Computing with Biological Models

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The concept of molecular computing has been motivated from the way how computing like activities take place in live cells. Recently there has been an increasing interest in the idea of performing computations at molecular level and hence several computational models for molecular computing have been proposed. The field of DNA based computing laid the foundation towards molecular computing.

A cell is a complex body with several compartments delimited by membranes of various types and the chemicals evolved in these compartments are of very diverse forms, from single ions to long DNA molecules. The membranes themselves are composed of chemicals and can interact with the chemicals, swimming in the aqueous solutions from the compartments. This whole process is governed by the biochemistry rules, applied nondeterministically in all compartments, in parallel to all objects.

A membrane structure is a hierarchical arrangement of membranes, all of them placed in a main membrane called skin membrane. This one delimits the system from its environment. The membrane should be understood as a three dimensional balloon. Each membrane precisely identifies a region, the space between it and all the directly inner membranes if any, exists. In the regions of a membrane we place multiset of objects. In the beginning objects are atomic and hence can be identified by symbols from a given alphabet. The objects evolve by means of given rules which are associated with a region. These rules specify both object transformation and object transfer from a region to another one. The passing of an object through a membrane is called a communication. Hence an object can be transformed into other objects, can pass through adjacent membranes and can dissolve the membrane in which it passes. Such a construct lead to a computing device called P-system. It starts with an initial configuration and evaluate until a halting configuration is obtained. The objects in a specified output membrane are the result of the computation.

P system is a construct

? $=(V,T,C,\mu,w_1,w_2,\ldots,w_n,(R_1,\rho_1),(R_2,\rho_2),\ldots,(R_m,\rho_m))$ where

i. V is an alphabet and its elements are called objects.

ii. $T \subset V$ called output alphabet.

iii. $C \subset V\text{-}T$ called catalyst.

Iv. μ is a membrane structure consisting of m membranes labeled as 1, 2, ... m. m is called the degree of ?.

v. $w_i : 1\leq i\leq m$ are strings which represent multisets over V associated with the region 1, 2, ... m of μ.

vi. $R_{i,}$ $1\leq i \leq m$ are finite sets of evolution rules over V associated with the regions 1, 2, ... m of μ. ρ_i is a partial order relation over R_i, $1\leq i\leq m$ specifying a priority relation among the rules of R_i. An evolution rule is a pair (u, v) which we write in the form u? v where u is a string over V and $v = v^1$ or $v = v^1\ \delta$ where ? v^1 is a string over $\{a_{here}, a_{out}, a_{in\,j}$: $a \in V\}$and δ is a special symbol not in V. length of u is called the radius of the rule.

If ? contains rules of radius greater than one, then we say that ? is a system with cooperation. Otherwise it is a non-cooperative system. The computation of is done in the following way. An initial configuration of ? is a (m+1) tuple $(\mu, w1_, w_2, \ldots, W_m)$.

For two configurations $C_1 = (\mu^1, w_{i1}{}^1, \ldots, w_{iik})$, C2= ($\mu$'', $w_{i1}, \ldots, w_{il}$'') of ? , we say that we have a transition from C_1 to C_2 if we can pass from C_1 to C_2 by using the evolution rules from $R_{i1}, R_{i2}, \ldots, R_{ik}$ in the regions $i_{1,} i_2, \ldots, I_k$.

A sequence of transitions between configurations of a given P system T is called a computation with respect to ? . Computation is successful if it halts, that is, there is no rule applicable to the objects present in the last configuration.

Let $T = \{a_1, a_2, \ldots, a_n.)$ For each string $w \in T^*$, we define a function $\psi_T : T^*$? N^n where N is a set of natural numbers such that $\psi_T(w) = (|w|_1, |w|_2, \ldots, |w|_n)$ where $|w|_j$ is the number of a_j's present in the string w. The result of a successful computation is $\psi_T(w)$ where w is the multiset of objects sent out of the skin membrane, when the computation stops. The set of all such vectors $\psi_T(w)$ is denoted by $P_s(\Pi)$ and we say that it is generated by Π.

In the family of sets of vectors $P_s(\Pi)$ generated by P systems with priority and catalyst coincides with the family of recursively enumerable sets of vectors. This approach is clearly motivated from a mathematical point of view, not only because it is natural to model the cell computation behavior, but also because the new computing model has several intrinsically interesting features.

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