HIERARCHICAL CLUSTERING 
WITH MEMBRANE COMPUTING

Mónica CARDONA, M. Angels COLOMER, Alba ZARAGOZA

Department of Mathematics
University of Lleida
Av. Alcalde Rovira Roure, 191. 25198 Lleida, Spain
e-mail: {colomer, alba, mcardona}@matematica.udl.es

Mario J. PéREZ-JIMÉNEZ

Research Group on Natural Computing
Department of Computer Science and Artificial Intelligence
University of Sevilla
Avda. Reina Mercedes s/n, 41012 Sevilla, Spain
e-mail: marper@us.es

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Abstract. In this paper we approach the problem of hierarchical clustering through membrane computing. A specific P system with external output is designed for each Boolean matrix associated with a finite set of individuals. The computation of the system allows us to obtain one of the possible classifications in a non-deterministic way. The amount of resources required in the construction is polynomial in the number of individuals and of characteristics analyzed.

Keywords: P systems, hierarchical clustering

1 INTRODUCTION

Many scientific investigations depend on many factors and this makes such investigations very complex. In order to simplify the problems and make them more
tractable it is necessary to group individuals with similar characteristics. The individuals are characterized by a high number of properties so the clustering according to their degree of similarity is not a simple task.

There are different methods of ranking the groups of individuals. We mention two types only here, the non-hierarchical and the hierarchical clustering. In non-hierarchical clustering homogenous groups are formed without establishing relations among them; in hierarchical clustering the individuals are grouped in levels. The inferior levels are contained in the superior levels. Hierarchical clustering is mostly used and it is dealt with in this paper.

Hierarchical clustering refers to the formation of a recursive clustering of the individuals by means of the partitions \( P_0, P_1, \ldots, P_m \) of the set of \( N \) individuals with \( 1 \leq m \leq N - 1 \). The partition \( P_0 \) consists of \( N \) groups, each one of them formed by a single individual. The groups that form this partition join progressively until arriving at the last partition, \( P_m \), that consists of a single group formed by all the individuals. In each step two most similar groups are joined according to a previously established criterion.

Researchers use clustering to characterize and to order a vast amount of information about variability of population of individuals. These populations are grouped in more or less homogenous clusters based on their properties. This methodology has been applied in fields as diverse as medicine, biology, classification of words and of fingerprints, artificial intelligence, etc. Recently clustering has been applied to the classification of musical genre \[13\], to predict essential hypertension \[12\], in the classification of material planning and control systems \[9\], of the ocean color \[1\], of the plants gens \[14\].

The different groups obtained by means of the classification are characterized by different levels of the measured variables. These values allow us to give common properties of the individuals belonging to the same group. The fact of having established groups allows us to identify the most similar cluster of a new individual. The characteristics measured of the individuals can be qualitative or quantitative variables. In most cases we are only interested in the presence or absence of certain qualitative characteristics. Thus, in this paper we consider the hierarchical clustering using dichotomizing variables, and this problem is approached within the framework of cellular computing with membranes. This approach is interesting because it allows us to treat some statistical topics within this new model of computation. The amount of used resources is polynomial in the number of individuals and the number of characteristics analyzed.

In the following, we assume that the reader is familiar with the basic notions of membrane computing; for details, refer to \[6, 7, 8, 15\].

### 2 HIERARCHICAL CLUSTERING

In order to obtain a hierarchical clustering we firstly need a set of individuals or observations.
Definition 1. A $k$-set over a metric space $(E, d)$, with $d(E \times E) \subseteq \mathbb{N}$ is a subset of $E^k$.

The elements of a finite $k$-set, $\Omega = \{\omega_1, \ldots, \omega_N\}$, are called individuals. The components of the individual $\omega_i$ (called characteristics or variables) is denoted by $\omega_{i1}, \ldots, \omega_{ik}$. Thus, the set of the individuals can be represented by the matrix $P_{Nk} = (\omega_{ij})_{1 \leq i \leq N, 1 \leq j \leq k}$.

The objective of clustering is to gather the individuals in similar groups whose members are all close to each other with various dimensions being measured. It will be necessary to establish criteria in order to measure the similarity between individuals and between groups. Obviously, the clustering that is obtained will depend on the similarity function that is chosen [10].

Definition 2. A similarity over a finite $k$–set, $\Omega = \{\omega_1, \ldots, \omega_N\}$, is a function $s$ of $\Omega \times \Omega$ in $\mathbb{R}^+$ that verifies

- $s$ is symmetric, that is $\forall (\omega_i, \omega_j) \in \Omega \times \Omega : s(\omega_i, \omega_j) = s(\omega_j, \omega_i)$
- $\forall \omega_i, \omega_j \in \Omega$ with $i \neq j : s(\omega_i, \omega_i) = s(\omega_j, \omega_j) \geq s(\omega_i, \omega_j)$.

In this paper we work with dichotomizing variables; their values are denoted by 0 and 1. One of the similarities most used for dichotomizing variables is that proposed by Sokal and Michener [2] and it is defined by:

$$s'(\omega_i, \omega_j) = \frac{1}{k} \cdot \sum_{r=1}^{k} (1 - |\omega_{ir} - \omega_{jr}|), \text{ for each } (\omega_i, \omega_j) \in \Omega \times \Omega. \quad (1)$$

In this paper the similarity that we use is a modification of the previous one. It represents the number of coincidences in the number of total characteristics and it is defined as follows:

$$s(\omega_i, \omega_j) = \sum_{r=1}^{k} (1 - |\omega_{ir} - \omega_{jr}|), \text{ for each } (\omega_i, \omega_j) \in \Omega \times \Omega. \quad (2)$$

We use this similarity because it is easier to implement with P systems and the result obtained is the same as those obtained with the similarity of Sokal and Michener.

In the case of the hierarchical clustering the groupings follow a hierarchy formed by partitions $P_0, P_1, \ldots, P_m$ that are called clusterings, and verify

$$P_0 \subseteq P_1 \subseteq P_2 \subseteq \ldots \subseteq P_m$$

with $1 \leq m \leq N - 1$. The sets that belong to the partitions are called clusters. The clusterings are constructed in a recursive manner. $P_0$ is formed by as many clusters as individuals. The following partitions are obtained by joining the two closest clusters belonging in the previous one. This process is done until we obtain a partition, $P_m$, with a single set formed by all the individuals.
Next we define the necessary mathematical concepts in the hierarchical clustering [11].

**Definition 3.** Let $\Omega = \{\omega_1, \ldots, \omega_N\}$ the $k$-set of $N$ individuals. A subset $H$ of the power set $\mathcal{P}(\Omega)$, is a hierarchy over $\Omega$ if it verifies:

- $\Omega \in H$
- $\{\omega\} \in H$ $(\forall \omega \in \Omega)$
- $\text{If } h \cap h' \neq \emptyset \Rightarrow h \subseteq h' \text{ or } h' \subseteq h$ $(\forall h, h' \in H)$
- $\bigcup\{h' \mid h' \in H, \; h' \subset h\} \in \{h, \emptyset\}$ $(\forall h \in H)$.

The elements of $H$ are called clusters. If $h_1, \ldots, h_p \in H$ with $\Omega = h_1 \cup \ldots \cup h_p$, then the set $\{h_1, \ldots, h_p\}$ is a clustering.

In order to construct a hierarchy it is necessary to have a similarity between individuals and another function that measures the similarity between clusters. The second function is called the aggregation index.

**Definition 4.** A symmetrical and nonnegative application $\delta$ from $\mathcal{P}(\Omega) \times \mathcal{P}(\Omega)$ to $\mathbb{R}$ is called an aggregation index between clusters if:

- $\delta(h_1, h_2) \geq 0$, for each $h_1, h_2 \in \mathcal{P}(\Omega)$.
- $\delta(h_1, h_2) = \delta(h_2, h_1)$, for each $h_1, h_2 \in \mathcal{P}(\Omega)$.

There are several aggregation indices [4] that depend on the similarity $s$ chosen. In this paper we use the aggregation index based on the minimum [5], defined by:

$$\delta(h_1, h_2) = \min\{s(\omega_i, \omega_j) \mid \omega_i \in h_1, \; \omega_j \in h_2\} \quad (3)$$

A hierarchy has associated an index that measures the homogeneity degree between the individuals belonging to the same cluster, and it is called hierarchical index. This index is always obtained by means of the aggregation index. In this paper we define the hierarchical index of a new cluster $h$ obtained from the union of two clusters $h = h_1 \cup h_2$, by means of $f(h) = \delta(h_1, h_2)$.

2.1 An Algorithm for the Construction of a Hierarchy

The algorithms that are used to obtain a hierarchy have the same structure, the only differences are the way to compute the similarities between individuals and the aggregation index between clusters [3].

In this paper we consider an algorithm whose input is a finite $k$-set $\Omega$, the similarity $s$, and the aggregation index $\delta$. The output is an indexed hierarchy $(H, f)$.

1. Place each individual of $\Omega$ in its own cluster (singleton), creating the list of clusters $L = P_0 = \{S_1 = \{\omega_1\}, S_2 = \{\omega_2\}, \ldots, S_N = \{\omega_N\}\}$. In this moment $\delta(S_i, S_j) = s(\omega_i, \omega_j)$, and $f(S_i) = k$ $(1 \leq i < j \leq N)$. 
2. Find the two closest clusters \( S_i, S_j \) \((1 \leq i < j \leq N)\), which will form a new class \( S_i = S_i \cup S_j \).
3. Remove \( S_j \) from \( L \).
4. Compute the aggregation index between all the pair of clusters in \( L \) by using equation (3).
5. Go to step 2 until there is only one set remaining.

**Remark 1.** If at step 2 there are more than one possibility, then one of them is chosen at random. So, the hierarchy obtained is not unique.

### 3 Hierarchical Clustering by Means of Membrane Computing

#### 3.1 Designing a P System

The goal of this paper is to obtain one hierarchical clustering of a finite \( k \)-set \( \Omega \), of \( N \) different individuals by using P systems. Each individual \( \omega_i \in \Omega \subseteq \{0, 1\}^k \) is denoted by \( \omega_i = (\omega_{i1}, \omega_{i2}, \ldots, \omega_{ik}) \), and we consider the similarity between individuals defined by (2).

Let \( P_{Nk} = (\omega_{ij})_{1 \leq i \leq N, 1 \leq j \leq k} \) be the matrix associated with the \( N \) individuals to classify. We define the P system of degree \( N \) with external output,

\[
\Pi(P_{Nk}) = (\Gamma(P_{Nk}), \mu(P_{Nk}), \mathcal{M}_1, \mathcal{M}_2, \ldots, \mathcal{M}_{N-1}, \mathcal{M}_N, R, \rho)
\]

associated with the matrix \( P_{Nk} \), as follows:

- **Working alphabet:**
  \[
  \Gamma(P_{Nk}) = \{e_{js}, d_{js} : 1 \leq j \leq N, 1 \leq s \leq k\} \cup \{a_s, b_s : 1 \leq s \leq k\} \cup \\
  \{S_{ij}, C_{ij} : 1 \leq i < j \leq N\} \cup \{\beta_i : 0 \leq i \leq k - 2\} \cup \\
  \{\alpha_{ijt}, X_{ijt} : 1 \leq i < j \leq N, 1 \leq t \leq k - 1\} \cup \{\gamma_i : 1 \leq i \leq N\} \cup \\
  \{\epsilon_i : 0 \leq i \leq 3k - 2\} \cup \{\eta_i : 0 \leq i \leq (N - 1)(3k - 1)\} \cup \{\sharp\}
  \]

- **Membrane structure:** \( \mu(P_{Nk}) = [N \ [1 \ [2 \ \ldots \ [N-1 \ ]N-1 \ ]].N \)

- **Initial multiset:**
  \[
  \mathcal{M}_i = \{a_s^{(N-1)\omega_{is}} : 1 \leq s \leq k \land 1 \leq i \leq N - 1\} \cup \\
  \{b_s^{(N-i)(1-\omega_{is})} : 1 \leq s \leq k \land 1 \leq i \leq N - 1\} \cup \\
  \{c_{js}^{\omega_{js}} : 1 \leq s \leq k \land i \leq j \leq N\} \cup \\
  \{d_{js}^{(1-\omega_{js})} : 1 \leq s \leq k \land i \leq j \leq N\} ; \quad 1 \leq i \leq N - 1
  \]

\[
\mathcal{M}_N = \{\gamma_N, \epsilon_0, \eta_0\} ;
\]
The set $R$ consists of the following rules:

- Rules in the skin membrane:

$$ r_0 = \{ \epsilon_0 \rightarrow \epsilon_1 \beta_0 \} \cup \{ \epsilon_i \rightarrow \epsilon_{i+1} : 1 \leq i \leq 3k-2 \land i \neq k \} \cup $$

$$ \{ \eta_i \rightarrow \eta_{i+1} : 0 \leq i \leq (N-1)(3k-1) - 1 \} \cup $$

$$ r_u = \{ \beta_{u-1} S^k\alpha \rightarrow \alpha_{\epsilon i (k-u)} : 1 \leq i < j \leq N \} \quad 1 \leq u \leq k-1 $$

$$ r'_{u} = \{ \beta_{u-1} \rightarrow \beta_{u} \} \quad 1 \leq u \leq k-1 $$

$$ r'_{k-1} = \{ \eta(N-1)(3k-1) \rightarrow (\epsilon, \text{out}) \} $$

$$ r_k = \{ \epsilon_i \gamma i \rightarrow \epsilon_{k+1} X_{ij}^{q-2} \gamma N (X_{ij}, \text{out}) : 2 \leq q \leq N, $$

$$ 1 \leq i < j \leq N, 1 \leq t \leq k-1 \} $$

$$ r'_k = \{ \epsilon_k \rightarrow \epsilon_{k+1} \} $$

$$ r_{k+1} = \{ X_{ij} S_p \rightarrow C_p X_{ij} : 1 \leq i < j \leq N, 1 \leq t \leq k-1 \} \cup $$

$$ \{ X_{ij} S_p \rightarrow C_p X_{ij} : 1 \leq i < j \leq N, 1 \leq t \leq k-1 \} \cup $$

$$ \{ X_{ij} S_p \rightarrow C_p X_{ij} : 1 \leq i < j \leq N, 1 \leq t \leq k-1 \} \cup $$

$$ r_{k+2} = \{ C_{ij} \rightarrow S_{ij} : 1 \leq i < j \leq N \} \cup $$

$$ \{ \epsilon_{k-1} X_{ij}^{q-2} \gamma N \rightarrow \epsilon_1 \beta_0 \gamma N : 1 \leq i < j \leq N, 1 \leq t \leq k-1 \} $$

$$ r'_{k+3} = \{ \epsilon_{k-1} \rightarrow \epsilon_1 \beta_0 \} $$

- Rules in the membrane labelled by $i \{ 1 \leq i \leq N-1 \}$:

$$ r_{k+4} = \{ a_s \epsilon_{js} \rightarrow (S_{ij}, \text{out}) : 1 \leq s \leq k, i + 1 \leq j \leq N \} $$

$$ r_{k+5} = \{ b_s d_{js} \rightarrow (S_{ij}, \text{out}) : 1 \leq s \leq k, i + 1 \leq j \leq N \} $$

- The partial order relation $\rho$ over $R$ consists of the following:

  - Priority relation in the membrane labelled by $i \{ 1 \leq i \leq N-1 \}$: $\rho_i = \emptyset$

  - Priority relation in the skin membrane:

$$ \rho_N = \{ r_1 > r'_1 > r_2 > r'_2 > \ldots > r_{k-1} > r'_{k-1} \} \cup \{ r_k > r'_k \} \cup $$

$$ \{ r_{k+1} > r_{k+2} > r_{k+3} > r'_{k+3} \} $$

### 3.2 An Overview of Computations

At the beginning of a computation the membrane labelled by $i \{ 1 \leq i \leq N-1 \}$ contains the objects $a_s, b_s, e_{js}, d_{js}$ ($1 \leq s \leq k$ and $i + 1 \leq j \leq N$). In this membrane the presence or absence of the objects $a_s, b_s$ (or $e_{js}, d_{js}$) encodes the values (0/1) of the individual $\omega_i$ (or components of the individuals $\omega_j$).

Initially, the skin membrane contains the objects $\gamma_N, \epsilon_0$ and $\eta_0$. The evolution of the object $\gamma_N$ allows us to know the number of clusters in all configurations of the
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P system: when the object $\gamma_i$ appears, then the individuals are grouped in $i$ clusters. We use the object $\epsilon_0$ in order to synchronize the loop in $3k - 1$ steps, and this allows us to join two clusters with maximum similarity. The object $\eta_0$ is a counter used to stop the P system in the configuration $(3k - 1)(N - 1)$ sending the object $\sharp$ to the environment.

In the initial configuration the only rules that can be applied in membrane $i$ ($1 \leq i \leq N - 1$) are the rules of the type $r_{k+4}$, $r_{k+5}$ that send the objects $S_{ij}(1 \leq i < j \leq N)$ to the skin membrane. The multiplicity of these objects allows us to know the similarity between individuals of the set $\Omega$. In the skin membrane, the rule $r_0$ produces the objects $\epsilon_1$, $\beta_0$.

After this configuration the computation of the P system is structured into loops with $3k - 1$ steps, each one formed by two stages. The first one takes $k$ steps and it begins with the object $\beta_0$. In these steps the object $S_{ij}$ with maximum multiplicity, $t$, is selected. In the $k$-th step of the loop the rule $r_k$ creates the objects $X_{ijt}$ in the skin membrane and sends a copy to the environment, and the object $\gamma_q$ is transformed in the object $\gamma_{q-1}$, encoding the fact that two clusters have been joined.

The second stage lasts $2k - 1$ steps. In the skin membrane there are the objects $X_{ijt}$ meaning that a new cluster labelled by $i$ is constructed by the union of the previous clusters $i, j$. The rules $r_{k+1}, r_{k+2}, r_{k+3}$ compute the similarities between new cluster $i$ and the other clusters, and this information is encoded by the multiplicity of the objects $S_{ip}$ ($1 \leq p \leq N, p \neq i$).

In the $(3k - 1)$-th step of the loop, the rule $r_{k+3}$ transforms the object $\epsilon_{3k-1}$ in $\beta_0$ and $\epsilon_1$ that allow us to go to the top of the loop.

The first partition consist of $N$ singletons, and in each loop two clusters are joined. So, $N-1$ loops are necessary to obtain the last partition (a cluster containing all $N$ individuals). For that, the loop is repeated $N-1$ times and the rule $r'_{k-1}$ is applied in the last step of any computation.

3.3 Formal Verification

In this section we show that the P system $\Pi(P_{Nk})$ is non-deterministic, and any computation we will provide a solution of the clustering problem.

First of all, let us list the necessary resources to construct the P system $\Pi(P_{Nk})$ from the matrix $P_{Nk}$.

- Size of the alphabet: $\Theta(N^2 \cdot k)$.
- Sum of the sizes of initial multisets: $\Theta(N \cdot k)$.
- Maximum of rules’ lengths: $\Theta(N)$.
- Number of rules: $\Theta(k \cdot N^3)$.
- Number of priority relations: $\Theta(k^2 \cdot N^6)$.
- Cost of time: $\Theta(N \cdot k)$.

Bearing in mind the recursive description of the rules and that the amount of resources is polynomial in $N, k$, it is possible to construct the system $\Pi(P_{Nk})$ from
the matrix $P_{Nk}$ by means of a deterministic Turing machine working in polynomial time.

Given a computation $C$ of the P system $Π(P_{Nk})$, for each $p ∈ N$ we denote by $C_p$ the configuration of the P system obtained after the execution of $p$ steps. For each membrane $l ∈ \{1, 2, \ldots, N\}$, we denote by $C_p(l)$ the multiset of objects contained in the membrane labelled by $l$ in $C_p$.

In what follows, $C$ will denote an arbitrary computation of the P system $Π(P_{Nk})$.

First, we show that in the configuration $C_1$, the multiplicity of the object $S_{ij}$ ($1 ≤ i < j ≤ N$) represents the similarity between the individuals $ω_i$ and $ω_j$.

**Proposition 1.** For every $i, j, t$ ($1 ≤ i < j ≤ N$, $1 ≤ t ≤ k - 1$), we denote $t_{ij}^{(1)} = \max \{ t : S_{ij}' \in C_t(N) \}$. Then, $t_{ij}^{(1)} = \sum_{s=1}^{k}(1 - |ω_{is} - ω_{js}|)$.

**Proof.** For every $i$ ($1 ≤ i ≤ N - 1$) we have:

$$C_0(i) = \left\{ a_s^{(N-i)}ω_{is}, b_s^{(N-i)(1-ω_{is})}, e_j^{ω_{js}}, d_j^{(1-ω_{js})} | i ≤ j ≤ N, ω_{is} ∈ \{0, 1\} \right\}.$$

Then, the only rules that can be applied are $r_{k+4}$ and $r_{k+5}$. The rule $r_{k+4}$ (or $r_{k+5}$) is only possible to apply when the component $s$ of the individuals $ω_i$ and $ω_j$ is equal to 1 (or to 0).

Whenever one of these rules is applied, the object $S_{ij}$ is sent to the skin membrane. Then, the multiplicity of the objects $S_{ij}$ in $C_1(N)$ will coincide with the number of equal components between the individuals $ω_i$ and $ω_j$. That is, $t_{ij}^{(1)} = \sum_{s=1}^{k}(1 - |ω_{is} - ω_{js}|)$. □

From now on, we denote by $t_{ij}^{(n)} = \max \{ t : S_{ij}' \in C_{1+(n-1)(3k-1)}(N) \}$ the maximum multiplicity of the objects $S_{ij}$ in the first step of the $n$-th loop of the computation.

**Proposition 2.** For each $n$ ($0 ≤ n ≤ N - 2$), we have:

a) $β_0 \in C_{1+n(3k-1)}(N)$.

b) If $1 ≤ j ≤ 3k - 1$, then $ε_j \in C_{1+n(3k-1)+(j-1)}(N)$.

**Proof.** We prove this proposition by induction on $n$.

- As $ε_0 \in C_0(N)$ we can apply one of the rules $r_0$ producing the objects $ε_1, β_0 \in C_1(N)$. In the following $k - 1$ steps the rules $r_0$ will be applied producing the object $ε_k \in C_k(N)$. If $α_{ijt}, γ_q \in C_k(N)$, then the rule $r_k$ (or the rule $r_k'$) will be applied. In both cases we obtain that $ε_{k+1} \in C_{k+1}(N)$. In successive configurations the rule $r_0$ transforms the objects $ε_j \in C_j(N), (k+1 ≤ j ≤ 3k-2)$ until we obtain the object $ε_{3k-1} \in C_{3k-1}(N)$.

- Let us suppose the hypothesis holds for $0 ≤ n < N - 2$. Then, $ε_{3k-1} \in C_{1+n(3k-1)+(3k-1-1)}(N) = C_{(n+1)(3k-1)}(N)$. If there is some object $X_{ijt}$ in that configuration, then the rules from $r_{k+3}$ will be applied, and in the opposite case,
the rule \( r'_{k+3} \) will be applied. In both cases the object \( \epsilon_{3k-1} \) is transformed in \( \epsilon_1 \), \( \beta_0 \in C_{1+(n+1)(3k-1)}(N) \). Applying \( k - 1 \) times the rules from \( r_0 \) we obtain that \( \epsilon_j \in C_{1+(n+1)(3k-1)+(j-1)}(N) \) (\( 1 \leq j \leq k \)). In \( C_{1+(n+1)(3k-1)+(k-1)}(N) \) the object \( \epsilon_k \) produces \( \epsilon_{k+1} \in C_{1+(n+1)(3k-1)+k}(N) \) by means of one rule from \( r_k \) or \( r'_k \). Then, applying the rules from \( r_0 \) successively we obtain that \( \epsilon_j \in C_{1+(n+1)(3k-1)+(j-1)}(N) \) (\( k + 1 \leq j \leq 3k - 1 \)).

**Corollary 1.** The objects \( X_{ijt} \) only can be sent to the environment at the moments \( 1 + n(3k - 1) + k \) (\( 0 \leq n \leq N - 2 \)).

**Proof.** The rule \( r_k \) is the only one that sends objects \( X_{ijt} \) to the environment, and from Proposition 2 we have \( \epsilon_k \in C_{1+n(3k-1)+k-1}(N) \) (\( 0 \leq n \leq N - 2 \)).

**Corollary 2.** There exists \( n \) (\( 0 \leq n \leq N - 2 \)) and there are objects \( X_{ijt} \) such that \( X_{ijt} \in C_{1+n(3k-1)+k}(N) \).

**Proposition 3.** The configuration \( C_{(N-1)(3k-1)} \) sends the halting object \( \sharp \) to the environment.

**Proof.** Applying \( (N - 1)(3k - 1) \) times the rules from \( r_0 \), the object \( \eta_0 \in C_0(N) \) produces \( \eta_{(N-1)(3k-1)} \in C_{(N-1)(3k-1)}(N) \). In this configuration the rule \( r'_{k-1} \) sends the halting object \( \sharp \) to the environment.

Next, we show that it is only possible to modify the environment in the \( k \)th step of the loop.

**Corollary 3.** For every \( n \) (\( 0 \leq n \leq N - 2 \)) the following assertions hold:

a) For every \( r \), \((1 + n(3k - 1) < r < 1 + n(3k - 1) + k) \) we have:

\[
C_r(env) = C_{1+n(3k-1)}(env).
\]

b) For every \( r \), \((1 + n(3k - 1) + k < r < 1 + n(3k - 1) + 3k - 1) \) we have:

\[
C_r(env) = C_{1+n(3k-1)+k}(env).
\]

**Proof.** The rule \( r_k \) is the only one sending objects to the environment before the halting configuration. From Corollary 1 we have \( X_{ijt} \in C_{1+n(3k-1)+k}(env) \). Thus, for every \( r \) \((1 + n(3k - 1) < r < 1 + n(3k - 1) + k) \) we have \( C_r(env) = C_{1+n(3k-1)}(env) \), and for every \( r \) \((1 + n(3k - 1) + k < r < 1 + n(3k - 1) + 3k - 1) \) we have \( C_r(env) = C_{1+n(3k-1)+k}(env) \).

In the following, we will show that in each loop one object \( X_{ijt} \) is sent to the environment and eventually there exists a loop which sends no object \( X_{ijt} \) to the environment. In this case, in next loops no further objects are sent to the environment.

Firstly we prove that if in the \( k \)-th step of the loop the rule \( r_k \) is not applicable, then also it is not applicable in the next loop.
**Proposition 4.** For every \( n \) (\( 0 \leq n \leq N - 2 \)) if the rule \( r_k \) cannot be applied in \( C_{1+n(3k-1)+k-1} \), then it cannot be applied in \( C_{1+(n+1)(3k-1)+k-1} \).

**Proof.** According to Proposition 2, for each \( n \) (\( 0 \leq n \leq N - 2 \)) we have \( \epsilon_k \in C_{1+n(3k-1)+k-1}(N) \). The objects \( \gamma_q \) always appear in the skin membrane. As the rule \( r_k \) is not applicable in \( C_{1+n(3k-1)+k-1} \), we have \( \alpha_{ij,t} \notin C_{1+n(3k-1)+k-1}(N) \).

Having in mind that objects \( \beta_u \) appear in \( C_{1+n(3k-1)+k+u}(N) \) (\( 1 \leq u \leq k - 1 \)) we deduce that \( S_{ij} \notin C_{1+n(3k-1)+u}(N) \). Hence the rule \( r_k \) cannot be applied to the configuration \( C_{1+n(3k-1)+k} \).

From step \( 1 + n(3k - 1) + k - 1 \) to step \( 1 + (n + 1)(3k - 1) + k - 1 \), any object \( S_{ij} \) is produced. Then, the rule \( r_k \) is not applicable to \( C_{1+(n+1)(3k-1)+k-1} \).

**Corollary 4.** Let \( n \) be such that \( 0 \leq n \leq N - 2 \). If \( C_{1+n(3k-1)+k(\text{env})} \) is equal to \( C_{1+(n+1)(3k-1)+k(\text{env})} \), then for each \( n' \) (\( n \leq n' \leq N - 2 \)) we have

\[
C_{1+n(3k-1)+k(\text{env})} = C_{1+n'(3k-1)+k(\text{env})}.
\]

**Corollary 5.** For each computation \( C \) there exists an unique \( \nu_C \) (\( 1 \leq \nu_C \leq N - 2 \)) such that the rule \( r_k \) is applicable to \( C_{1+(\nu_C-1)(3k-1)+k-1} \), but it is not applicable to \( C_{1+\nu_C(3k-1)+k-1} \).

**Proof.** It follows from Corollary 2, Proposition 4, and Corollary 4.

The following result allows us to give a meaning to the value \( t \) associated with the object \( X_{ij,t} \).

**Proposition 5.** Let \( X_{i_{n,j_{n}}t_{i_{n,j_{n}}}^{(n)}} \) be the object that is sent to the environment by applying the rule \( r_k \) to the configuration \( C_{(k+1)+n(3k-1)-1} \). Then, we have

\[
t_{i_{n,j_{n}}}^{(n)} = \max \{ t \mid S_{ij}^t \in C_{1+n(3k-1)}(N), \ 1 \leq i < j \leq N \}.
\]

**Proof.** As the rule \( r_k \) is applicable to \( C_{(k+1)+n(3k-1)-1} \), we have the object \( \alpha_{i_{n,j_{n}}t_{i_{n,j_{n}}}^{(n)}} \) belongs to \( C_{(k+1)+n(3k-1)-1} \). That object is obtained from the application of one of the rules \( r_{k-\ell}^{(n)} \) over the object \( S_{ij}^{t_{i_{n,j_{n}}}^{(n)}} \), where \( t_{i_{n,j_{n}}}^{(n)} \) is the maximum of the multiplicities of the objects \( S_{ij} \). If there exists \( t' > t_{i_{n,j_{n}}}^{(n)} \) such that \( S_{ij}^{t'} \in C_{1+n(3k-1)}(N) \), then rules from \( r_{k-t'} \) have been applied. So, rules from \( r_{k-t_{i_{n,j_{n}}}^{(n)}} \) will not be applicable.

Next, we show that the maximum multiplicity of the objects \( S_{ij} \) belonging to the skin membrane in any loop \( n \) is always greater than or equal to the multiplicity of the objects \( S_{ij} \) of the following loop \( n + 1 \).

**Proposition 6.** Let \( w_n = \max \{ t : S_{ij}^t \in C_{1+n(3k-1)}(N), 1 \leq i < j \leq N \} \), with \( 0 \leq n \leq N - 2 \). Then \( w_n \geq w_{n+1} \), for each \( n \).
Proposition 8. Let us suppose that $X_{i_1j_1}^{(1)}, \ldots, X_{i_nj_n}^{(n)} \in C_{1+n(3k-1)}(\text{env})$ with $1 \leq n \leq \nu_C$, and $t_{ij}^{(n)} = \max \{ t : S_{ij}^t \in C_{1+n(3k-1)}(\text{N}) \}$. Then,
• If $i_n \notin \{i, j\}$, then $t^{(n+1)}_{ij} = t^{(n)}_{ij}$.
• If $1 \leq i_n < j_n < p \leq N$, then $t^{(n+1)}_{i_n p} = \min \{t^{(n)}_{i_n p}, t^{(n)}_{j_n p}\}$.
• If $1 \leq i_n < p < j_n \leq N$, then $t^{(n+1)}_{i_n p} = \min \{t^{(n)}_{i_n p}, t^{(n)}_{j_n p}\}$.
• If $1 \leq p < i_n < j_n \leq N$, then $t^{(n+1)}_{p i_n} = \min \{t^{(n)}_{p i_n}, t^{(n)}_{p j_n}\}$.

Proof. The pairs $(S_{i_n p}, S_{j_n p}), (S_{i_n p}, S_{p j_n}), (S_{p i_n}, S_{p j_n})$ are transformed in the objects $C_{i_n p}, C_{j_n p}, C_{p i_n}, C_{p j_n}$, respectively, by applying the rule $r_{k+1}$ to $C_{k+(n-1)(3k-1)}$. After that, the rule $r_{k+2}$ removes the objects $S_{i_n p}, S_{j_n p}, S_{p i_n}, S_{p j_n}$. Thus, the multiplicity of the objects $C_{i_n p}, C_{j_n p}, C_{p i_n}, C_{p j_n}$ is equal to $\min \{t^{(n)}_{i_n p}, t^{(n)}_{j_n p}\}, \min \{t^{(n)}_{i_n p}, t^{(n)}_{j_n p}\}$, and $\min \{t^{(n)}_{p i_n}, t^{(n)}_{p j_n}\}$, respectively. Finally, we note that the objects $S_{i j}$ are produced from the objects $C_{i j}$ by applying the rule $r_{k+3}$. 

Let us consider a $C$ a computation of the P system $\Pi(P_{N k})$. We recursively construct a sequence of partitions $\Delta^c_0, \Delta^c_1, \ldots, \Delta^c_{N_c}$ of the set of the individuals, as follows:

• $\Delta^c_0 = \{B^0_{q^0_0}, \ldots, B^0_{q^0_N}\}$ with $q^0_0 = i$ and $B^0_i = \{\omega_i\} \equiv \{i\} \ (1 \leq i \leq N)$.
• The partition $\Delta^c_1$ is constructed from the object $X_{i_1 j_1 t^{(1)}_{i_1 j_1}} \in C_{k+1}($env$)$ with $1 \leq i_1 < j_1 \leq N$, as follows:
  - We have $\{i_1, j_1\} \subseteq \{q^1_0, \ldots, q^1_N\}$. If $i_1 = q^u_s$ and $j_1 = q^v_s$, with $1 \leq u < s \leq N$, then the new cluster is $B^1_{q^u_0} = B^0_{q^u_0} \cup B^0_{q^v_0}$ with $q^1_0 = q^0_s, B^0_{q^v_0} \notin \Delta^c_1$, and $B^1_l = B^0_l$ for $l \in \{q^1_0, \ldots, q^1_N\} - \{q^0_u, q^0_v\}$.

Then $\Delta^c_1 = \{B^1_{q^1_0}, \ldots, B^1_{q^1_{N-1}}\}$.

• We construct $\Delta^c_{n+1}$ from $\Delta^c_n = \{B^0_{q^u_n}, \ldots, B^0_{q^v_n}\}$ and $X_{i_{n+1} j_{n+1} t^{(n+1)}_{i_{n+1} j_{n+1}}}$, as follows:
  - From Proposition 7, we deduce that $\{i_{n+1}, j_{n+1}\} \subseteq \{q^1_n, \ldots, q^{N-n}_n\}$. If $i_{n+1} = q^u_n$ and $j_{n+1} = q^v_n$, with $1 \leq u < s \leq N$, then the new cluster is $B^1_{q^u_n} = B^0_{q^u_n} \cup B^0_{q^v_n}$ with $q^1_n = q^1_s, B^0_{q^v_n} \notin \Delta^c_{n+1}$, and $B^1_l = B^1_l$ for $l \in \{q^1_n, \ldots, q^{N-n}_n\} - \{q^1_n, q^1_s\}$.

Then $\Delta^c_{n+1} = \{B^1_{q^1_n}, \ldots, B^1_{q^{N-n+1}_n}\}$.

Next, we show that $t^{(n)}_{i j}$ is the aggregation index between clusters.
Theorem 1. For every \( i, j, n \) (\( 1 \leq i < j \leq N, 1 \leq n \leq \nu_C \)), \( t_{ij}^{(n)} \) is the minimum similarity between any pair of individuals belonging to \( B_i^{n-1} \cup B_j^{n-1} \). That is,

\[
t_{ij}^{(n)} = \min \left\{ t_{ij}^{(1)} : i', j' \in B_i^{n-1} \cup B_j^{n-1} \right\} = \delta(B_i^{n-1}, B_j^{n-1}).
\]

Proof. By induction on \( n \).

- From Proposition 1, if \( S_{ij}^{(1)} c \in C_1(N) \), then \( t_{ij}^{(1)} \) corresponds to the similarity between individuals \( i, j \).
- Let us suppose that the result holds for \( n \) with \( 1 \leq n < \nu_C \). Let \( X_{i_n}^{(n)} \in C_{i_n} \) be the object sent to the environment in the configuration \( C_{i+n(3k-1)+k} \), and let \( \Delta_{n-1}^{C} = \left\{ B_i^{n-1}, \ldots, B_j^{n-1} \right\} \).
  - If \( i_n \notin \{i, j\} \), then from Proposition 8 we have \( t_{ij}^{(n+1)} = t_{ij}^{(n)} \). The result follows from the construction of \( \Delta_{n}^{C} \) and the induction hypothesis.
  - If \( 1 \leq i < i_n < j_n \), then from Proposition 8 we deduce that \( t_{i_n}^{(n+1)} = \min \{ t_{i_n}, t_{j_n} \} \). The result follows from the construction of \( \Delta_{n}^{C} \) and the induction hypothesis.
  - The proof is similar in the remaining cases.

Proposition 9. For each \( n \) (\( 0 \leq n \leq \nu_C - 1 \)), let us suppose that the partition \( \Delta_{n}^{C} = \left\{ B_i^{n}, \ldots, B_j^{N-n} \right\} \) is constructed from the object \( X_{i_n}^{(n)} \). If we denote by \( f \) the hierarchical index function, then \( f(B_i^{n}) = t_{i_n}^{(n)} \), and for each \( B \in \Delta_{n}^{C} \), we have \( f(B) \geq t_{i_n}^{(n)} \).

Proof. By induction on \( n \).

- Let us recall that \( \Delta_{0}^{C} = \left\{ \{\omega_1\}, \ldots, \{\omega_N\} \right\} \) and \( f(\{\omega_i\}) = k \) (\( 1 \leq i \leq N \)).
- From construction, \( \Delta_{1}^{C} = \left\{ B_{q_1}^{1}, \ldots, B_{q_{N-1}}^{1} \right\} \) with \( B_{q_1}^{1} = \{\omega_{i_1}, \omega_{j_1}\} \) and \( B_{q_{N-1}}^{1} = \{\omega_j\} \) (\( \forall j \neq i_1 \)). Then \( f(B_{j_1}^{1}) = k \) with \( j \neq i_1 \) and \( f(B_{i_1}^{1}) = t_{i_1,j_1}^{(1)} \) (because \( s(\omega_{i_1}, \omega_{j_1}) = t_{i_1,j_1}^{(1)} \leq k-1 \)).
- Let us suppose that the result holds for \( n \) (\( 1 \leq n < \nu_C \)). We have \( t_{i_n+1,j_n+1}^{(n+1)} \leq t_{i_n,j_n}^{(n)} \).
  - If \( i_n+1, j_n+1 \in B_{q_{n+1}}^{n} \), then \( B_{q_{n+1}}^{n+1} = B_{q_{n+1}}^{n} \). From the induction hypothesis we deduce that \( f(B_{q_{n+1}}^{n+1}) = t_{i_n,j_n}^{(n)} \), \( f(B_{i_n+1}^{n+1}) = t_{i_n+1,j_n+1}^{(n+1)} \), and \( \delta(B_{i_n+1}^{n}, B_{j_n+1}^{n}) = t_{i_n+1,j_n+1}^{(n+1)} \), then \( f(B_{n+1}^{n+1}) = t_{i_n+1,j_n+1}^{(n+1)} \).
Proposition 10. The P system $\Pi(P_{Nk})$ allows us to construct a hierarchical clustering associated with any computation of the P system.

**Proof.** Let $C$ be a computation of the P system $\Pi(P_{Nk})$. Let $\Delta^C_0$, $\Delta^C_1$, ..., $\Delta^C_\nu$ be the partition associated with it. By Proposition 9 all the clusters of the partition $\Delta^C_n$ have a hierarchical index greater than or equal to $t^{(n)}_{i_1,i_2}$ (denoted by $t_n$ in advance).

We construct the partition of the hierarchy $P_0, P_1, \ldots, P_m$ as follows:

- $P_0 = \Delta_0 = \{\{\omega_1\}, \{\omega_2\}, \ldots, \{\omega_N\}\}$.
- If the partitions $\Delta_1, \Delta_2, \ldots, \Delta_{p_1}$ have associated the same hierarchical index, then $P_1 = \Delta_{p_1}$.
- If the partitions $\Delta_{p_1+1}, \Delta_{p_1+2}, \ldots, \Delta_{p_2}$ have associated the same hierarchical index, then $P_2 = \Delta_{p_2}$.
- We continue in this way until we have one of the following situations:
  - if $\Delta_{\nu_C}$ has a hierarchical index $t_{\nu_C} = k - 1$, then $P_m = \Delta_{\nu_C} = \Omega$.
  - if $\Delta_{\nu_C}$ has a hierarchical index $t_{\nu_C} < k - 1$, then $P_{m-1} = \Delta_{\nu_C}$ and $P_m = \Omega$.

\[\square\]

4 CONCLUSIONS

One of the central issues when we have a set of individuals, each of them characterized by a $k$-tuple, is to obtain a cluster that allows us to group similar individuals.

In this paper we propose a non-deterministic P system with external output to obtain a hierarchical clustering. This P system gives one of the possible solutions to the problem. We present an efficient (semi-uniform) solution to the problem of clustering in the framework of the cellular computing with membranes. The solution is semi-uniform because for each matrix formed by the values of the individuals, a specific P system with external output is designed. The solution is efficient, because it is polynomial in order of the number $N$ of individuals and of the number $k$ of characteristics. The amount of resources initially required to construct the system is polynomial in $N$ and $k$.

The mechanisms of the formal verification of P systems are often a very hard task. Therefore, to have new examples where this task is accomplished is always interesting, in order to find systematic processes of formal verification in a model of computation oriented to machines, like the P systems. The paper provides such a new example of formal verification of P systems designed to solve a problem, following a specific methodology valid in cases as that considered in the paper.

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Mónica Cardona received her degree in mathematics from the Barcelona University. She is associated professor of applied mathematics at the University of Lleida. Her main research areas are in stochastic process and membrane computing. She has published 3 scientific papers.

M. Angels Colomer received her doctor degree in mathematical sciences by the Polytechnic University of Catalonia. In the past, she was associated professor at the Polytechnic University of Catalonia. She is titular Professor of statistic and operative research at the University of Lleida. Her main research areas are in stochastic process and membrane computing. She has published seven books in statistics and control quality, two book chapters of applications of stochastic models, and 15 scientific papers.

Mario J. Pérez-Jiménez received his degree in mathematics from the Barcelona University and doctor degree in mathematics from the Sevilla University. In the past, he was associated professor at the University of Barcelona. Currently, he is titular professor of computer science and artificial intelligence at the University of Sevilla, where is the head of the Research Group on Natural Computing. His main research areas are computational complexity theory, unconventional models of computation, natural computing, membrane computing, bioinformatics, and computational modelling for systems biology. He has published twelve books in computer science and mathematics, and over 100 scientific papers in international journals (collaborating with many researchers worldwide). He has served as reviewer for various prestigious ISI–journals (e.g. BioSystems, Discrete Applied Mathematics, Informatica Lithuan, International Journal of Foundations of Computer Science, International Journal of Computer Mathematics, Neurocomputing, Pattern Recognition Letters, SoftComputing, Theoretical Computer Science, Theory of Computing Systems). He is a member of editorial boards of the journals Soft Computing, and International Journal of Computers, Communications and Control. He is the main researcher in various European, Spanish and Andalusian research grants. He has been and independent expert to the evaluation of NEST (New and Emergent Science and Technology) proposals under the Sixth Framework Programme of the European Community, and he is an European Science Foundation peer reviewer.
Alba Zaragoza received her degree in mathematics from the Autonomous University of Barcelona and doctor degree from Lleida University. She is an associate professor of applied mathematics at the University of Lleida. Her main research areas are in stochastic processes and membrane computing. She has published a book on control quality and 4 scientific papers.