Krajowa Konferencja Zastosowań Matematyki w Biologii i Medycynie

Jastrzębia Góra, 16th–20th September 2013

ARITHMETICAL ANALYSIS OF BIOMOLECULAR FINITE AUTOMATON

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ABSTRACT

We present the result of the article [1], in which a theoretical analysis of extension of the finite automaton built on DNA (introduced by the Shapiro team) to an arbitrary number of states and symbols is given. The Shapiro automaton action is based on cyclic cutting and ligating of DNA molecules. Its distinctive features included the fact that it was programmable (it means we may choose arbitrarily transitions of any two-state automaton), as well as autonomous (the activity of the automaton does not require man's intervention during calculations). However the Shapiro automaton was only 2-state 2-symbol finite automaton. The first two authors proposed in [2] use a new idea of several restriction enzymes instead of one to extend numbers of states in Shapiro automaton. In the article [1] we present conditions for the existence of such extensions in terms of ingredients used in the implementation. We give arithmetical conditions for numbers of states, symbols, length of codes, the number of used restriction enzymes and length of leaving sticky ends under which it would be possible to construct more powerful biomolecular computers. We also analyze from theoretical point of view the idea of increasing the complexity of this automata by using many restriction enzymes (instead of one) in the same mixture. Another theoretical analysis, precisely computational power of the Shapiro automata (called by the authors the Benenson automata) was given by Soloveichik and Winfree [3].

Our next future work will be concentrated on construction of algorithms and computer software to build elements of DNA finite automaton in the form of DNA strands (satisfying required conditions) for laboratory experiments.

ACKNOWLEDGEMENTS

This project is supported by the National Science Centre of Poland (NCN). Grant number: DEC2011/01/B/NZ2/03022.

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