Dendritic Artificial Immune Network Model for Computing

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Abstract

Today, a large number of methods and models of intelligent information processing have been developed, among which artificial immune systems (AIS) can be distinguished, which are used to solve various practical problems. At the same time, existing models of AIS have a number of disadvantages, the main of which are low productivity and relatively low accuracy. Therefore, the work sets out the task of building such an AIS model that would provide better calculation characteristics both in terms of speed and accuracy. A new model of an AIS in the form of a dendritic artificial immune network (DaiNET) is proposed, which is built using graph theory and allows increased speed, ensures acceptable accuracy of results, and reduces the complexity of the antibody network formation process. The formation of the dendritic structure of the immune network is considered an example of solving the object clustering problem, which is one of the main areas of the practical application of AIS. It is proposed to form a *k*-connected graph of antibodies, in which the affinity of antibodies is used as a measure that determines the strength of the connection between antibodies in the immune network. The determination belonging to the clusters of antibodies of the immune network is based on the values of their avidity for each of the clusters, which are based on the affinity between immune objects. The general scheme of the data clustering algorithm based on the DaiNET immune model is considered, which is represented by the sequential execution of the stages of preparation, formation of a *K*-connected immune network, and network interaction. The peculiarities of the work of immune operators of the DaiNET model are considered. The results of a comparative analysis of the proposed DaiNET immune model with existing immune models and other clustering methods on different data sets are presented, which showed that it outperforms other immune models both in terms of speed and accuracy of object grouping.

Keywords

Dendritic Artificial Immune Network, Antibodies, Model, Clustering, Affinity, Avidity, Graph, Level of Stimulation

1. Introduction

The theory of artificial immune systems (AIS) is one of the directions in the organization of artificial intelligence systems [1-3]. To date, there are several common AIS models that are used to solve various practical problems [4, 5]: a) negative/positive selection model, b) clonal selection model, c) artificial immune network (AIN) model. These models differ from each other in the ways of editing the antibody population, ways of organizing immune operators, and in the possibilities of interaction between immune objects.

Among the listed immune models, the most promising for practical application is the AIN model, since it involves the organization of interaction not only between populations of antibodies and antigens but also the interaction between antibodies within one population [2]. This makes it possible to use this

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model not only for solving practical problems with supervised learning but also for solving problems with self-learning [3, 6]. In addition, due to the possibility of interaction between antibodies, the AIN model is easier to modify than the other listed models and allows the formation of hybrid models that operate on the basis of various biological and non-biological approaches for organizing calculations.

It should be noted that the existing AIN models, such as Artificial Immune Networks (aiNET) and Resource Limited Artificial Immune Networks (RLAIN) [2, 3] have a number of disadvantages, which increases the relevance of the task of modifying them for solving practical problems. The main disadvantages of the aiNet model are low performance and relatively low accuracy, which manifests itself, for example, in solving problems of classification, clustering, and pattern recognition. The RLAIN model also has a number of disadvantages associated with high implementation complexity, high depending on the method for determining the level of antibody stimulation, and narrow specialization expressed in solving problems of data classification with supervised learning.

In accordance with this, the task is to build a tree-type immune network model using graph theory, which will solve the problem of increasing the speed of the aiNet model, provide acceptable accuracy of the results, and also reduce the complexity of the process of forming a network of antibodies and recognition areas, which is typical for the RLAIN model.

2. Formation of the dendritic structure of the immune network

We will consider the formation of the dendritic structure of the immune network using the example of solving the object clustering problem, which is one of the main areas of the practical application of AIS [2, 3]. It is proposed to form a connected graph of antibodies. The concept of affinity is used as a measure that determines the strength of the connection or similarity between AIN antibodies [1]:

$$aff = \left(1 + d_{ij}\right)^{-1} , \tag{1}$$

where d_{ij} is the Euclidean or Manhattan distance between the features of the i th and j th immune objects. According to this, before the formation of a dendritic network of antibodies, affinities are calculated between all initial antibodies within a certain feature space. The process of forming the dendritic structure of the immune network is multi-stage. In the first stage, the antibody network is formed as a graph [7], where each vertex is connected to all other vertices of this graph (see Figure 1).

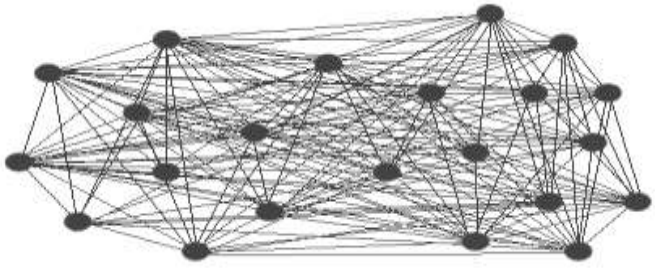

Figure 1: The first stage of the formation of a dendritic immune network

The process of forming a network of antibodies is a process of optimizing a fully connected graph of objects, the vertices of which are antibodies, and the edges are the affinities between them. Optimization means reducing the number of connections between antibodies in order to reduce the number of computational operations between pairs of antibodies. At the same time, the value of the Natural Affinity Threshold (NAT), which is the average affinity between all antibodies in the population, is used as a criterion that regulates the number of affinity connections between antibodies:

$$NAT(AB) = \frac{\sum_{i=1}^{n}\sum_{j=1}^{n-1} aff\left(ab_i, ab_j\right)}{n(n-1)}, \tag{2}$$

where n is the number of antibodies in the population; $aff\left(ab_i, ab_j\right)$ is the affinity value between the i th and j th antibodies according to (1).

Accordingly, connections between antibodies are removed if their affinities do not exceed the NAT value. Thus, due to the use of NAT in immune training and self-regulation of the network, the number of edges in the fully connected graph of antibodies is significantly reduced, which allows the speed of the operation of the immune network. In addition, to reduce the number of calculations in the dendritic immune network of antibodies, objects characterized by a high level of stimulation are selected. Levels of antibody stimulation are determined based on the closest antibody affinities of the dendritic immune network. Selected objects, characterized by a high level of stimulation, participate in solving the task of classification, clustering, skeletonization, and pattern recognition. Other antibodies are not amenable to cloning, mutation, and suppression, which leads to a reduction in the number of computational operations and increases the speed of the immune model.

Thus, the reduction of the number of connections between antibodies occurs due to the removal of connections characterized by minimum values of affinities. According to the expression used to define affinity (1), the range of affinity values is measured within (0.0; 1.0]. At the same time, the smaller the affinity value, the weaker the connection between objects, that is, the smaller the similarity between an increase in the affinity value means a stronger bond between a pair of immune objects.

When reducing the number of connections between antibodies of a dendritic immune network, it is assumed to use some input parameter K that limits the number of connections between antibodies of the network. That is, each antibody can create no more than connections with other antibodies in the network, other connections created by this antibody are removed. This idea is borrowed from the method of classification of k Nearest Neighbors (kNN) [8, 9]. Accordingly, during the formation of a dendritic network of antibodies, each antibody can form no more than K connections characterized by maximum affinities. Figure 2 shows a dendritic K-connected network of antibodies with parameter K = 3.

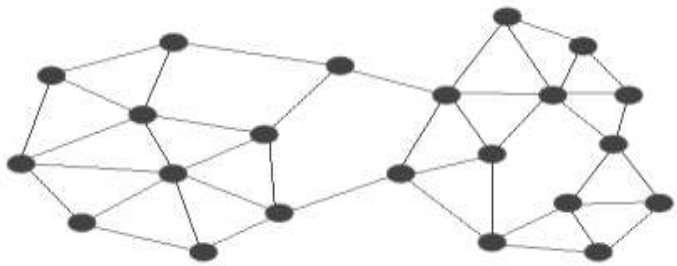

Figure 2: Dendritic K-connected network of antibodies (K = 3)

It should be noted that the parameter can vary in the range from 2 to many connections. At the same time, an increase in the number of active connections that remain during the construction of a dendritic immune network leads to a significant decrease in the speed of the immune clustering algorithm. However, a decrease in the number of connections between antibodies of the dendritic immune network leads to a decrease in the accuracy of clustering and the appearance of a significant number of immune object grouping errors.

However, as a result of the formation of a dendritic network, some immune objects located in clusters of antibodies may have a large number of connections exceeding the value of K. This happens because such an antibody independently forms K bonds and accepts additional bonds from other antibodies that are in close proximity according to its affinity. Thus, thanks to the reduction of the number of connections between antibodies in the network, a dendritic structure of the antibody network is formed from the initial graph with complete connections between objects, in which cluster centers are subsequently selected.

At the second stage, after the formation of a K-linked network of antibodies, the level of stimulation of each antibody is calculated based on its affinity with other immune objects forming the network [10]:

$$s_i = \frac{1}{K}\sum_{j=1}^{K} aff\left(ab_i, ab_j\right), \tag{3}$$

where s_i is the value of the stimulation level of the ith antibody to the antibodies associated with it; K is a parameter that determines the number of antibody connections in the network.

Candidates for cluster centers are determined based on the value of the antibody S_i stimulation level. At this stage of the formation of the dendritic immune network, a set of antibodies is formed, which are characterized by high levels of stimulation and the number of connections exceeding the value of the parameter K. The set of antibodies obtained in this way forms a set of candidate objects for cluster centers (see Figure 3). It should be noted that the number of such selected candidate cells for cluster centers may exceed the number of clusters determined at the beginning of the clustering process.

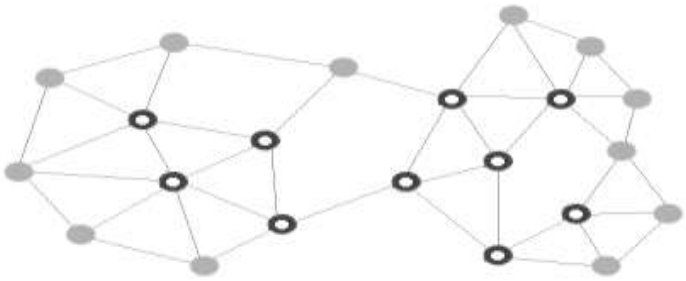

Figure 3: Determination of antibodies with a high level of stimulation

In Figure 3, which shows the result of selecting candidate antibodies for cluster centers, objects with a minimum level of stimulation that cannot be selected as cluster centers are marked in light gray, and antibodies that are characterized by a large number of strong affinity bonds and with a high level of stimulation, are displayed as white peaks with a dark gray outline. Thus, in the process of choosing potential centers of clusters, antibodies located on the periphery of the AIN do not participate, which leads to an increase in the speed of the object clustering algorithm.

Cluster centers are selected using a parameter that regulates the number of clusters that should be selected as a result of clustering [11, 12]. The value of the threshold affinity of NAT (2), which is determined at the first stage of the formation of the dendritic immune network, also takes part in this process. During the selection of cluster centers, the antibody is characterized by the maximum number of connections with other antibodies in the network, and the maximum level of stimulation is chosen for the centers from all candidate antibodies. Such an antibody is chosen as the center of the first cluster.

The centers of other clusters are determined relative to the selected center of the first cluster. According to this, in order for a candidate object for cluster centers to be selected as the center of a new cluster, the value of its affinities with other antibodies - the centers of clusters that were determined earlier should not exceed the value of the threshold affinity of the NAT network [13]. If the affinity between the candidate antibody for the cluster centers exceeds the NAT threshold with at least one of the selected cluster centers, this antibody is excluded from the set of candidate objects for the cluster centers. Thanks to this, only a small number of the farthest antibodies, which are characterized by a weak affinity between them, are selected from the entire set of potential cluster centers.

Fig. 4 presents the result of the selection of cluster centers for a dendritic immune network with K connections. At the same time, all affinity connections between antibodies in the network are marked in light gray color, candidate objects for cluster centers are marked with white vertices with a dark gray outline, and objects selected as the centers of formed clusters are marked in green. It should be noted that in this case the formation of two clusters is expected in the clustering process.

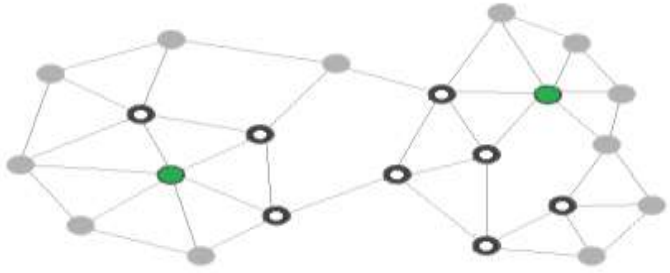

Figure 4: The result of the selection of cluster centers

In the fourth stage, after the distribution of the centers of the clusters, the process of determining the belonging of the antibodies of the immune network to them takes place. First, the immune objects that are characterized by a strong affinity connection with antibodies are clustered, which are the centers of the clusters, that is, the objects that have direct connections with the clusters in the tree-shaped immune network with K connections.

It should be noted that at this stage, the processes of immune modification of the network, which are accompanied by cloning, mutation, and editing of the population of grouped antibodies, are not performed. This is due to the high computational complexity and significant time costs that inevitably arise when conducting these immune processes. Therefore, to increase the speed of clustering, all antibodies that have a strong affinity to one of the selected cluster centers are joined to the same cluster with which they are associated. Thus, after the clustering of antibodies that are close to the centers of the clusters, groups consisting of a limited set of immune objects are formed. Clusters of this type are called clusters with centers of strong condensation.

Further, in order to carry out clustering of other antibodies that are not characterized by a strong affinity connection with any of the centers of the formed clusters, their affinities to each of the clusters and its antibodies that form the center of strong condensation are determined. The definition of avidity is based on the affinity between immune objects [14]. The avidity of an antibody with other antibodies belonging to the same cluster is defined as the sum of affinities between them:

$$av_i = \sum_{j=1}^{m} aff\left(ab_i, ab_j\right), \tag{4}$$

where av_i is the value of the avidity of the i th antibody with other antibodies of the cluster; m – the number of antibodies in the cluster; $aff\left(ab_i, ab_j\right)$ - affinity value between antibodies of the same cluster according to (1). The avidity determined in this way reflects the level of strength of the immune connection between the objects of the cluster and this antibody.

The concept of avidity antibodies and antigens, or between antibodies in an immune network, is often used in aiNet models that are used to solve classification, clustering, and data analysis problems [14]. Figure 5 shows the result of the grouping of immune objects that have a direct strong affinity relationship with antibodies selected as the centers of the formed clusters in the dendritic immune network. Cluster center antibodies are marked in green, antibodies associated with two different cluster centers are marked in blue and yellow, and the rest of the antibodies are shown in light gray.

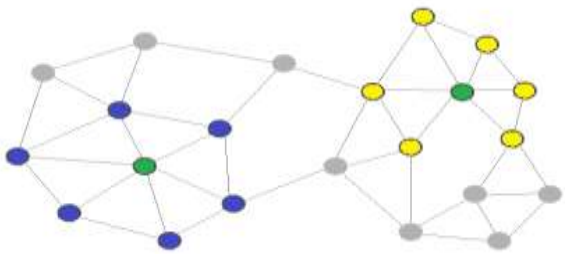

Figure 5: Clustering of objects associated with cluster centers

After determining the avidities between the antibodies that form the center of strong cluster condensation, these values are averaged. The average avidity obtained in this way determines the cluster and will be used in the clustering of other objects of the dendritic immune network that do not have a direct strong immune connection with the center of any cluster.

In the fifth stage, clustering of other objects occurs, triggering immune processes in a dendritic immune network of antibodies thanks to the operators of cloning, mutation and the use of suppression of clones and the network of antibodies that do not belong to any cluster. At the same time, for each clone, after its mutation, affinities with target objects are determined, which are clustered antibodies and which form clusters with a center of strong condensation.

During selection, for each cloned antibody, one object is selected from the entire set of its clones, characterized by maximum avidity antibodies forming the center of a cluster of strong condensation. This clone replaces the antibody from which it was created during the operation of the population

suppression operator of antibodies with undefined cluster membership. It should be noted that the immune process of cloning, mutation, suppression of clones, and suppression of antibodies of the dendritic immune network will be completed in the event that there is no antibody left in the network that has an avidity to one of the cluster centers, which will be lower than the avidity in the clusters with centers of strong condensation.

Thus, the process of clustering of objects that do not participate in the formation of centers of strong condensation and cannot be selected as the center of a new cluster occurs through the process of immune self-regulation of the antibody network and is determined by using the avidities of antibody generations. At the same time, such antibodies are created thanks to the use of immune operators, which determine the formation of a generation of antibodies on iterations of the process of immune self-regulation of the antibody dendritic network.

In Figure 6 shows the clustering result of the artificial immune dendritic network of antibodies distributed between two defined clusters.

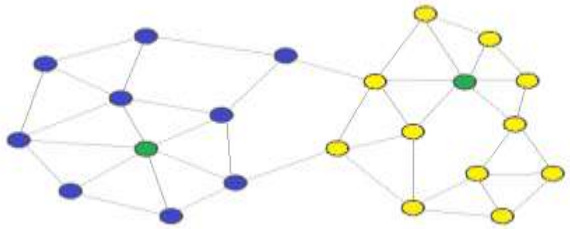

Figure 6: The result of antibody network clustering

Thus, the use of the graph theory model to create a dendritic model of the DaiNET immune network allows solving the problem of low performance of the aiNET immune model, as well as reducing the complexity of the process of forming the antibody network and recognition regions, which is characteristic of the RLAIN immune model.

3. General scheme of the data clustering algorithm based on the DaiNET immune model

The process of clustering a set of input objects based on the DaiNET immune model can be represented as a sequence of the following stages:

1. Setting the clustering parameters and obtaining the initial set of objects.
2. Determination of the scales of characteristics of the studied objects.
3. Formation of a K-linked dendritic immune network.
4. Selection of cluster centers.
5. Determination of cluster identities.
6. Immune self-regulation of the network.
7. Conclusion about the clustering of objects.

Since the most common model of AIN operation is the aiNET model, it is the basis for building immune models using AIS principles. Despite their versatility and the possibility of self-regulation and learning, most immune methods cannot be used without additional modifications when solving the tasks of classification and clustering of objects. To increase the speed of immune learning in the proposed DaiNET immune model, the main immune operators were modified: primary selection operator, mutation operator, clone suppression, and antibody suppression operators.

To improve the quality of clustering and increase the speed of the object grouping process, it is advisable to carry out additional work with a set of objects from which the initial population of antibodies is formed. In the course of preparatory work, it is necessary to determine the scales of features of objects. This happens if these scales are not defined before the start of the clustering process. When examining the scales of the initial data, the ranges of possible values for all features that characterize the set of objects for clustering are determined [15, 16]. Accordingly, for each group of features, when determining the data scales, the maximum and minimum possible values that can be taken by this or that feature during the mutation of the immune object are determined. This must be

done so that during the mutation, the characteristics of the clones do not take on values that go beyond the permissible range of values, because this can lead to a significant decrease in the speed of clustering.

To increase the speed of data clustering, operators of data scaling and the formation of a K-connected dendritic network of antibodies, an operator for determining the initial centers of clusters, as well as an operator for determining affinities, which is used at the final stage of object grouping during antibody clustering, have been added to the operation of the DaiNET immune model that do not form centers of strong cluster condensation. It should be noted that the scaling operator is not necessary and data clustering can occur without its use. However, the use of this operator leads to an increase in the speed of network self-regulation and, as a result, leads to an increase in the speed of clustering.

Accordingly, at the level of immune operators, the DaiNet immune model is represented by the sequential execution of the corresponding stages given by the expression (5):

$$
\begin{aligned}
DaiNet(AB, K, c) = {} & {}^{PRP}\begin{bmatrix} Scaling(AB)\rightarrow \\ Presentation(AB)\rightarrow \\ NATCalculation(AB) \end{bmatrix} \Rightarrow \\
\Rightarrow {} & {}^{DKN}\begin{bmatrix} DKnetCreation(AB, K)\rightarrow \\ CalcStimulation(AB)\rightarrow \\ CentersSelection(AB, c, NAT)\rightarrow \\ DendricClustering(AB') \end{bmatrix} \Rightarrow \\
\Rightarrow {} & {}^{NET}\begin{bmatrix} Cloning(AB'', CL)\rightarrow \\ Mutation(CL)\rightarrow \\ Presentation(CL, AB', AB'')\rightarrow \\ CLSupression(CL, AB', AB'')\rightarrow \\ NetSupression(CL, AB'')\rightarrow \\ AvCalculation(AB'')\rightarrow \\ ClusterSelection(AB'') \end{bmatrix},
\end{aligned}
\qquad (5)
$$

In this expression, DaiNet (AB, K, C) is a notation for the method of clustering input AB objects using a dendritic K-linked immune antibody network, and the criterion C used to indicate the number of clusters formed.

The stage of preparation for clustering is denoted by the abbreviation *PRP* and contains several operators: operator *Scaling(AB)* – is used for scaling objects; operator *Presentation(AB)* – used to determine the affinities between antibodies of the formed immune network; operator *NATCalculation (AB)* – used to determine the threshold affinity of NAT in the population of antibodies.

The stage of work aimed at forming a K-connected immune network has the conventional designation *DKN* and contains the following operators: operator *DKnetCreation (AB, K)* – is used to form a K-connected tree network of antibodies; operator *CalcStimulation (AB)* – used to determine the level of antibody stimulation; operator *CentersSelection (AB, c, NAT)* – used to select cluster centers; operator *DendricClustering (AB')* – used to form clusters of strong condensation.

The stage of network interaction has the designation NET and contains the following operators: cloning operator *Cloning (AB'', CL)* - used to spread the population of antibodies not related to any of the formed clusters; mutation operator *Mutation (CL)* – is used to change the characteristics of clones; target object presentation operator *Presentation (CL, AB', AB'')* – used to determine the affinities between clones and objects that form clusters of strong condensation; clone suppression operator *CLSupression (CL, AB', AB'')* – used to edit the clone population; antibody network suppression operator *NetSupression (CL, AB')* – used to reduce the number of objects in the immune network; the operator for determining the avidity antibodies and clusters of strong condensation *AvCalculation (AB'')* – used to distribute non-clustered objects between the clusters being formed; operator *ClusterSelection* (*AB'')* – used to determine whether antibodies belong to clusters.

The proposed organization of calculations based on the DaiNET immune model in the example of solving the object clustering problem, according to the formal representation at the level of immune operators (5), consists of the following main steps.

Step 1. Preparatory stage:

- Conducting scaling for the population of immune objects.
- Presenting antibodies to each other.
- Determination of the *NAT* affinity threshold for the population of antibodies.

Step 2. Construction of a dendritic K-connected immune network:

- Selection of *K*-connections with maximum affinities in the network.
- Determination of antibody stimulation levels.
- Selection of cluster centers based on stimulation levels and *NAT*.
- Formation of clusters of strong thickening.

Step 3. Self-regulation and clustering of antibodies, the cycle of execution of operators:

- Cloning of antibodies that did not determine belonging to the cluster.
- Mutation of formed clones.
- Presentation of clusters of strong concentration of clone population.
- Suppression of clones.
- Suppression of cloned antibodies.
- Determination of avidities for antibodies with an undefined cluster.
- Determining whether antibodies belong to clusters based on avidities.

As a result of the operation of the DaiNET model, clustering of the initial population of antibodies occurs. At the same time, these objects belong to one of the selected clusters in the process of immune interaction of the dendritic K-linked network of antibodies. Carrying out the stage of determining avidities allows the clustering of antibodies clusters of strong condensation.

4. Peculiarities of work of immune operators in the DaiNET model

Features of the work of immune operators on the DaiNet model, given in (5), play a major role in increasing the speed and accuracy of calculations. In the DaiNet model, both the immune operators and some principles of the aiNET model have been transformed. Therefore, let's consider in more detail the immune operators used in the DaiNET model.

The antibody presentation operator *Presentation (AB)* is used at the initial stage of the clustering algorithm. At the same time, an initial population of antibodies is formed from a set of initial objects, and affinities between all antibodies are determined. The use of affinity allows forming an immune network of antibodies for further clustering.

The *NATCalculation (AB)* operator is used to calculate the value of the *NAT* threshold affinity, which is used at various stages of the formation of the *K*-linked dendritic immune network and to determine the initial cluster centers, on the basis of which the strongly thickened clusters will be formed.

The operator *DKnetCreation (AB, K)* allows you to form a network of antibodies with a limited number of connections between objects. At the same time, affinity is the main indicator of the strength of the connection between antibodies. To speed up the network, the number of connections between antibodies is reduced using the external parameter *K*. As a result of the operation of this operator, a *K*-linked network of antibodies is formed for the further determination of the initial centers of clusters, as well as the formation of strongly thickened clusters.

The operator *CalcStimulation (AB)* is used to determine the level of antibody stimulation of the immune network. The use of stimulation levels makes it possible to distinguish from the initial population of antibodies, immune objects that are characterized by a large number of strong affinity connections with the antibodies of the network. Thus, the antibodies of the immune network stimulate these immune objects and cluster around them. From these groups of antibodies, clusters of strong condensation are subsequently formed.

The operator *CentersSelection (AB, c, NAT)* is used to form clusters of strong condensation. At the same time, the search for the initial centers of clusters takes place, after which clusters with a center are formed. Then, all antibodies that are associated with this center form clusters with a center of strong

condensation. At the same time, the centers of clusters can only be immune objects characterized by the maximum number of connections exceeding the number of *K*. These antibodies are sorted by the value of the stimulation level in ascending order. The center of the first cluster is the antibody that has the maximum level of stimulation and the number of connections with other antibodies in the network exceeding the *K* value.

Other cluster centers are determined iteratively. After determining the first cluster center, the center of the second cluster in its group should be characterized by a high level of stimulation, and also have an affinity with the center of the first cluster, less than the *NAT* value that was previously determined. In the next iteration, from the remaining antibodies, with a high level of stimulation, an antibody is selected that has affinities with previously selected cluster centers lower than the *NAT* value. If no antibody has a large number of connections, but meets the *NAT* value requirements, it can be selected as the center of a new cluster.

The operator $DendricClustering\,(AB')$ forms clusters of strong condensation from initial clusters with a selected center. This stage of DaiNet work is carried out exclusively thanks to the affine connections of the dendritic network without starting the network self-regulation mechanism, that is, without using operators of cloning, mutation and editing of the population of clones and antibodies of the network. The formation of clusters with centers of strong condensation takes place by joining to clusters of antibodies connected to their center by strong affinity bonds.

The cloning operator $Cloning\left(AB'', CL\right)$ creates a population of clones that are identical to the cloned antibodies. It should be noted that an increase in the number of clones leads to a decrease in the speed of immune training due to the fact that each formed clone undergoes mutation and is presented to target objects, which increases the time of immune training. Thus, as a result of the operation of the cloning operator, the number of generated clones for each antibody should not be too large or too small, because this will negatively affect the time of immune training. Therefore, DaiNet uses proportional cloning with increased affinity, which allows to form the population of clones in the best way. Accordingly, the number of clones during cloning is determined as follows:

$$Nc_i = M \cdot C_m \cdot \max aff\left(ab_i, ag_j\right), \tag{6}$$

where Nc_i is the number of clones of the *i*-th antibody; *M* – total number of antibodies; C_m – affinity amplification factor; $\max aff\left(ab_i, ag_j\right)$ – maximum affinity with one of the target objects. It should be noted that the affinity gain coefficient C_m is an integer value that is used in the DaiNet model as an input argument and takes values in the range [1;10].

The clone mutation operator Mutation (CL) is used to make changes to the characteristics of clones. In the DaiNet model, the inversely proportional mutation is used with the limitation of the lower threshold for determining the mutation coefficient. At the same time, the lower limit of the range of possible values used to determine this coefficient is limited. The mutation coefficient is determined according to the following expression:

$$\mu = rand\left[\frac{1}{2}\left(1 - aff\left(ab, AB\right)\right); 1 - aff\left(ab, AB\right)\right], \tag{7}$$

where $aff\left(ab, AB\right)$ – affinity between the parent antibody and a set of target objects or antigens. Thanks to this, the maximum change in the characteristics of clones depending on the change in affinity is achieved, while minimizing the probability of loss of specificity of antigens or other target objects.

The operator $Presentation\left(CL, AB', AB''\right)$ is used at the stage of self-regulation of the dendritic immune network and is used to represent antibodies that did not determine belonging to one or another cluster or to antibodies that form centers of strong condensation of clusters. On the set of unclassified antibodies, there are other antibodies that form clusters of strong condensation, previously isolated. This leads to a significant increase in performance and an increase in the speed of object clustering.

The clone suppression operator $CLSupression\left(CL, AB', AB''\right)$ edits the population of clones after mutation. The affinities of clones with their target objects are used, which are chosen as antibodies that form the centers of clusters of strong condensation. Editing of a set of clones is carried out by comparing their stimulation levels, and as a result of the operation of the clone suppression operator, one object

with the best stimulation level remains in the population. Thanks to this, the speed of immune learning increases without losing classification accuracy.

After the immune network is formed and clones selected as a result of suppression are added to it, it is edited using the network suppression operator $NetSupression(CL, AB'')$. At the same time, the criteria regulating the process of network suppression are the levels of stimulation of cloned antibodies. If the level of stimulation of an antibody by one or another center of a cluster of strong condensation is lower than the corresponding level of a clone formed from this antibody, this antibody is removed and replaced by a clone. Otherwise, the clone is removed, and the antibody remains in the population and is again exposed to the action of the cloning operator. Thus, only antibodies with maximum levels of stimulation to the centers of cluster condensation remain in the network.

After the operation of the network suppression operator is completed, the affinities between antibodies and the selected centers of clusters of strong condensation are determined based on the operator $AvCalculation(AB'')$, whose work is completed by determining the affinities with all antibodies that form clusters of strong condensation. The self-regulation cycle of the DaiNET model is completed by the operation of the operator $ClusterSelection(AB'')$, during which each antibody determines whether it belongs to one or another cluster based on the value of avidities with antibodies that form the centers of strong condensation of clusters and avidities determined within the clusters. The conclusion that the antibody belongs to one or another cluster is made if the avidity between this antibody and the cluster is not less than the avidity between the antibodies of the center of strong condensation of the cluster.

The main condition for the completion of training is the achievement of full specificity of antibodies to the formed clusters. Large populations of antibodies are required to achieve this state. At the same time, it is mathematically impossible to determine the number of populations necessary to achieve full specificity, so the DaiNet model uses a static stopping criterion that determines the maximum number of antibody populations that are formed in the process of immune learning and network self-regulation.

5. Experimental results of object clustering based on the DaiNET model

For a comparative analysis of the proposed DaiNET immune model with existing immune models and other common data clustering methods, three sets of objects with a limited number of features were formed. These sets differ in the number of objects and the number of clusters that should be obtained as a result of clustering. The characteristics of the data sets are given in Table 1.

Table 1

Sets of objects for clustering

Identifier	Number	
	Objects	Clusters
Set 1	100	3
Set 2	500	5
Set 3	2500	10

The given sets of objects are used in two ways: 1) as initial data sets for clustering algorithms; 2) as control samples to check the quality of classification. This happens because the specified data sets are already classified, but can be used without specifying the initial belonging of this or that object to some class or cluster.

A comparison of the proposed approach with other immune and non-immune methods of data grouping is given in the table. 2. When analyzing the performance of the proposed DaiNet model, reference clustering methods MST (Minimum Spanning Tree) and C-means [8, 9], as well as immune models Clonalg and aiNet [2] were used. When comparing algorithms, two main metrics were used: *T* is the time spent by the clustering algorithm on grouping the initial set of objects; *A* is the accuracy of clustering, which is determined as a result of comparing the clusters formed during the operation of the clustering algorithm and the belonging of a set of objects to the input classes.

Table 2
Results of object clustering

Algorithm		Set 1	Set 2	Set 3
MST	*T*	38%	36%	39%
	A	88%	85%	82%
C-means	*T*	72%	74%	72%
	A	100 %	100 %	100 %
Clonalg	*T*	100 %	100 %	100 %
	A	80%	83%	81%
aiNet	*T*	98%	95%	93%
	A	52%	50%	50%
DaiNet	*T*	48%	46%	47%
	A	95%	93%	96%

According to the clustering results given in Table 2, we note that the C-means algorithm is characterized by the maximum accuracy of the grouping of objects *A*, and the Clonalg algorithm by the worst speed *T*. Therefore, these algorithms were chosen as the absolute maximum values (100%). On the other hand, the MST method is characterized by the best performance, that is, when using this method, clustering takes the least time, approximately 4 times less than clustering using the Clonalg method. But at the same time, the MST method is significantly inferior to other methods in terms of the accuracy of the grouping of the studied set of objects.

It should be noted that the use of the proposed DaiNet model for data clustering is characterized by high grouping accuracy. According to this characteristic, it is inferior only to the C-means method by a few percent. However, the DaiNet model outperforms the C-means method in terms of performance by almost 10% and is inferior only to the MST method in terms of this indicator. hen comparing the DaiNET model with other immune models that are usually used to solve data classification and clustering problems, it should be noted that the DaiNet model outperforms other immune models both in terms of speed and accuracy of object grouping. This makes the proposed model the most adapted to the organization of calculations for solving practical problems based on the use of the immune approach.

6. Conclusions

The theory of AIS is currently one of the areas of intelligent information processing, which is used to solve various practical problems. Among the existing immune models, the most promising for practical use is the artificial immune network model, which involves the organization of interaction not only between populations of antibodies and antigens, but also the interaction between antibodies within the same population. The existing models of artificial immune networks aiNET and RLAIN have a number of disadvantages, the main of which are low speed and relatively low accuracy. To increase the speed, ensure acceptable accuracy of the results, and reduce the complexity of the antibody network formation process, a new IIS model has been proposed in the form of a DaiNET dendritic artificial immune network, which is built using graph theory.

The formation of the dendritic structure of the immune network is considered in the example of solving the object clustering problem. It is proposed to form a K-connected graph of antibodies, in which the strength of the connection between the antibodies of the immune network is determined by the affinity of the antibodies. A *NAT* threshold affinity value is used to regulate the number of affinity connections between immune network antibodies. To reduce the number of calculations in the antibody tree network, objects characterized by a high level of stimulation, which is determined on the basis of

the closest affinities of the antibodies forming the network, are selected. Based on the value of the level of stimulation of antibodies, the centers of clusters are determined, and the determination belonging to clusters of other antibodies of the immune network is based on the values of their affinities to each of the clusters. The general scheme of the data clustering algorithm based on the DaiNET immune model and the peculiarities of its immune operators are considered. The DaiNET model is represented at the level of immune operators by the sequential execution stages of preparation, formation of a *K*-linked immune network, and network interaction of antibodies. The practical significance of the obtained results lies in the development of software modules for the implementation of the proposed DaiNET model, which can be used to solve a wide range of practical problems. Experimental studies of the proposed DaiNET immune model for solving the problem of clustering on various data sets were carried out and its comparison with existing immune models and other clustering methods was carried out, which showed that the DaiNET model is superior to other immune models both in terms of speed and accuracy of the grouping of objects.

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