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FUZZY ACS WITH BIOLOGICAL *CATALYSTS* ON MEMBRANES IN CHEMICAL REACTIONS

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Abstract: **A computing model called Fuzzy abstract rewriting system on multisets, close to reality is recently designed by introducing fuzziness on computation [2]. As an extension of this model a device Fuzzy Artificial cell system with proteins on membrane is developed for which the structure is analyzed on its parameters. The proposed model can be (further) monitored to the case of living organisms.**

Keywords: . P system, Abstract Rewriting System, Artificial Cell System, Fuzzy ARMS, Fuuzy ACS, Proteins on membranes.

I. Introduction

Formal languages study the structure of the words and the relationship among the languages. A fuzzy formal language is a formal language where each word has a degree of membership to the language. Multisets are really useful structures as interesting models of computations are built upon them. Membrane computing is a model of computation that is built around the notion of multiset rewriting rules. More specifically, it is a computational paradigm that was inspired by the way of cells live and function [5]. A P system is a conceptual computational device whose functionality is based on an abstraction of the cell. It consists of porous of membranes that are populated with multisets of objects which are usually materialized as strings of symbols. In addition, there are rules that are used to change the configuration of the system.

Fuzzification of P system is a quiet reasonable development. Rigid mathematical models employed in biology are not completely adequate for the interpretation of biological information. This fact has led to the adoption of fuzzy models and methodologies. Also it has been shown that P systems with fuzzy multiset rewriting rules are equivalent to fuzzy Turing machines. An orthogonal approach to the fuzzification of both multisets and hybrid sets are presented by Apostolos Syropoulos [9]. Y. Suzuki and H. Tanaka have introduced the multiset rewriting system, "Abstract rewriting System on multisets" (ARMS). Based on this system, they have developed a molecular computing model called Artificial Cell System which consists of a multiset of symbols, a set of rewriting rules and membranes [7, 8]. These correspond to a class of P systems which is a parallel molecular computing model proposed by Gh. Paun and is based on the processing of multisets of objects in cell-like membrane structures [5].

P systems with proteins on membranes are inspired closely switching protein channels. The maximal parallelism way of processing different species of molecules in the membrane structure is not very close to reality. A model that is limiting the parallelism through the modeling of the trans-membrane proteins (protein channels) observed in nature. P system with proteins on membranes is introduced and the power of the system is examined. [4, 6]

Following chemical reactions, the possible mechanism was proposed for the kinetics of the sulfoxidation reactions, mimiking biological systems by A. M. I. Jayaseeli and Rajagopal [3]. Recently, the computational studies of the above mentioned work, based on membrane computing is proposed and *Kinetic ARMS* in Artificial Cell System with hierarchically structurable membrane ($KACSH$)[1] is developed.

Fuzzy ARMS called as $FARMS$ .with fuzzy multiset rewriting rules and fuzzy data viewed as a computational device is introduced[2]. The above mechanism of Artificial Cell System with hierarchically structurable membrane is developed with fuzzy multiset evolution rules with fuzzy data. In this paper we have introduced a new system called $FACSP$(*Fuzzy ARMS* in Artificial Cell System with

proteins on membranes) and its behaviour is studied. We believe that the new system would be of use in the modeling of living organisms.

II. Preliminaries

We first recall the basic structural ingredients of the computing device.

A. P System with Fuzzy Data [9]

A P system with fuzzy data is a construct

$$\Pi_{FD} = (O, \mu, w^{(1)}, ..., w^{(m)}, R_1, ..., R_m, i_0, \lambda)$$

where

- O is an alphabet (i.e., a set of distinct entities) whose elements are called objects;
- μ is the membrane structure of degree $m \geq 1$; membranes are injectivelly labeled with succeeding natural numbers starting with one;
- $w^{(i)} : O \rightarrow N_0 \times I, 1 \leq i \leq m$ are functions that represent multi-fuzzy sets over O associated with each region i; N_0 is the set of all natural numbers including $0, I \in [0, 1]$;
- $R_i, 1 \leq i \leq m$ are finite sets of multiset rewriting rules (called evolution rules) over O. An evolution rule is of the form $u \rightarrow v, u \in O^*$ and $v \in O^*_{TAR}$ where $O_{TAR} = O \times TAR, TAR = \{here, out\} \cup \{in_{(j)} | 1 \leq j \leq m\}$. The effect of each rule is the removal of the elements of the left-hand side of each rule from the current compartment and the introduction of the elements of right-hand side to the designated compartments;
- $i_0 \in \{1, 2, ..., m\}$ is the label of an elementary membrane (i.e., a membrane that does not contain any other membrane), called the output membrane;
- $\lambda \in [0, 1]$ is a threshold parameter, which is used in the final estimation of the computational result.

B. P System with Fuzzy Multiset Rewriting Rules [9]

A P system with fuzzy multiset rewriting rules and crisp data is just an ordinary P system that has, in addition, a corresponding fuzzy set for each set R_i of multiset rewriting. A P system with fuzzy multiset rewriting rules will compute a number to some degree. Clearly, such systems must also obey the so called maximal parallelism principle, that is the rules should be selected in such a way that only optimal output will be yielded. Thus, P systems with fuzzy data differ fundamental from P systems with probabilistic rewriting rules in that there is no bias in the selection of the rules. When a P system with fuzzy multiset rewriting rules halts, the result of the computation to some degree is equal to the cardinality of the multiset contained in the output compartment. Clearly, it is also necessary to know how to compute the truth degree that is associated with the computational result.

C. ARMS (Abstract Rewriting System on Multisets) [7]

$ARMS$ is like a chemical solution in which molecules floating on it can interact with each other according to reaction rules. Technically, a chemical solution is a finite multiset of elements denoted by $A^k = \{a, b, ..\}$; these elements correspond to molecules. Reaction rules that act on the molecules are specified in ARMS by rewriting rules. In fact, this system can be thought of as an underling algorithmic chemistry [1].

Let A be an alphabet whose elements are called objects; the alphabet itself is called a set of objects. A multiset over a set of objects A is a mapping $M : A \rightarrow N_0$. The number $M(a)$ for $a \in A$ is the multiplicity of object a in the multiset M. We do not accept here an infinite multiplicity. We denote by $A^\#$ the set of all multisets over A including the empty multiset ϕ defined by $\phi(a) = 0$ for all $a \in A$. A multiset rewriting rule (evolution rule) over the set A of objects is a pair (M_1, M_2) of elements in $A^\#$(which can be represented as a rewriting rule $w_1 \rightarrow w_2$ for two strings $w_1, w_2 \in A^\#$ such that $M_{w_1} = M_1$ and $M_{w_2} = M_2$). We use to represent such a rule in the form $M_1 \rightarrow M_2$.

An abstract rewriting system on multisets ($ARMS$) is a pair $\Gamma = (A, (R, \rho))$ where A is a set of objects; R is a finite set of multiset evolution rules over A; ρ is a partial order relation over R specifying a priority relation among rules of R. With respect to an $ARMS$ Γ, we can define over $A^\#$ a relation: ($\Rightarrow$): for $M, M' \in A^\#$ we write $M \Rightarrow M'$ iff $M' = (M - (M_1 \cup \cdots \cup M_k)) \cup (M'_1 \cup \cdots \cup M'_k)$ for some $M_i \rightarrow M'_i \in R, 1 \leq i \leq k, k \geq 1$, and there is no rule $M_s \rightarrow M'_s \in R$ such that $M_s \subseteq (M - (M_1, \cup ... \cup M_k))$; at most one of the multisets $M_i, 1 \leq i \leq k$, may be empty. With respect to an $ARMS$ $\Gamma = (A, R)$ we can define various types of multisets: A multiset $M \in A^\#$ is dead if there is no $M' \in A^\#$ such that $M \Rightarrow M'$. This is equivalent to the fact that there is no rule $M_1 \rightarrow M_2 \in R$ such that $M_1 \subseteq M$. A multiset $M \in A^\#$ is initial if there is no $M' \in A^\#$ such that $M' \Rightarrow M$.

In $ARMS$, all the reaction rules are applied in parallel. In every step, all the rules are applied to all objects in every membrane that can be applied. If there are more than one applicable rule that can be applied to an object then one rule is selected randomly.

D. Fuzzy ARMS [2]

Recently we have proposed a computing device that based on Abstract Rewriting systems on multisets closely related to P system with fuzzy multiset rewriting rules and fuzzy data which is called as $FARMS$.

1) Definition

A *Fuzzy ARMS* ($FARMS$) is a quintuple

$$\Gamma = \{A, (R, \rho), J, \mu\}$$

where

- A is a set of objects,
- R is a finite set of multiset rewriting rules over A,
- ρ is a partial order relation over R, specifying a priority relation among the rules of R,
- $J = \{r_j / j = 1 \text{ to } n, n = \text{cardinality of } R\}$ i.e. the number of multiset rewriting rules over A,
- $\mu : J \to [0,1]$ is the membership function in R such that $\mu(r_j) = i, i \in [0,1]$.

In $FARMS$, reaction rules are applied in parallel. When there are more than one applicable rules then one rule is selected randomly.

A *Fuzzy ARMS* generates a *Fuzzy ARMS language* $L(FARMS)$ as follows. An object $x \in A^*$ is said to be in $L(FARMS)$ iff it is derivable from any object $S \in A$ and the grade of membership $\mu_{L(FARMS)}(x)$ is greater than 0, where

$$\mu_{L(FARMS)}(x) = \begin{pmatrix} max \\ 1 \le k \le n \end{pmatrix} \left[\begin{pmatrix} min \\ 1 \le i \le l_k \end{pmatrix} \mu(r_i^k) \right]$$

where $x \in A^*$ and n is the number of different derivatives that x has in $FARMS$, l_k is the length of the k^{th} derivative chain, r_i^k denotes the label of the i^{th} multiset rewriting rule used in the k^{th} derivative chain, $i = 1, 2, \ldots, l_k$.

Clearly, $\mu_{L(FARMS)}(x)$ = Strength of the strongest derivative chain for S to x for all $x \in A^*$.

2) *Example*

Consider the *Fuzzy ARMS*

$$\Gamma = \{A, (R, \rho), J, \mu\}$$

where

$A = \{a, b, c, d, f\}$,

$$R = \left\{ \begin{array}{lll} r_1 : & a^m, f \to b^m, c^m & \text{with } \mu(r_1) = 0.8 \\ r_2 : & c^m, d \to a^m, c^m & \text{with } \mu(r_2) = 0.5 \end{array} \right\},$$

$J = \{r_j \in R / j = 1, 2\}$,

$\mu : J \to I$ is the membership function s.t. $\mu(r_j) = i, i \in [0,1]$,

$\rho = \phi$.

We do not assume priority among the rules $\{r_1$ and $r_2\}$. In $FARMS$, reaction rules are applied in parallel. When there are more than one appliicable rules, then one rule is selected randomly. Let us take $\{a^m, f, d : m \ge 1\}$ as an initial state.

If $m = 1$, the rule r_1 is applied in parallel and $\{a, f, d\}$ is transformed in to $\{b, c, d\}$ with $\mu(r_1) = 0.8$. Since r_1 cannot be applied on this multiset, r_2 is applied. resulting into the multiset $\{a, b, c\}$ with $\mu(r_2) = 0.5$. As there is no rule that can transform the multiset further, the system is in a dead state. Thus the grade of membership value $\mu_{L(FARMS)}(a, b, c)$ is

$$\begin{pmatrix} max \\ 1 \le k \le n \end{pmatrix} \left[\begin{pmatrix} min \\ 1 \le i \le l_k \end{pmatrix} \{0.8, 0.5\} \right] = 0.5$$

If $m = 2$, the rule r_1 is applied in parallel and $\{a, a, f, d\}$ is transformed in to $\{b, b, c, c, d\}$ with $\mu(r_1) = 0.8$. Since r_1 cannot be applied on this multiset, r_2 is applied, resulting into the multiset $\{a, a, b, b, c, c\}$ with $\mu(r_2) = 0.5$. As before, there is no rule that can transform the multiset further. So, the system is in a dead state. Thus the grade of membership value $\mu_{L(FARMS)}(a, a, b, b, c, c)$ is

$$\begin{pmatrix} max \\ 1 \le k \le n \end{pmatrix} \left[\begin{pmatrix} min \\ 1 \le i \le l_k \end{pmatrix} \{0.8, 0.5\} \right] = 0.5$$

proceeding like this, we obtain the language as $L(FARMS) = \{a^n, b^n, c^n / n \ge 1\}$ with $\mu_{L(FARMS)}(a^n, b^n, c^n) = 0.5$.

E. Kinetic Studies of the Sulfoxidation reactions

Establishing model compounds enhances the study of enzymic intermediates. Therefore over the part three decades biomimetic approaches towards mimicking the catalytic role of these enzymes on the oxygenation reaction have been focused [3]. A. M. I. Jayaseeli et al. established an eco-friendly redox system which serve as peroxidase model by opting hydrogen peroxide as oxygen source for the iron(III)–salen catalysed oxidation of sulfides and sulfoxides. The progress of the reaction was followed using UV-visible spectro photometric techniques. Michaleis-Menton behaviour was observed when the rate of the reaction followed kinetically. Taking into consideration of the substituents effect of complexes as well as substrates, the rates of the reactions are tabulated and a suitable mechanism was proposed.

F. Computing with Proteins on membranes [6]

A kind of model on P systems with membranes is considered where the main information to process is encoded in the multisets from the regions of P system, but these objects evolve under the control of a bounded number of proteins placed on membranes. Also, the rules used are very restrictive: move objects across membranes under the control of membrane proteins, changing or not the objects and/or the proteins during these operations. The reason for considering both extensions was that in biology, many reactions taking place in the compartments of living cells are controlled /catalysed by the proteins embedded in the membranes bilayer. In the P systems two types of objects, proteins and usual objects are used; the former are placed on

the membranes, the latter are placed in the regions delimited by membranes. The fact that a protein p on a membrane (with label) i is written in the form $[_i p|\quad]_i$. Both the regions of a membrane structure and the membranes can contain multisets of objects and of proteins, respectively. The following type of rules are introduced in [4] where a, b, c, d are objects, p is a protein, and i is a label (cp means change protein).

Type	Rule	Effect
$1cp$	$[_i p\|a]_i \to [_i p'\|b]_i$ $a[_i p\|]_i \to b[_i p'\|]_i$	modify an object, but not move
$2cp$	$[_i p\|a]_i \to a[_i p'\|]_i$ $a[_i p\|]_i \to [_i p'\|a]_i$	move an object, but not modify
$3cp$	$[_i p\|a]_i \to b[_i p'\|]_i$ $a[_i p\|]_i \to [_i p'\|b]_i$	modify and move one object
$4cp$	$a[_i p\|b]_i \to b[_i p'\|a]_i$	interchange two objects
$5cp$	$a[_i p\|b]_i \to c[_i p'\|d]_i$	interchange and modify two objects

An intermediate case can be that of changing proteins from p to $\bar{p}$ and back (like in the case of bistable catalysts). Rules with such flip-flop proteins are denoted by $nff, n = 1, 2, 3, 4, 5$.

1) P System with Proteins on Membranes

A system with Proteins on membranes (in the sequel simply P system, if not stated otherwise) is a system of the form,

$$\Gamma = \{O, P, \mu, w_1/z_1, \cdots, w_m/z_m, E, R_1, \cdots, R_m, i_0\}$$

where

- m is the degree of the system (the number of membranes)
- O is the set of objects
- P is the set of proteins (with $O \cap P = \phi$)
- μ is the membrane structure
- w_i are the (strings representing the) multisets of objects present in the m regions of μ
- z_i are the multisets of proteins present on the membranes of μ
- $E \subseteq O$ is the set of objects present in the environment (in an arbirarily large number of copies each)
- R_i are finite set of rules associated with the m membranes of μ
- $i_0 \in \{1, 2, \cdots, m\}$ is the label of the output membrane.

Reaction rules are applied in the following manner: In each step, a maximal multiset of rules is used, that is, no rule is applicable to the objects and the proteins which remain unused by the chosen multiset. At each step we have the condition that each object and each protein can be involved in the application of at most one rule, but the membranes are not considered as involved in the rule applications except the division rules, hence the same membrane can appear in any number of rules of types 1-5 at the same time. By halting computation we understand a sequence of configurations that ends with a halting configuration (there is no rule that can be applied considering the objects and proteins present at that moment in the system). With a halting computation we associate a result, in the form of the multiplicity of objects present in region i_0 at the moment when the system halts. We denote by $N(\Pi)$ the set of numbers computed in this way by a given system Π. We denote in the usual way by $NOP_m(pro_r; list\ of\ types\ of\ rules)$ the family of sets of numbers $N(\Pi)$ generated by systems with at most m membranes using rules as specified in the *list of types of rules*, and with at most r proteins present on a membrane. When parameters m or r are not bounded, we use $*$ as a subscript.

III. Fuzzy Artificial Cell System with Proteins on Membranes

We now introduce a mechanism of Artificial Cell System with Proteins on Membranes having fuzzy multiset evolution rules and fuzzy data.

A. Definition

A *Fuzzy ACS* with Proteins on membranes $FACSP$ is a construct,

$$\Gamma = \{O, P, \mu, w_1/z_1, \cdots, w_m/z_m, E, (R_p, \rho), i_0, J, \omega\}$$

where

- m is the degree of the system (the number of membranes)
- O is the set of objects
- P is the set of proteins (with $O \cap P = \phi$)
- μ is the membrane structure

- w_i are the (strings representing the) multisets of objects present in the m regions of μ where $i = 1$ to m
- z_i are the multiset of proteins (biological Catalysts) present on the membranes of μ where $i = 1$ to m
- E is the set of objects present in the environment (in an arbitarily large number of copies each)
- R_p is a set of Fuzzy multiset evolution rules over$A, p = 1$ to m of μ
- ρ is the partial order relation over R_p
- $i_0 \in \{1, 2, \cdots, m\}$ is the elementary membrane (output)
- $J = \{R_{pq} \in R_p / p = 1, \ldots, m, q \geq 1\}$, $q =$ cardinality of R_p
- $\omega : J \rightarrow [0, 1]$ is the membership function s.t. $\omega(R_{pq}) = i, i \in [0, 1]$.

The rules are used in the non-deterministic maximally parallel way:

The same rules are applied to every membrane. There are no rules specific to a membrane. All the rules are applied in parallel. In every step, all the rules are applied to all objects in every membrane that can be applied. If there are more than one applicable rule that can be applied to an object and protein then one rule is selected randomly. If a membrane dissolves, then all the objects in its region are left free in the region immediately above it. All objects and proteins not specified in a rule and which do not evolve are passed unchanged to the next step. At each step we have the condition that each object and each protein can be involved in the application of at most one rule, but the membranes are not considered as involved in the rule applications except the division rules, hence the same membranes can appear in any number of rules at the same time.

By halting computation we understand a sequence of configurations that ends with a halting configuration (there is no rule that can be applied considering the objects and proteins present at that moment in the system). With a halting computation we associate a result in the form of the multiplicity of objects present in region i_0 at the moment when the system halts.

A *Fuzzy ACS* with proteins on membranes generates a language $L(FACSP)$ as follows: An object $x \in O^*$ which is present in the region i_0 at the moment when the system halts is said to be in $L(FACSP)$ iff it is derivable from any object $S \in O$ and the grade of membership $\omega_{L(FACSP)}(x)$ is greater than 0, where

$$\omega_{L(FACSP)}(x) = \begin{pmatrix} max \\ 1 \leq k \leq n \end{pmatrix} \left[\begin{pmatrix} min \\ 1 \leq i \leq l_k \end{pmatrix} \omega(R_i^k) \right]$$

where $x \in O^*$ and n is the number of different derivatives that x has in $FACSP$, l_k is the length of the k^{th} derivative chain, R_i^k denotes the label of the i^{th} multiset evolution rule used in the k^{th} derivative chain, $i = 1, 2, \ldots, l_k$. Clearly, $\omega_{L(FACSP)}(x) =$ Strength of the strongest derivative chain for S to x for all $x \in O^*$.

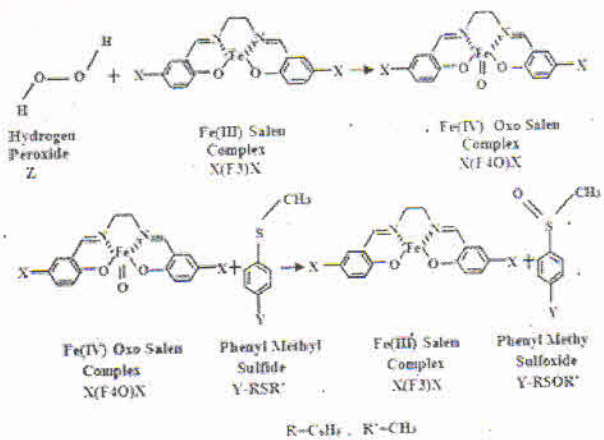
We denote in the usual way by $L_{FACSP_m}(pro_r, list\ of\ types\ of\ rules)$ the family of languages $L(FACSP)$ generated by systems Π with at most m membranes, using rules as specified in the *list of types of rule* and with at most r proteins present on a membrane. When parameters m or r are not bounded, we use $*$ as a subscript.

B. FACSP in Oxidation of Sulfides

1) Process A:

We describe the formation of intermediate between complex and the oxidant.

(a). $Z + X(F3)X \rightarrow X(F4O)X$;
$X(F4O)X + Y\text{-}RSR' \rightarrow X(F3)X + Y\text{-}RSOR'$



A simple abstract reaction scheme is followed.
Case $I : X = H$
Following convention is used to do the computation.
$Y = H = L, Y = OCH_3 = M, Y = CH_3 = N$,
$Y = F = P, Y = Cl = Q, Y = Br = U, Y = NO_2 = V$.
Now (a) will have the following reaction rules

1. $Z + H(F3)H \rightarrow H(F4O)H$;
$H(F4O)H + L\text{-}RSR' \rightarrow H(F3)H + L\text{-}RSOR'$

2. $Z + H(F3)H \rightarrow H(F4O)H$;
$H(F4O)H + M\text{-}RSR' \rightarrow H(F3)H + M\text{-}RSOR'$

3. $Z + H(F3)H \rightarrow H(F4O)H$;
$H(F4O)H + N\text{-}RSR' \rightarrow H(F3)H + N\text{-}RSOR'$

4. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + P\text{-}RSR' \rightarrow H(F3)H + P\text{-}RSOR'$

5. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + Q\text{-}RSR' \rightarrow H(F3)H + Q\text{-}RSOR'$

6. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + U\text{-}RSR' \rightarrow H(F3)H + U\text{-}RSOR'$

7. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + V\text{-}RSR' \rightarrow H(F3)H + V\text{-}RSOR'$

2) *BEHAVIOUR OF FACSP - A:*

Case-I Consider the $FACSP$

$$\Gamma = (O, P, \mu, w_1/z_1, w_2/z_2, E, (R_p, \rho), i_0, J, \omega)$$

where

- $O = \{Z, A_1, B, S_i, P_i, i = 1, \ldots, 7\}$,
- $P = \{A_1, B\}$,
- $\mu = [_1[_2]_2]_1$,
- w_1, w_2 are the multisets of objects present in the regions $1, 2$ of μ, $w_1 = \{Z, S_i, i = 1, \ldots, 7\}, w_2 = \{\phi\}$,
- z_1, z_2 are the multisets of proteins present on the membranes $1, 2$ of μ, $z_1 = \{A_1\}, z_2 = \{\phi\}$,
- $E = \{\phi\}$,
- R_p is a finite set of Fuzzy multiset evolution rules over $A; p = 1, 2$
- $\rho = \phi$,
- $i_0 = 2$ is the output membrane,
- $J = \{R_{pq} \in R_p / p = 1, 2. q = 1 \text{ to } 7\}$, $q =$ cardinality of R_p.
- $\omega : J \rightarrow [0, 1]$ is the membership function s.t. $\omega(R_{pq}) = i, i \in [0, 1]$, where

$$\omega_{L(FACSP)}(x) = \left(\underset{1 \le k \le n}{max}\right)\left[\left(\underset{1 \le i \le l_k}{min}\right)\omega(R_i^k)\right]$$

and $x \in O^*$

$R_p = \{R_1, R_2\}$ consists the following evolution rules.

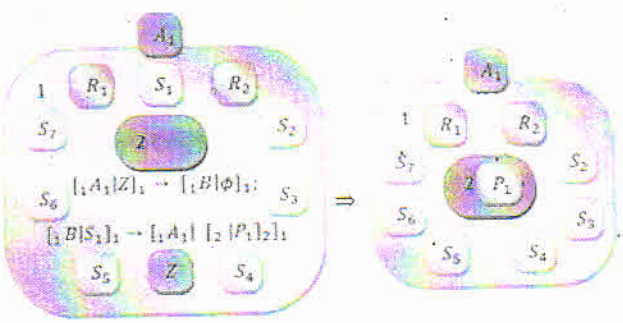
$$R_1 = \left\{\begin{array}{lccc}
R_{11}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_1]_1 & \rightarrow & [_1A_1|\ [_2\ |P_1]_2]_1 \\
 & \text{with } \omega(R_{11}) & = & 0.0025 \\
R_{12}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_2]_1 & \rightarrow & [_1A_1|\ [_2\ |P_2]_2]_1 \\
 & \text{with } \omega(R_{12}) & = & 0.01 \\
R_{13}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_3]_1 & \rightarrow & [_1A_1|\ [_2\ |P_3]_2]_1 \\
 & \text{with } \omega(R_{13}) & = & 0.0059 \\
R_{14}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_4]_1 & \rightarrow & [_1A_1|\ [_2\ |P_4]_2]_1 \\
 & \text{with } \omega(R_{14}) & = & 0.0016 \\
R_{15}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_5]_1 & \rightarrow & [_1A_1|\ [_2\ |P_5]_2]_1 \\
 & \text{with } \omega(R_{15}) & = & 0.0011 \\
R_{16}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_6]_1 & \rightarrow & [_1A_1|\ [_2\ |P_6]_2]_1 \\
 & \text{with } \omega(R_{16}) & = & 0.0009 \\
R_{17}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\
 & [_1B|S_7]_1 & \rightarrow & [_1A_1|\ [_2\ |P_7]_2]_1 \\
 & \text{with } \omega(R_{17}) & = & 0.00027.
\end{array}\right\}$$

$R_2 = \phi$.

In its initial configuration, the system contatins 2 membranes with 8 objects $(Z, S_i, i = 1, \ldots, 7)$ and a biological protein A_1 on membrane 1. It has two steps. In the first step, any one of the 7 rules is selected randomly. Let the rule R_{11} be applied. Then the protein A_1 is changed into B. In the second step, the protein change back from B to A_1 and the object S_1 evolved into P_1 and move to membrane 2. Since there is no rule that can transform the object in membrane 2 further, the process halts. The resulting object in the output membrane 2 is P_1.

$$\underset{1 \le k \le n}{max}\left[\underset{1 \le i \le l_1}{min}\ (0.0025)\right] = 0.0025;$$

$$\omega_{L(FACSP)}(P_1) = 0.0025$$



FACSP -A

Similar process will be done when other rules are applied.

As a result, we have

$$\omega_{L(FACSP)}(P_i) = \left\{ \begin{array}{ccc} 0.0025 & \text{if} & i = 1 \\ 0.01 & \text{if} & i = 2 \\ 0.0059 & \text{if} & i = 3 \\ 0.0016 & \text{if} & i = 4 \\ 0.0011 & \text{if} & i = 5 \\ 0.0009 & \text{if} & i = 6 \\ 0.00027 & \text{if} & i = 7 \end{array} \right\}$$

Hence $L(FACSP) = \{P_i / i = 1 \text{ to } 7\}$

We obtain different languages with corresponding membership values for different complexes $(A_i, i = 1 \text{ to } 7)$.

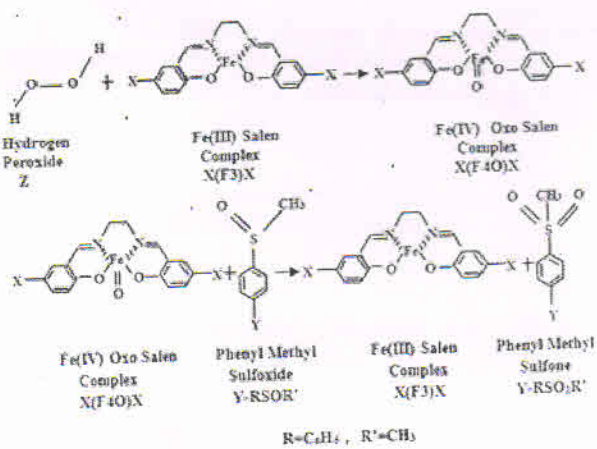
We denote by $L(FACSP)(pro_1; 7ffp)$ the family of languages $L(FACSP)$ generated by Γ with atmost 2 membranes using rules as specified in the $7ffp$ rules and with atmost one protein.

C. FACSP in Oxidation of Sulfoxides

1) Process B:

First, we describe the formation of intermediate between complex and the oxidant.

(a). $Z + X(F3)X \rightarrow X(F4O)X;$
$X(F4O)X + Y\text{-}RSOR' \rightarrow X(F3)X + Y\text{-}RSO_2R'$



A simple abstract reaction scheme is followed.
Case $I : X = H$
Following convention is used to do the computation.
$Y = H = L, Y = OCH_3 = M, Y = CH_3 = N,$
$Y = F = P, Y = Cl = Q, Y = Br = U.$
Now (a) will have the following reaction rules

1. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + L\text{-}RSOR' \rightarrow H(F3)H + L\text{-}RSO_2R'$

2. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + M\text{-}RSOR' \rightarrow H(F3)H + M\text{-}RSO_2R'$

3. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + N\text{-}RSOR' \rightarrow H(F3)H + N\text{-}RSO_2R'$

4. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + P\text{-}RSOR' \rightarrow H(F3)H + P\text{-}RSO_2R'$

5. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + Q\text{-}RSOR' \rightarrow H(F3)H + Q\text{-}RSO_2R'$

6. $Z + H(F3)H \rightarrow H(F4O)H;$
$H(F4O)H + U\text{-}RSOR' \rightarrow H(F3)H + U\text{-}RSO_2R'$

2) BEHAVIOUR OF FACSP - B:

Case-I Consider the $FACSP$

$$\Gamma = (O, P, \mu, w_1/z_1, w_2/z_2, E, (R_p, \rho), i_0, J, \omega)$$

where

- $O = \{Z, A_1, B, SO_i, P_i, i = 1, \ldots, 6\}$
- $P = \{A_1, B\}$,
- $\mu = [_1[_2]_2]_1$
- w_1, w_2 are the multisets of objects present in the regions $1, 2$ of μ, $w_1 = \{Z, SO_i, i = 1, \ldots, 6\}, w_2 = \{\phi\}$
- z_1, z_2 are the multisets of proteins present on the membranes $1, 2$ of μ, $z_1 = \{A_1\}, z_2 = \{\phi\}$,
- $E = \{\phi\}$
- R_p is a finite set of Fuzzy multiset evolution rules over $\Lambda; p = 1, 2$
- $i_0 = 2$ is the output membrane,
- $\rho = \phi$,
- $J = \{R_{pq} \in R_p / p = 1, 2, q = 1 \text{ to } 6\}$, $q =$ cardinality of R_p.
- $\omega : J \rightarrow [0, 1]$ is the membership function s.t. $\omega(R_{pq}) = i, i \in [0, 1]$, where

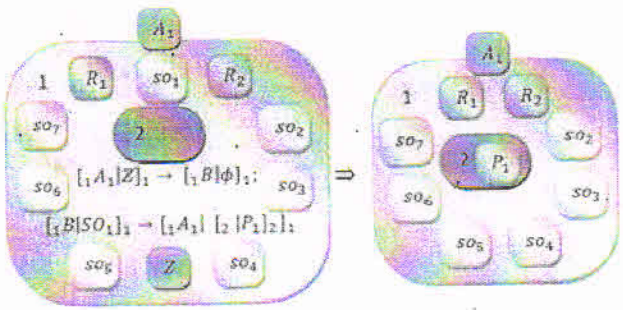
$$\omega_{L(FACSP)}(x) = \left(\begin{array}{c} max \\ 1 \leq k \leq n \end{array} \right) \cdot \left[\left(\begin{array}{c} min \\ 1 \leq i \leq l_k \end{array} \right) \omega(R_i^k) \right]$$

and $x \in O^*$

$R_p = \{R_1, R_2\}$ consists the following evolution rules.

$$R_1 = \left\{ \begin{array}{lccl} R_{11}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\ & [_1B|SO_1]_1 & \rightarrow & [_1A_1|\ [_2\ |P_1]_2]_1 \\ & \text{with } \omega(R_{11}) & = & 0.00017 \\ R_{12}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\ & [_1B|SO_2]_1 & \rightarrow & [_1A_1|\ [_2\ |P_2]_2]_1 \\ & \text{with } \omega(R_{12}) & = & 0.00028 \\ R_{13}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\ & [_1B|SO_3]_1 & \rightarrow & [_1A_1|\ [_2\ |P_3]_2]_1 \\ & \text{with } \omega(R_{13}) & = & 0.00022 \\ R_{14}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\ & [_1B|SO_4]_1 & \rightarrow & [_1A_1|\ [_2\ |P_4]_2]_1 \\ & \text{with } \omega(R_{14}) & = & 0.00013 \\ R_{15}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\ & [_1B|SO_5]_1 & \rightarrow & [_1A_1|\ [_2\ |P_5]_2]_1 \\ & \text{with } \omega(R_{15}) & = & 0.00012 \\ R_{16}: & [_1A_1|Z]_1 & \rightarrow & [_1B|\phi]_1; \\ & [_1B|SO_6]_1 & \rightarrow & [_1A_1|\ [_2\ |P_6]_2]_1 \\ & \text{with } \omega(R_{16}) & = & 0.00011. \end{array} \right\}$$

$R_2 = \phi$.



FACSP-B

The computation is done as in $FACSP$ - A. As a result, we get

$$\omega_{L(FACSP)}(P_i) = \left\{ \begin{array}{lll} 0.00017 & \text{if} & i = 1 \\ 0.00028 & \text{if} & i = 2 \\ 0.00022 & \text{if} & i = 3 \\ 0.00013 & \text{if} & i = 4 \\ 0.00012 & \text{if} & i = 5 \\ 0.00011 & \text{if} & i = 6 \end{array} \right\}$$

Hence $L(FACSP) = \{P_i / i = 1 \text{ to } 6\}$.

Similarly, we obtain different languages with corresponding membership values for different complexes $(A_i, i = 1$ to $6)$.

We denote by $L(FACSP)(pro_1; 6ffp)$ the family of languages $L(FACSP)$ generated by Γ with atmost 2 membranes using rules as specified in the $6ffp$ rules and with atmost one protein.

IV. Conclusion

A new membrane computing model $FACSP$ (Fuzzy ARMS in Artificial Cell System with Proteins on membranes) have been proposed. It is a preliminary research work on P systems with proteins on membranes. It is worth examining the proposed system in the modeling of living organisms. It remains to explore the properties and applications of Fuzzy $ARMS$ in Artificial cell system with proteins on membranes.

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