IEEE Access
Multidisciplinary | Rapid Review | Open Access Journal

Received January 31, 2020, accepted February 19, 2020, date of publication February 28, 2020, date of current version March 13, 2020.

Digital Object Identifier 10.1109/ACCESS.2020.2976875

Negative Selection Algorithm Based on Antigen Density Clustering

CHAO YANG[1,2,3], LIN JIA[1], BING-QIU CHEN[1], AND HAI-YANG WEN[1]

[1]School of Computer Science and Information Engineering, Hubei University, Wuhan 430062, China
[2]Hubei Education Informatization Engineering Technology Research Center, Wuhan 430062, China
[3]Hubei Key Laboratory of Applied Mathematics, Faculty of Mathematics and Statistics, Hubei University, Wuhan 430062, China

Corresponding author: Chao Yang (stevenyc@hubu.edu.cn)

This work was supported in part by the National Natural Science Foundation of China under Grant 61977021, and in part by the Open Project of Hubei Key Laboratory of Applied Mathematics under Grant HBAM201902.

ABSTRACT The negative selection algorithm (NSA) is one of the basic algorithms of the artificial immune system. In the traditional negative selection algorithm, candidate detectors are randomly generated without considering the uneven distributions of self-antigens and nonself-antigens, thereby resulting in many redundant detectors, and it is difficult for these detectors to fully cover the area of nonself-antigens. To overcome the problem of low detector generation efficiency, a negative selection algorithm that is based on antigen density clustering (ADC-NSA) is proposed in this paper. The algorithm divides the process of detector generation into three steps: the first step is to calculate the density of the antigens by using the method of antigen density clustering to select nonself-clusters. The second step is to prioritize the abnormal points (nonself-antigens that are not clustered) as the centers of candidate detectors and to generate the detectors via calculation. The third step is to generate the detectors via the traditional algorithm. Detector generation via these three steps can reduce the randomness of the detector generation in the traditional algorithm, thereby improving the efficiency of detector generation. The experimental results demonstrate that on the BCW and KDD-Cup datasets, the negative selection algorithm that is based on antigen density clustering can effectively increase the detection rate while reducing the false-positive rate compared with the traditional negative selection algorithm (RNSA) and two improved algorithms at the same expected coverage.

INDEX TERMS Artificial immunity, negative selection algorithm, antigen density clustering, detector.

I. INTRODUCTION

The artificial immune system (AIS) is a computational paradigm that is inspired by the biological immune system [1]. The artificial immune system has been widely used in computer security, anomaly detection and prediction [2], [3], [23], [24]. The negative selection algorithm is one of the basic algorithms of AIS. This algorithm was proposed by Forrest [4] in 1994 and has been applied to intrusion detection and data classification.

The negative selection algorithm has been widely used in the fields of network intrusion detection, spam detection, medical diagnosis, and fault detection [5]–[8]. However, the negative selection algorithm has the disadvantages of high detector repeat coverage and loopholes. [9], [10], [11]. In response to these disadvantages, many scholars have proposed improved algorithms. For example, Gonzalez *et al.* [12] proposed a real-valued negative selection algorithm (RNSA) with an immutable radius. Antigens and antibodies belong to the $[0, 1]^n$ value space to maximize the coverage of nonself-regions to improve the detection efficiency. Ji and Dasgupta [13] proposed a variable-radius negative selection algorithm (V-Detector). The main strategy is to randomly generate the detector center x, find the nearest self-antigen to x, calculate the distance r between them, and dynamically generate detectors with x as the center and r as the radius. Chen *et al.* [14] proposed a negative selection algorithm that was based on hierarchical clustering of self-sets (CB-RNSA). After the hierarchical clustering of self-sets, cluster centers are used to replace self-points, which effectively reduces the computational cost of distance calculations. Liu *et al.* [15] proposed SDS-RNSA, which uses a subspace density search algorithm to calculate the sample subspace region and directly generates detectors in its subspace to increase the detection rate.

The associate editor coordinating the review of this manuscript and approving it for publication was Ting Li.

Zhengjun *et al.* [16] proposed a negative selection algorithm that was based on soft subspace clustering of antigens (ASSC-NSA), which uses clustering to calculate the key features and weights of various types of antigens, thereby reducing the influence of redundant features on the detector, which effectively guides the generation of mature detectors. In 2018, Abid *et al.* [10] designed a layered real-valued NSA (LRNSA). Different layers are formed according to the distance of candidate detectors from the self-antigens, and the detectors belonging to far-self layer are generated by clustering optimization method. In addition, the algorithm makes the detectors stay apart from each other in order to maximize the coverage and decrease the number of mature detectors. In 2019, Fan *et al.* [11] proposed ASTC-RNSA, the algorithm first uses the Delaunay triangulation method from the perspective of computational geometry to divide its space into simple units for determining the position of the detector. Then the overlap between the simple unit and the self-antigen is removed to form a set of triangulation coverage areas, and finally detectors are generated within this area. Avoid the time-consuming self-tolerance process of traditional NSAs.

According to the discussion above, the focus of improving the NSA algorithm has been on the efficient generation of detectors. Many scholars have improved the traditional algorithm in response to the problems of high redundancy and loopholes that are caused by the random generation of candidate detectors via the traditional algorithm.

This paper proposes a negative selection algorithm that is based on antigen density clustering (ADC-NSA). Partial detectors are generated via density clustering to reduce the repeated coverage and loopholes that are caused by randomly generated detectors in the traditional algorithm. In this paper, the generation of a detector via antigen density clustering is divided into three steps: the first step is to cluster the antigen via the antigen density clustering algorithm and to select the clustered nonself-clusters as the mature detectors; the second step is to use nonself-antigens that are not clustered as abnormal points to generate mature detectors via training; and the third step is to use traditional algorithms to randomly generate candidate detectors and to train them to generate mature detectors. This process reduces the generation of redundant detectors and enables the algorithm to cover the nonself-area with as few detectors as possible, thereby effectively overcoming the problems of high detector repeat coverage and loopholes.

II. PROBLEM DESCRIPTION

Traditional negative selection algorithms generate mature detectors (antibodies) by judging whether the candidate detector matches the self-antigens. Then, the data to be detected are matched with the mature detectors. If the matching is successful, the data are abnormal. The basic definitions and process of the algorithm are as follows:

Definition 1: Antigen set. The antigen set is $A_g = \{x_1, x_2, x_3, \ldots, x_n\}$, where $x_i \in [0, 1]$, n represents the total number of sample points, x_i represents the normalized value of sample point i, and A_g represents the set of normalized values of all sample points.

Definition 2: Self-antigen and nonself-antigen., Self-antigen self $\in A_g$ represents the positive sample of the sample, and nonself-antigen nonself $= A_g - self$ represents the negative sample of the sample. The area that is covered by the self-antigens in the range of the value space is called the self-region, and the area not covered is called the nonself-region.

Definition 3: Affinity. The Euclidean distance $\mathrm{dist}(x_i, x_j) = \sqrt{\sum_{d=1}^{D} (x_i^d - x_j^d)^2}$ between two points represents the affinity between the two points, where x_i and x_j represent the i-th and j-th sample points, d represents a feature dimension of the sample points, D represents the total number of feature dimensions of the sample points, and x_i^d represents the d-th dimension feature of the i-th sample point.

Definition 4: Detectors. A detector is denoted by $d_e(z_i, r_i)$, where z_i represents the randomly generated candidate detector center, r_i represents the distance from the center to its nearest self-cell, and the circle that is formed by z_i and r_i corresponds to the mature detector.

As illustrated in Figure 1, the traditional negative selection algorithm simulates the negative selection process in which the immune system recognizes self-cells and nonself-cells. The algorithm randomly generates candidate detectors, and by removing the detectors that have detected the self-antigens, the detectors that can detect any nonself-cell are retained. Finally, a mature detector set is generated for data detection. The main advantages are that no prior knowledge is required and an unlimited number of nonself-antigens can be detected with a limited number of self-antigens [17], [18]. The main disadvantage is that the traditional negative selection algorithm generates random detectors in the detector generation step [11], [19], which leads to problems such as high repeat coverage and loopholes.

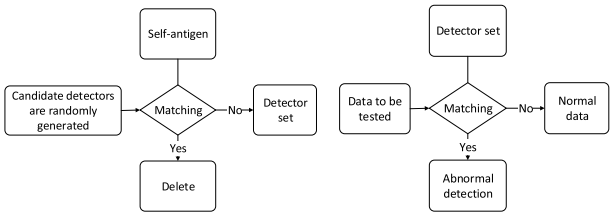


FIGURE 1. (a) Detector generation (b) Data detection.

In Figure 2, the pentagram represents the self-set, and the open circles represent the mature detectors. All regions except the self-set are nonself-regions. The traditional negative selection algorithm expects that the detectors can cover as many nonself-regions as possible. However, when the antigens are unevenly distributed in the sample space, where the antigens are densely distributed, the gaps between the sample points are narrow, which hinders the efficient generation of detectors. Where antigens are sparse, the randomly generated candidate detectors will inevitably be highly redundant,

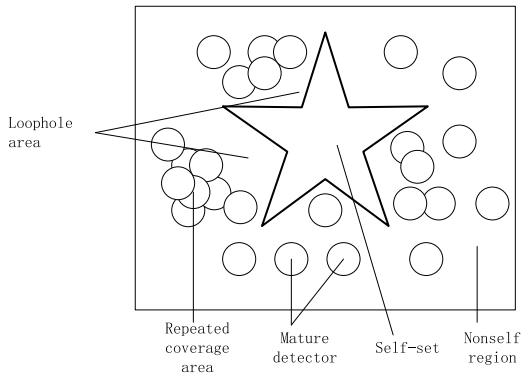


FIGURE 2. Generation of the detectors via the traditional algorithm.

thereby resulting in high repeat coverage of the detectors, and loopholes will form in areas that are difficult to cover.

III. ADC-NSA ALGORITHM IMPLEMENTATION STRATEGY

The traditional negative selection algorithm does not consider the uneven distribution of antigens in the sample space [20]; as a result, detectors cover each other and cause substantial redundancy. For overcoming this challenge, the ADC-NSA is proposed in this paper. First, the clustering algorithm is used to identify high-density regions, and the clustered nonself-clusters are directly used as mature detectors. Second, in the low-density regions, the abnormal points (nonself-antigens that are not clustered) are preferentially used as the candidate detector centers to generate detectors after calculating the radius. Finally, candidate detectors are randomly generated via the traditional algorithm. The generation of detectors via these three steps can reduce the randomness of the detector generation in the traditional algorithm, thereby effectively overcoming the problems of high detector repeat coverage and loopholes and improving the efficiency detector generation.

A. ADC-NSA BASIC DEFINITION

Definition 1: The Euclidean distance d_{ij} between sample points x_i and x_j is:

$$d_{ij} = \sqrt{\sum_{d=1}^{D} (x_i^d - x_j^d)^2} \tag{1}$$

The antigen set $A_g = \{x_1, x_2, x_3, \ldots, x_n\}$ contains n sample points, and each sample point has D-dimensional feature attributes and is expressed as $x_i = \{x_i^1, \ldots, x_i^d, \ldots, x_i^D\}$. x_i^d represents the d-th dimension feature of the i-th sample point, and the distance between any two sample points x_i and x_j in the antigen set is calculated using the Euclidean distance, which is also called antigen affinity calculation.

Definition 2: The local density ρ_i of the sample point x_i is:

$$\rho_i = \sum_{x_i \in A_g} M(d_{ij} - d_c) \tag{2}$$

where d_c represents the cutoff distance (clustering radius). In [25], [27], a d_c was selected so that the average number of neighbors in each sample point was about 2% of the total number of sample points, and $M_{(m)} = \begin{cases} 1, & m \le 0 \\ 0, & m > 1 \end{cases} (m = d_{ij} - d_c)$. If d_{ij} is greater than d_c, ρ_i is not changed, whereas ρ_i is incremented by one if d_{ij} is less than the d_c. This function is used to calculate the true density of x_i.

Definition 3: The sample point distance δ_i is defined as follows:

If ρ_i is smaller than ρ_j:

$$\delta_i = \min\left(d_{ij}\right) \ (x_i, x_j \in A_g, j \neq i \quad \text{and } \rho_j > \rho_i) \tag{3}$$

If ρ_i is maximal:

$$\delta_i = \max\left(d_{ij}\right) \quad (x_i, x_j \in A_g, j \neq i) \tag{4}$$

Definition 4: The cluster center c_i is determined by the size of the cluster center weight γ_i. Sort γ_i in descending order and set the sample points that correspond to the first K values of γ_i as c_i [26].

Definition 5: The cluster center weight γ_i is defined as:

$$\gamma_i = \delta_i \times \rho_i \tag{5}$$

Definition 6: The abnormal point a_i is determined according to δ_i and ρ_i. A point with small ρ_i and relatively large δ_i is called an abnormal point. In this paper, the nonself-antigens that satisfy these conditions and are not clustered are called abnormal points, which will be preferred as the candidate detector centers.

Definition 7: The cluster discriminant F_i is defined as:

$$F_i = \begin{cases} 1 & \dfrac{\sum_{i=1}^{n} g(x_i)\,(non - self)}{n\,(total)} > \varepsilon \\ 0 & else \end{cases}$$
$$g(x) = \begin{cases} 1 & non - self \\ 0 & self \end{cases} \tag{6}$$

If $F_i = 1$, the cluster is a nonself-cluster; otherwise, it is a self-cluster. The ε is the category judgment threshold, and it takes 0.99 in this experiment.

Definition 8: The expected coverage c_p is defined as:

$$c_p(p, t, m) = \begin{cases} -1 & if\ t \ge G \\ 0 & else\ if \dfrac{m}{\sqrt{t \times p \times (1-p)}} - \sqrt{\frac{t \times p}{1-p}} < Z_a \\ 1 & else \end{cases} \tag{7}$$

The calculation termination condition is Flag $= c_p$. If Flag $= -1$, set $t = m = 0$ and start counting again. Z_a is a very small constant. In this experiment, the value of Z_a is set as 0.001, and $G > \max\left(\frac{5}{p}, 5/(1-p)\right)$.

B. ADC-NSA ALGORITHM

The basic process of the negative selection algorithm that is based on antigen density clustering is presented as Algorithm 1 and Figure 3:

Algorithm 1 ADC-NSA Algorithm

Input: set $A_g = \{x_1, x_2, x_3, \ldots, x_n\}$, cutoff distance d_c, expected coverage c_p

Output: *Detectors*

<1>: Detectors = ∅, self ∪ nonself =A_g, self∩nonself = ∅.

<2>: Use the antigen density clustering algorithm to calculate d_{ij}, δ_i, and ρ_i of each sample point, abnormal point a_i and nonself-clustering center c_i.

<3>: Add the nonself-cluster that is composed of c_i and d_c as the first type of mature detector into set *Detectors*.

<4>: Select the abnormal point a_i as the center of the candidate detector preferentially, calculate the distance between a_i and the nearest self-antigen, record it as R, and add the circle with a_i as the center and R as the radius as the second type of mature detector to *Detectors*.

<5>: Randomly generate candidate detectors within the collection, and add the third type of mature detectors, which are generated using the traditional detector generation algorithm, to *Detectors*.

<6>: Reach c_p and terminate of the algorithm. Thus, the generation of *Detectors* ends.

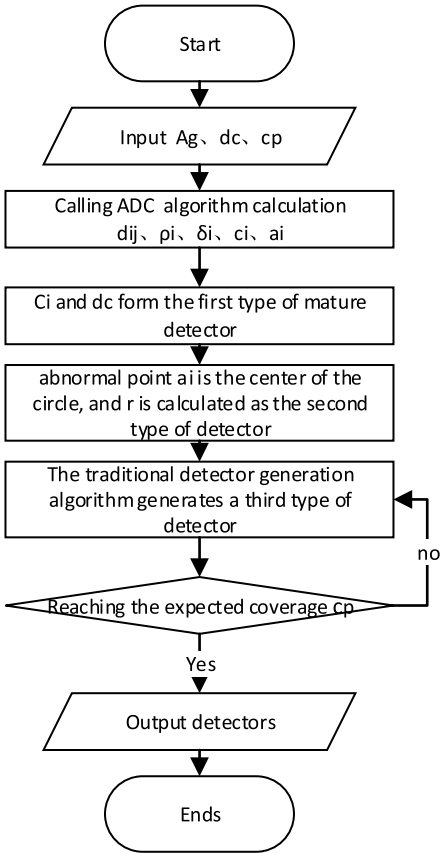


FIGURE 3. ADC-NSA algorithm flowchart.

1) ANTIGEN DENSITY CLUSTERING ALGORITHM

The antigen density clustering algorithm clusters antigens based on the density of the antigen distribution, in preparation for the generation of the detectors. The algorithm is based on the following assumptions: (1) The density of the clustering center point is higher than that of the surrounding sample points. (2) The distance between the clustering center point and the higher density point is relatively large.

The process of the antigen density clustering algorithm is presented as Algorithm 2:

Algorithm 2 Antigen Density Clustering Algorithm

Input: set $A_g = \{x_1, x_2, x_3, \ldots, x_n\}$ and cutoff distance d_c

Output: nonself-clustering center c_i and abnormal point a_i

<1>: Calculate Euclidean distance d_{ij} according to formula (1).

<2>: Calculate local density ρ_i according to formula (2).

<3>: Calculate δ_i according to formulas (3) and (4).

<4>: Calculate γ_i according to formula (5) and select c_i according to definition 4.

<5>: Select the abnormal point a_i that satisfies the condition in definition 6.

<6>: Determine the cluster category according to formula (6), and select the nonself-clusters.

2) DETECTOR GENERATION ALGORITHM

The generation of the detector is divided into three main steps: (1) Use the nonself-clusters that are calculated via antigen density clustering as detectors. (2) Use the abnormal point a_i preferentially as a candidate detector center to generate a detector via calculation. (3) Use the traditional algorithm to generate the detectors. The generation process of the detectors is illustrated in Figure 4, and the process is presented as Algorithm 3:

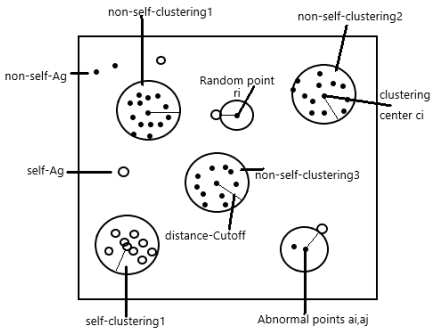


FIGURE 4. Detector generation process.

If a detector that is composed of an abnormal point a_i and a radius r_i includes other abnormal points a_j, then remove a_j. If there are randomly generated candidate detector points in the self-antigens or other mature detectors, then remove these points. At this time, the number of repeated detectors is $m+1$; otherwise, the number of mature detectors is $t+1$. Calculate

Algorithm 3 Detector Generation Algorithm

Input: Expected coverage c_p, self-antigens, nonself-cluster center c_i, and abnormal point a_i

Output: *Detectors*

<1>: self $\in A_g$, detectors $= \emptyset$.

<2>: Use the nonself-cluster-center c_i as the center of the circle and d_c as the radius to form detectors, and add them into *Detectors* as the first category of mature detectors.

<3>: Calculate the distance r_i between a_i and the nearest self-antigen, generate detectors with point a_i as the center and r_i as the radius, and add them as the second category of mature detectors into *Detectors*.

<4>: Randomly generate a candidate detector center z_i within the set. Calculate the minimum distance r_i between z_i and the self-antigen, and generate the detector with the point z_i as the center of the circle and r_i as the radius. Add it as the third category of mature detectors into *Detectors*.

<5>: Stop generating detectors if c_p has been reached.

the termination condition Flag $=c_p$ according to the statistical hypothesis testing method [13] of formula (7).

In Figure 4, hollow dots represent self-antigens with a specified radius, solid dots represent nonself-antigens, large circles represent clustering results, and the regions with self-antigens are nonself-regions. The generated mature detectors should cover as many nonself-regions as possible. Among them are nonself-clusters 1, 2, and 3 and self-cluster 1. These four groups of clusters are calculated via the antigen density clustering algorithm according to the distribution of the antigens. Nonself-clusters 1, 2 and 3 (each of which is defined by a cluster center c_i and a cutoff distance d_c) are selected as the first category of mature detectors according to the cluster discrimination formula (6). a_i is preferentially used as the center of the candidate detector. Then, calculate the distance between a_i and the nearest self-antigen; this distance is regarded as R_i. If the detector that is defined by the abnormal point a_i and the radius R_i contains other abnormal points a_j, then remove a_j and select the detector as the second category of mature detectors. If a randomly generated candidate detector point is in the self-antigen or other mature detectors, then remove it. As illustrated in the figure, the candidate detector center z_i is randomly generated, and the closest self-antigen distance r_i is selected as the radius. At this time, the generated detector is used as the third category of mature detectors. Three categories of mature detectors have been generated.

IV. EXPERIMENT AND ANALYSIS OF THE RESULTS

A. DATASETS AND EVALUATION INDICATORS

The datasets that are used in this paper are from the UCI database [21]. Classic datasets BCW and KDD-Cup99, which are often used for anomaly detection and machine learning, are selected. The BCW dataset originates from breast cancer data that were provided by foreign medical institutions. This dataset has 2 categories, 9 attributes, 241 abnormal data, and 458 normal data. This experiment standardizes and normalizes the data, and divides the testing set and training set of the BCW dataset by using a partition function, As shown in Table 1. The KDD-Cup99 dataset originates from 9-week network data connection information that was collected by a foreign LAN. This dataset includes a training dataset and a test dataset. In this experiment, the experimental data are extracted at a ratio of 1:1. Each connection record in the training dataset contains 41 fixed feature attributes and a class identifier. The data features include basic features, network features and content features.

As shown in Table 2.

TABLE 1. Details of THE BCW dataset in the experiment.

Data type	Label	Total number	Experimental training data	Experimental test data
Normal	2	458	Random 70%	Random 30%
Abnormal	4	241	Random 70%	Random 30%

TABLE 2. Details of the KDD dataset in the experiment.

Data type	Description	Attack in training set	Attack in testing set	Experimental training data	Experimental test data
Normal	Normal access	None	None	10%	10%
DOS	Denial of service attack	Nepture,back, sumrf, land etc.	apache2, udpstorm, mailbomb etc.	5%	5%
Probe	Detection attack	Portsweep, ipsweep, satan etc.	Mscan, sait etc.	50%	50%
R2L	Remote unauthorized access	Ftpwrite, guess_passwo rd etc.	Sendmail, named, snmpguess etc.	50%	50%
U2R	Illegal elevation of user rights	buffer_overfl ow, loadmodule, etc.	Xterm, httptunnel etc.	50%	50%

The evaluation indices are the detection rate (DR) and the false-positive rate (FPR), which are commonly used in the classic binary classification problem.

$$\mathrm{DR} = \frac{TP}{TP + FN} \tag{8}$$

$$\mathrm{FPR} = \frac{FP}{FP + TN} \tag{9}$$

In these expressions, TN denotes the number of true-negative types, which are correctly recognized as self-antigens; TP denotes the number of true-positive types, which are correctly recognized as nonself-antigens; FN denotes the number of false-negative types, which are incorrectly recognized as self-antigens; and FP denotes the number of false-positive types, which are incorrectly recognized as nonself-antigens.

B. EXPERIMENTAL DATA PREPROCESSING

This experiment uses the most common z-score normalization (zero-mean normalization) method, also known as standard deviation standardization. This method gives the mean and standard deviation of the original data to standardize the data.

The processed data conforms to the standard normal distribution, that is, the mean is 0, the standard deviation is 1, and its conversion function is: $x* = x - \mu\sigma$. Where μ is the mean of all sample data and σ is the standard deviation of all sample data. There are two benefits after data normalization: ① Improve the convergence speed of the model, ② Improve the accuracy of the model.

Due to the large KDD-CUP data set, this paper uses Principal Component Analysis (PCA) to reduce the dimension of this data set, while maintaining the characteristics of the largest variance contribution in the data set. The main steps are: The features are recombined into uncorrelated principal components, which are used to represent the original information. This method can effectively reduce the dimensionality of the sample and improve the calculation accuracy [22].

The key statement in the code is as follows: sklearn. decomposition.PCA (n_components = 99.9, copy = True, whiten = False).

① n_components: If the value is assigned to string, such as n_components = 'mle', the number of features will be automatically selected to meet the required percentage of variance; if no value is assigned, the default is None and the number of features will not change (the feature data will be changed). In this experiment, the percentage of variance is set to 99.9%, that is, the similarity with the feature data before dimensionality reduction is 99.9%.

② copy: True or False, the default is True, that is, whether the original training data needs to be copied.

③ whiten: True or False, the default is False, that is, whether to whiten, so that each feature has the same variance.

C. EXPERIMENTAL PARAMETER SETTINGS

The main parameters of this experiment are the expected coverage c_p and the cutoff distance d_c. The experimental results are presented in Figures 5, 6, 7 and 8. Figures 5 and 6 plot the detection rate and the false-positive rate when c_p is 90%-99%. Figures 7 and 8 plot the detection rate and the false-positive rate when c_p is 99% and d_c is 0.1-0.55.

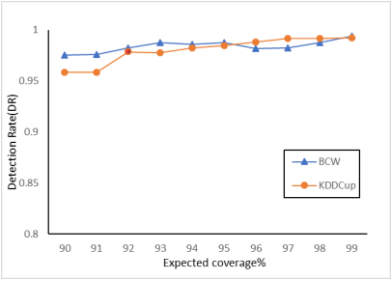


FIGURE 5. Effect of the expected coverage c_p on the detection rate.

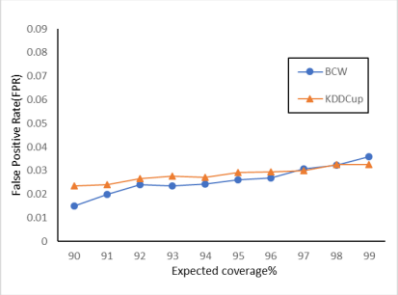


FIGURE 6. Effect of the expected coverage c_p on the false-positive rate.

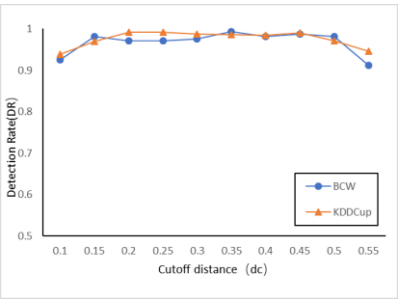


FIGURE 7. Effect of the cutoff distance d_c on the detection rate.

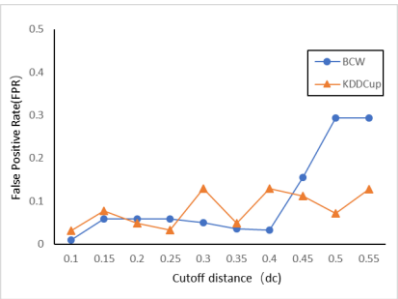


FIGURE 8. Effect of the cutoff distance d_c on the false-positive rate.

The experimental parameters are the best parameters that were identified in the analysis of the experimental results. According to the figure, in the BCW dataset, when c_p is 99% and d_c is 0.35, the detection rate of this algorithm reaches its maximal value and the false-positive rate is relatively low. At this time, the detection rate is 99.41%, and the false-positive rate is 3.54%.

In the KDD-Cup dataset, the algorithm performs best when c_p is 99% and d_c is 0.25. The detection rate reaches 99.24%, and the false-positive rate is 3.25%.

The final parameter settings are listed in Table 3:

D. COMPARATIVE ANALYSIS EXPERIMENT

To further evaluate the performance of the algorithm, this paper compares it with three algorithms, namely, RNSA [12], V-Detector [13], and ASSC-NSA [16], on the BCW and KDD-Cup datasets. The statistics are presented in Table 4, and the results of the comparative experiments are presented in Figures 9, 10, 11, and 12.

TABLE 3. ADC-NSA parameter settings on two datasets.

dataset	c_p	self-radius	d_c	DR	FPR
BCW	99%	0.002	0.35	0.9941	0.0355
KDD-Cup	99%	0.02	0.25	0.9924	0.0325

TABLE 4. Comparison of four algorithms on the bcw and KDD-Cup datasets.

algorithm	B C W		KDD-Cup	
	DR	FPR	DR	FPR
ADC-NSA	0.9941	0.0354	0.9924	0.0325
ASSC-NSA	0.9797	0.0367	0.9388	0.0426
V-D	0.9367	0.0419	0.8256	0.0446
RNSA	0.8481	0.0620	0.7469	0.0519

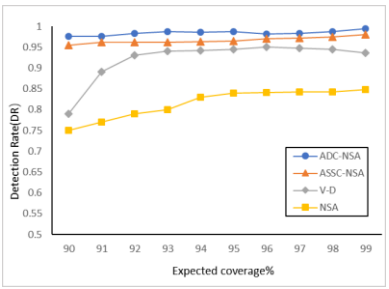


FIGURE 9. Comparison of the detection rates of four algorithms on BCW.

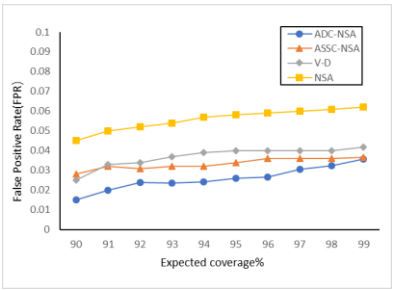


FIGURE 10. Comparison of the false-positive rates of four algorithms on BCW.

These results are the averages of the detection rates and the false-positive rates that were obtained via multiple experiments with c_p equal to 99%. In this experiment, the detection rate is 99.41% and the false-positive rate is 3.54% on the BCW dataset. On the KDD-Cup dataset, based on PCA dimension reduction, the detection rate is 99.24% and the false-positive rate is 3.25%. It is concluded that ADC-NSA, which is proposed in this paper, realized a higher detection rate and a lower false-positive rate than the three compared algorithms.

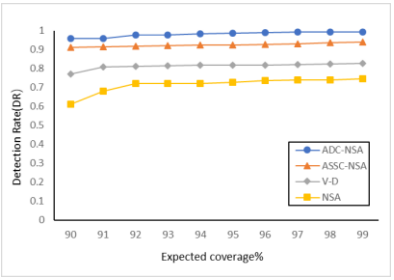


FIGURE 11. Comparison of the detection rates of four algorithms on KDD-Cup.

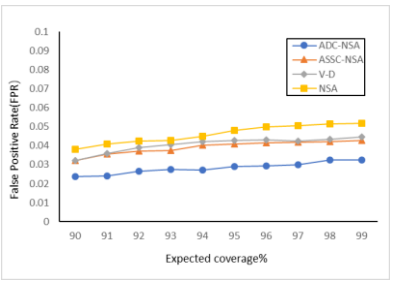


FIGURE 12. Comparison of the false-positive rates of four algorithms on KDD-Cup.

TABLE 5. Time complexit of each algorithm.

NSA	time -complexity
RNSA	$O\left(-\frac{\lvert D\rvert * N_s}{(1-P_m)^{N_s}}\right)$
V-Detector	$O\left(-\frac{\lvert D\rvert * N_s}{(1-P_m)^{N_s}}\right)$
ASSC-NSA	$O((N_s+N_n)^3 * d^3 * m)$
ASTC-RNSA	$O(N_s * \log N_s + N_s^{d/2} + \lvert D\rvert * d^2)$
ADC-NSA	$O((N_s+N_n)^2 * d)$

E. TIME COMPLEXITY ANALYSIS

Based on this experiment, the following assumptions are made: N_s is the number of self-antigens, N_n is the number of nonself-antigens, d is the dimension, M is the number of nonself-clusters, and P is the number of abnormal points. By analyzing definitions 1 through 7, we can get that the time complexity of antigen density clustering algorithm is $O((N_s+N_n)^2)$. Combined with the detector generation algorithm, the time complexity of this experiment is $O((N_s+N_n)^2 * d)$. Compared with other experiments [11], the time complexity is shown in Table 5.

As shown in Table 5, compared with RNSA and V-Detector, the time complexity of ADC-NSA is much lower than the traditional exponential level [14]. Under the same conditions, the time complexity of this algorithm is better than the improved ASSC-NSA. As the dimension d increases, the time complexity of this algorithm will also be better than the improved ASTC-RNSA. Overall, the time complexity of the algorithm is slightly lower.

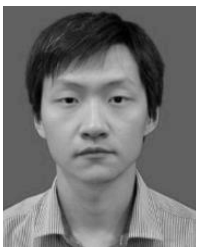
V. CONCLUSION

The traditional negative selection algorithm ignores the influence of the antigen distribution on the generation of detectors during the detector generation stage, thereby resulting in low efficiency of detector generation. Therefore, this paper proposes a negative selection algorithm that is based on antigen density clustering (ADC-NSA): First, the clustering algorithm is used to identify high-density regions, and the clustered nonself-clusters are directly used as mature detectors. Second, the abnormal points are selected as the centers of candidate detectors preferentially in low-density regions, and detectors are generated via training. Finally, detectors are generated via the traditional algorithm. The algorithm can effectively generate detectors in regions with various densities; hence, the algorithm has a higher detection rate and a lower false-positive rate.

At present, the algorithm still has two problems: 1. In the clustering step, the selection of the cutoff distance d_c during clustering still depends on artificial experience; 2. When the detection is performed, the points that fall into the loopholes are not clear. The next research work is how to achieve adaptiveness in the selection of d_c and conduct further research on the determination of the data to be detected that falls into the loopholes.

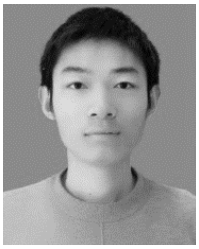
REFERENCES

[1] X. K. Gang and X. Xinying, "Overview of artificial immune system and algorithm," *Comput. Eng. Appl.*, vol. 41, no. 20, pp. 77–80,2005.
[2] G. Dozier, D. Brown, H. Hou, and J. Hurley, "Vulnerability analysis of immunity-based intrusion detection systems using genetic and evolutionary hackers," *Appl. Soft Comput.*, vol. 7, no. 2, pp. 547–553, Mar. 2007.
[3] S. T. Powers and J. He, "A hybrid artificial immune system and self organising map for network intrusion detection," *Inf. Sci.*, vol. 178, no. 15, pp. 3024–3042, Aug. 2008.
[4] S. Forrest, A. S. Perelson, L. Allen, and R. Cherukuri, "Self-nonself discrimination in a computer," in *Proc. IEEE Comput. Soc. Symp. Res. Secur. Privacy*, May 1994, pp. 202–212.
[5] M. E. Pamukov, V. K. Poulkov, and V. A. Shterev, "Negative selection and neural network based algorithm for intrusion detection in IoT," in *Proc. 41st Int. Conf. Telecommun. Signal Process. (TSP)*, Jul. 2018, pp. 1–5.
[6] H. Xiao-juan, L. Lei, and Q. Ning-jia, "A novel spam categorization algorithm based on active leaning method and negative selection algorithm," *Acta Electronica Sinica*, vol. 1, no. 1, pp. 203–209,2018.
[7] S. Le and B. Wenyang, "New negative selection algorithm and its application in disease diagnosis," *J. Frontiers Comput. Sci. Technol.*, vol. 1, pp. 36–42,2015.
[8] X. Song, F. Gao, Z. Chen, and W. Liu, "A negative selection algorithm-based identification framework for distribution network faults with high resistance," *IEEE Access*, vol. 7, pp. 109363–109374, 2019.
[9] J. Kim, P. J. Bentley, U. Aickelin, J. Greensmith, G. Tedesco, and J. Twycross, "Immune system approaches to intrusion detection-a review," *Natural Comput.*, vol. 6, pp. 413–466, Jan. 2007.
[10] A. Abid, M. T. Khan, and C. W. de Silva, "Layered and real-valued negative selection algorithm for fault detection," *IEEE Syst. J.*, vol. 12, no. 3, pp. 2960–2969, Sep. 2018.
[11] Z. Fan, C. Wen, L. Tao, C. Xiaochun, and P. Haipeng, "An antigen space triangulation coverage based real-value negative selection algorithm," *IEEE Access*, vol. 7, pp. 51886–51898, 2019.
[12] F. A. Gonzalez, D. Dasgupta, and L. F. Nino, "A randomized real-valued negative selection algorithm," in *Proc 2nd Int. Conf. Artif. Immune Syst.*, pp. 261–272, 2003.
[13] Z. Ji and D. Dasgupta, "V-detector: An efficient negative selection algorithm with probably adequate detector coverage," *Inf. Sci.*, vol. 179, no. 10, pp. 1390–1406, Apr. 2009.
[14] W. Chen, T. Li, X. Liu, and B. Zhang, "A negative selection algorithm based on hierarchical clustering of self set," *Sci. China Inf. Sci.*, vol. 56, no. 8, pp. 1–13, Oct. 2011.
[15] Z. Liu, T. Li, J. Yang, and T. Yang, "An improved negative selection algorithm based on subspace density seeking," *IEEE Access*, vol. 5, pp. 12189–12198, 2017.
[16] L. Zhengjun, G. Jiangjin, and Y. Tao, "Improved negative selection algorithm based on antigen soft subspace clustering," *Appl. Res. Comput.*, vol. 35, no. 3, pp. 680–684, Mar.2018.
[17] Z. Z. Jin, M. H. Liao, and G. Xiao, "Survey of negative selection algorithms," *J. Commun.*, vol. 34, no. 1, pp. 159–170, 2013.
[18] J. Zhou and D. Dasgupta, "Real-valued negative selection algorithm with variable-sized detectors," in *Proc. GECCO*, 2004, pp. 287–298.
[19] G. Jiangjin and Y. Tao, "Immune evolution negative selection algorithm," *Appl. Res. Comput.*, vol. 34, no. 5, pp. 1293–1297, May 2017.
[20] Z. Fan, Y. Jin, L. Tao, and Z. Fangdong, "DnyNSA: A novel real-value based negative selection algorithm," in *Proc. IEEE Symp. Ser. Comput. Intell. (SSCI)*, Nov. 2018, pp. 1104–1109.
[21] *UCI Data Set*. [Online]. Available: http://archive.ics.uci.edu/ml/index.php
[22] N. Lei and S. Zhong-lin, "PCA-AKM algorithm and its application in intrusion detection system," *Comput. Sci.*, vol. 45, no. 2, pp. 226–230,2018.
[23] A. da Silva, I. S. Guarany, B. Arruda, E. C. Gurjao, and R. S. Freire, "A method for anomaly prediction in power consumption using long short-term memory and negative selection," in *Proc. IEEE Int. Symp. Circuits Syst. (ISCAS)*, May 2019, pp. 1–5.
[24] A. Lasisi, N. Tairan, R. Ghazali, W. K. Mashwani, S. N. Qasem, H. Kumar G R, and A. Arora, "Predicting crude oil price using fuzzy rough set and bio-inspired negative selection algorithm," *Int. J. Swarm Intell. Res.*, vol. 10, no. 4, pp. 25–37, Oct. 2019.
[25] Z. Yuan and L. Zhong, "Fuzzy density peaks clustering algorithm based on k-nearest neighbors," *Comput. Eng. Softw.*, vol. 38, no. 4, Aug. 2017.
[26] M. C. Lai, S. Hong, and M. Tao, "A density peak clustering algorithm based on the automatic selection of cluster center points," *Comput. Sci.*, vol. 43, no. 7, pp. 255–258, 2016.
[27] A. Rodriguez and A. Laio, "Clustering by fast search and find of density peaks," *Science*, vol. 344, no. 6191, pp. 1492–1496, Jun. 2014.

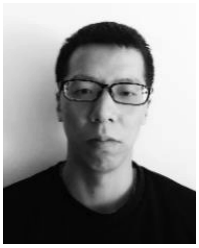


CHAO YANG received the Ph.D. degree in information security from Wuhan University, Hubei, China, in 2012. He is currently an Associate Professor with the School of Computer Science and Information Engineering, Hubei University. He is also a Researcher with the Hubei Education Informatization Engineering Technology Research Center and the Hubei Key Laboratory of Applied Mathematics. His research interests include information security, artificial intelligence, and artificial immune systems.

LIN JIA received the B.E. degree in IoT engineering from the Luojia College, Wuhan University, in 2018. She is currently pursuing the M.S. degree in computer application technology with Hubei University, Hubei, China. Her research interests include artificial immune systems and machine learning.



BING-QIU CHEN received the B.S. degree in information and computing science from Huanggang Normal University, in 2017. He is currently pursuing the M.E. degree in computer technology with Hubei University, Hubei, China. His research interests include artificial immune systems and machine learning.



HAI-YANG WEN received the B.E. degree in software engineering from the Hubei University of Economics, in 2018. He is currently pursuing the M.E. degree in computer technology with Hubei University, Hubei, China. His research interests include artificial immune systems and machine learning.