AN ARTIFICIAL IMMUNE ALGORITHM FOR SPECTRUM RECOGNITION OF HYPERSPECTRAL DATA

Yanfei Zhong [a, *], Liangpei Zhang [a], Pingxiang Li [a], Xin Huang [a]

[a] State Key Laboratory of information Engineering in Surveying Mapping and Remote Sensing, Wuhan Univerity 129 Luoyu Road, Wuhan, Hubei, 430079, China – zhongyanfei@lmars.whu.edu.cn

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ABSTRACT:

An intelligent approach based on artificial immune systems (AIS) is proposed in this paper to perform the task of spectrum recognition in hyperspectral data analysis. Although traditional spectral matching techniques have provided some confirmatory information to aid the interpretation of hyperspectral data, the improvement is yet to be made because of the complexity of the spectra. The immunological algorithm for spectral reactions is described in which a population of memory cells for each of the possible laboratory-derived spectral is evolved using artificial immune operators, such as, clone, mutation, and selection. In specially, the clonal and the mutation operators are two foremost processes. The clonal process can draw the evolutionary process closer to the goal. It raises the average affinity value and gives the following steps a good change to further move towards the solution, i.e. the known spectra. The mutation step generates random changes of single features to the individual solutions and helps the proposed algorithm to avoid local optimal value. By the above training process, a small well-trained specialist library is established for testing their pattern recognition ability. The recognition in the proposed algorithm is the automatic process to find all possible spectral responsible for the observed spectrum, analogous to the antibody's recognizing antigen in the natural immune system. Whenever a spectrum is recognized for the first time, a copy of it is reserved as a new memory cell for the spectrum. Therefore, when it appears a second time, it can be easily recognized by the antibodies created during its first appearance. Consequently, the proposed method provides a learning methodology for pattern recognition. The proposed algorithm is compared with two well known spectral matching algorithms: binary coding and spectral angle mapper algorithms using simulated and real hyperspectral data. Experimental results demonstrate that the proposed approach can better recognize the unknown spectra than traditional algorithms based on a well-established specialist library obtained by different immune operators, and hence provide an effective option for spectrum recognition of hyperspectral data.

1. INTRODUCTION

The development of hyperspectral remote sensing is one of great technology breakthroughs made by human in the area of the earth observation, and it is the advanced technique of the contemporary remote sensing (Landgrebe, 2002). The value of using a hyperspectral imaging spectrometer or spectroradiometer measurements lies in its ability to provide a high-resolution reflectance spectrum for each picture element in the image or each material of interest on the ground. These captured spectral data with sufficient resolution sometimes can directly identify those materials by the techniques of spectrum recognition. For instance, the spectral matching technique (Richards and Jia, 1999) is an important approach of these methods, and considerable attention has been given to develop library matching techniques that allow remote sensing-derived spectral to be compared with spectral that were previously collected in the field or in the laboratory. Spectral angle mapper and binary encoding (Richards and Jia, 1999) are two traditional spectral matching algorithms. They can identify classify the hyperspectral remote sensing image by comparing with the stored laboratory-derived spectra successfully. However, they don't obtain well results when the unknown materials are too similar or the samples of each material are too small in hyperspectral remote sensing image.

To solve the above problem, an intelligent approach based on artificial immune systems (AIS) (Dasgupta, 1999a; De Castro and Timmis 2002a) is proposed here as an alternative way to perform the task of spectrum recognition in hyperspectral data analysis when using the single spectrum from spectral library or the number of samples is too small. AIS inspired by the vertebrate immune systems, use the immunological properties to support a wide range of applications including pattern recognition (Carter 2000, Dasgupta *et al.* 1999b), intrusion detection (Kim and Bentley, 2001), clustering (Timmis *et al.*, 2000), and optimization (De Castro and Von Zuben, 2002b). AIS has strong capabilities of pattern recognition, learning and associative memory, hence it is natural to view AIS as a powerful information processing and problem-solving paradigm in both the scientific and engineering fields (Hart and Timmis, 2008). Artificial immune systems (AIS) possess nonlinear classification properties along with the biological properties such as positive and negative selection, clonal selection, and immune memory. Therefore, AIS, like genetic algorithms and neural nets, is an intelligent tool for advanced pattern recognition. Specially, Clonal selection algorithm has proved useful for pattern classification in several applications ((De Castro and Von Zuben, 2002a) and negative selection algorithm has been widely applied for anomaly detection (Forrest *et al.*, 1994). AIS models exploit the following features by utilizing the immunological properties, such as clonal selection, immune

* Corresponding author.

memory and immune network: (1)AIS are data-driven self-adaptive methods as they adjust themselves to the data without any explicit specification of functional or distributional form for the underlying model; (2) AIS are universal functional approximators since they can approximate any functional with arbitrary accuracy; (3) AIS are nonlinear models, and hence are flexible in modeling complex real word relationships; (4) AIS inherit the memory property of human immune system and can recognize the same or similar antigen quickly at different times. However, so far, few papers concern applications of AIS in hyperctral data processing because apply AIS to hyperspectral data is very difficult because of its characteristics of huge volume data (Zhong *et al.*, 2006). In this paper, some initial investigations are conducted to employ artificial immune systems for spectrum recognition of hyperspectral data.

The proposed algorithm simulates the recognition process of AIS to recognize the unknown spectra by utilizing the negative selection algorithm and clonal selection algorithm. By the self/non-self recognition mechanism of negative selection algorithm and the optimal capacity of clonal selection algorithm, the proposed algorithm can fit an optimal detector population to each spectrum rather than traditionally try for a single optimum detector to allow for flexible coverage of feature space and the fitting of multiple local optima. Finally, these detectors are used to recognize the spectra. The proposed algorithm was experimented with several simulated or real-world spectral datasets. Experimental results demonstrate that the proposed algorithm outperforms the traditional spectral matching algorithm when only few known spectra may be used to classification, and thus provides an effective option to spectrum recognition of hyperspectral data.

The remainder of the paper is organized as follows: Section 2 overviews the vertebrate immune system and Section 3 deals with the negative selection algorithm and clonal selection algorithm of AIS. Section 4 describes the proposed algorithm. In Section 5, the experimental results are provided. Finally, the conclusion is given in Section 6.

2. VERTEBRATE IMMUN SYSTEM

The vertebrate immune system is a complex system of cells, molecules and organs that represent an identification mechanism capable of perceiving and combating dysfunction from our own cells and the action of exogenous infectious microorganisms. The vertebrate immune system protects our bodies from infectious agents such as viruses, bacteria, fungi and other parasites. Any molecule that can be recognized by the adaptive immune system is known as an antigen (Ag).The basic component of the immune system is the lymphocytes or the white blood cells. Lymphocytes exist in two forms, B cells and T cells. These two types of cells are rather similar, but differ with relation to how they recognize antigens and by their functional roles, B-cells are capable of recognizing antigens free in solution, while T cells require antigens to be presented by other accessory cells. Each of this has distinct chemical structures and produces many Y shaped antibodies form its surfaces to kill the antigens. Ab's are molecules attached primarily to the surface of B cells whose aim is to recognize and bind to Ag's (Jerne, 1973).

The immune system possesses several properties such as self/nonself discrimination immunological memory, positive /negative selection, immunological network, clonal selection and learning which performs complex tasks. When an antigen invades the immune systems, the immune systems firstly discriminate the antigen between self and nonself by negative selection. When a B-cell receptor recognizes a nonself antigen with a certain affinity, it is selected to proliferate and produce antibodies in high volumes. The antibodies are soluble forms of the B-cell receptors that are released from the B-cell surface to cope with the invading nonself antigen. Antibodies bind to antigens leading to their eventual elimination by other immune cells. Proliferation in the case of immune cells is asexual, a mitotic process; the cells divide themselves. During reproduction, the B-cell clones undergo a hyper mutation process that, the Ag stimulates the B cell to proliferate and mature into terminal Ab secreting cells, named plasma cells. The process of cell division generates a clone. In addition to proliferating and differentiating into plasma cells, the activated B cells with high antigenic affinities are selected to become memory cells with long life spans. These memory cells circulate through the blood, lymph, and tissues. When exposed to a second antigenic stimulus, commence to differentiate into plasma cells capable of producing high-affinity Ab's, preselected for the specific Ag that had stimulated the primary response, Figure1 illustrates the negative selection, clonal selection, expansion, and affinity maturation processes.

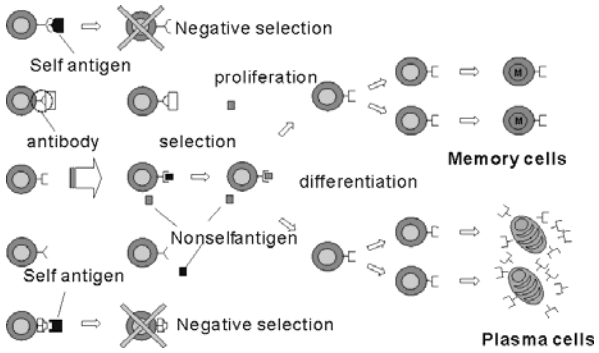


Figure1. The principle of vertebrate immune system

3. ARTIFICIAL IMMUNE SYSTEMS

3.1 Negative selection algorithm

From an information processing perspective, negative selection presents an alternative paradigm to perform pattern recognition by storing information about the complement set (nonself) of the patterns to be recognized (self). A negative selection algorithm has been proposed in the literature (Forrest *et al.*, 1994). with applications focused on the problem of anomaly detection, such as computer and network instrusion detection, time series prediction, image inspection and segmentation, and hardware fault tolerance.

Given an appropriate problem representation, define the set of patterns to be protected and call it the *self- set* (P). Based upon the negative selection algorithm, generate a set of *detectors* (M) that will be responsible to identify all elements that do not belong to the self-set, i.e., the nonself elements. The negative selection algorithm runs as follows (De Castro and Von Zuben, 2002a):

Step 1: Generate random candidate elements (C) using the same representation adopted;

Step 2: Compare (match) the elements in C with the elements in P. If a match occurs, i.e., if an element of P is recognised by an element of C, then discard this element of C; else store this element of C in the detector set M.

Step 3: After generating the set of detectors (M), the next stage of the algorithm consists in *monitoring* the system for the presence of nonself patterns. In this case, assume a set P* of patterns to be protected. This set might be composed of the set P plus other new patterns, or it can be a completely novel set. For all elements of the detector set, that corresponds to the nonself patterns, check if it recognizes (matches) an element of P* and, if yes, then a nonself pattern was recognized and an action has to be taken.

3.2 Clonal selection algorithm

De Castro and Von zuben developed the Clonal Selection Algorithm on the basis of clonal selection theory of the immune system (De Castro and Von zuben, 2002b). It was proved that can perform pattern recognition and adapt to solve multi-modal optimization tasks. The CLONALG algorithm can be described as follows:

Step 1: Randomly initialize a population of individual (M);

Step 2: For each pattern of P, present it to the population M and determine its affinity with each element of the population M;

Step 3: Select n of the best highest affinity elements of M and generate copies of these individuals proportionally to their affinity with the antigen. The higher the affinity, the higher the number of copies, and vice-versa;

Step 4: Mutate all these copies with a rate proportional to their affinity with the input pattern: the higher the affinity, the smaller the mutation rate;

Step 5: Add these mutated individuals to the population M and reselect m of these maturated individuals to be kept as memories of the systems;

Step 6: Repeat steps 2 to 5 until a certain criterion is met.

4. THE ARTIFICIAL IMMUNE ALGORITHM FOR MIXTURE SPECTRUM RECOGNITION

Interpretation of a spectrum (like mixture mineral spectrum) has been a difficult and very time-consuming task for remote sensing researchers. Although traditional spectral matching techniques have provided some confirmatory information to aid the interpretation, the improvement is yet to be made. An intelligent approach based on AIS is described here as an alternative way to perform the task of spectrum recognition in hyperspectral data analysis. Table 1 summarizes the mapping between the immune system and the proposed algorithm.

The immune system	The proposed algorithm
Self-antigens	A set of known spectra S.
Nonself-antigens	A set of unknown spectra or the classified hyperspectral image *X*.
antibody	Any evolved population, which uniquely recognizes one of the self antigen (known spectra)
Matching	An antigen and antibody are said to match if the similarity between antigen and antibody is larger than the set threshold T.

Table 1. Mapping between the immune system and the proposed algorithm

The proposed algorithm consists of the following steps:

4.1 Input the known spectra and unknown data

Based on the characteristics of the spectral library or the hyperspectral remote sensing image and application purpose, the set of known spectra is inputted to the proposed algorithm. As shown in Table 1, in the proposed algorithm, the known spectra are represented by the set of self-antigens, where $S=\{S_i \mid i=1,2,\Lambda\ ,m\}$, m represents the number of the known spectra. Hyperspectral remote sensing data $X=\{x_1,x_n,\Lambda\ ,x_n\}$ through N_b bands as the set of nonself-antigens are observed, where *n* represents the size of the image or the number of unknown spectra.

4.2 Training and evolving process

Next, an immunological model for spectral reactions is described in which a population of memory cells for each of the possible laboratory-derived spectral is evolved using artificial immune operators, such as, clone, mutation, selection, and displacement. For each of the known spectra S_i, the following processes are carried out.

Step 1: Initialization. An antibody population AB_i for S_i is randomly produced, $AB_i=\{ab_{ir} \mid r=1,\Lambda\ ,N\}$, where AB_i uniquely recognizes S_i, *N* is the number of antibodies. ab_{ir} has the an equal length of channels, N_b.

Step 2: Calculation of affinity. According to the initial antibody population, the affinity $F(ab_{ir},S_i)$ between each antibody ab_{ir} in the antibody population AB_i and S_i is calculated using the equation (1) by the Spectral Angle Mapper (SAM) (Kruse *et al.*, 1993). The higher the affinity, the better the matching.

$$F(ab_{ir},S_i)=\exp(-SAM(ab_{ir},S_i)/2) \tag{1}$$

$$SAM(ab_{ir},S_i)=\alpha=\cos^{-1}\left[\frac{\sum_{l=1}^{N_b}ab_{ir}(l)S_i(l)}{\left[\sum_{l=1}^{N_b}(ab_{ir}(l))^2\right]^{\frac{1}{2}}\left[\sum_{l=1}^{N_b}(S_i(l))^2\right]^{\frac{1}{2}}}\right] \tag{2}$$

where S_i is a known spectrum, ab_{ir} is a antibody of AB_i. According to the Equations (1) and (2), $SAM(x,y)\in[0,\pi/2]$, and $affinity(x,y)\in[0.485,1]$

Step 3: Selection. If the affinity between ab_{ir} and S_i is within a

user-specified threshold T_1, ab_{ir} is removed from the antibody population AB_i, where T_1 controls the affinity between the antibodies and antigen. Only these antibodies with the high affinity may go to the next evolving step. The removed antibodies from AB_i are composed of the remaining population, $AB_{\{R\}}$.

Step 4: Purification. To uniquely recognize a self antigen S_i, it is necessary to expose the selected antibodies to other self antigens environment. So we need to put the selected antibodies into a pool consisting of $\{S_k \mid 1 \le k \le m, k \ne i\}$ for purification, this time we only want to keep those unmatched self antigen S_k. That is, if the affinity between ab_{ir} and S_k is within a user-specified threshold T_2, ab_{ir} is preserved in the antibody population AB_i. Other antibodies are removed from AB_i to the population of the remaining antibodies $AB_{\{R\}}$.

Step 5: If the number of the antibodies in AB_i is still equal to *N*, that is, no antibodies is removed, the process jumps to Step 9. Otherwise, the proposed algorithm executes the next step.

Step 6: Clone. All antibodies in $AB_{\{R\}}$ are cloned, which each antibody has two clonal antibodies. The total number of clones generated N_c is defined in equation (3) as follow:

$$N_c = 2n_R \tag{3}$$

where n_R is the number of antibodies in $AB_{\{R\}}$. The clonal and the mutation operators are two foremost processes. The clonal process can draw the evolutionary process closer to the goal. It raises the average affinity value and gives the following steps a good change to further move towards the solution, i.e. the known spectra.

Step 7: Mutation. The proposed algorithm allows each cloned antibodies the opportunity to produce mutated offspring. The higher the affinity, the smaller the mutation rate. The mutation rate is adaptively determined by equation (4) as follows:

$$mutate\_rate = 1 - (F(ab, S_i)/2) \tag{4}$$

To decrease the computational costs, the proposed algorithm utilizes the Cauchy mutation to produce the mutated offspring according to the equation (5) because of its higher probability of making longer jumps (Yao *et al.*, 1999).The mutation step generates random changes of single features to the individual solutions and helps the proposed algorithm to avoid local optimal value.

$$ab_k'(j) = ab_k(j) + \eta_k(j)\delta_j \tag{5}$$

where δ_j is a Cauchy random variable and is generated anew for each value of j, $j = 1,2,\Lambda\ ,N_b$.

Step 8: Reselection. The mutated antibodies are added to AB_i, which they satisfy the condition of step 3 and step 4. Then, $AB_{\{R\}}$ is updated by the mutated antibodies and the process returns to step 5.

Step 9: Once the antibody population AB_i has been obtained, training on this particular antigen S_i is completed. The next self antigen (known spectra) is then selected and the training process proceeds from step 1 to step 9. This process continues until all self antigens have been trained in the proposed algorithm. After the process, the antibody population AB is generated, $AB = \{AB_i \mid i = 1,\Lambda\ ,m\}$, where m represents the number of the known spectra.. The process is similar to the innate immune recognition.

4.3 Spectrum Recognition

By the above training process, a small well-trained specialist library AB is established for testing their pattern recognition ability. The recognition in the proposed algorithm is the automatic process to find all possible spectral responsible for the observed spectrum, analogous to the antibody's recognizing antigen in the natural immune system. The process is as follows:

Step 1: Input the unknown spectrum x_j orderly from the hyperspectral data $X = \{x_1, x_n, \Lambda\ , x_n\}$, where n represents the size of the image or the number of unknown spectra.

Step 2: Calculate the affinity between x_j and the antibodies of AB.

Step 3: Find all antibodies, which the affinity is larger than the user-specified threshold T_2.

Step 4: Output all possible known spectra and the unknown spectrum is matched to the class of the antibody that has the maximum affinity.

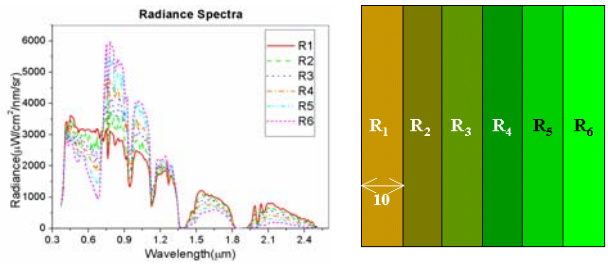
5. EXPERIMENTS AND ANALYSIS

The proposed algorithm and traditional spectral matching algorithms were tested on different types of remote sensing images. Two experiments were conducted to test performances. Consistent comparisons were also carried out among the proposed algorithm, Binary coding and Spectral angle Mapper (SAM) in all experiments.

5.1 Experiment 1- Simulated Data

The first experimental data is a simulated data using two spectral signatures (soil and vegetation) extracted from a 1997 AVIRIS image scene of Jasper Ridge, CA region (Plaza, 2002). A simple 60 × 60-pixle hyperspectral simulated data with six signatures (R1, R2, R3, R4, R5, R6) has been generated by using artificially generated mixtures between the above-mentioned spectra with different abundance fractions (Plaza, 2002). Random noise was used to simulate contributions from

ambient and instrumental sources, which was created by using numbers with a standard normal distribution obtained from a pseudorandom number generator and added to each pixel to generate a signal-to noise ratio (SNR) of 30:1. Figure 2 (a) shows the radiance curves of six signatures. Figure 2 (b) shows the experimental data.



(a) (b)

R1: Soil; **R2:** 0.8*Soil+0.2Veg; **R3:** 0.6*Soil+0.4*Veg; **R4:** 0.4*Soil+0.6*Veg; **R5:** 0.2*Soil+0.8*Veg; **R6:** Veg

Figure 2. (a) The Radiance spectra of two signatures; (b) Simulated data (Plaza, 2002)

The configuration for the proposed algorithm is as follows: the number of antibodies *N*=10; $T_1 = 0.95$; $T_2 = 0.9$. Figure 3 (c) illustrates the matching result using the proposed algorithm. In order to compare the classification result, Figure 3 (a) and (b) describe the matching using binary coding and spectral angle mapper, respectively. Table 2 shows the matching accuracy for three algorithms.

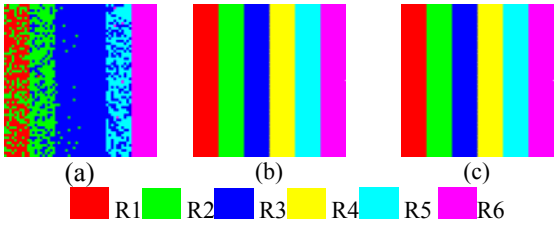


Figure 3. The spectral matching results for simulated data (a) binary coding (b)SAM (c)the proposed algorithm

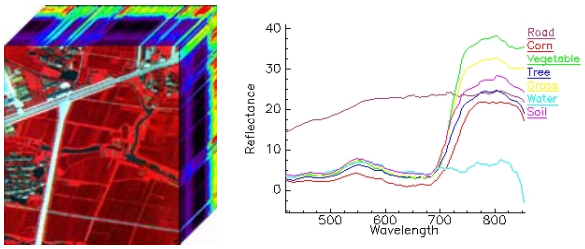
As shown in Table 2, the proposed algorithm and SAM have the satisfied results, which the overall accuracy is 100% and Kappa coefficient is 1. That is, they recognize correctly all unknown spectra. Although the simulated data is simple, binary coding produces the worst accuracy with the overall accuracy and Kappa coefficient, 66.17% and 0.5940 respectively. In addition, the R4 class is lost, which all spectra of R4 are mismatched to R3 class. The simple binary code does not always provide reasonable separability between the spectra in a library. The experimental result evinces the proposed algorithm is a good spectral matching algorithm.

Accuracy	**Algorithms**		
	Binary coding	SAM	The proposed algorithm
Overall	66.1667%	100%	100%
Kappa	0.5940	1	1

Table 2 Comparison of three spectral matching algorithms in experiment 1

5.2 Experiment 2: Xiaqiao PHI hyperspecral image

The dataset used in this experiment was acquired from the Xiaqiao test site, a mixed agricultural area in China, using the Pushbroom Hyperspectral Imager (PHI). 80 bands of the PHI image (340×390 pixels) were tested, and their spectral ranges were from 0.417 to 0.854μm. Figure 4 (a) shows the experimental PHI image cube. Seven known spectra are shown in Figure 4 (b), which represent the Road, corn, vegetable, tree, grass, water, and soil spectrum respectively.(Zhang *et al.*, 2007).



(a) (b)

Figure 4 (a) Xiaqiao PHI image. (b) Spectra of the seven classes.

The configuration for the proposed algorithm is as follows: the number of antibodies *N*=10; $T_1 = 0.98$; $T_2 = 0.9$. Figure 5 (c) illustrates the matching result using the proposed algorithm. In order to compare the classification result, Figure 5 (a) and (b) describe the matching results using binary coding and SAM, respectively. To evaluate the classification accuracy, a test field map was provided in Figure 5(d) based on the ground truth data. The matching accuracy for three algorithms is given in Table 3.

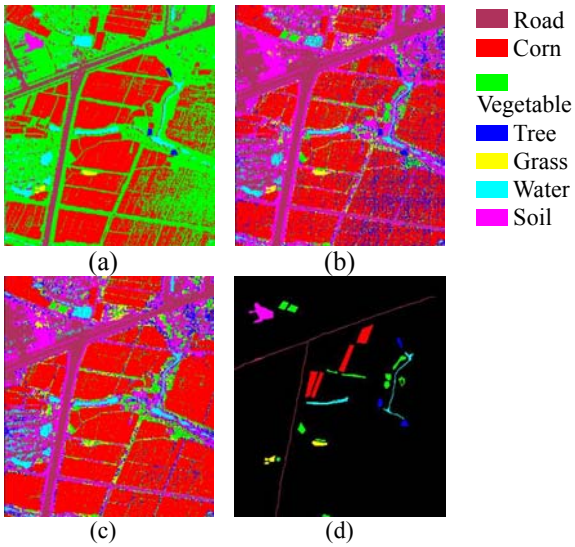


Figure 5. The spectral matching results for PHI data (a) binary coding (b)SAM (c)the proposed algorithm (d) Image for test fields

Accuracy	**Algorithms**		
	Binary coding	SAM	The proposed algorithm
Overall	63.17%	70.34%	76.18%
Kappa	0.55	0.643	0.702

Table 3 Comparison of three spectral matching algorithms in experiment 2

As shown in Figure 5, it is hard for binary coding algorithm to differentiate between vegetables and other classes, with many other class pixels mismatched as vegetable pixels. SAM finds it hard to distinguish between corn and tree, which many corn class pixels are mismatched as tree pixels. However, the proposed algorithm achieves the best visual results for all classes. In addition, Table 3 shows that the proposed algorithm produces a better result than two traditional spectral matching algorithms. The details are as follows: the proposed algorithm based on artificial immune systems achieves the highest overall accuracy and Kappa coefficient among the three algorithms. It improves the overall accuracy from 63.17% using binary coding algorithm, 70.34% using SAM to 76.18% (i.e. by 13.01% and 5.84%) and Kappa coefficient from 0.55, 0.643 to 0.702 (i.e. by 0.152 and 0.059). The main reason for the comparatively high accuracy achieved by the proposed algorithm is that it can adjust itself to the data to approximate the known spectra with arbitrary accuracy by different immune operators, such as clone, mutation. By the immunological evolving process, the proposed algorithm may obtain a set of antibodies for each known spectra. So, in the process of spectrum recognition, the proposed algorithm can improve the matching accuracy because each known spectrum has many memorial antibodies to recognize it. This demonstrates that the proposed algorithm is an excellent spectral matching algorithm for hyperspectral data.

6. CONCLUSIONS

A novel spectrum recognition algorithm based on artificial immune systems was proposed in this paper. When a known spectrum was inputted, the proposed algorithm trained the known spectrum to find a set of antibodies for the known spectrum by different immune operators, such as clone, mutation. By the above training process, a small well-trained specialist library was established for testing their pattern recognition ability. The immune memorial set of antibodies for all known spectra was utilized to recognize these unknown spectra. A series of experiments have been carried out to test the performance of our algorithm using different types of images. Two experiments were carried out to test the performance of our algorithm using simulated and real hyperspectral data. Compared with two conventional spectral matching algorithms, the proposed algorithm has demonstrated its better performance. Consequently, the proposed algorithm provides an effective option for spectral matching or spectrum recognition of hyperspectral data. In our future work, AIS and the proposed algorithm will be further explored for more extensive remote sensing applications.

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REFERENCES

Dasgupta, D.,1999a. *Artificial Immune Systems and Their Applications*. Germany: Springer.

Dasgupta, D., Cao Y., and Yang C.,1999b. Immunogenetic approach to spectra recognition. *In: Proc GECCO'99*, San Francisco, CA , USA, 149- 155.

De Castro, L. N. and Timmis, J.,2002a. *Artificial Immune systems: A New Computational Intelligence Approach*, London, Springer-Verlag.

De Castro, L. N. and Von Zuben, F. J.,2002b. Learning and optimization using the clonal selection principle. *IEEE Transactions on Evolutionary Computation*, 6(3), pp. 239-250.

Forrest, S., Perelson, A. S., Alledn L., and Cherukuri, R.,1994. Self-nonself discrimination in a computer, *Proceedings of IEEE Symposium on Research in Security and Privacy*, pp. 202-212.

Hart, E., and Timmis, J.,2008. Applications areas of AIS: The past, the present and the future, *Applied soft computing*, 8(1), pp. 191-201.

Jerne, N. K.,1973. The Immune System, *Scientific American*, 229(1), pp. 52-60.

Kim, J., and Bentley, P.,2001. Towards an artificial immune system for network intrusion detection: An investigation of clonal selection with a negative selection operator. *In Proceedings of the congress on evolutionary computation (CEC)*, Seoul, Korea, 2, pp. 1244-1252.

Kruse, F. A., Lefkoff, A. B., Boardman, J. W., Heidebrecht, K. B., Shapiro, A. T., Barloon, P. J. and Goetz, A. F. H.,1993. The spectral image processing system (SIPS) – interactive visualization and analysis of imaging spectrometer data, *Remote Sensing of Environment*, 44, pp.145-163.

Landgrebe, D. A.,2002. Hyperspectral image data analysis. *IEEE Signal Processing Magazine*, 19(1), pp.17 – 28.

Plaza, A., Martínez, P., Pérez, R. M., and Plaza, J.,2002. Spatial/spectral Endmember Extraction by Multidimensional Morphological Operations, *IEEE Transactions on Geoscience and Remote Sensing*, 40(9), pp. 2025-2041.

Richards, J. A., and Jia, X. P.,1999. *Remote Sensing Digital Image Analysis*, *An Introduction*, 3rd revised and enlarged edition, Springer-Verlag, Berlin.

Timmis, J., Neal M., and Hunt, J.,2000. An artificial immune system for data analysis. *Biosystem*, 55(1/3), pp. 143-150.

Yao, X., Liu, Y., and Lin, G.,1999. Evolutionary programming made faster, *IEEE Transactions on evolutionary computation*, 3(2), pp.82-102..

Zhang, L., Zhong, Y., Huang, B., and Li, P.,2007. A resource limited artificial immune algorithm for supervised classification of multi/hyper-spectral remote sensing image. *International Journal of Remote Sensing*, 28(7), pp. 1665-1686.

Zhong, Y., Zhang, L., Huang, B. and Li, P.,2006. An unsupervised artificial immune classifier for multi/hyperspectral remote sensing imagery, *IEEE Transactions on Geoscience and Remote Sensing*, 44(2), pp. 420-431.