Current Developments on Computational Modeling Using P Systems

Agustín Riscos-Núñez⋆

Research Group on Natural Computing, Department of Computer Science and
Artificial Intelligence, University of Sevilla, Avda. Reina Mercedes s/n, 41012, Sevilla,
Spain
`ariscosn@us.es`

Abstract. A P system based general framework for modeling ecosystems dynamics will be described. Roughly speaking, the idea is to use several regions (environments) that can be connected, each of them containing a probabilistic P system with active membranes (having identical skeleton for every environment).

Some real case studies will be displayed, discussing the usefulness of this tool in simulating complex ecosystems dynamics to aid managers, conservationists and policy-makers in making appropriate decisions for the improvement of management and conservation programs.

Membrane Computing is a quite active research field, initiated by Păun in 1998 [6]. 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 models, 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).

Recently, P systems are being used as tools for modeling purposes, adapting their semantics in an appropriate way. Indeed, interesting achievements are being obtained, which show that membrane computing can be an alternative to classical modeling frameworks (e.g. those based on differential equations). 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.

The talk will try to provide a general overview of modeling frameworks for systems biology and population dynamics based on P systems (see e.g. [1,7]), displaying some real case studies [2,3]. 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 [4,5].

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