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A Computing Model for Biochemical Reactions

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Recent developments on the theory of reaction automata ([4,5,6]) are surveyed. In these years, Ehrenfeucht and Rozenberg have introduced a formal model, called reaction systems ([2]), for investigating interactions between biochemical reactions. Reaction systems provide a formal framework suited for investigating at an abstract level the way of biochemical functioning. Meanwhile, the notion of a multiset has frequently appeared and been investigated in many areas of computer science and related fields ([1,7]) because of its usefulness. In fact, identifying a volume of compound chemicals as a multiset makes it possible that a multiset rewriting provides a natural way to express chemical reactions. Combining two notions of a reaction system and of a multiset rewriting, we have introduced reaction automata as computing devices for accepting string languages ([4]), in order to model and analyze the behaviors of biochemical reactions in the computational framework.

The notion of reaction automata is an extension of reaction systems in which reaction rules are defined by triples consisting of reactants, inhibitors, and products. A computation process of a reaction automaton is performed in such a way that each time receiving one symbol from an input string, a reaction automaton changes its memory (multiset) by applying reaction rules to the multiset. Since reaction automata are a computing model based on multiset rewriting that accepts string languages, their modeling capability for chemical reactions can be investigated in terms of the theory of computation ([3]).

It is shown that reaction automata are computationally Turing universal. Further, Computational complexity issues for some classes of reaction automata are explored in comparison to language classes in the Chomsky hierarchy.

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