

# Population P Systems a Model for the Behaviour of Systems of Bio-Entities

John Auld<sup>1</sup>, Luca Bianco<sup>2</sup>, Gabriel Ciobanu<sup>3</sup>, Marian Gheorghe<sup>1</sup>,  
Dario Pescini<sup>4</sup>, and Francisco J. Romero-Campero<sup>5</sup>

<sup>1</sup>Department of Computer Science, The University of Sheffield  
Regent Court, Portobello Street, Sheffield S1 4DP, UK  
E-mail: [acp05jma@sheffield.ac.uk](mailto:acp05jma@sheffield.ac.uk), [M.Gheorghe@dcs.shef.ac.uk](mailto:M.Gheorghe@dcs.shef.ac.uk)

<sup>2</sup>Department of Computer Science, University of Verona  
Strada Le Grazie 15, 37134 Verona, Italy  
Email: [bianco@sci.univr.it](mailto:bianco@sci.univr.it)

<sup>3</sup>Romanian Academy, Institute of Computer Science,  
Blvd. Carol I nr. 8, 700505 Iasi, Romania E-mail: [gabriel@info.uaic.ro](mailto:gabriel@info.uaic.ro)

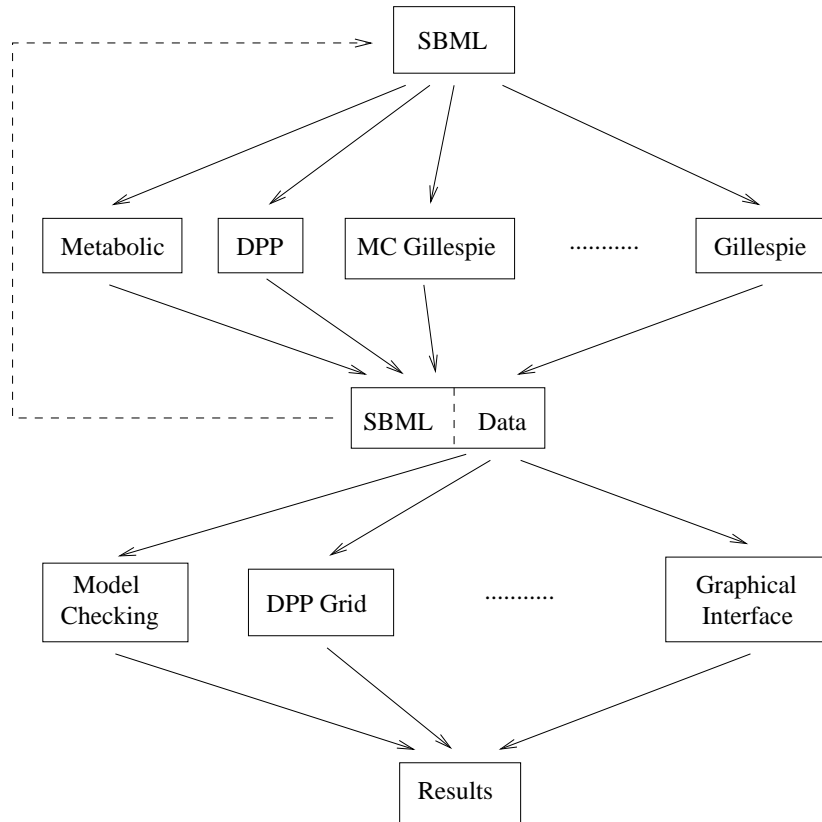
<sup>4</sup>Department of Informatics, Systems, and Communications  
Università degli Studi di Milano-Bicocca  
Via Bicocca degli Arcimboldi 8, 20126 Milano, Italy  
Email: [pescini@disco.unimib.it](mailto:pescini@disco.unimib.it)

<sup>5</sup>Research Group on Natural Computing  
Department of Computer Science and Artificial Intelligence  
University of Seville, Avda. Reina Mercedes, 41012 Sevilla, Spain  
E-mail: [fran@us.es](mailto:fran@us.es)

## 1 Introduction

Membrane computing is an emerging branch of natural computing which deals with distributed and parallel computing devices of a bio-inspired type, which are called *membrane systems* or *P systems* ([15], [16], [20]). P systems, originally devised by Gh. Păun in [15], are introduced as computing devices which abstract from the structure and functioning of living cells - they are defined as a hierarchical arrangement of regions delimited by membranes (*membrane structure*), with each region having associated a multiset of objects and a finite set of rules. The structure of a P system is usually represented as a tree describing the hierarchical architecture based on membranes. P systems are a very powerful computational model equivalent to Turing machines, able to efficiently to solve NP complete problems, that exhibit very promising interactions to other similar computational paradigms [16]. A wealth of P system variants have been published and theoretical properties intensively studied [16], [14], [11], [20].

Apart from the main stream of research involving the study of the computational capabilities of different variants of P systems and applications in biology, there were investigations into formally defining the semantics of the behaviour and evolution of such systems. In [2] an operational semantics for a class of P systems is defined and its implementation in Maude is described. A step further has been taken by providing a structural operational semantics for a class of P



**Fig. 1.** The project.

systems with correctness proofs for each set of inference rules [3]. A Petri net semantics for a basic class of P systems has been also provided [13]. All these approaches refer to P systems evolving in a maximally parallel manner, which is the cornerstone of most of the variants of the model.

Recent researches have been instead dedicated to the study of P systems as a modelling tool for biological systems [9], [8], [17], [7], [10], [18]. In this case P systems are not used as a computing paradigm, but rather as a formalism for describing the behaviour of the system to be modelled. Therefore, there is a growing interest in developing implementations for the membrane computing paradigm in order to be able to execute a P system model, run simulations of biological phenomena, and verify certain properties of the model. In this respect, a number of tools have already been produced (some of them are available from [20]).

## 2 Population P Systems

A natural generalisation of the P system model can be obtained by considering P systems where the structure of the system is defined by an arbitrary graph. Each node in the graph represents a membrane, which gets assigned a multiset of objects and a set of rules for modifying these objects and communicating them alongside the edges of the graph [16]. These networks of communicating membranes are also known as tissue P systems because, from a biological point view, they can be interpreted as an abstract model of multicellular organisms. They collaborate with each other to form a multitude of different tissues, arranged into organs performing various functions [1]. This model may be also regarded as an abstraction of a population of bio-entities aggregated together in a more complex bio-unit. In this respect the model addresses not only the cellular and tissue levels, but also the case of various colonies of more complex organisms like bacteria, ants, bees etc. A basic computational model of this type, called population P systems, has been introduced and its power established [4]. A specific class of systems inspired by the quorum sensing mechanism occurring in bacterium colonies has been devised and its power investigated [5]. These models of populations of individuals resemble the work on colonies started in the last decade [19].

This work will show the main results concerning the computational power of different variants of population P systems [4], [5] and their relevance to self-assembly processes [12], [6]. A simple specification language, that is designed to be used in systems biology modelling, with its semantics, and an integrated simulation tool (see Figure 1) together with a graphical interface (see Figure 2) will be presented.

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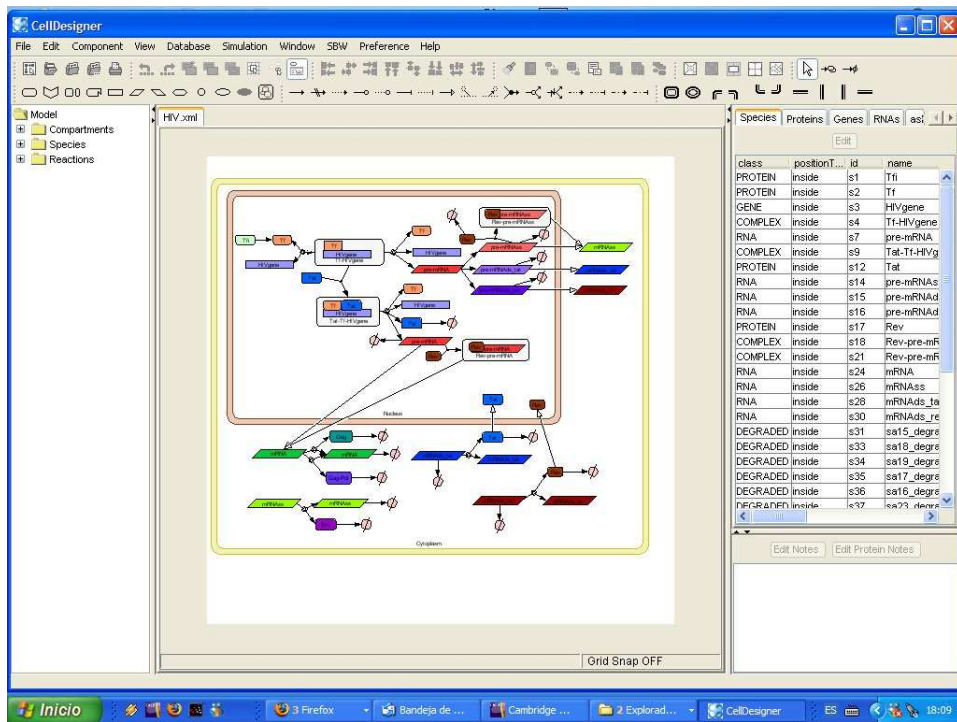


Fig. 2. The CellDesigner Interface