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COMPLEXITY MEASURES FOR BINDING-BLOCKING AUTOMATA [1, 2]

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ABSTRACT

We define three complexity measures for binding-blocking automata (BBA) namely, blocking number, blocking instant and blocking quotient. We also study some hierarchical structures of BBA arising out of it.

Keywords: Peptide-antibody interaction, binding-blocking automata, complexity measures

1. Introduction

Recently various computing models are being explored, of which DNA computing is one. In [1], L. Adleman took a small instance of a graph and using DNA strands he showed how to check whether the graph is Hamiltonian graph or not. Some of the other papers which followed [1] are [5, 10]. A complete survey can be found in [6, 9, 11, 12].

In a similar way to DNA hybridization, antibodies which specifically recognize peptide sequences can be used for calculation [4, 8]. In [8], H. Hug et al. introduced the concept of peptide computing via peptide-antibody interaction and solved the well known NP-complete problem – the satisfiability problem. In [4], we proved the computational completeness of peptide computing and also showed how to solve two well-known NP-complete problems namely, the Hamiltonian path problem and the exact cover by 3-set problem (a variation of the set cover problem [7]) using the interactions between peptides and antibodies.

Peptide is a sequence of amino acids attached by covalent bonds called peptide bonds. A peptide consists of recognition sites called *epitopes* for the antibodies to bind to them. A peptide can contain more than one epitope for the same or different antibodies. For each antibody which attaches to a specific epitope there is a binding

[1] Major part of this work was done when the author was in Department of Computer Science and Engineering, Indian Institute of Technology Madras, Chennai – 600036, India.

[2] Full version of a submission presented at the 4th Workshop on *Descriptional Complexity of Automata, Grammars and Related Structures* (London, Ontario, Canada, August 21–24, 2002).