The Improved Hierarchical Clustering Algorithm by a P System with Active Membranes

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Abstract: - In this paper an improved hierarchical clustering algorithm by a P system with active membranes is proposed which provides new ideas and methods for cluster analysis. The membrane system has great parallelism. It could reduce the computational time complexity and is suitable for the clustering problem. Firstly an improved hierarchical algorithm was presented which introduced the K-medoids algorithm. The distance of clusters is defined as the distance between the medoids of these clusters instead of the mean distance between them. Secondly a P system with all the rules to solve the above hierarchical algorithm was constructed. The specific P system is designed for the dissimilarity matrix associated with n objects. The computation of the system can obtain one possible classifications in a non-deterministic way. Through example test, the proposed algorithm is appropriate for cluster analysis. This is a new attempt in applications of membrane system.

Key-Words: - Clustering algorithm; the hierarchical clustering; K-medoids algorithm; Membrane computing; P System; Membrane system

1 Introduction

Clustering is a very important problem in machine learning, statistics, biology, data mining and many other many fields. Through the process of clustering, data set are partitioned into clusters with intra-cluster data similar and inter-cluster data dissimilar.

Many fields like combinatorial problem, finite state problems and graph theory have applied membrane computing. For many combinatorial problems membrane computing approaches are very suitable used on account of the vast parallelism. The time complexity parallelism of the computing will be lessened so it can meet the requirement of improving the processing speed of the big data [1, 2].

These two above are combined in this paper to solve the typical clustering problem: N objects are clustered into k clusters by the hierarchical clustering algorithm. The subscript i of the point a_i represents the i-th object of the original objects and the dissimilarity of any two original objects defines the distance of corresponding points a. Different clusters are represented by different membranes and the traditional hierarchical algorithm are improved. First, each object composes one cluster. The distance between clusters is the same as the distance between the objects. Second, find the closest two membranes and merge them into one. Then put the information out into the output membrane and compute distances between medoids as the distance between clusters. And then find the closest two membranes...... and so on, until only one cluster left. This strategy makes a new use of membrane computing.

2 The Improved Hierarchical Clustering Algorithm

The hierarchical clustering algorithm is a very classical partitioning algorithm. It can cluster the data set $X = \{x_1, x_2, ..., x_n\}$ with n objects into k clusters.

Firstly, an n*n distance matrix D_{nn}' is defined to show the distance between any two objects:

$$D_{nn}' = \begin{pmatrix} w_{11}' & w_{12}' & .. & w_{1n}' \\ w_{21}' & w_{22}' & .. & w_{2n}' \\ & & ... & \\ w_{n1}' & w_{n2}' & .. & w_{nn}' \end{pmatrix} \quad (1)$$

Where, w_{ij}' is the dissimilarity between x_i and x_j[3].

Secondly, the matrix elements w_{ij}' are changed into integer w_{ij} for membrane computing by rounding. The new matrix D_{nn} is as follows [4]:

$$D_{nn} = \begin{pmatrix} w_{11} & w_{12} & .. & w_{1n} \\ w_{21} & w_{22} & .. & w_{2n} \\ & & \cdots & \\ w_{n1} & w_{n2} & .. & w_{nn} \end{pmatrix} \qquad (2)$$

Then, the steps of hierarchical clustering algorithm are as follows:

1. Every object composes one cluster in the beginning. The distance between the clusters is just the distance between these objects.
2. Find the nearest two clusters and combine them into one cluster.
3. Compute distances between the present clusters again.
4. Repeat the steps 2 and 3 until one cluster is left [5].

Four measures to get the distance between clusters are widely used now. They are average distance, mean distance, minimum distance and maximum distance, respectively. The maximum distance is the method which uses the maximum distance of the points in different clusters to represent the distance of the two clusters and the minimum distance is the method which uses the minimum distance to represent it. So these two methods are sensitive to the outliers or the noise data. The mean distance is a little better. The average distance can put up with the outliers. But it is different to compute.

So, the mean distance is improved to the medoids distance in this paper. It is more robust to noise and outliers and easier to compute. The medoids distance is the distance between the medoid of two clusters. A medoid can be defined as one object of a cluster, whose total distance to all the objects in the cluster is minimal. That is to say, it is a most centrally located point in the given data set.

3 P Systems with Active Membranes

According to the process of cells managing chemical substances, P system is abstracted as a new membrane computing model. There are different biochemical reactions in tissues or biological cells. On the basis of these, three kinds of models are proposed: Cell-like P Systems, Tissue-like P Systems and Neural-like P Systems. Cell-like P System imitates the function and structure of the cells, and it includes the membrane structure, rules and objects as basic elements. Membranes divide the whole system into different regions. The skin membrane is the outermost membrane. A membrane is a basic membrane if there are no membranes in it and a membrane is a non-elemental membrane otherwise. Rules and objects exist in regions. Usually the objects are indicated by strings or characters. Rules are used to process objects or membranes in corresponding region. The rules are executed uncertainly and maximum concurrently. P System can be divided into three types from the angle of kinds of rules: transition P system, P system with communication rules and P system with active membranes [6]. The basic membrane structure is shown in Fig.1.

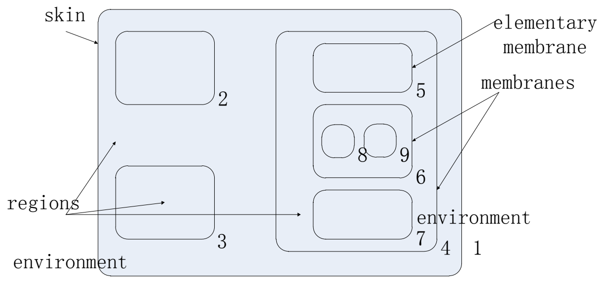

Fig.1. the basic membrane structure

P systems with active membranes change the membrane structure when executing rules. So space of exponential growth can be generated in linear operation steps. This is very helpful to solve the computationally hard problems within feasible time.

In general, a P system with active membranes of degree m is a construct:

$$\prod = (O, \mu, w_1, w_2, \ldots, w_m, R_1, R_2, \ldots, R_m, i_o) \qquad (3)$$

Where:

1. O is an alphabet. Elements in it are called objects;
2. μ is a membrane structure, each membrane has its label, $H = \{1, 2, ..., m\}$ is the label set ;
3. $w_i\,(i = 1, 2, ..., m)$ is the objects in membrane i ;

$R_i\,(i = 1, 2, ..., m)$ is the rules of membrane i

The basic rule is in the form of $(u \to v)_r$ [7]. u is a string composed of objects in O and v is a string in the form of $v = v'$ or $v = v'\delta$. v' is a string over $\{a_{here}, a_{out}, a_{in_j} \mid a \in O, 1 \le j \le m\}$. δ is a symbol not in O . It means after executing the rule this membrane will be dissolved. r is the promoters or the inhibitors and it is in the form of r=r' or $r = \neg r'$ .A rule can execute only when the promoters

r' appear and a rule can stop only when the inhibitors appear. The radius of this rule $u \to v$ is the length of u. R_i is the set of the rules in region i. ρ_i is the precedence relation which defines the partial order relation over R_i .High priority rule is executed prior. [8].The active membranes have rules as follows:

(a) object evolution rules:

$[_h a \to v]_h^e, h \in H, e \in \{+,-,0\}, a \in O, v \in O^*$

Object a evolves into v when the electric charge of membrane $h^\#$ is e. The electric charge of membrane $h^\#$ can be ignored if it is 0 which means that membrane $h^\#$ has no polarity.

(b) communication rules:

$a[_h\,]_h^{e_1} \to [_h b]_h^{e_2}, [_h a]_h^{e_1} \to [_h\,]_h^{e_2} b,$

$h \in H, e_1, e_2 \in \{+,-,0\}, a, b \in O$

Object a out of membrane h changes to object b and enters the membrane or object a in membrane h changes to object b and comes out of the membrane when the electric charge of membrane $h^\#$ is e_1. And the polarization of the membrane can be changed, but the label of membrane cannot.

(c) dissolving rules:

$[_h a]_h^e \to b \;\; h \in H, e_1, e_2 \in \{+,-,0\}, a, b \in O$

Membrane h will be dissolved with all objects in membrane h be kept except object a which is changed to object b when electric charge in membrane $h^\#$ is e.

(d) Division rules:

$[_h a]_h^{e_1} \to [_h b]_h^{e_2} [_h c]_h^{e_3}$

$h \in H, e_1, e_2, e_3 \in \{+,-,0\}, a, b, c \in O$

Membrane h can be separated into two membranes h with all objects duplicated except object a which is changed to object b and c respectively w hen the electric charge in membrane $h^\#$ is e_1 .These two new membranes may have different polarizations.

(e) Fusion rules:

$[_h b]_h^{e_2} [_h c]_h^{e_3} \to [_h a]_h^{e_1}$

$h \in H, e_1, e_2, e_3 \in \{+,-,0\}, a, b, c \in O$

This rule is opposite to the division rules shown above.

5. i_o is the output membrane which is used to save the final calculation result[6].

The rules are used maximum parallel and uncertainly in each membrane when calculating. The P system will halt after some steps if no more rules can be executed and these objects in output membrane is the final result. The P system will not halt if rules are always executed, then this calculation is invalid, and there is no result being outputted.

4 A P System for the Hierarchical Clustering Method

4.1 The P System for the Hierarchical Clustering Method

A P system for the improved hierarchical algorithm is proposed. Its structure is depicted in Fig.2.

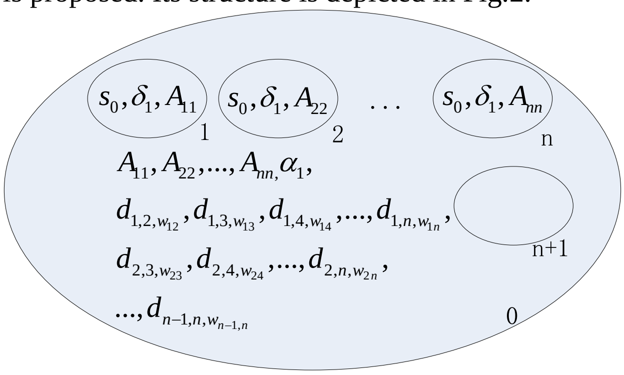

Fig.2 the P system for the k-medoids clustering method

It use the subscript i of the points a_i to represent the i-th object of the original objects and use the matrix D_{nn} to compare the similarity between the n objects. The specific algorithm is followed:

First, it set the maximum data in the matrix D_{nn} Max, the minimum data in the matrix D_{nn} Min and set the absolute value of these two Abs for convenience.

The P system for clustering is defined as follows:

$$\prod = (O, \mu, M_0, M_1, ..., M_n, M_{n+1}, R_0, R_1, ..., R_n, R_{n+1}, \rho) \quad (4)$$

Where:

1) $0 = \{A_{11}, A_{22}, ..., A_{nn,} \alpha_1, d_{1,2,w_{12}}, d_{1,3,w_{13}}, d_{1,4,w_{14}}, ..., d_{1,n,w_{1n}}, \; d_{2,3,w_{23}}, d_{2,4,w_{24}}, ..., d_{2,n,w_{2n}}, ..., d_{n-1,n,w_{n-1,n}}, s_0, \delta_1\}$

0 represents the collection of objects in the P system.

2) $\mu = [_0 [_1\,]_1 [_2\,]_2 ... [_n\,]_n [_{n+1}\,]_{n+1}\,]_0$

μ represents the membrane structure of the P system.

3) $M_0 = \{A_{11}, A_{22}, ..., A_{nn}, \alpha_1, d_{1,2,w_{12}}, d_{1,3,w_{13}}, d_{1,4,w_{14}}, ..., d_{1,n,w_{1n}}, d_{2,3,w_{23}}, d_{2,4,w_{24}}, ..., d_{2,n,w_{2n}}, ..., d_{n-1,n,w_{n-1,n}}\}$

$M_1 = \{s_0, \delta_1, \mathrm{A}_{11}\}, M_2 = \{s_0, \delta_1, \mathrm{A}_{22}\}, ..., M_n = \{s_0, \delta_1, \mathrm{A}_{nn}\}\ M_{n+1} = \{\lambda\}$

M represents the collection of initial objects in each membrane. M_{n+1} is the output membrane of this P system.

The rules in R_0 [9,10]:

$r_1 = \{(\eta_{ij} A_{ip} A_{jq} d_{i,j,t} \to \eta_{i(j+1)} A_{ip} A_{jq} d_{i,j,w_{pq}}) \bigcup (\eta_{ij} \to \eta_{i(j+1)})_{\neg(A_{ip} \cup A_{jq})} \mid 1 \le i, j, p, q \le n, -1 \le t \le Max\}$

$r_2 = \{\eta_{i(n+1)} \to \eta_{(i+1)(i+2)} \mid 1 \le i \le n-1\}$

$r_3 = \{\eta_{n(n+1)} \to \lambda\}$

$r_4 = \{(([A_{ip}]_i [s_0, \delta_1, A_{jq}]_j \to b_{ij} [A_{ip}, a_q, \alpha_t]_i) \bigcup (A_{ip} A_{jq} \to \lambda)$
$\bigcup (\alpha_t \to d_{tij})_{in_{n+1}})_{(d_{i,j,0}) \cup \alpha_t} \mid 1 \le i, j, p, q \le n, 1 \le t \le n-1\} \bigcup \{(\alpha_n \to \#)_{in_{n+1}})_{(d_{i,j,0}) \cup \alpha_n} \mid 1 \le i, j, p, q \le n\}$

$r_5 = \{(d_{j,t,p} \to d_{-1,-1,-1})_{b_{ij}} \bigcup (d_{i,j,0} \to d_{-1,-1,-1})_{b_{ij}} \mid 1 \le i, j, t \le n, -1 \le p \le Max\}$

$r_6 = \{b_{ij} \to \lambda \mid 1 \le i, j \le n\}$

$r_7 = \{d_{i_1, j_1, t_1} d_{i_2, j_2, t_2} ... d_{i_{\frac{n(n-1)}{2}}, j_{\frac{n(n-1)}{2}}, t_{\frac{n(n-1)}{2}}} \to d_{i_1-1, j_1-1, t_1-1} d_{i_2-1, j_2-1, t_2-1} ... d_{i_{\frac{n(n-1)}{2}}-1, j_{\frac{n(n-1)}{2}}-1, t_{\frac{n(n-1)}{2}}-1} \mid 1 \le i, j \le n, 1 \le t \le Max\}$

The rules in $R_i (1 \le i \le n)$:

$r_1' = \{\alpha_t \delta_i a_i \to \alpha_t \zeta_i O_i \mid 1 \le i \le n\} \bigcup \{(\alpha_t \delta_i \to \alpha_t \delta_{i+1})_{\neg a_i} \mid 1 \le i \le n, 1 \le t \le n-1\}$

$r_2' = \{s_t O_i a_j A_{hp} \to b_j O_i s_{t+w_{ij}-w_{pj}} A_{hp} \mid 1 \le i, j, p, h \le n, |t| \le nAbs\}$

$\mathrm{r}_3' = \{s_i A_{jp} O_h \to s_0 A_{jh} a_p \mid -nAbs \le i < 0, 1 \le j, p, h \le n\} \bigcup \{s_i A_{jp} O_h \to s_0 A_{jp} a_h\} \mid 0 \le i \le nAbs, 1 \le j, p, h \le n\}$

$r_4' = \{b_i \to a_i \mid 1 \le i \le n\}$

$r_5' = \{\zeta_i \to \delta_{i+1} \mid 1 \le i \le n\}$

$r_6' = \{\delta_{n+1} A_{jp} \alpha_t \to (\alpha_{t+1} A_{jp} \eta_{11}, out) \delta_1 A_{jp}\ \# \mid 1 \le j, p \le n\}$

$\rho = \{r_i > r_j \mid 1 \le i < j \le 7\} \bigcup \{r_i' > r_j' \mid 1 \le i < j \le 6\}$

4.2 An Overview of Computations

Membranes 1 to n represent the n clusters in initial condition. The object A_{ii} shows that the medoid of i-th cluster is x_i at this time. Rules in membrane 0 execute firstly. The object $d_{i,j,t}$ shows that the distance between membrane i and membrane j is t. Let all the third subscript t decrease at the same until one of them is zero (An object $d_{i,j,0}$ appears). It means that cluster i and cluster j are the nearest clusters. (If more than one $d_{i,j,0}$ appear at the same time, one of them is chose uncertainly.) Next the object A_{jq} in cluster j changes to a_q (Because there is only one medoid in one membrane, it is set the medoid of membrane i. The medoid of membrane j changes to ordinary point.) and all objects in membrane j is merged into cluster i. The object α_t enters into membrane i to active rules in membrane i to re-determine the medoid because there are new points entered. At the same time, A_{ip} and A_{jq} disappear, all objects $d_{i,j,t}$ and $d_{j,t,m}$ are changed to $d_{-1,-1,-1}$ because membrane j has disappeared and d_{tij} is sent to membrane n+1 to show that membrane i and membrane j is merged in circle t. To this, the two nearest clusters are merged.

If any membrane from 1 to n accepts an object α_t, this membrane should re-determine its medoid. Each point will be set as the new medoid from a_1 .Then calculate the difference between the dissimilarity between the new medoid and the remaining point and the dissimilarity between the original medoid and the remaining point and add the data to the subscript of object S. If the subscript of S is less than 0 after calculating all the dissimilarity with remaining points, the point a_1 can reduce the total consumption. So it is set as the new medoid. Else the original center point is maintained, rename object O_h to a_h. The object δ_{i+1} is produced to go to the next cycle to compare the object a_2 and the medoid and so on until all the objects a_i are compared. Last objects in this membrane are restored to initial state and the information of the medoid and the object α_{t+1} (This shows the hierarchical clustering algorithm goes into the next circle.) and η_{11} are put out. The object # is used to stop the computation step.

The object η_{11} actives rules in membrane 0. The objects $d_{i,j,t}$ are re-valued according to the new medoids. Then, it goes to the second circle. When there is only one cluster left, the computation is over.

5 Test and Analysis

To illustrate how the membrane system shown in Fig.2 run specifically, the 7 integral points (1,1), (2,1), (2,2), (3,4), (4,2), (4,3), (5,4) shown in Fig.3 is considered:

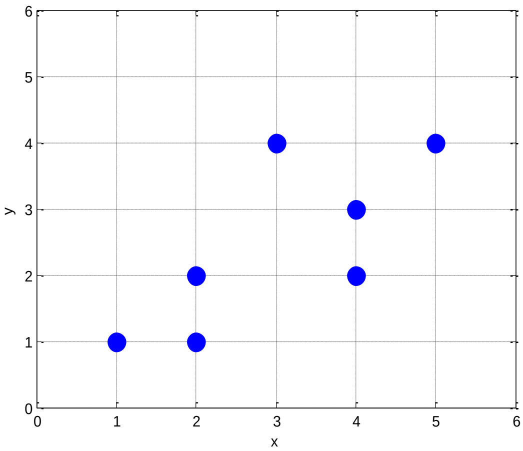

Fig.3 the 7 points waiting for being clustered

First of all, it defines the dissimilarity matrix D_{77}'. In this example, it uses the distance between any two points as the dissimilarity. Because the points are integral points, matrix D_{77} is the same to matrix D_{77}':

$$D_{77} = D_{77}' = \begin{pmatrix} 0 & 1 & 2 & 13 & 10 & 13 & 25 \\ 1 & 0 & 1 & 10 & 5 & 8 & 18 \\ 2 & 1 & 0 & 5 & 4 & 5 & 13 \\ 13 & 10 & 5 & 0 & 5 & 2 & 4 \\ 10 & 5 & 4 & 5 & 0 & 1 & 5 \\ 13 & 8 & 5 & 2 & 1 & 0 & 2 \\ 25 & 18 & 13 & 4 & 5 & 2 & 0 \end{pmatrix} \quad (5)$$

The membrane system clustering these seven numbers into two classes is shown in Fig.4:

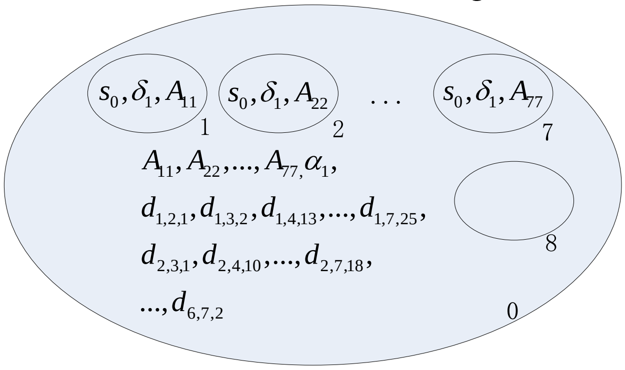

Fig.4 the P system clustering seven numbers into two classes

Steps of two circulations of the clustering are listed in Table 1 and Table 2. Because the steps are almost the same, only parts of them are listed here.

Table 1 steps of the first circulation of the clustering

membrane number	0	1	2	$n+1$
t_0:	$A_{11}, A_{22}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_1, d_{1,2,1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{2,3,1}, d_{2,4,10}, d_{2,5,5}, d_{2,6,8}, d_{2,7,18}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,5}, d_{6,7,2}$	s_0, δ_1, A_{11}	s_0, δ_1, A_{22}	λ
t_1:	$A_{11}, A_{22}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_1, d_{1,2,0}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{2,3,0}, d_{2,4,9}, d_{2,5,4}, d_{2,6,7}, d_{2,7,17}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1} (r_7)$	s_0, δ_1, A_{11}	s_0, δ_1, A_{22}	λ
t_2:	$A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, d_{1,2,0}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{2,3,0}, d_{2,4,9}, d_{2,5,4}, d_{2,6,7}, d_{2,7,17}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, b_{12} (r_4)$	$s_0, \delta_1, A_{11}, \alpha_1, a_2$	$\times$	d_{112}
t_3:	$A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, d_{-1,-1,-1}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-1}, d_{2,4,9}, d_{2,5,4}, d_{2,6,7}, d_{2,7,17}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, b_{12} (r_5)$	$s_0, \delta_2, A_{11}, \alpha_1, a_2 (r_1')$	$\times$	d_{112}

Table 1(continued) steps of the first circulation of the clustering

membrane number	0	1	2	$n+1$
t_4:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{2,5,4},d_{2,6,7},d_{2,7,17},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},b_{12}(r_5)$	$s_0,A_{11},\alpha_1,\zeta_2,O_2(r_1')$	$\times$	d_{112}
t_5:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{2,6,7},d_{2,7,17},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},b_{12}(r_5)$	$s_0,A_{11},\alpha_1,\zeta_2,a_2(r_3')$	$\times$	d_{112}
t_6:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{2,7,17},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},b_{12}(r_5)$	$s_0,A_{11},\alpha_1,\delta_3,a_2(r_5')$	$\times$	d_{112}
t_7:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},b_{12}(r_5)$	$s_0,A_{11},\alpha_1,\delta_4,a_2(r_1')$	$\times$	d_{112}
t_8:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1}(r_6)$	$s_0,A_{11},\alpha_1,\delta_5,a_2(r_1')$	$\times$	d_{112}
t_9:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1}$	$s_0,A_{11},\alpha_1,\delta_6,a_2(r_1')$	$\times$	d_{112}
t_{10}:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1}$	$s_0,A_{11},\alpha_1,\delta_7,a_2(r_1')$	$\times$	d_{112}
t_{11}:	$A_{33},A_{44},A_{55},A_{66},A_{77},d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1}$	$s_0,A_{11},\alpha_1,\delta_8,a_2(r_1')$	$\times$	d_{112}
t_{12}:	$A_{11},A_{33},A_{44},A_{55},A_{66},A_{77},\alpha_2,d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},\eta_{11}$	$s_0,A_{11},\delta_1,a_2(r_6')$	$\times$	d_{112}

Table 2 steps of the second circulation of the clustering

membrane number	0	5	6	$n+1$
t_0:	$A_{11},A_{33},A_{44},A_{55},A_{66},A_{77},\alpha_2,d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},\eta_{11}$	s_0,δ_1,A_{55}	s_0,δ_1,A_{66}	d_{112}
t_1:	$A_{11},A_{33},A_{44},A_{55},A_{66},A_{77},\alpha_2,d_{-1,-1,-1},d_{1,3,1},d_{1,4,12},d_{1,5,9},d_{1,6,12},d_{1,7,24},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},\eta_{12}(r_1)$	s_0,δ_1,A_{55}	s_0,δ_1,A_{66}	d_{112}
...				
t_7:	$A_{11},A_{33},A_{44},A_{55},A_{66},A_{77},\alpha_2,d_{-1,-1,-1},d_{1,3,2},d_{1,4,13},d_{1,5,10},d_{1,6,13},d_{1,7,25},d_{-1,-1,-1},d_{-1,-1,-1},$ $d_{-1,-1,-1},d_{-1,-1,-1},d_{-1,-1,-1},d_{3,4,4},d_{3,5,3},d_{3,6,4},d_{3,7,12},d_{4,5,4},d_{4,6,1},d_{4,7,3},d_{5,6,0},d_{5,7,4},d_{6,7,1},\eta_{18}(r_1)$	s_0,δ_1,A_{55}	s_0,δ_1,A_{66}	d_{112}

Table 2(continued) steps of the second circulation of the clustering

membrane number	0	5	6	$n+1$
t_8:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{23}(r_2)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_9:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{23}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
...				
t_{14}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{28}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{15}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{34}(r_2)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{16}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{35}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{17}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{36}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{18}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{37}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{19}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{38}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{20}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{45}(r_2)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{21}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{46}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{22}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{47}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{23}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{48}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{24}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, \eta_{56}(r_2)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}

Table 2(continued) steps of the second circulation of the clustering

membrane number	0	5	6	$n+1$
t_{25}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1},$ $d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,4}, d_{6,7,1}, \eta_{57}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{26}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1},$ $d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,5}, d_{6,7,1}, \eta_{58}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{27}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1},$ $d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,5}, d_{6,7,1}, \eta_{67}(r_2)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{28}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1},$ $d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,5}, d_{6,7,2}, \eta_{68}(r_1)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{29}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1},$ $d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,5}, d_{6,7,2}, \eta_{78}(r_2)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{30}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-1}, d_{1,3,2}, d_{1,4,13}, d_{1,5,10}, d_{1,6,13}, d_{1,7,25}, d_{-1,-1,-1}, d_{-1,-1,-1},$ $d_{-1,-1,-1}, d_{-1,-1,-1}, d_{-1,-1,-1}, d_{3,4,5}, d_{3,5,4}, d_{3,6,5}, d_{3,7,13}, d_{4,5,5}, d_{4,6,2}, d_{4,7,4}, d_{5,6,1}, d_{5,7,5}, d_{6,7,2}(r_3)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{31}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}(r_7)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{32}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{66}, A_{77}, \alpha_2, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}(r_7)$	s_0, δ_1, A_{55}	s_0, δ_1, A_{66}	d_{112}
t_{33}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{5,6,0}, d_{5,7,4}, d_{6,7,1}, b_{56}(r_4)$	$s_0, \delta_1, A_{55}, a_6, \alpha_2$	$\times$	d_{112}, d_{256}
t_{34}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}, b_{56}(r_5)$	$s_0, \delta_2, A_{55}, a_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}
t_{35}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}(r_6)$	$s_0, \delta_3, A_{55}, a_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}
t_{36}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \delta_4, A_{55}, a_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}
t_{37}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2},$ $d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \delta_5, A_{55}, a_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}

Table 2(continued) steps of the second circulation of the clustering

membrane number	0	5	6	$n+1$
t_{38}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \delta_6, A_{55}, a_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}
t_{39}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \zeta_6, A_{55}, O_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}
t_{40}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \zeta_6, A_{55}, a_6, \alpha_2(r_3')$	$\times$	d_{112}, d_{256}
t_{41}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \delta_7, A_{55}, a_6, \alpha_2(r_5')$	$\times$	d_{112}, d_{256}
t_{42}:	$A_{11}, A_{33}, A_{44}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}$	$s_0, \delta_8, A_{55}, a_6, \alpha_2(r_1')$	$\times$	d_{112}, d_{256}
t_{43}:	$A_{11}, A_{33}, A_{44}, A_{55}, A_{77}, d_{-1,-1,-2}, d_{1,3,1}, d_{1,4,12}, d_{1,5,9}, d_{1,6,12}, d_{1,7,24}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{-1,-1,-2}, d_{3,4,4}, d_{3,5,3}, d_{3,6,4}, d_{3,7,12}, d_{4,5,4}, d_{4,6,1}, d_{4,7,3}, d_{-1,-1,-1}, d_{5,7,4}, d_{-1,-1,-1}, \eta_{11}, \alpha_3$	$s_0, \delta_1, A_{55}, a_6, \alpha_2(r_6')$	$\times$	d_{112}, d_{256}

4 Conclusion

This paper improves the hierarchical algorithm and constructs a P system to realize it. This algorithm is suitable for cluster analysis by example test, but it needs to be further studied whether it is suitable for cluster analysis of large amount of data. Speaking from a theoretical point of view, the P system has great parallelism. So it can reduce the time complexity of computing and increases the computational efficiency. The following research work will focus on the theoretically analyze of the algorithm's time complexity. Additionally, membrane computing is a new biological computing method. Now its theoretical research is mature, but its application is not particularly extensive. A lot of applications will emerge in various fields in the future. The application in cluster proposed in this paper is one example. There are many clustering method and this paper only use the hierarchical algorithm. Membrane computing can be applied to a variety of other clustering methods.

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