

## A Clonal Selection Algorithm for Classification of Mangroves Remote Sensing Image

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### **Abstract**

*As a new computational intelligence model based on artificial immune systems, clonal selection algorithm has been widely utilized for data analysis and pattern recognition. Recently it was applied to remote-sensing image classification. However, due to the similar spectral feature between mangroves and other land cover types such as agricultural land and forests, serious misclassification and confusion can develop in mangroves classification using conventional methods. This paper proposes a clonal selection based supervised classification algorithm which takes into account not only spectral feature but also geographical feature and image feature. The proposed algorithm searches the best cluster centers for various types of training samples by the improved clonal selection algorithm. The antibody represents the candidate solution, while antigen is reflected by affinity function. The antibody is encoding by decimal way. The inner superiority and the outer superiority together are used to measure the superiority of antibody. The selection operator and mutation operator are designed to guarantee the diversity and global optimality. Experiments are performed and the results show that the proposed method can improve the extraction accuracy of mangroves effectively.*

**Keywords:** *Artificial immune, Classification, Clonal Selection, Mangroves, Remote Sensing*

### **1. Introduction**

As the important component of the world's coastal ecosystems, mangroves have most significant ecological and economic values, and have been commonly concerned in the researches of environment and resources [1]. Detection and analysis of the distribution of mangroves are the important work for their protection. Remote sensing technology now gives people a new way for mapping and monitoring the dynamic change of mangrove forest resources, as it allows information to be gathered from the forbidding environment of mangrove forests. The classification is the core issue in the application of mangroves remote sensing [2]. Because of the similar spectral feature between mangroves and other land cover

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types such as agricultural land and forests, the phenomena of “same object with different spectrums” and “same spectrum foreign matter” are widespread in spectral images. As a result misclassification and leakage points are common, which led to a low classification accuracy [3]. It is significant to find new technologies to improve the classification accuracy of mangroves remote sensing image.

Artificial immune system (AIS) is a new intelligent system imitating biological immune system. Now it is a solution to complex and distributed problems, and has drawn increased attention from the artificial intelligence community. Recently it has been exploited for a wide spectrum of applications such as pattern recognition [4], machine learning [5], clustering [6], and optimization[7]. However the application of AIS to remote sensing image classification has been rather limited. Few papers have concerned how to apply it to remote sensing imagery classification. Also AIS has not been explicitly applied to satellite data processing in an attempt to discriminate mangrove vegetation from neighboring ecosystems. Zhong and etc. try to apply AIS to unsupervised and supervised remote-sensing image classification [8-10]. A clonal selection based remote sensing image classification algorithm was attempted in ref. [10], and the experiments showed that the method is superior to traditional algorithms. However, due to the similar spectral features between mangroves and other land cover types, when we applied this method to mangrove remote sensing image, the accuracy is unsatisfactory. Therefore this paper proposed an improved clonal selection algorithm (ICSA) for the classification of mangrove remote sensing image. Geographical feature and image feature together with spectral feature were integrated as decision making features, the best cluster centers for various land cover types were calculated in parallel, and finally the minimum distance method was called to perform the classification. The antibody is encoding by decimal way which is suited for remote sensing data. The inner superiority and the outer superiority together are used to measure the superiority of antibody. The selection operator and mutation operator are designed to guarantee the diversity and global optimality. Experiments are performed on the TM remote sensing image of Zhangjiang estuary in southeastern China. The results show the proposed method can improve the extraction accuracy of mangroves effectively.

## 2. Clonal Selection Algorithm

As a kind of artificial immune algorithm, clonal selection algorithm is derived from the clonal selection principle [11]. Clonal selection principle simulates b cells protect the human body against attacks from antigens (such as viruses, bacteria and other parasites) and eliminate the infected cells. The whole process of antigen recognition, cell proliferation, and differentiation is called the clonal selection principle which is used to explain the basic features of an adaptive immune response to an antigenic stimulus. Clonal selection principle establishes the idea that only those cells that recognize the antigens are selected for proliferation. The selected cells are subject to an affinity maturation process, which improves their affinity to the selective antigens. CLONALG is the general clone selection algorithm proposed by De Castro and Von Zuben [12]. The description of the CLONALG is shown in Figure 1.

```
BEGIN  
Construct the initial population of antibodies  
REPEAT  
  Evaluate antibodies to calculate their affinities  
  Select the  $n$  best affinity antibodies and clone them  
  Mature the clones and evaluate them  
  Allow the best antibody from each subpopulation to survive  
  Replace the  $d$  lowest affinity antibodies with new antibodies randomly produced  
UNTIL A termination criterion is satisfied or the maximum generation number is reached  
END
```

**Figure 1. The description of the CLONALG**

The antibody in Figure 1 means B-cell. After an antigen is recognized by an antibody with certain affinity, the antibody is stimulated and will start to proliferate by cloning. The cloning rate is proportional to the antigenic affinity. After cloning operation, the new cloned cells are subject to a hypermutation process inversely proportional to their affinity; the higher the affinity the smaller the mutation rate. Hence, the mutation rate of a clone is inversely proportional to the fitness of its parent. This hypermutation process enables the new cells to match the antigen more closely. The antibodies with high affinities are selected to differentiate into memory cells which do not secrete antibodies but instead remember the antigenic pattern. The antibodies that are not stimulated as they do not match any antigens will eventually die. As a relatively novel optimization algorithm, the CLONALG has been successfully applied to solve various engineering problems [13, 14].

### **3. The Proposed Method**

The processing of the proposed algorithm for the classification of mangroves remote sensing image is developed into 3 steps:

Step 1: preparing the sample set and determining the features for decision-making.

Step 2: calling the improved clonal selection algorithm to get the cluster center for each land-cover type.

Step 3: calling the minimum distance method to perform the classification.

#### **3.1. Preparing the sample set and determining the features for decision-making**

Spectral feature is foundational data of remote sensing image. The spectrums of TM image: band1~band7 are the original features. The Normalized Difference Vegetation Index (NDVI), Digital Elevation Model (DEM) and texture information are integrated to be the decision-making features for classification, which has been proved to improve the classification accuracy effectively [15, 16].

Mangrove forests are constrained by topographic factors. Field investigations validate that mangrove forests were not distributed above 8 meter elevation. Therefore, the digital elevation model (DEM) can be used to exclude non-mangroves pixels that had similar spectral attributes with mangroves pixels, but were above the elevation limiting line. Texture contains important information about the structural arrangement of surfaces and their relationship to the surrounding environment. By analyzing the false color composite image of TM data, we know that the texture of mangroves is being fine and smooth, while other green vegetations are coarse and rippled such as the Agricultural lands. Gray-level co-occurrence matrix (GLCM) is effective way to quantitatively evaluate textural parameters and represent

the texture. Leen-Kiat Soh et al. formulated 10 features of GLCM in ref [17]. This paper take 3 of them (Variance, second moment and dissimilarity) to be the texture features which are proved to be useful for mangroves classification by experiments. Therefore there are 12 features for each sample in this study. Let  $F$  to be the number of the features for each training sample, then  $F=12$ . This means each sample is a 12-dimensional vector.

Given that there are  $K$  different kinds of Land-cover types in remote sensing image. The training samples are composed of various land cover types samples. For each land-cover type, the same number of training samples are taken, let  $T$  be the number, then the total number of the training samples is  $N = K \times T$ . Given that  $X = \{X^{(1)}, X^{(2)}, \dots, X^{(K)}\}$  is the training sample set, where  $X^{(i)} = \{X^{(i)_1}, X^{(i)_2}, \dots, X^{(i)_T}\}$  is a subset of  $X$ , and it just consists of the samples of the  $i^{th}$  kind of land-cover type.  $X^{(i)_j} = (x^{(i)_j,1}, x^{(i)_j,2}, \dots, x^{(i)_j,F})$  is the  $F$  dimensional feature vector of the  $j^{th}$  sample in the  $i^{th}$  class training sample set.  $x^{(i)_j,k}$  is the real-valued of the  $k^{th}$  feature of  $X^{(i)_j}$ .

### 3.2. Immune algorithm for learning the cluster centers

By the training sample set, the improved clonal selection algorithm (ICSA) is called to get the optimal cluster center for each land-cover type. The following discuss the processing of the ICSA step by step.

#### 1) Generating the initial antibody population

In ICSA, the antibody corresponds to the candidate solution of the problem. The coding way of antibody is one of the important issues to ICSA. Unlike the coding way in ref.[10], ICSA introduces real encoding method for antibody which consists of the cluster centers for all the land cover types. The coding way is intuitive, more effective and suitable for remote sensing data, and can avoid repeating the operation of encoding and decoding for binary code.

The antibody  $Ab=(C_1, C_2, \dots, C_K)$  is composed by the clustering centers for all the  $K$  land cover types, where  $C_i (i=1, 2, \dots, K)$  is the cluster center of the  $i^{th}$  land cover type. Therefore  $C_i = (c_{i,1}, c_{i,2}, \dots, c_{i,F})$  is a  $F$  dimensional vector. At the beginning of ICSA, the initial antibody population  $Ab_{[N_{ab}]}$  and memory cell  $Ab_{[M]}$  are generated. Where  $N_{ab}$  is the number of the antibodies in antibody population, and  $M$  is the number of the antibodies in memory set. The  $C_i$  of the initial antibody in  $Ab_{[N_{ab}]}$  or  $Ab_{[M]}$  is generated by taking a sample randomly from the training samples set of the  $i^{th}$  kind of land-cover type, this is to say that  $C_i = X^{(i)_j} = (x^{(i)_j,1}, x^{(i)_j,2}, \dots, x^{(i)_j,F})$ , where  $j \in [1, T]$  is a random number.

The evolution of the immune algorithm is to get the optimal cluster centers for all land cover types, which can well represent their training samples respectively. The antibodies in the memory set will converge to the optimal cluster centers step by step during the progressing of the algorithm.

#### 2) Calculating the affinities of the antibodies

The antigen represents the problem to be solved, which is represented by Ag-Ab affinity function. The evolutionary search in immune algorithm is based on the affinity function which is used to measure the superiority of antibody. Affinity function determines the convergence speed of the algorithm, and affects the searching of optimal solution. Based on the coding way above, we know that each cluster center in the antibody should effectively represent its training samples, also the difference between any two classes should be as great as possible. We call them as the inner superiority and the outer superiority of antibody respectively. Therefore we synthetically considered these properties in the design of affinity function.

Firstly, the distance between the cluster center and the geometric center of its samples is used to determinate whether the cluster center  $C_i$  can well represent the training samples of the  $i^{th}$  land cover type. Eq. 1 shows this.

$$S_i = \sqrt{\|C_i - \bar{X}^{(i)}\|^2} \quad (1)$$

Where  $\bar{X}^{(i)} = \frac{1}{T} \sum_{j=1}^T X^{(i)}_j = (\bar{x}^{(i)}_1, \bar{x}^{(i)}_2, \dots, \bar{x}^{(i)}_F)$  is the geometric center of the  $i^{th}$  land cover type samples, and  $\bar{x}^{(i)}_j = \frac{1}{T} \sum_{k=1}^T x^{(i)}_{k,j}$  is the geometric center of  $j^{th}$  feature in  $i^{th}$  land cover type samples. The better  $C_i$  has the smaller value of  $S_i$ .

Secondly, in order to measure the outer superiority of antibody, the Euclidean distance between two cluster centers is used to measure their differences. The difference between  $C_i$  and  $C_j$  is calculated by Eq. 2.

$$d(C_i, C_j) = \|C_i - C_j\| = \sqrt{\sum_{k=1}^F (c_{i,k} - c_{j,k})^2} \quad (2)$$

For the  $C_i$  in a antibody, We define the function  $f(C_i)$  to measure the fitness of  $C_i$ . See Eq. 3

$$f(C_i) = R_i = \max_{j \neq i} \left\{ \frac{S_i + S_j}{d(C_i, C_j)} \right\} \quad (3)$$

Eq. 3 shows the better  $C_i$  has the smaller value of  $f(C_i)$ , for the small value of  $f(C_i)$  means we can get both the better inner superiority and the better outer superiority. For an antibody  $Ab$ , because it is composed by the cluster centers of all the classes, the fitness of the antibody  $Ab$  is defined as the sum of all the  $f(C_i)$  ( $i=1..K$ ). Eq. 4 shows this.

$$f(Ab) = \frac{1}{K} \sum_{i=1}^K R_i = \frac{1}{K} \sum_{i=1}^K \max_{j \neq i} \left\{ \frac{S_i + S_j}{d(C_i, C_j)} \right\} \quad (4)$$

Therefore, the better  $Ab$  has the smaller value of  $f(Ab)$ .

Finally the Ag-Ab affinity function is showed in Eq. 5.

$$Fit(Ab) = \frac{1}{f(Ab)} \quad (5)$$

The excellent antibody has higher values of affinity function, and is to be more favorable for classification.

### 3) Implement the clone and selection operations

In immune algorithm, clone selection operator can not only ensure the diversity of antibodies but also generate the antibody with high affinity has better chance to enter the next generation. Based on the affinity function, ISCA calculates the affinities of all the antibodies in antibodies population. Given  $max\_Fit$  to be the maximum value of the affinity function in antibody population. The probability of the antibody  $Ab$  to be selected is calculated by Eq. 6.

$$p(Ab) = \frac{1}{\|Fit(Ab) - max\_Fit\|} \quad (6)$$

Eq. 6 shows that the selection rate is proportional to the affinity of the antibody, the antibody which is closer to the optimal antibody has the higher opportunity to be selected. This enables the new antibodies to match the antigen more closely.

By the select operator,  $n$  individuals from the antibody population are selected to be the select population  $Ab_{\{Select\}}$ . Then the selected antibodies are submitted to perform the clone operation. The clone size is an increasing function of the antibody affinity. Fig. 7 shows the number of the antibody  $Ab$  in  $Ab_{\{Select\}}$  to be cloned.

$$N_{clone}(Ab) = round(\frac{\beta \times n}{i}) \quad (7)$$

Where  $n$  is the number of the antibodies in  $Ab_{\{Select\}}$ ,  $\beta$  is the cloning coefficient, and  $i$  is the ranking of the affinity of  $Ab$  in the  $Ab_{\{Select\}}$ . For example, if  $n = 100, \beta = 1.0$ , the antibody with the highest affinity ( $i=1$ ) will be cloned 100 times, and the second is 50 times. The clone selection ensures the antibodies to evolve toward the cluster centers.

**4) Perform random hyper-mutation operator on the select population  $Ab_{\{Select\}}$**

Mutation operator is very important to artificial immune algorithm. It enables the new antibodies to match the antigen more closely, and avoid falling into local optimal solution. Here a random hyper-mutation operator is used, which is compatible with the decimal coding way.

For a given mutation probability  $P_m$ , ICOSA selects the mutation antibody randomly from  $Ab_{\{Select\}}$ , supporting the mutation antibody is  $Ab = (C_1, C_2, \dots, C_{N_c})$ . Then ICOSA chooses the mutation element of  $Ab$  randomly. Supposing the element is  $C_k (k=1, 2, \dots, N_c)$ , and the offspring antibody generated by random hyper-mutation is  $Ab' = (C_1, C_2, \dots, C'_k, \dots, C_{N_c})$ , where  $C'_k$  is built by the following way:

Firstly, select several features from  $C_k = (c_{k,1}, c_{k,2}, \dots, c_{k,N_f})$  randomly. Secondly, for the selected feature  $c_{k,i} (i=1, 2, \dots, N_f)$ , do the mutation by Eq. 8 to get the new antibody.

$$c'_{k,i} = c^L_{k,i} + r \cdot (c^U_{k,i} - c^L_{k,i}) \quad (8)$$

Where  $c^U_{k,i}$  and  $c^L_{k,i}$  are upper bound and lower bound of  $c_{k,i}$  respectively,  $r$  is a random value within the range  $[0,1]$ .

During the evolution of immune algorithm, ICOSA control the value of mutation probability  $P_m$  by Eq. 9.

$$p_m = P_m \cdot (1 - r^{\frac{(1-t)}{M}}) \quad (9)$$

where  $t$  is the iteration number,  $r$  is a random value within the range  $[0,1]$ ,  $M$  is the maximal iteration number. With the increasing of  $t$ , the value of  $P_m$  will tend to 0.

After finishing the random hyper-mutation on the select population  $Ab_{\{Select\}}$ , the matured antibody population  $Ab_{\{mutation\}}$  is generated.

**5) Reselect the improved individuals from  $Ab_{\{mutation\}}$  to update the memory set  $Ab_{\{M\}}$**

In this step, ICOSA reselect the improved individuals from the matured antibody population  $Ab_{\{mutation\}}$ , and compares with antibodies in memory set  $Ab_{\{M\}}$ . Some members of  $Ab_{\{M\}}$  can be replaced by the improved members of  $Ab_{\{mutation\}}$ .

**6) Update the antibody population  $Ab_{\{N_{ab}\}}$**

In order to ensure that the higher affinity antibodies have the higher probabilities to enter the next generation, ICSA replaces  $d$  lowest affinity antibodies of  $Ab_{\{N_{ab}\}}$  by the  $d$  largest affinity antibodies in  $Ab_{\{mutation\}}$  and  $Ab_{\{M\}}$ , which guarantees the convergence of the immune algorithm. The lower affinity cells have higher probabilities of being replaced.

**7) Perform the evolution by executing the loop from step 2 to step 6**

The algorithm repeats from step 2 to step 6 until the termination criterion is satisfied or the predetermined generation number is reached. After each loop, there has one antibody generation.

**8) Get optimal cluster center for each land-cover type**

By selecting the optimal antibody from the memory cell  $Ab_{\{M\}}$ , the  $C_i$  ( $i=1..K$ ) of the optimal antibody is the optimal cluster center of the  $i^{\text{th}}$  land-cover type.

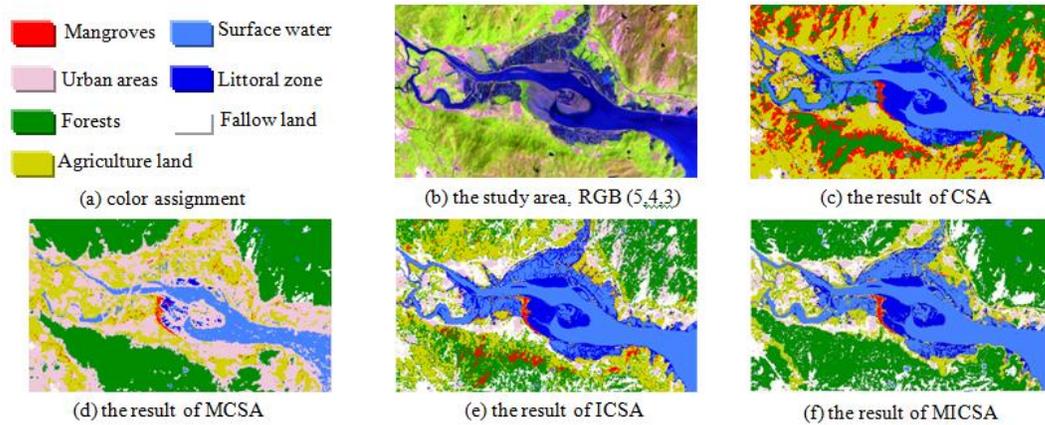
**9) Classification**

After achieving the cluster centers of the various land-cover types, the Minimum Distance method is used to classify the remote sensing image. For a test sample  $Y$ , if  $C_i = \arg \min_{C_j} (dis(C_j, Y))$ , then  $Y$  is classified to the  $i^{\text{th}}$  land-cover type. Instead of Euclidean distance, the distance function  $dis()$  is Mahalanobis distance. The reason is that Mahalanobis distance takes into account the linkages between various properties and independence of the measure scale. It is an effective calculation method for the similarity of two unknown sample.

## 4. Experiment and Analysis

The experiment was performed using a multispectral Landsat TM image of the Zhangjiang estuary in southeastern China, a national mangrove reserve. The reserve is bounded by  $22^{\circ}53'45''\text{N} \sim 23^{\circ}56'00''\text{N}$  and  $117^{\circ}24'07''\text{E} \sim 117^{\circ}30'00''\text{E}$ . The TM data was acquired on September 25, 2006, with 30-m resolution (Figure 2(a)). According to field investigation in the area, the land-cover type is defined by seven categories. They were mangroves ( $C_1$ ), agricultural land ( $C_2$ ), forests ( $C_3$ ), surface water ( $C_4$ ), urban areas ( $C_5$ ), littoral zone ( $C_6$ ), and fallow land ( $C_7$ ). In order to evaluate the efficiency of the proposed algorithm (ICSA) we compare with the clonal selection algorithm introduced in ref. [10], which is named it by CSA and was implemented in accordance with the presentation in ref. [10].

For validating the effect of multi-features fusion, experiments are executing on the spectral feature and the fusion of multi-features respectively. Therefore the experiments are divided into 4 situations: Spectral feature based clonal selection algorithm (CSA), Multi-features fusion clonal selection algorithm (MCSA), Spectral feature based improved clonal selection algorithm (ICSA) and Multi-features fusion improved clonal selection algorithm (MICSA). The algorithms were all programmed in matlab. The images of the classification results are shown in Figure 2(c)-(f).



**Figure 2. The study area and the classification result images**

As shown in Figure 2, CSA, ICSA and MICSA can get better classification results on surface water and littoral zones. However the mixing misclassified points among forests, agricultural land and mangroves for CSA are serious, also CSA misclassified many fallow land points into urban areas points. MCSA can well identify agricultural land and mangroves, but the mixing misclassification among urban areas, littoral zone and agricultural land are serious. ICSA misclassified many forests and agricultural land points into mangroves, and also misclassified many forests points into agricultural land. All 4 methods are able to identify the major mangrove areas, but a lot of samples of agricultural land and forests are wrongly identified as mangroves in CSA and ICSA. Comparing with MICSA, MCSA has many mangrove leakage and misclassified points. Therefore MICSA is more capable of differentiating the mangroves from other classes, and it can achieve better results visually.

For implementing the classification assessment, confusion matrix is used to evaluate the classification performances of the algorithms. By field sampling and high resolution image, 200 samples are taken randomly for each land cover category as the ground truth samples to build the confusion matrices. The confusion matrices for classification results of the 4 algorithms are listed in Table 1.

**Table 1. The error confusion matrix for each classification method**

CSA									MCSA								
Class	C1	C2	C3	C4	C5	C6	C7	Total	Class	C1	C2	C3	C4	C5	C6	C7	Total
C1	156	29	84	0	0	0	1	270	C1	164	0	12	0	20	14	56	266
C2	2	41	79	0	12	0	62	196	C2	0	67	0	0	0	0	0	67
C3	41	129	37	6	0	7	0	220	C3	0	0	82	0	0	0	0	82
C4	0	0	0	171	0	39	0	210	C4	13	84	68	200	75	31	0	471
C5	0	0	0	0	188	0	85	273	C5	0	5	38	0	101	0	1	145
C6	1	1	0	23	0	154	19	192	C6	4	44	0	0	4	155	0	207
C7	0	0	0	0	0	0	33	33	C7	19	0	1	0	0	0	143	162
Total	200	200	200	200	200	200	200	1400	Total	200	200	200	200	200	200	200	1400
ICSA									MICSA								
Class	C1	C2	C3	C4	C5	C6	C7	Total	Class	C1	C2	C3	C4	C5	C6	C7	Total
C1	167	0	0	0	2	110	23	302	C1	152	0	1	0	0	0	14	167
C2	7	87	0	10	0	10	0	114	C2	8	166	0	28	0	3	0	205
C3	0	0	161	0	12	0	3	176	C3	0	0	163	0	0	0	1	164
C4	2	93	0	190	0	0	0	285	C4	0	33	0	172	0	0	0	205
C5	0	0	39	0	184	0	0	223	C5	0	0	36	0	200	0	0	236
C6	11	20	0	0	0	64	0	95	C6	31	1	0	0	0	197	1	230
C7	13	0	0	0	2	16	174	205	C7	9	0	0	0	0	0	184	193
Total	200	200	200	200	200	200	200	1400	Total	200	200	200	200	200	200	200	1400

The elements of main diagonal in confusion matrix are the number of samples which are classified correctly. Table 1 shows that the sum of main diagonal elements in MICSA is largest. This means the proposed MICSA can improve the classification accuracy effectively. The Kappa coefficient and overall accuracy is showed in table 2. We can see that the multi-features fusion can improves the overall classification accuracy. The overall classification accuracy of MICSA is 88.3%, and the Kappa coefficient is 0.863, which indicates that it can improve overall classification accuracy effectively. All of these results prove that the proposed clonal selection algorithm is a very competent method for mangroves remote sensing image classification.

**Table 2. Comparison of overall accuracy**

	CSA	MCSA	ICSA	MICSA
Overall	55.7%	65.1%	73.4%	88.3%
<i>Kappa</i>	0.483	0.593	0.689	0.863

## 5. Conclusions

Great success has been achieved in the mapping of mangroves areal extent from space by previous researches. However there remain a number of limitations in various classification algorithms. As Blasco *et al.* pointed out, "Some technical 'groping' is always necessary before the most appropriate digital processing method, compatible with local features, is found" [18]. This paper proposed an artificial immune algorithm for classification of mangroves remote sensing image. By using the improved clonal selection algorithm, the optimal cluster center for each land-cover type was found, and then minimum distance method was called to perform the classification. The decimal encoding way of antibody, the design of affinity function, and the implementations of selection operator and mutation operator are all the core contents of the algorithm. A series of experiments were carried out on TM image to test the performances. The results indicate that the proposed method can improve the precision of mangroves remote sensing image classification effectively. More evaluation experiments on the algorithm performance are certainly necessary, and more effective method would be carried out to discern different types of mangrove forests.

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