

Introduction to the DNA Computing (new computing paradigms)

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Friday 5th May 2017, 11:30 a.m.

Room 2, Via Archirafi 34, 90123 Palermo

In 1994 L. Adleman was the first who solved the combinatorial problem of the existence of a Hamilton path in a graph by means of adequately designed chains of DNA molecules (DNA is a polymer which encodes genetic information in living organisms) and using well-known biochemical operations on them. Since that time there have appeared many scientific papers which have offered solutions to other problems known in computer science with the use of DNA. For example DNA computation has been used to solve Knight problem, the tic-tac-toe algorithm, or general SAT problem. Major challenges in DNA computing are constructions of models according to the Chomsky hierarchy e.g. Turing machines, pushdown automata and finite automata. A part of the above constructions present only theoretical solutions, while other ones were tested in laboratories. As regards this domain, the elaboration of a 2-state 2-symbol autonomous and programmable finite automaton by a team of scientists of the Weizmann Institute, led by E. Shapiro, was a significant event. The automaton built on DNA, was tested in a laboratory. Its 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 2-state automaton), as well as autonomous (the activity of the automaton does not require man's intervention during calculations). In the lecture will be presented results of the research in the DNA Computing area and elements of classical automata theory, languages and computation e.g. finite automata, pushdown automata and so on.

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All interested people, in particular students, are invited to participate