

Annotation on PhD Thesis

Title: On the Power and Universality of Biologically-inspired Models of Computation

Author: Sergiu Ivanov

Institute: Université Paris Est, France

Defence date: June 23, 2015



Keywords: computational completeness, universality, insertion-deletion systems, networks of evolutionary processors, controlled insertion-deletion systems, register machines, Petri nets.

Objective: Consider the problems of computational completeness and universality for several biologically-inspired models of computation: insertion-deletion systems, networks of evolutionary processors, and multiset rewriting systems. The presented results fall into two major categories: study of expressive power of the operations of insertion

and deletion with and without control, and construction of universal multiset rewriting systems of low descriptional complexity.

Novelty: The thesis focuses on novel models of computation inspired by the biological cell and gives original techniques of analysis of the expressive power of these models as well as of optimisation of their descriptional complexity.

Results: In the first part of the thesis we focus on insertion-deletion systems and we show that allowing one-symbol insertion and deletion rules to check a two-symbol left context enables them to generate all regular languages. Moreover, we prove that allowing longer insertion and deletion contexts does not increase the computational power. We further consider insertion-deletion systems with additional control over rule applications and show that the computational completeness can be achieved by systems with very small rules.

The second part of the thesis is concerned with the universality problem, which consists in finding a fixed element able to simulate the work any other computing device. We start by considering networks of evolutionary processors (NEPs), a computational model inspired by the way genetic information is processed in the living cell, and construct universal NEPs with very few rules. We then focus on multiset rewriting systems, which model the chemical processes running in the biological cell. For historical reasons, we formulate our results in terms of Petri nets. We construct a series of universal Petri nets and give several techniques for reducing the numbers of places, transitions, inhibitor arcs, and the maximal transition degree. Some of these techniques rely on a generalisation of conventional register machines, proposed in this thesis, which allows multiple register checks and operations to be performed in a single state transition.

Software contributions: The construction of small universal Petri nets (multiset rewriting systems) was supported by software developed by the author with the goal of automating solutions to some combinatorial and optimisation problems. Programmatic definitions of

the discussed models of computing were given and are available online¹.

Applicative value: The applicative value of the thesis has two principal aspects. On the one hand, the results concerning insertion-deletion systems contribute directly to understanding of the complexity of the biological processes this model was inspired by, whereas the described small universal objects may serve as a theoretical foundation for the construction of simple but computationally universal biological computers. On the other hand, the thesis proposes a number of original approaches to the discussed problems, which can be generalised and applied in a different context.

¹<https://github.com/scolobb/computing-devices>