Dualistic open problems in membrane computing*

Luca Manzoni and Antonio E. Porreca

Dipartimento di Informatica, Sistemistica e Comunicazione
Università degli Studi di Milano-Bicocca
Viale Sarca 336/14, 20126 Milano, Italy
{luca.manzoni,porreca}@disco.unimib.it

Summary. We present some high-level open problems in the complexity theory of membrane systems, related to the actual computing power of confluence vs determinism, semi-uniformity vs uniformity, deep vs shallow membrane structures, membrane division vs internal evolution of membranes.

1 Confluence vs determinism

P systems solving decision problems (*recogniser P systems* [14]) are usually required to be *confluent* [14] rather than strictly deterministic. That is, they are allowed to have multiple computation, as long as all of them agree on the final result, acceptance or rejection.

This sometimes simplifies the presentation of some algorithms. For instance, a classic membrane computing technique [12, 19] consists in generating all 2^n truth assignments of n variables by using membrane division rules of the form $[x_i]_h \to [t_i]_h\ [f_i]_h$, with $1 \leq i \leq n$. The membrane division is triggered separately in each membrane with label h by one of the objects x_i, nondeterministically chosen at each computation step. Irrespective of all such nondeterministic choices, the end result is invariably a set of 2^n membranes, each containing a different truth assignment.

Notice, however, that this kind of nondeterminism can be completely avoided by serialising the generation of truth assignments for each variable: first all instances of x_1 trigger the division, then all instances of x_2, and so on. This can be achieved by adding an extra subscript to each object, which counts down to zero and only then starts the division process.

It is often the case that confluent nondeterminism can be avoided in a similar way, although this is usually proved by exhibiting a deterministic

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algorithm, rather than showing how to remove the nondeterminism from existing algorithms. It is then natural to ask whether this is indeed always the case, or if there exists a variant of P system where confluent nondeterminism is strictly stronger than determinism.

For powerful enough P systems (e.g., able to efficiently simulate deterministic Turing machines, or stronger than that) we feel that the existence of such a variant would be very surprising, although there do exist confluent nondeterministic algorithms with no known deterministic version. For instance, the currently known proof of efficient universality (i.e., the ability to simulate any Turing machine with a polynomial slowdown) of P systems with active membranes using elementary membrane division [1] relies on a massive amount of nondeterministic choices performed at each simulated step; these are due to the fact that send-in communication rules cannot differentiate among membranes having the same label and electrical charges.

2 Semi-uniformity vs uniformity

Recogniser P systems usually appear in families $\boldsymbol{\Pi} = \{\Pi_x : x \in \Sigma^\star\}$, where each member of the family is associated to a string x and accepts if and only if x belongs to a given language.

A family of P systems is usually required to be at least *semi-uniform*, that it, to have an associated Turing machine M with some suitable resource bound (usually, polynomial time) such that M on input x outputs a suitable encoding of Π_x [14, 9].

A more restrictive condition on families of P systems is full-fledged *uniformity* [14, 9]: there exist *two* Turing machines F and E (again, usually with polynomial runtime) such that F on input $n = |x|$ constructs a P system "skeleton" Π_n, valid for all strings of length n, and E on input x produces a multiset w encoding x, which is then placed inside the input region of Π_n, giving the P system Π_x that computes the answer.

It is known [10] that, for restrictive enough resource bounds, uniformity is weaker than semi-uniformity. However, when polynomial-time semi-uniform solutions to problems sometimes appear in the literature first, polynomial-time uniform solutions usually follow.

We conjecture that polynomial-time uniformity and semi-uniformity do indeed coincide for powerful enough P systems, such as standard P systems with active membranes [12]. The idea here is that a semi-uniform family could be made uniform by simulating the "semi-uniform portion" of the construction, depending on the actual symbols of $x \in \Sigma^n$, with the P system constructed for all strings of length n.

3 Membrane division vs internal evolution

The computing power of a *single* membrane (for cell-like P systems) or cell (for tissue-like P systems) working in polynomial time usually has a **P** upper bound, as already proved by the "Milano theorem" [19]; the only way to exceed this bound would be to include *really overly powerful* rules (e.g., rules able to perform an **NP**-complete task in a single step). The **P** upper bound can actually be achieved by having cooperative rewriting rules (even minimal cooperation [18, 17] suffices) or rules able to simulate them indirectly (e.g., active membrane rules with membrane charges [8]). Several techniques for simulating polynomial-time Turing machines using a single membrane are known [7].

Any additional power beyond **P** of models presented in the literature is due to membrane division, first exploited in order to solve **NP**-complete problems in polynomial time [12]. Membrane division enables us to create exponentially many processing units working in parallel; by using communication rules, these can synchronise and exchange information (this is the famous space-for-time trade-off in membrane computing).

It is reasonable to expect that P system variants where the power of a single membrane working in polynomial item coincides with **P** can be standardised in a "Turing machine normal form": each membrane performs a Turing machine simulation[2], and the communication and division rules implement a network, whose shape can be exploited to simulate nondeterminism, alternation, or oracle queries [7].

Notice that what previously described does not necessarily carry over to variants of P systems with weaker rules internal to the membranes, such as "P conjecture systems" [13, Problem F] (active membranes without charges), which do not seem able to simulate cooperation [2], or with communication restricted to a single direction, either send-out [5, 6, 16] or send-in only [15].

4 Deep vs shallow membrane structures

Let us now consider cell-like P systems with membrane division, for instance P systems with active membranes [12]. It has already been shown that the nesting depth of membranes (more specifically, the nesting depth of membranes with associated division rules, which we might call *division depth*) is one of the most influential variables when establishing the efficiency of these P systems.

Indeed, P systems without membrane division (i.e., with division depth 0) are known to characterise the complexity class **P** in polynomial time [19]. At the other end of the spectrum, we have P systems with active membranes with elementary and non-elementary division rules (i.e., with polynomial division depth), which characterise **PSPACE** in polynomial time.

[2] This can be trivially implemented by having each membrane simulate a Turing machine which, in turn, simulates the original membrane via a Milano theorem.

When only elementary membrane division is allowed (i.e., division depth 1), then the intermediate complexity class $\mathbf{P}^{\#\mathbf{P}}$ is characterised in polynomial time [3, 6]. This class contains all decision problems solved by deterministic polynomial-time Turing machines with oracles for counting problems in the class $\#\mathbf{P}$ [11].

It has been proved that moving from any constant division depth d to division depth $d+1$ allows the P systems to simulate Turing machines with more powerful oracles [4]. We conjecture that this is in fact a proper hierarchy. This result would require proving the upper bounds corresponding to the known lower bounds.

It also remains open to characterise the computing power of polynomial-time P systems with other division depths, such as $O(\log n)$.

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