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Algorithmic Analysis of LS-systems: Solving the 3-SAT problems in a logarithmic space*

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Abstract

The computation model of "LS-systems" is proposed as a formal system of a kind of molecular computing based on kinase-guided signaling pathways. The central idea of the computing process is to equip the mechanism of problem solving itself with the high degree of complexity. This mechanism is autonomous and controllable in theory.

We take the 3-SAT problem as the test-bed for studies of the algorithm derived from LS-systems denoted as $\Im_{LS}$. After we carried out the algorithmic analysis of $\Im_{LS}$, we get the following conclusion:

Proposition 1:

The cost of solving the 3-SAT problems by $\Im_{LS}$ is dependent on the size of the neighborhood, the probability of the operators of interactions and uniformity of the global sampling.

The neighborhood is randomly set at each step. So the average size is the simplest way to measure the size of neighborhood. The operations of interactions are exerted uniformly, but the probability varies according to the situation of variables in different clauses. Besides the initiation of the candidates, the granularity of the computing units can be modified dynamically with respect to the global scope of candidates sampling. Provided that the process for molecular computing be constructed by the signaling pathways in cells, the main target of controller will be the set of kinases.

By the algorithm $\Im_{LS}$, the whole space of problem solving varies as a reduction process from a set of graphs into a set of trees that represent the set of final solutions. We have that:

Proposition 2

Let m be the number of clauses, n be the number of variables, we have achieved the space complexity as O(int(log(n))) and the time complexity as O(m), where int(.) refers to the integer value of the corresponding variable and the set of kinases is recursively generated in an autonomous ways.

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