A linear–time tissue P system based solution for the 3–coloring problem

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Abstract

In the literature, several examples of the efficiency of cell-like P systems regarding the solution of **NP**-complete problems in polynomial time can be found (obviously, trading space for time). Recently, different new models of tissue-like P systems have received important attention from the scientific community. In this paper we present a linear-time solution to an **NP**-complete problem from graph theory, the 3–coloring problem, and we discuss the suitability of tissue-like P systems as a framework to address the efficient solution to intractable problems.

Key words: Membrane Computing, Tissue P Systems, cell division, 3–coloring problem.

1 Introduction

Membranes are involved in many reactions taking place inside various compartments of a cell, and they act as selective channels of communication between different compartments as well as between the cell and its environment [1].

This paper is enclosed in the Natural Computing framework. More precisely, in the study of the structure and functioning of cells as living organisms able to process and generate information. Assuming this starting point, two different disciplines within Natural Computing can be found in the literature: *Membrane Computing* and *Brane Calculi*.

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Brane Calculi were recently introduced in [6], under the assumption that in living cells membranes are not merely containers, but they are actually highly dynamic and participate actively in the cell life. In this way, "computation" happens on the membranes, not inside them.

On the other hand, Membrane Computing starts from the assumption that the processes taking place within the compartmental structure of a living cell can be interpreted as computations [19].

This emergent cross-disciplinary branch of Natural Computing was introduced by Gh. Păun in [18]. It has received important attention from the scientific community since then, with contributions by computer scientists, biologists, formal linguists and complexity theoreticians, enriching each others with results, open problems and promising new research lines. In fact, Membrane Computing has been selected by the Institute for Scientific Information, USA, as a fast *Emerging Research Front* in Computer Science, and [20] was mentioned in [30] as a highly cited paper in October 2003.

The computational devices in Membrane Computing are called *P systems*. Roughly speaking, a P system consists of a membrane structure, in the compartments of which one places multisets of objects which evolve according to given rules in a synchronous non-deterministic maximally parallel manner [5].

In the last years, many different models of P systems have been proposed. The most studied variants are characterized by a *cell-like* membrane structure, where the communication happens between a membrane and the surrounding one. In this model we have a set of nested membranes, in such a way that the graph of neighborhood relation is a tree.

One of the topics in the field is the study of the computational power and efficiency of P systems. In particular, different models of these cell-like P systems have been successfully used in order to design solutions to **NP**-complete problems in polynomial time (see [10] and the references therein). These solutions are obtained by generating an exponential amount of workspace in polynomial time and using parallelism to check simultaneously all the candidate solutions. Inspired in living cells, cell-like P systems abstract the way of obtaining new membranes, mainly from two biological processes: *mitosis* (membrane division) and *autopoiesis*, see [14] (membrane creation). Both ways of generating new membranes have given rise to the corresponding P systems model: *P systems with active membranes*, where the new workspace is generated by membrane division and *P systems with membrane creation*, where the new membranes are created from objects.

Both models are universal from a computational point of view, but technically, they are pretty different. In fact, nowadays there does not exist any theoretical result which proves that these models can simulate each other in polynomial time.

Under the hypothesis **P**$\neq$**NP**, Zandron et al. [29] established the limi-

[5] A layman-oriented introduction can be found in [21] and further bibliography at [31].

tations of P systems that do not use membrane division concerning the efficient solution of **NP**-complete problems. This result was generalized by Pérez Jiménez et al. [25] obtaining a characterization of the **P**≠**NP** conjecture by the polynomial time unsolvability of an **NP**-complete problem by language accepting P systems (without using rules that allow to construct an exponential number of membranes in polynomial time).

We shall focus here on another type of P systems, the so-called (because of their membrane structure) *Tissue P Systems*. Instead of considering that membranes are hierarchically arranged, the membranes are placed in the nodes of a graph. This variant has two biological inspirations (see [17]): intercellular communication and cooperation between neurons. The common mathematical model of these two mechanisms is a net of processors dealing with symbols and communicating these symbols along channels specified in advance. The communication among cells is based on symport/antiport rules[6]. Symport rules move objects across a membrane together in one direction, whereas antiport rules move objects across a membrane in opposite directions.

From the seminal definition of Tissue P systems [16,17], several research lines have been developed and other variants have arisen (see, for example, [2,5,7,12,13,27]). One of the most interesting variants of Tissue P systems was presented in [22]. In that paper, the definition of Tissue P systems is combined with the one of P systems with active membranes, yielding *Tissue P systems with cell division*.

One of the main features of such Tissue P systems with cell division is related to their computational efficiency. In [22], a polynomial-time solution to the **NP**-complete problem SAT is shown. In this paper we go on with the research in this variant and present a linear-time solution to another well-known **NP**-complete problem: the 3–coloring problem.

The paper is organized as follows: first we recall some preliminaries and the definition of Tissue P systems with cell division. Next, recognizer Tissue P systems are briefly described. A linear–time solution to the 3–coloring problem is presented in the following section, with a short overview of the computation and the necessary resources. Finally, the main results, some conclusions and new open research lines are presented.

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