

KATEDRA INFORMATIKY FAKULTA MATEMATIKY, FYZIKY A INFORMATIKY UNIVERZITA KOMENSKÉHO, BRATISLAVA

BIOLOGICKY MOTIVOVANÉ VÝPOČTOVÉ MODELY

(Dizertačná práca)

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Vedúci: doc. RNDr. Damas Gruska, PhD. Bratislava, 2011

Čestne prehlasujem, že som túto dizertačnú prácu vypracoval samostatne s použitím citovaných zdrojov.

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Poďakovanie

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Abstrakt

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Práca začína definovaním základných pojmov a končí interaktívnou prílohou.

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

Obsah

Zoznam obrázkov

Zoznam tabuliek

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

Kapitola 2

Membrane computing

Membranes intro

Natural computing is a recent field of research wchi tries to imitate nature in the way it "computes", learning new computing models and computing paradigms experimented for billions of years by nature.

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 [?] 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.

P systems

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

3.1 Definitions

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

• V is the alphabet of symbols,

- μ is a membrane structure consisting of m membranes labeled with numbers $1, 2, \ldots, m$,
- $w_1, w_2, \dots w_m$ are multisets of symbols present in the regions $1, 2, \dots, m$ of the membrane structure,
- $R_1, R_2, \ldots R_m$ are finite sets of the rewriting rules associated 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 $a \to b$ and in the second membrane there is a rule $b \to aa$. 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 applied to result of previous step S_{i-1} . So when $S_i = (C_j, C_{j+1}), S_{i-1} = (C_{j-1}, C_j)$.

Result of computation is multiset of symbols that left the skin membrane in the configuration after the last computation step. For one initial configuration there can be multiple possible results. It follows from the fact that there exist more than one maximal multiset of rules that can be applied in each step.

P system defines a parikh image of a language: the set of possible results of computations.

TODO:

How is P system defined. Mostly taken from my article. Multiset rewriting. Accepting vs generating model, active or passive membranes, quality vs

quantity aspects.

3.2 P system variants

We are interested in computation power of various variants of P systems. Especially those that are universal (Turing completeness).

3.2.1 Parallelism options

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

3.2.2 Contextivity rules

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

- 3.2.3 Priority rules
- 3.2.4 Energy of membranes
- 3.2.5 Calculi of Looping Sequences

3.3 Case studies

Vultures in Pyrenees, Scavangers of Pyrenees.

Záver

Literatúra

[1] Gheorghe Păun. Computing with membranes. Technical Report 208, Turku Center for Computer Science-TUCS, 1998. (www.tucs.fi).

Štatistiky

Tu budú štatistiky.