

SNUPS – A SIMULATOR FOR NUMERICAL MEMBRANE COMPUTING

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ABSTRACT. *Various phenomena and processes that take place in nature and in living entities have been taken as inspiration sources for developing innovative computing methodologies. P systems represent a branch of natural computing in which the membrane structure and functioning of a biological cell are imitated to provide a powerful computational model. There are numerous theoretical studies on different types of P systems which have been shown to be computationally universal. Various application areas have been successfully proposed, ranging from modeling of biological and biochemical processes, to economics and cryptography. However, there are very few simulators of P systems available and fully documented in the public domain and this fact limits the scope of possible new applications. No numerical P systems simulators have been designed and made available so far and it is the purpose of this paper to present the structure and functionalities of SNUPS, the first and only one simulator of numerical P systems available.*

Keywords: Natural computing, Biomembranes, Numerical P systems, Simulation, Java

1. Introduction. Natural computing is an emerging research area in which novel computing paradigms and problem-solving techniques are proposed and implemented by taking inspiration from various natural phenomena and information-processing structures. Natural computing includes among other techniques, evolutionary algorithms, neural networks, molecular computing and quantum computing. Natural computing also refers to those applications in which computer hardware and software are used to replicate or synthesize natural processes and also to the use of natural materials to compute.

Particle Swarm Optimization (PSO) and respectively Ant Colony Optimization (ACO) are two prominent swarm intelligence based problem solving methods and have been used with good results in a variety of application areas. For example, PSO algorithms were used for designing DNA sequence sets [1]. DNA computing (or molecular computing, in general) is a form of natural computing which is based on using DNA, biochemistry and molecular biology, and its power comes from the fact that it has great potential of massive data storage and processing computation over data in parallel [2]. In [3], it is proposed a new biological molecular model using the Adleman-Lipton model. In [4], a new forecasting methodology inspired by natural selection and combining mathematical, computational and biological sciences, which includes fuzzy logic, DNA encoding, polymerase chain reaction and DNA quantification was proposed.

It is considered that the first cell appeared when a membrane formed. Biomembranes regulate the traffic across the boundary between the cell and the rest of the world and divide the internal space of the cell into discrete compartments to segregate processes and components [5]. More, the boundaries are central to energy conservation and cell-to-cell