A Bioinspired Computing Approach to Model Complex Systems

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Abstract. The use of models is intrinsic to any scientific activity. In particular, formal/mathematical models provide a relevant tool for scientific investigation. This paper presents a new Membrane Computing based computational paradigm as a framework for modelling processes and real-life phenomena. P systems, devices in Membrane Computing, are not used as a computing paradigm, but rather as a formalism for describing the behaviour of the system to be modelled. They offer an approach to the development of models for biological systems that meets the requirements of a good modelling framework: relevance, understandability, extensibility and computability.

Keywords: Membrane Computing · Multienvironment P systems · Multicompartimental P systems · Population Dynamics P systems

1 Introduction

Scientists regularly use abstractions with the aim to describe and understand the reality they are examining. Computational modelling is the process of representing real world problems in mathematical terms in an attempt to find solutions to their associated complex systems. A formal model is an abstraction of the real-world onto a mathematical/computational domain that highlights some key features while ignoring others that are assumed to be secondary. A formal model should not be considered as representation of the truth, but instead as a statement of our current knowledge of the phenomenon under research.

It is desirable for a model to fulfill four properties: *relevance*, *understandability*, *extensibility* and *computability* [19]. A formal model must be relevant capturing the key features while ignoring others assumed to be secondary. The abstract formalism used should adecquately match the informal concepts and ideas from the investigated phenomenon. Mathematical models should also be extensible to higher level of organizations, like tissues, organs, organisms, etc, in the case of cellular systems. Finally, a formal model should be able to be implemented in a computer so that we can run simulations to study the dynamics of the system in different scenarios, as well as the qualitative and quantitative reasoning about its properties.

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One of the main objectives of any model is to provide a predictive capability, that is, the possibility to make guesses in terms of plausible hypotheses related to the dynamics of the observed phenomenon in different scenarios that are of interest to experts.

Cellular systems and population biology often depend on many parameters related to the observed behaviours. Since they define the dynamics of the system, parameters must satisfy some conditions, which can be referred to as the invariants of the associated behaviour. Some of these invariants can be expressed by rules and can be obtained by carrying out experiments, while others cannot be measured or they are very expensive to estimate. Therefore, before simulations can be performed in order to make predictions, we need to *calibrate* our model. Several parameters values are tested by calibration and the results corresponding to the state parameters are compared with the observed/expected behaviour of the system for the same state parameters. In some cases, the design of the model has to be reconsidered [15].

Nowadays ordinary/partial differential equations (ODEs/PDEs) constitute the most widely used approach in modelling complex systems. Nevertheless, in some cases such as molecular interaction networks in cellular systems, any model described by means of a system of ODEs/PDEs is based on two assumptions: (a) cells are assumed to be well stirred and homogeneous volumes so that concentrations do not change with respect to space; and (b) chemical concentrations vary continuously over time in a deterministic way. This assumption is valid if the number of molecules specified in the reaction volume are sufficiently large and reactions are fast.

Membrane Computing is an emergent branch of Natural Computing introduced by G. Paun at the end of 1998. This new computing paradigm starts from the assumption that processes taking place in the compartmental structure of a living cell can be interpreted as computations. In contrast to differential equations, P systems explicitly correspond to the discrete character of the components of a complex system and use rewriting/evolution rules on multisets of objects which represent the variables of the system. The inherent stochasticity, external noise and uncertainty in cellular systems is captured by using stochastic or probabilistic strategies. A general bioinspired computing modelling framework, called *multienvironment P systems* is introduced.

The paper is structured as follows. First, the framework of multienvironment P systems is defined in a formal way. Section 3 is devoted to multicompartmental P systems, the stochastic approach. Besides, four case studies at cellular level are presented in this Section. Population dynamics P systems, the probabilistic approach, are studied in Section 4 and three case studies related to real ecosystems are described. Finally, some conclusions are drawn.

2 Multienvironment P System

A *multienvironment P system* of degree (m, n, q) taking T time units is a tuple

$$(G, \Gamma, \Sigma, \mu, T, \Pi_1, \ldots, \Pi_n, \mathcal{R}, E_1, \ldots, E_m, \mathcal{R}_E)$$

where:

- $G = (V, S)$ is a directed graph. Let $V = \{e_1, \ldots, e_m\}$ whose elements are called environments;
- Γ is the working alphabet and $\Sigma \subsetneqq \Gamma$.
- μ is a rooted tree with q nodes.
- T is a natural number that represents the simulation time of the system;
- $\Pi_k = (\Gamma, \mu, \mathcal{M}_{1,k}, \ldots, \mathcal{M}_{q,k}, \mathcal{R})$, $1 \leq k \leq n$, is a basic P system of degree q, and $\mathcal{R}$ is a finite set of rules of the type $u[v]_i^{\alpha} \longrightarrow u'[v']_i^{\beta}$.
- $E_j \in M_f(\Sigma)$, $1 \leq j \leq m$.
- $\mathcal{R}_E$ is a finite set of communication rules among environments of the following forms $(x)_{e_j} \longrightarrow (y_1)_{e_{j_1}} \ldots (y_h)_{e_{j_h}}$ and $(\Pi_k)_{e_j} \longrightarrow (\Pi_k)_{e_{j'}}$.
- No rules from $\mathcal{R}$ and $\mathcal{R}_E$ compete for objects.
- Each rule of the system has associated a computable function whose domain is $\{0, \ldots, T\}$.

A multienvironment P system can be viewed as a finite set of environments and a finite set of P systems, such that: (a) the links between environments are given by the arcs taken from a directed graph; (b) each P system has the same working alphabet, the same membrane structure and the same evolution rules; and (c) each environment contains several P systems, where each evolution rule has associated a computable function and each one of them has an initial multiset which depends on the environment; and (d) there is a finite set of rules among the environments. Furthermore, inside the environments, only objects from a distinguished alphabet can exist.

It is worth pointing out that this bioinspired computational approach has some qualitative advantages with respect to ordinary/partial differential equations approach:

- They use a language closer to experts than differential equations.
- They are not affected by the usual constraints present when defining differential equations based models.
- They are modular, that is, once an initial version of the model is designed, adding modifications is relatively easy. On the one hand, small changes in the system entails small changes in the model. On the other hand, when using differential equations most times we have to start from scratch.

3 Stochastic Approach: Multicompartmental P Systems

A multienvironment P system of degree (m, n, q) taking T time units, is said to be stochastic if:

(a) the computable functions associated with the rules of the P systems are *propensities*: they are computed from *stochastic constants* by applying the law of mass-action law (the reaction rate depends proportionally on the product of the concentrations of the reactants), and the stochastic constants are obtained from the kinetic constants in an easy way [18]; these rules depend on time but not on the environment;

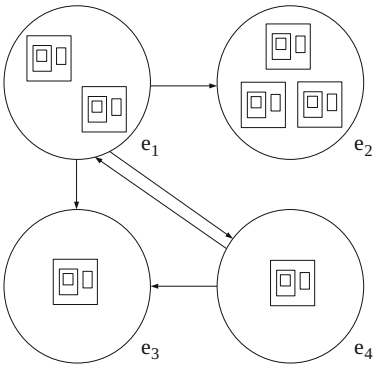

Fig. 1. A multienvironment extended P system

(b) at the initial moment, the P systems $\Pi_1, \ldots, \Pi_n$ are ramdomness distributed between the m environments; for instance, as in the picture.

These kind of P systems are called *multicompartmental P systems.*

The dynamics of these systems is captured by either the *multicompartmental Gillespie's algorithm* [18] or the *deterministic waiting time algorithm* [2]. Gillespie's algorithm [10–13] provides an exact method for the stochastic simulation of systems of bio-chemical reactions; the validity of the method is rigorously proved and it has been already successfully used to simulate biochemical processes and it is based on the inversion method of Monte Carlo theory. The deterministic waiting time algorithm is based on the fact that in vivo chemical reactions take place in parallel in a asynchronous manner. The time taken for the formation of each molecule, called waiting time, is calculated and the rule (reaction) with the least waiting time is applied, changing the concentration in their respective compartments. Each time there is a change in the concentration of a molecule in any compartment, the waiting time for reactions "using" that molecule needs to be recalculated for the compartment.

Infobiotics workbench is a computational framework implementing a synergy among multicompartmental stochastic simulations, formal model analysis and structural/parameter model optimisation for computational systems and synthetic biology (http://www.infobiotics.org/index.html)

In this section some practical examples of multicompartmental P systems applications for modelling cellular systems are presented.

3.1 Apoptosis Mediated by FAS Protein

The FAS-induced apoptotic signalling pathway was shown to be one of the most relevant processes for understanding and combating cancer, AIDS and neurodegenrative diseases such as Parkinson's disease, Alkzheimer, etc.

Two pathways activated by FAS have been identified [23], and are referred to as type I (*death receptor pathway*) and type II (*mitochondrial pathway*), where caspases play a crucial role for both the initiation and execution of apoptosis (*programmed cell death*). The pathways diverge after activation of initiator caspases and converge at the end by activating executor caspases. In the type I pathway, initiator caspases activate executor caspases directly. In the type II pathway, a more complicated cascade is activated involving the disruption of mitochondrial membrane potential.

We have designed a multicompartmental P system with only one environment that consists of 53 objects and 99 evolution rules (see [2] for details) in order to study when a cell chooses the mitochondrial pathway or the death receptor pathway to produce apoptosis.

A *Java* simulator has been implemented and it accepts as input a *Systems Biology Markup Language* (SBML) file containing the rules to be simulated and initial concentrations for the molecules in the system. We used the *Cell Designer* package to generate the SBML source file for the reactions (Cell Designer is a structured diagram editor for drawing gene-regulatory and biochemical networks). The simulator engine mimics the biological cell and it is designed in a modular way so that it can use different strategies for different pathways if needed. The specific strategy, based on the deterministic waiting time algorithm, will be executed depending on the initial concentrations of various objects present in the system. A simulator designed in *Scilab*, a scientific software package for numerical computations providing a powerful open computing environment for engineering and scientific applications [23], using the multicompartmental Gillespie algorithm has been also considered [2].

The consistency between the framework and the experimental results in the paper [14] validates our model. We have stated that our discrete methods handle low levels of molecules in a different way that ODE/PDE techniques. To further investigate the differences between discrete and ODE/PDE methods, we have chosen to focus on one rule from the FAS-mediated pathway (a transformation)

Multicompartmental P systems constitute an alternative to ordinary/partial differential equations methods. We have argued that the discrete nature of our technique might be better for simulating the evolution of systems involving low numbers of molecules.

3.2 Gene Regulation Systems in Lac Operon in E. coli

In most bacteria, gene expression is highly regulated in order to produce the necessary proteinic machinery to respond to environmental changes. Therefore, at a given time, a bacterial cell synthesises only those proteins necessary for its survival under the particular conditions of that time.

Many of the genes in Escherichia coli (E. coli) are expressed constitutively; that is, they are always turned on. Others, however, are active only when their products are needed by the cell, so their expression must be regulated. The most direct way to control the expression of a gene is to regulate its rate of transcription. Adding a new substrate to the culture medium may induce the formation of new enzymes capable of metabolising that substrate. An example of this phenomenon happens

when we take a culture of E. coli that is feeding on glucose and transfer some of the cells to a medium containing lactose instead. In this case a revealing sequence of events takes place.

A multicompartmental P system modelling the gene expression control in the Lac Operon has been designed (see [20] for details). Specifically, the system has only one environment, the total number of symbols in the working alphabet is 51 and there are 55 evolution rules. The novelty of this design is that the objects can be symbols or strings over the alphabet. In this context, finite multisets of strings within membranes represent the genetic information encoded in DNA and RNA. The central dogma of molecular cell biology states that genetic information is stored in the DNA. This information is transcribed into mRNA which in turn is translated into proteins. It is worth pointing out that transcription and translation have been modelled as rewriting and concurrent processes on strings.

Using the Multicompartmental Gillepie's Algorithm and a simulator developed in *Scilab*, we have studied the behaviour of the system for different environmental conditions to see how the system is able to sense the presence of different substrate (glucose and lactose).

The delay between the sensing of the signal and the expression of different genes is not explicitly modelled but emerges as a consequence of the formulation of our approach. Our results agree well with experimental observations and results obtained by using other approaches.

3.3 Quorum Sensing in Vibrio Fischeri

Bacteria are generally considered to be independent unicellular organisms. Nevertheless, in some circumstances bacteria exhibit coordinated behaviour which allows an entire population of bacteria to regulate the expression of specific genes depending on the size of the population.This phenomenon is called *quorum sensing*, that is, a cell density dependent gene regulation system. It was first investigated in the marine bacterium *Vibrio Fischeri*. The bacteria colonise specialised light organs in the squid which cause it to become luminescent. Vibrio Fischeri only causes luminescence when colonising the light organs and do not emit light when in the planktonic free-living state. Luminescence in the squid is involved in the attraction of prey, camouflage and communication between different individuals.

Bacteria colonies behave like multicellular organisms. Each bacterium must be able to sense and communicate with other units in the colony to express some specific genes in a coordinated way. The cooperative activities carried out by members of the colony generate a *social intelligence* [17].

In this case, we have designed a multicompartmental P system of degree $(25, n, 1)$, with 25 environments containing each of them an ordinary P system only having the skin membrane (see [21] for details) This model has been represented in the *Systems Biology Markup Language* using *Cell Designer* [9].

The emergent behaviour of the system has been studied for three colonies of different size (10, 100 and 3000 bacteria) to examine how bacteria can sense the number of individuals in the colony and produce light only when such number is big enough.

Our simulations show that Vibrio fischeri has a quorum sensing system where a single bacterium can guess that the size of the population is big enough and start to produce light. This bacterium starts to massively produce signals, but if the signal does not accumulate in the environment it means that the guess was wrong and it switches off the system. In contrast, if the signal does accumulate in the environment meaning that the number of bacteria in the colony is big enough, a recruitment process takes place that causes the entire population of bacteria to become luminescent. Let us stress that this emergent behaviour is a result of local interactions in the environments between different simple agents, the bacteria, which are only able to produce and receive molecular signals. These results agree well with in vitro observations.

4 Probabilistic Approach: Population Dynamics P Systems (PDP Systems)

A multienvironment functional P system with active membranes of degree (q, m, n) taking T time units, is said to be probabilistic if:

(a) the computable functions associated with the rules of the systems are *probability functions* verifying some conditions (these rules depend on the environment but not on the time, they are constant functions);
(b) the total number of P systems Π_k is equal to the number of environments: each environment contains one P system; and
(c) the rules among environments are only of the form: $(x)_{e_j} \longrightarrow (y_1)_{e_{j_1}} \dots (y_h)_{e_{j_h}}$

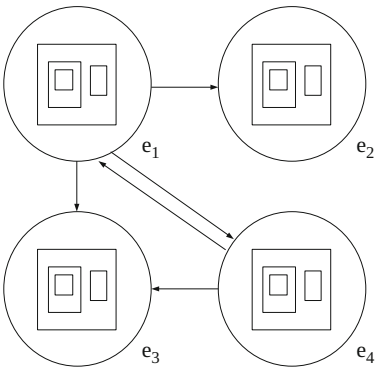

Fig. 2. A Population Dynamics P system

This kind of P systems are called *Population Dynamics P systems* [5]. The dynamics/semantics of these systems is captured by *ad hoc* algorithms such as *Binomial block based simulation algorithm* (BBB) [1], *Direct Non Deterministic distribution with Probabilities algorithm* (DNDP) [7] and *Direct distribution based on Consistent Blocks algorithm* (DCBA) [16], among others.

The BBB algorithm follows a strategy based on the binomial distribution and blocks of rules with the same left-hand side. In general, each simulation step is divided into two main stages: *selection* and *execution*. In the first one, the algorithm decides which rules will be applied, and the number of applications for each one (taking into account their left-hand sides and the available objects in the current configuration). In the second stage, the selected rules are applied, consuming the multisets of the rules' left-hand sides and adding the multisets of the rules' right-hand sides the selected number of times, and possibly changing the polarization of membranes.

The DNDP algorithm performs a non-deterministic distribution of objects along the rules, but considering the probabilities. The algorithm is split into two phases, selection and execution. This time, selection phase is divided into two micro-phases: selection phase 1 (consistency) and selection phase 2 (maximality). Together with an initialization phase, it has a total of four phases. The first selection phase calculates a multiset of consistent applicable rules. This is performed by looping the rules in a random order, and applying each one (if consistent with the already selected rules) using the binomial distribution according to the probabilities. The second selection phase eventually increases the multiplicity of some of the rules in the previous multiset to assure maximal application, obtaining a multiset of maximally consistent applicable rules. Again, there is a loop over the remaining rules, checking the maximality condition. Although the DNDP algorithm achieves better results than its predecessor (BBB), the behaviour still produces some distortion in many situations (it is biased towards the rules with the highest probabilities).

The DCBA algorithm is based on the idea of proportionally distributing the amount of objects along the rule blocks. A proportional calculus is made in such a way that rules requesting for more objects are penalized. However, this calculation can be adapted to the biological semantics to be captured by the model. Probabilities are applied to rule blocks locally. The simulation algorithm consists on two phases, selection and execution. But this time, selection is split into three micro-phases: phase 1 (distribution), phase 2 (maximality), and phase 3 (probabilities). Selection phase 1 uses a distribution table, where rows represent objects inside regions, and columns are rule blocks. A normalized distribution of the objects is performed over the rows. Phase 2 iterates the remaining rule blocks assuring maximality, and phase 3, once rule blocks have been selected, calculates multinomial distributions for each one (according to the selected number for it, and the probabilities of the corresponding rules). DCBA is able to reproduce the desired semantics for the model of PDP systems. However, its efficient implementation is a challenge (the distribution table can be very large).

P-Lingua (http://www.p-lingua.org/wiki/index.php/Main_Page) is a programming language for Membrane Computing which aims to be a standard to

define P systems, in particular, population dynamics P systems. `MeCoSim` (http://www.p-lingua.org/mecosim/) is a visual environment to model, simulate, analyse and verify solutions based on P systems, by defining custom apps for virtual experimentation under different scenarios.

In what follows some practical examples of PDP systems applications for modelling real ecosystems are presented.

4.1 Bearded Vulture

The Bearded Vulture is a cliff-nesting and territorial large scavenger distributed in mountains ranges in Eurasia and Africa. This is one of the rarest raptors in Europe (150 breeding pairs in 2007). This endangered species feeds almost exclusively on bone remains of wild and domestic ungulates. Its main food source is bone remains of dead small and medium-sized animals.

The ecosystem to be modelled is in the Pyrenean and Prepyrenean mountains of Catalonia (NE Spain) and it is composed of 13 species: (a) three avian scavengers (Bearded vulture,the Egyptian vulture and the Griffon vulture as predator species); (b) six wild ungulates (Pyrenean Chamois, Red deer, Fallow deer, Roe deer, Mouflon and Wild boar); and (c) four domestic ungulates (sheep, cow, goat and horse) that are found in an extensive or semi-extensive regime providing carrion for the avian scavengers and considered as prey species. Prey species are herbivores and their remains form the primary food resource for the avian scavengers in the study area.

In order to model this real ecosystem, a population dynamics P system with two environments containing each of them an ordinary P system of degree 2 has been considered (see [3] for details). The model addresses:

(a) the population dynamics previously mentioned;
(b) the interactions among the 13 species;
(c) the presence of two zones in the study area;
(d) the communication protocol between the two areas; and
(e) the ecosystem maximum load capacity for each of the areas.

The algorithmic scheme of the proposed model is shown in Figure 3 and it is structured following a series of modules which are run sequentially corresponding to the passing of 1 year in the ecosystem.

We have studied the dynamics of the ecosystem modifying the initial conditions in order to analyse how the ecosystem would evolve if different biological factors were modified either by nature or through human intervention. We have designed a population dynamics P system with only one environment and 49 types of rules. For each type of animal the number of biological parameters are related to reproduction, mortality, feeding and other general processes of the species itself. We have shown the robustness of the model with respect to a modified order of application of the different processes modules.

`MeCoSim` software has been used for the execution of the model. The population trend of the three scavenger species and the six wild ungulates has been obtained by

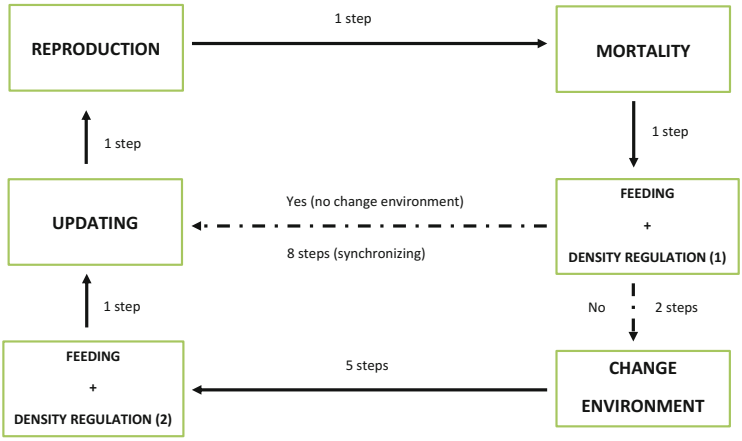

Fig. 3. Algorithmic scheme of the Bearded vulture model [3]

the model with respect to data recovered by direct censuses from 1994 to 2008. The model has been experimentally validated with data experimentally obtained corresponding to the years from 1994 to 2008 (the input being the number of animals in 1994) covering a period of 14 years.

4.2 Pyrenean Chamois

Pyrenean Chamois (*Rupicapra p. pyrenaica*) is an ungulate species inhabiting the Catalan Pyrenees. It is of great interest, not only from a hunting standpoint, but also naturalistic and touristic. In recent years, several diseases have caused a drastic decrease in the number of individuals. In particular, the disease associated to a pestivirus is having a very important impact on a social and economic scale in the Pyrenees. Since they provide significant economic contributions in the area and constitutes an important food resource for obligate and facultative scavengers, it is very interesting to provide a model in order to facilitate the management of their ecosystems.

We have given the first computational model of a real ecosystem from the Catalan Pyrenees involving the Pyrenean Chamois. Specifically we have designed a population dynamics P system model [6] which consists of four environments containing each of them an ordinary P system of degree 11. The system uses 47 types of rules and considers four separated areas in the Catalan Pyrenees where the species lives. Weather conditions, especially in winter (particularly the thickness of the snow layer), influences the values of biological parameters of the Pyrenean Chamois species[8]. Causes of death for this species include: natural death, hunting and diseases. Only Pestivirus infection has been taken into account.

The algorithmic scheme of the proposed model is shown in Figure 4. The algorithm has been sequenced, but all animals evolve in parallel. The processes to be

modelled will be the weather conditions (snow), reproduction, regulation of density, food, natural mortality, hunting mortality and mortality due to a disease.

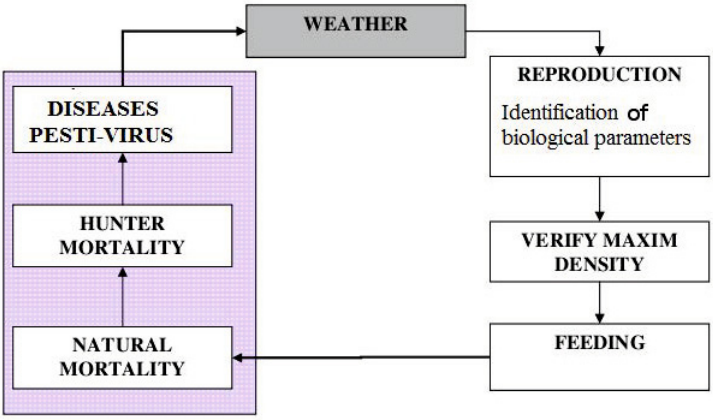

Fig. 4. Algorithmic scheme of the Pyrenean Chamois model [6]

We have shown the robustness of the model with respect to the order of application of different rules.

There are experimental data available from 1988 on, although censuses where not carried out annually so that, experimental series is not a continuous one. Using the censuses in 1988 as input for the model, 22 years have been simulated repeating the process 50 times for each of the years simulated. In general, the model behaves well in all cases.

4.3 Zebra Mussel

The Zebra Mussel (*Dreissena polymorpha*) is a long known invasive species in Middle East, Europe or even Northern USA rivers and fresh water lakes. This species provokes serious ecological and socioeconomic impacts. It is an agent of radical ecologic change, threatening colonized ecosystems in the short and half terms by modifying certain water and sediments parameters, causing the displacement of autochthonous species.

In Spain, its colonization began in Ebro river, in the summer of 2001 [22], threatening not only the infrastructure of several reservoirs but also tourism and the ecological sustainability of the affected ecosystems.

The ecosystem to be modelled is very complex as a consequence of the combined effect of different features: the biological cycle of Zebra Mussels, the heterogeneity of the physical environment, the size of the reservoir, and its water turnover. Thus, the variations in the level of water can be considered negligible. As a result, the application of conventional techniques for modelling may be unfeasible.

In order to study the population dynamics of the Zebra Mussel in the fluvial reservoir of Riba-roja, the following factors have been considered:

(1) The basic biological processes of the species, determined by the thermal conditions and the substrate suitability in the reservoir;
(2) the features of the special habitat under study, that is, an artificial reservoir with water currents and eddies, and changes in water renewal depending on the depth and time of year, according to the reservoir management for hydropower and characteristics of incoming water;
(3) the possibility of external larvae entering from an upstream reservoir and the transfer of individuals to the reservoir by boats.

The algorithmic scheme of the proposed model is shown in Figure 5. Each individual may initiate the loop at different times. The processes sequenced in the figure are run in parallel in an area at the same time. The processes are out of sync between areas. The passing of a year is represented by running the loop twice.

A population dynamics P system based model for the Zebra Mussel at the Ribarroja reservoir (Spain) has been presented [4]. The system consists of 17 environments containing each of them an ordinary P system of degree 40. The system uses 55 types of rules. The main goal of this model is to provide a management tool to aid in the decision-making process, with the aim of controlling (eradicating or decreasing) the population of these invasive mussels.

Three different scenarios have been studied:

- The first set of simulations is addressed to determine the effect of the current water flow on the reservoir.
- The goal of the second set of simulations is to obtain a water flow (water turnover) that allows the elimination of the Zebra Mussel in the reservoir, keeping the other conditions constant.
- The last set of simulations aimed to test one of the main hypotheses concerning the invasion of the Zebra Mussels in the reservoir. It studies the effect of the external introduction of larvae considering the current hydrological regime.

The software tool `MeCoSim` has been used to design the simulator interface. Input values (i.e., parameters and value variables of the model) are introduced directly into the interface of the simulator. In order to study the behaviour of the model in a specific scenario, we simply need to change the input values in this interface.

The results obtained by the simulation of the presented model under the given scenarios are consistent with those published by other authors and observed by the experts responsible for the monitoring and management of the population of Zebra Mussels in the reservoir of Riba-roja.

5 Conclusions

In this paper, a general bioinspired computing modelling framework, called multienvironment P systems, is introduced. The framework is based on Membrane Computing and two approaches are described: stochastic approach which is usually applied to model *micro*-level systems (such as signalling pathways, gene expression

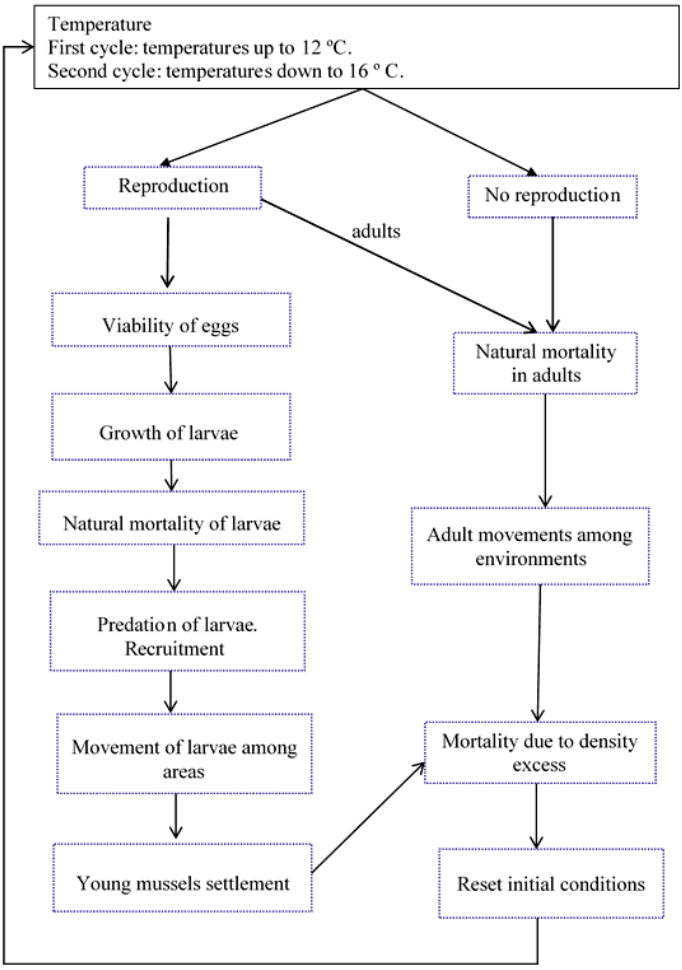

Fig. 5. Algorithmic scheme of the Zebra Mussel model [4]

control, bacteria colonies, etc.), and the probabilistic approach which is normally used for *macro*-level modelling (such as real ecosystems). Stochastic multienvironment P systems are called multicompartmental P systems, and probabilistic multienvironment P systems are called population dynamics P systems. The dynamics of multicompartmental P systems is captured by either the multicompartmental Gillespie's algorithm or the deterministic waiting time algorithm. The dynamics of the population dynamics P systems is captured by *ad hoc* algorithm such as binomial block based simulation algorithm (`BBB`), direct non Deterministic distribution with probabilities algorithm (`DNDP`), the direct distribution based on consistent blocks algorithm (`DCBA`).

Several case studies are presented in order to illustrate the bioinspired computing modelling framework. Specifically, three cases for multicompartmental P systems (apoptosis mediated by FAS protein, gene regulation system in Lac Operon in E. coli and quorum sensing in Vibrio Fischeri) and three cases for population dynamics P systems (real ecosystems related to bearded vulture, Pyrenean Chamois and Zebra Mussel).

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