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A DETAILED STUDY OF A DNA COMPUTER WITH MULTIPLE ENDONUCLEASES.

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ABSTRACT

We propose general approach for construction different models of a DNA computers, e.g. finite state machines [1, 2], push-down automata (computer with memory) [3]. We constructed in laboratory conditions a DNA computer [1, 5] and presented a detailed experimental verification of its feasibility. We described the effect of the number of states, the length of input data, and its nondeterminism on the computing process. Moreover, we have presented the reaction optimization and the methods of eliminating certain biochemical problems occurring in the implementation of a DNA computer. The problem with two copies of the same transition molecule ligating with one another could be eliminated by using different techniques to prevent self-ligation of DNA or by expanding the genetic alphabet – using unnatural nucleotides, e.g. isocytosine (dC), isoguanine (dG), 5-(2,4-diaminopyrimidine) (dj), and xanthosine (dX). This approach has the additional interesting property that the alphabet for codes of symbols could be expanded from four nucleotides (alphabet is Σ = {A, T, G, C}) to, e.g. eight nucleotides (the alphabet is Σ = {A, T, G, C, dC, dG, dj, dX}). Thus, using unnatural base pairs, it will be possible to increase the complexity a DNA computers.

In the next approach [4, 6] we presented an algorithmic method for the construction of transition molecules in a DNA computer with multiple endonucleases. This is an ad hoc approach to assembling multiple restriction enzymes for the construction of a DNA computers. This method allows the rapid construction of the main element (transition molecules) of a DNA computers and can be used in the future for automatic construction of other models of computation, e.g. pushdown automata or Turing machines made of biomolecules. This method has an additional interesting property consisting of the possibility to increase the number of states in the previously prepared model by adding subsequent restriction enzymes and appropriate encoding of the transition molecules. We apply this method to construct a DNA computer with exactly four (viz. *Bbv*I,

*Acu*I, *Bae*I, *Mbo*II) commercially available endonucleases as hardware. Furthermore, we describe an experimental realization of the above theoretical model of a DNA computer made of four endonucleases. One of the tested endonucleases (*Bae*I) cuts double-stranded DNA molecules in both directions (to the left and to the right). Our laboratory experiments provide a new way to use endonucleases which cut DNA molecules in both directions in laboratory implementations of more powerful computational devices, e.g. push-down automata [3].

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