

Membrane Computing (Tutorial)

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The aim of the tutorial is to give a general overview of the Membrane Computing paradigm [2,5]. Membrane Computing is a quite active research field, initiated by Gh. Păun in 1998 [3]. It is a theoretical machine-oriented model, where the computational devices (known as *P systems*) are in some sense an abstraction of a living cell. There exist a large number of different definitions of P systems, but most of them share some common features: a *membrane structure* (defining in a natural way a number of regions or compartments), and an alphabet of *objects* that are able to evolve and/or move within the membrane structure according to a *set of rules* (emulating the way substances undergo biochemical reactions in a cell).

Many of the first P systems specifications that were investigated proved to be *universal* or *computationally complete* (i.e. equivalent to Turing Machines). Besides, the quest for *efficiency* has been another research direction, yielding in many cases cellular solutions to **NP**-complete problems working in polynomial time (making a space-time trade-off and using the inherent massive parallelism of P systems). The first session of the tutorial will formalize these concepts, presenting a computational complexity theory for Membrane Computing.

Another completely different approach is to concentrate on the evolution of the P systems itself, instead of focusing on the output of the computation and the number of steps. This research direction is getting an increasing attention recently. For instance, P systems have been used to model biological phenomena within the framework of cellular systems and population biology presenting models of oscillatory systems, signal transduction, gene regulation control, quorum sensing, metapopulations, and real ecosystems.

The second session of this tutorial will introduce a P systems based general framework for modelling complex dynamical phenomena.

Phenomena under investigation are described by means of multienvironment P systems consisting of a finite number of environments, each of them having a specific P system with active membranes. Each rule has associated a computable function which depends on the left-hand side of the rule and the run time. The inherent randomness and uncertainty of biological processes is captured by using probabilistic or stochastic strategies.

Applications of Membrane Systems in Computational Systems and Synthetic Biology

As mentioned above, P systems are being used as tools for modelling purposes, adapting their semantics in an appropriate way. Works on this direction rely on the development of associated simulation software, since P systems have not yet been implemented neither in hardware nor in biological means.

It is interesting to note that some biological parameters of the modeled processes can be obtained experimentally by biologists or ecologists (and therefore they can be taken into account when designing the model), while some other relevant constants may be unknown. Software tools are thus necessary to enable virtual experimentation, as well as for the process of model validation.

Specifically, membrane computing, offers a modelling framework for multi-compartmental stochastic and discrete systems that allows us to design and assess bacterial synthetic gene circuits operating at the multi-cellular level [4]. The third session of this tutorial will present a specification/modelling language based on P systems that allows researchers to design synthetic gene circuits in a parsimonious and incremental manner. In this respect, membrane computing assists in one of the goals of synthetic biology, the incorporation of engineering principles into the pipelines used in the design and in vivo implementation of gene circuits exhibiting desirable behaviour or phenotypes.

The last session of the tutorial will illustrate the general modelling framework for systems biology and population dynamics based on P systems, by displaying some real case studies, and their associated software tools [1].

Acknowledgments. The authors acknowledge the support of the projects TIN2008-04487-E and TIN2009-13192 of the *Ministerio de Ciencia e Innovación* of Spain, cofinanced by FEDER funds, and the support of the Project of Excellence with *Investigador de Reconocida Valía* of the *Junta de Andalucía*, grant P08-TIC-04200.

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