

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.

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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

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 [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.

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

3.1 Definitions

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

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.