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Biologicky motivované výpočtové modely

(Dizertačná práca)

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Poďakovanie

Osobitná vďaka patrí vedúcemu diplomovej práce doc. RNDr. Damasovi Gruskovi PhD. za cenné rady, námety, podnetné pripomienky a všestrannú pomoc, ktorú si hlboko vážim. Len vďaka mnohým prínosným konzultáciam a intenzívnej spolupráci som bol schopný napísať toto dielo. Nesmiem zabudnúť ani na RNDr. Branislava Rovana, CSc. a spolužiakov za to, že si na dizertačnom seminári našli čas, aby si vypočuli moju prezentáciu dizertačnej práce. Ďalšie poďakovania venujem rodičom a známym, ktorí to so mnou dokázali vydržať posledné týždne pred odovzdaním.

Abstrakt

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Práca začína definovaním základných pojmov a končí interaktívnou prílohou.

Kľúčové slová: Mariáš, Teória hier, Minimax, Neúplna informácia.

Obsah

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Úvod

About computational models inspired by biology. Neural networks, evolution algorithms, membrane systems.

V teoretickej informatike je veľa oblastí, ktoré sú motivované inými vednými disciplínami. Veľkú skupinu tvoria modely motivované biológiou. Patria sem napríklad neurónové siete, výpočtové modely založené na DNA, evolučné algoritmy, ktoré si už našli svoje významné uplatnenie v informatike a dokázali, že sa oplatí inšpirovať biológiou. L-systémy sú špecializované na popisovanie rastu rastlín, ale našli si uplatnenie aj v počítačovej grafike, konkrétne vo fraktálnej geometrii. Ďalšie rozvíjajúce sa oblasti ešte čakajú na svoje významnejšie uplatnenie.

Jednou z nich sú membránové systémy. Je pomerne mladá oblasť - prvý článok bol publikovaný v roku 2000 (see [**?**])

Kapitola 1

Preliminaries

1.1 Formal languages theory

Our study is based on the classical theory of formal languages. We will recall some definitions:

Definition 1.1.1 *An* **alphabet** *is a finite nonempty set of symbols. Usually it is denoted by* Σ *or* V*.*

Definition 1.1.2 *A* **string** *over an alphabet is a finite sequence of symbols from alphabet.*

We denote by V^* the set of all strings over an alphabet V. By $V^+ = V^* - \{\varepsilon\}$ we denote the set of all nonempty strings over V.

Definition 1.1.3 *A* **language** *over the alphabet* V *is any subset of* V^**.*

1.2 Register machines

Definition 1.2.1 *A* n**-register machine** *is a tuple* $M = (n, P, i, h)$*, where:*

- n *is the number of registers,*
- P *is a set of labeled instructions of the form* $j : (op(r), k, l)$*, where* $op(r)$ *is an operation on register* r *of* M*, and* j*,* k*,* l *are labels from the set* $Lab(M)$ *(which numbers the instructions in a one-to-one manner),*

- *i is the initial label, and*
- *h is the final label.*

The machine is capable of the following instructions:

- $(add(r), k, l)$: Add one to the contents of register r and proceed to instruction k or to instruction l; in the deterministic variants usually considered in the literature we demand $k = l$.
- $(sub(r), k, l)$: If register r is not empty, then subtract one from its contents and go to instruction k, otherwise proceed to instruction l.
- *halt* : This instruction stops the machine. This additional instruction can only be assigned to the final label h.

A deterministic m-register machine can analyze an input $(n_1, \ldots, n_m) \in N_0^m$ in registers 1 to m, which is recognized if the register machine finally stops by the halt instruction with all its registers being empty (this last requirement is not necessary). If the machine does not halt, the analysis was not successful.

1.3 Multisets

Definition 1.3.1 *A multiset over a set X is a mapping $M : X \to \mathbb{N}$.*

We denote by $M(x), x \in X$ the multiplicity of x in the multiset M.

Definition 1.3.2 *The* **support** *of a multiset M is the set $supp(M) = \{x \in X | M(x) \geq 1\}$.*

It is the set of items with at least one occurence.

Definition 1.3.3 *A multiset is* **empty** *when it's support is empty.*

A multiset M with finite support $X = \{x_1, x_2, \ldots, x_n\}$ can be represented by the string $x_1^{M(x_1)} x_2^{M(x_2)} \ldots x_n^{M(x_n)}$.

Definition 1.3.4 *Multiset inclusion. We say that mutiset M_1 is included in multiset M_2 if $M_1(x) \leq M_2(x) \forall x \in X$. We denote it by $M_1 \subseteq M_2$.*

Definition 1.3.5 *The* **union** *of two multisets* $M_1 \cup M_2 : X \to \mathbb{N}$ *is defined as* $(M_1 \cup M_2)(x) = M_1(x) + M_2(x)$.

Definition 1.3.6 *The* **difference** *of two multisets* $M_1 - M_2 : X \to \mathbb{N}$ *is defined as* $(M_1 - M_2)(x) = M_1(x) - M_2(x)$.

Definition 1.3.7 *Product of multiset* M *with natural number* $n \in \mathbb{N}$ *is* $(n \cdot M)(x) = n \cdot M(x)$.

1.4 Multiset languages

The number of occurences of a given symbol $a \in V$ in the string $w \in V^*$ is denoted by $|w|_a$.

Definition 1.4.1 $\Psi_V(w) = (|w|_{a_1}, |w|_{a_2}, \ldots, |w|_{a_n})$ *is called a Parikh vector associated with the string* $w \in V^*$, *where* $V = \{a_1, a_2, \ldots a_n\}$.

Definition 1.4.2 *For a language* $L \subseteq V^*$, $\Psi_V(L) = \{\Psi_V(w) | w \in L\}$ *is the Parikh mapping associated with* V.

Example 1.4.1 Consider an alphabet $V = \{a, b\}$ and a language $L = \{a, ab, ba\}$. $\Psi_V(L) = \{(1, 0), (1, 1)\}$. Notice that Parikh image of L has only 2 element while L has 3 elements.

Definition 1.4.3 *If FL is a family of languages, by PsFL is denoted the family of Parikh images of languages in FL.*

Kapitola 2

Membrane computing

Recently, an interdisciplinary research between the fields of Computer Science and Biology has been rapidly growing.

Bioinformatic has undergone a fast evolving process, especially the areas of genomics and proteomics. Bioinformatics can be seen as the application of computing tools and techniques for the management of biological data. Just to mention a few, the design of efficient algorithms for sequence alignment, the investigation of methods for prediction of the 3D structure of molecules and proteins and the development of data structures to effectively store huge amount of structured data.

On the other hand, the birth of biologically inspired frameworks started the investigation of mathematical models and their properties and technological requirements for their implementation by biological hardware. Those frameworks are inspired by the nature in the way it "computes", and has gone through the evolution for billions of years.

Neural networks, genetic algorithms and DNA computing are already well established research fields.

However, nature computes not only at the neural or genetic level, but also at the cellular level. In general, any non-trivial biological system has a hierarchical structure where objects and information flows between regions, what can be interpreted as a computation process.

The regions are typically delimited by various types of membranes at different levels from cell membranes, through skin membrane to virtual membranes which delimits different parts of an ecosystem. This hierarchical system can be seen in other field such as distributed computing, where again well delimited computing units coexist and are hierarchically arranged in complex

systems from single processors to the internet.

Membranes keep together certain chemicals or information and selectively determines which of them may pass through.

From these observations, Paun [1] introduces the notion of a membrane structure as a mathematical representation of hierarchical architectures composed of membranes. It is usually represented as a Venn diagram with all the considered sets being subsets of a unique set and not allowed to be intersected. Every two sets are either one the subset of the other, or disjoint.

Kapitola 3

P systems

In previous chapter we introduced the notions of membrane and membrane structure.

The next step is to place certain objects in the regions delimited by the membranes. The objects are identified by their names, mathematically symbols from a given alphabet.

Several copies of the same object can appear in a region, so we will work with multisets of objects.

In order to obtain a computing device, we will allow the objects to evolve according to evolution rules. Any object, alone or together with another objects, can be transformed in other objects, can pass through a membrane, and can dissolve the membrane in which it is placed.

All objects evolve at the same time, in parallel manner across all membranes.

The evolution rules are hierarchizes by a priority relation, which is a partial order.

These aspects all together forms a P system as introduced in [1].

In section 3.1 we will provide formal definition of a P system.

3.1 Definitions

P system is a tuple $(V, \mu, w_1, w_2, \ldots, w_m, R_1, R_2, \ldots, R_m)$, where:

- V is the alphabet of symbols,

- μ is a membrane structure consisting of m membranes labeled with numbers $1, 2, \ldots, m$,
- $w_1, w_2, \ldots w_m$ are multisets of symbols present in the regions $1, 2, \ldots, m$ of the membrane structure,
- $R_1, R_2, \ldots R_m$ are finite sets of the rewriting rules asssociated with the regions $1, 2, \ldots, m$ of the membrane structure.

Each rewriting rule may specify for each symbol on the right side, whether it stays in the current region, moves through the membrane to the parent region or through membrane to one of the child regions. An example of such rule is the following: $abb \rightarrow (a, here)(b, in)(c, out)(c, here)$.

A **configuration** of a P system is represented by it's membrane structure and the multisets of objects in the regions.

A **computation step** of P system is a relation $\Rightarrow$ on the set of configurations such that $C_1 \Rightarrow C_2$ iff:

For every region in C_1 (suppose it contains a multiset of objects w) the corresponding multiset in C_2 is the result of applying a multiset of maximal simultaneously applicable multiset rewriting rules in R_w^{msap} to w.

In other words, a maximal multiset of rules is applied in each region.

For example, let's have two regions with multisets aa and b. In the first region there is a rule $a \rightarrow b$ and in the second membrane there is a rule $b \rightarrow aa$. The only possible result of a computation step is bb, aa. The first rule was applied twice and the second rule once. No more object could be consumed by rewriting rules.

Computation of a P system consists of a sequence of steps. The step S_i is appied to result of previous step S_{i-1}. So when $S_i = (C_j, C_{j+1})$, $S_{i-1} = (C_{j-1}, C_j)$.

There are two possible ways of assigning a result of a computation:

1. By considering the multiplicity of objects present in a designated membrane in a halting configuration. In this case we obtain a vector of natural numbers. We can also represent this vector as a multiset of objects or as Parikh image of a language.
2. By concatenating the symbols which leave the system, in the order they are sent out of the skin membrane (if several symbols are expelled at the same time, then any ordering of them is accepted). In this case we generate a language.

The result of a computation is clearly only one multiset or a string, but for one initial configuration there can be multiple possible computations. It follows from the fact that there exist more than one maximal multiset of rules that can be applied in each step.

3.2 P system variants

Besozzi in his PhD thesis (see [2]) formulates three criteria that a good P system variant should satisfy:

1. It should be as much realistic as possible from the biological point of view, in order not to widen the distance between the inspiring cellular reality and the idealized theory.

2. It should result in computational completeness and efficiency, which would mean to obtain universal (and hence, programmable) computing devices, with a powerful and useful intrinsic parallelism;

3. It should present mathematical minimality and elegance, to the aim of proposing an alternative framework for the analysis of computational models.

3.2.1 Accepting vs generating

3.2.2 Active vs passive membranes

Most of the studied P system variants assumes that the number of membranes can only decrease during a computation, by dissolving membranes as a result of applying evolution rules to the objects present in the system. A natural possibility is to let the number of membranes also to increase during a computation, for instance, by division, as it is well-known in biology. Actually, the membranes from biochemistry are not at all passive, like those in the models briefly described above. For example, the passing of a chemical compound through a membrane is often done by a direct interaction with the membrane itself (with the so-called protein channels or protein gates present in the membrane); during this interaction, the chemical compound which passes through membrane can be modified, while the membrane itself can in this way be modified (at least locally).

In [3] Paun considers P systems with active membranes where the central role in the computation is played by the membranes: evolution rules are associated both with objects and membranes, while the communication through membranes is performed with the direct participation of the membranes; moreover, the membranes can not only be dissolved, but they also can multiply by division. An elementary membrane can be divided by means of an interaction with an object from that membrane.

Each membrane is supposed to have an electrical polarization (we will say charge), one of the three possible: positive, negative, or neutral. If in a membrane we have two immediately lower membranes of opposite polarizations, one positive and one negative, then that membrane can also divide in such a way that the two membranes of opposite charge are separated; all membranes of neutral charge and all objects are duplicated and a copy of each of them is introduced in each of the two new membranes. The skin is never divided. If at the same time a membrane is divided and there are objects in this membrane which are being rewritten in the same step, then in the new copies of the membrane the result of the evolution is included.

In this way, the number of membranes can grow, even exponentially. As expected, by making use of this increased parallelism we can compute faster. For example, the SAT problem, which is NP complete, can be solved in linear time, when we consider the steps of computation as the time units. Moreover, the model is shown to be computationally universal.

3.2.3 Parallelism options

Maximal parallelism, minimal parallelism, n-parallelism, sequential models.

3.2.4 Contextivity rules

Context rules vs cooperational rules, catalytic rules, symmetric cooperational rules, catalytic rules, promoters, inhibitors, context-free rules.

3.2.5 Priority rules

3.2.6 Energy of membranes

3.2.7 Calculi of Looping Sequences

3.3 Case studies

Vultures in Pyrenees, Scavangers of Pyrenees.

Záver

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Štatistiky

Tu budú štatistiky.