- [6] J. Faro and S. Velasco, "Studies on A Recent Class of Network Models of the Immune System", *J.Theor. Biol.* 164, 271-290, 1993.
- [7] Hiroyuki Fujita, Kazuyuki Aihara, "A Distributed Surveillance and Protection System in Living Organisms." *T. IEE Japan*, Vol. 107-C, NO. 11, pp.1042-1048, 1987.
- [8] R.Hightower, S. Forrest, and A.S. Perelson, "The evolution of secondary organization in immune gene libraries." *Proc. Second European Conference on Artificial Life*, 1993.
- [9] S.Forrest, B.Jovornik, R.E. Smith, and A.S. Perelson, "Using genetic algorithms to explore pattern recognition in the immune system." *Evolutionary computation*, NO.1, pp.191-211,1993.
- [10] J.D.Farmer, N.H.Packard, A.S.Parelon, "The Immure System, Adaptation, and Machine Learning", *Physical*, D 22, 187-204, 1986.
- [11] J.D. Farmer, "A Rosetta Stone for Connectionism." *Physic*, No. D42, pp.153-187, 1990.
- [12] H. Bersini and F. J. Varela, "The immune recruitment mechanism: A selective evolutionary strategy," *Proc. ICGA-91*, pp.520-526, 1991.
- [13] Z. Tang, H. Hebishima, K. Tashima, D. Ishizuka and K. Tanno, "An immune network based on biological immune response network and its immunity," *IEICE Trans. Fundamentals*, *IEICE Trans.*, vol.J80-A, No.11, pp.1940-1950, Nov.1997.
- [14] K. Takenaka, Z. Tang, K. Tashima, D.Ishizuka and K.Tanno,"An ImmuneNetwork for Pattern Recognition," In *Proc.NOLTA'97*,vol.1,pp189-192,1997.
- [15] K. Tashima, Z. Tang, K. Takenaka, D.Ishizuka and K.Tanno,"A self-organized Immune Network," In *Proc.NOLTA'97*,vol.1,pp.193-196,1997.
- [16] Z. Tang, T. Yamaguchi, K. Tashima, O. Ishizuka, K. Tanno, "A Multiple-Valued Immune Network and Its Applications", *IEICE Trans., Fundamentals*, Vol. E82-A, NO.6 June, 1999.
- [17] T. Yamaguchi, Z. Tang, O. Ishizuka, K. Tanno, "Adaptive Multi-Valued Immune System", *I.IEE Japan*. Vol.121-C, No.11, pp.1747-1754, 2001.
- [18] Z. Tang, K. Tashima, Q. P. Cao, "A Pattern Recognition System Using Clonal Selection-Based Immune Network", *IEICE Trans.*, vol. J84-D, No. 12, pp. 2615-2622, Dec. 2001.
- [19] Inman, J. K., *The Antibody Combining Region: Speculations on the Hypothesis of General Multispecificity*. In G.I.Bell, A.S.Perelson, and J.G.H.Pimbley (Eds.), *Theoretical immunology*, pp.243-278. NY: Marcel Dekker, 1978.