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BioMASS: a Biological Multi-Agent Simulation System

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***Abstract*—This article presents an agent based model for the simulation of biological systems. The approach consists mainly of providing individual based models for each of the functional groups that conform an ecosystem. Functional groups (a term commonly used by ecologists) may represent a group of individuals (from the same or from different species) that share relevant attributes. This provides flexibility to configure different kinds of populations by parametrization without the need of programming, something useful for biologists. Additionally, a simulation tool implemented as a multi-agent system facilitates the analysis and understanding of ecological complexity. Multi-agent systems are proposed to address heterogeneity and autonomy demanded by the interdisciplinary individual-based modeling methodology. The objective of the system is to explore the intricate relationships among population and individuals, in an ecosystem approach. The main difference with other tools is the ability of incorporating individual decisions, based on metabolism and environmental conditions.**

I. INTRODUCTION

SIMULATION by means of computational tools is a widely used resource for ecologists to test hypotheses given the difficulty to carry out experiments directly in the natural environment. Some of the problems typically faced are those related to the impact of human activity on ecosystem health. Computational experimentation enables researchers to test their working hypotheses quickly, repeatedly and without affecting the environment. Given the large number of organisms and interactions that make up the most simple ecosystem, until recently the simulation tools have been based on numerical solutions to equations in which entire populations or groups of individuals are represented by means of statistical parameters. This is the case of Ecopath [1], a software tool that computes numerical solutions for a mass balance equation to estimate the changes in the biomass of an ecosystem such as reproduction and mortality rates, migration, predation and biomass extraction by anthropogenic activity. Ecopath models are initialized with data describing the groups of organisms belonging to the ecosystem under study. If there is available information about the spatial distribution of these populations, it is possible to subdivide the study area in a grid and apply the computational tool for calculating time and space fluctuations of biomass for each population group inside the domain under study.

Ecopath is the most popular computer simulation tool for Ecology but is not unique. There are other tools such as EcoSim [2] or Goldsim [3] that use Monte Carlo techniques to simulate the uncertainty inherent to the environmental systems. However, despite its enormous value as research tools, models based on numerical calculations reduce to statistical parameters the description of the populations of organisms, leaving out of the model important information about the many and different forms of relationships among the individuals within an ecosystem. For example, Ecopath only considers one kind of relationship, predator-prey, and yet this is parameterized in the form of biomass transferred among as many food items in the diet. Many other relationships such as competition or symbiosis are ignored even if their importance in the functioning of an ecosystem might be substantial. But more importantly, these models ignore the ability of individuals within a population to interact with the environment, modify it while at the same time adapting to it.

Individual-based modeling (IBM) has appeared [4] to support more flexibility and analysis abilities when modeling ecosystems. IBM, rather than global parameters about the populations use descriptions at the individual level to build an ecosystem model and allocates computational resources to simulate the development of every organism included in the model, making explicit the relations that each one might establish with other organisms and the environment. The behavior exhibited by the populations, their statistical indicators and the cause-effect relationship with respect to the environment are properties that must *emerge* from the aggregation of the activities and interactions of all the individuals. It is expected that the macro-scale predictions produced by IBM show high concordance with those obtained by the numerical models. But models that are based on individuals are able to produce much more detailed information about the simulated entities and their interrelationships, both, in time and space scale. To model a biomass transfer between two population groups in an IBM it is necessary to define the process of hunting-

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capture-ingestion that may occur when two individuals become spatially close at a given time. Similarly it is possible to model the corresponding menace detection-avoidance process. Thus, the predator-prey relationship is modeled with richer detail than in traditional numerical modeling. Just as this, in an IBM it is possible to model many other kinds of relationship for reproduction, competition for space, for collaboration, etc.

In the case of the Mexican Caribbean coast, there is great concern about the effect that the intense tourist activity in this area has on the health of the ecosystems associated with this area's coastal reefs. These reefs are part of the Mesoamerican Reef System which is the second largest barrier reef in the world after the Great Barrier Reef located on the northeast coast of Australia. In a typical application of numerical modeling programs, Arias-Gonzales et al [5] studied the relationship between fishing activities and the health of the coastal reef ecosystems at three locations of the Mexican Caribbean using the simulation tool Ecopath. The study provides statistical evidence on the negative effect of fishing activities on coral reef health and the ecosystems that sustain them. However, the computational tool cannot yield information about the intimate mechanisms that might explain the connecting thread between cause and effect.

The long-term goal of this project is to find explanations for the statistically-proven interrelated phenomena of human activity and the decline of coastal marine ecosystems of the Mexican Caribbean. To this end we initiated the construction of the BioMASS software tool for simulation of biological ecosystems by applying the IBM approach. This tool is based on a strict model for mass and energy transfer using a rich predator-prey relationship. This allows the study of trophic chains within ecosystems while allowing the specification of many other types of relationships among organisms.

The next section describes the IBM approach and proposes a set of techniques for its successful implementation under the paradigm of multi-agent systems. Section III presents the class structure that supports the simulation system and the composition relationships among the objects involved. It also describes the energy transfer, individual growth and emergent statistical information gathering mechanisms. Section IV shows the user interface on a prerelease version of the system and how it is used to set up an experiment. Section V presents some experimental results using a rather simple hypothetical ecosystem. Section VI addresses some conclusions and describes future work.

II. INDIVIDUAL BASED MODELING

IBM is a term used in Ecology to name a class of models that describes individual organisms as computational entities. These models are the foundation for a new methodology to address the complexity of ecological systems [6].

Traditionally, ecological systems are studied by formulating simplified representations of these systems using mathematical equations. The equations are formally solved to answer the questions the model was devised for. However, to keep the mathematical equations explicitly soluble, analytically or numerically, the assumptions of the models are very simple. These assumptions are symbolized through variables characterizing the state of the whole system. In this sense, traditional models are more like a macro perspective of a system limited to properties descriptions at this level.

On the other hand, IBM promotes computer simulation models that are suited to observe how unforeseen system level properties emerge from the adaptive behavior of individual organisms. IBM also allows ecologists to study how this macro-structural emergent phenomena influences individuals behavior, that is, the macro-micro causality. Thus, computer simulation can be an effective tool to build less simplified models overcoming certain limitations of traditional techniques to explain patterns, processes and to predict the behavior of a system in response to individual changes and their interactions.

In IBM, individual organisms belonging to a system and their autonomous behavior are explicitly represented. These individuals are also called agents and are commonly implemented as software objects. According to the IBM paradigm, agents should be described as heterogeneous and autonomous entities that exhibit adaptive behavior, usually through learning skills, adjusting their behavior to each other and to the changing environment. The agents interact locally, meaning they interact spatially only within a given neighborhood. Autonomous means that they act without a central direction or control, rather pursuing their goals, as organisms strive to survive and reproduce in nature. Being heterogeneous implies being unique among a population. This uniqueness should be described using its genetic content, its morphological and physiological characteristics, the physical space that occupies (two individuals cannot be situated at the same place at the same time) and the local nature of its interactions with its environment.

Despite the several advantages of IBM over mathematical theorizing, IBM is more complex to develop because IBM requires computer-programming abilities by the modeler. An IBM has to be implemented as a system of software agents and the individual uniqueness should be reflected as a set of computational attributes. Another issue related with IBM is the difficulty to analyze and understand the simulation model results, a hard task that requires multiple model executions over time and systematically varying initial conditions in order to assess the robustness of the results set.

To overcome these difficulties IBMs can be developed as a Multi-Agent Systems (MAS), a paradigm that came from the field of distributed artificial intelligence (DAI). A multi-agent system is a collection of software agents developed mostly to solve tasks in a distributed manner. Each one of these agents is a computer system situated in a given environment that is capable of autonomous action in order to meet its design objectives [7]. It t has proof to be appropriate for the representation of ecological dynamics, which state modeling problems in terms of representations, communication and controls [8]. The abstractions of this paradigm are especially adequate to simulate at the individual level the physiological processes, the life cycle, the decision-making mechanisms, the interactions with other individuals and with the environment, and other processes that determine the local state of an organism. There are many theories, methodologies, mechanisms and tools from the Agent Oriented Software Engineering (AOSE) to design and implement MAS [9]. Also there is another trend to provide discipline specific MAS developing tools, such as agent-based social simulation tools, agent-based computational economics simulation tools, and so on [10]. However, it is important to be especially careful with the selection of these tools since many of them lack the artifacts to achieve the mentioned autonomy and uniqueness.

The BioMASS tool is a Java application based on the Repast agent-based modeling and simulaton plaform[11] with the purpose of building individual based models (IBMs) for ecological systems. It considers that for implementing IBM under the MAS paradigm, IBM simulation software should meet the following requirements as formulated in [12]:

1) The capacity of the model to represent each individual (not a collection) by means of a dedicated software agent.
2) The capacity of the model to endow each individual with distinctive traits to ensure the uniqueness of each entity inside the temporal and spatial context of the simulation (this guarantees that each individual might be different with respect not only to others but with itself at different moments)
3) The ability of the model to represent the way the individual utilizes resources by means of its local and direct interaction with its environment.
4) The ability of the model to reflect the phases through which the individual goes along its life cycle.
5) The size of a population and all other statistical variables of the simulation may be computed at any time from the result of the aggregated accounting of the single individuals and not from inference.
6) The population dynamics (of cyclical nature) must emerge from the integration of the life cycle of its individuals (which rather than cyclical is lineal) through generational change.

The above characteristics guarantee individual's heterogeneity and are attained through the computational artifacts of the BioMASS tool. Thus, the agents instantiated by this tool automatically conform to the above criteria. Autonomy is also achieved within the simulation tool by a thought design, providing scheduling mechanisms that allow agents to freely behave without central coordination. Using the BioMASS tool, the development of an IBM for an ecological system would then consist on defining and instantiating a population of agents with some distribution of initial states and during the simulation execution each individual will follow a differentiated and autonomous living path.

III. AGENTS MODEL: STRUCTURE AND DYNAMICS

One purpose of the BioMASS ecosystem tool is to facilitate biologists to create their specific models. As they may not be experts on computing programming, the tool provides a set of assistants that should help them to define the species in an ecosystem, their deployment, and other simulation parameters. Therefore, the agent model should be general enough to satisfy the requirements of a wide set of species and well-structured to facilitate its extensibility when needed.

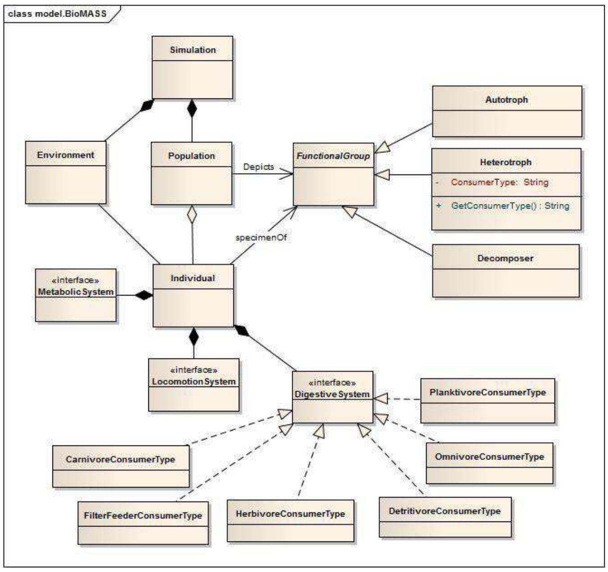


Fig. 1. BioMass class model excerpt

The BioMASS model depicted in Fig. 1 is inspired on previous work by Parrott and Kok [13], but modified in three senses. First, rather than simulating a specific ecosystem, this paper presents a software tool that enables the non programmer to model different types of ecosystems. Second, this paper emphasizes the definition of functional groups (a term commonly used by ecologists) that may represent a group of individuals (from the same or from different species) that share relevant attributes in the context of the simulation. Third, we have turned to an architecture based on a set of interrelated objects to represent a living organism (an individual of a functional group) and a set of interchanchable modules representing the different systems that compose it. To this end, the *Individual* class consists of a set of well defined interfaces such as *DigestiveSystem*, *MetabolicSystem* and *LocomotionSystem* interfaces which will be realized by concrete implementation classes following the special characteristics of each functional group. Thus, an individual organism, as shown in Fig. 1, is made of several components. There is a taxonomy of classes of organisms which is expressed as inheritance relationships with *FunctionalGroup* abstract class on the top and the *Autotroph*, *Heterotroph* and *Decomposer* classes underneath. Each new functional group results as the instantiation of one of these classes and adjusting a set of attributes to characterize all its individuals. During the simulation a *Population* class object will be instantiated as well for each functional group required in the model under study, which in turn will spawn the *Individual* objects representing the organisms of such population.

Microorganisms are considered as part of the environment modeled as a Repast Context, which provides methods to estimate their density and to account on the effect of these microorganisms, such as the decomposition of death organisms by bacterial activity, or the biomass primary production by phytoplankton activity.

All organisms have a location in the environment, a mass and a volume. They follow a life-cycle from birth to death and then decompose. During their life-cycle they pass through different phases or states following a path determined for their species. The state has influence on different factors such as growth rates, the ability to reproduce, or physical shape.

The agents have been defined taking into account the main activities that are relevant for the biomass flow through an ecosystem. These activities are shown in Fig. 2. As depicted in this activity diagram, the organism may be alive, in which case, at each simulation cycle, it will have to spend a certain amount of energy for living, following the model explained in section III-A. Then it has to check its surrounding and depending on the urgency of avoiding a threat or the need for food, the agent will decide to escape or will attempt to capture some prey. These actions imply energy consumption for moving, and in the case of feeding, also for the metabolic functions. Then individuals can wander around, grow and reproduce depending on their state. These activities also imply some additional energy expenditure, and in consequence, changes of mass. Feeding and reproduction imply as well mass exchanges with the environment as explained in section III-A. These activities have been used to identify the components of the individual agent, which is seen as a set of systems: locomotion, sensorial, digestive, etc. It has been considered as well a decision system for the agent to have some memory of past events and some ability to reasoning and adaptation, although this has not been implemented yet.

As IBM has gained in popularity, software tools have appeared to implement them. There are various ecological-oriented agent-based simulation (ABS) platforms comparable with the one proposed in this work, such is the case of Mimosa [14], CORMAS [15] and VLS [16]. Mimosa is a framework based on ontologies for knowledge representation in a discrete-event system simulation, in this framework ecologists must first describe the concepts or categories they are using to describe the target system. CORMAS is a multi-agent simulation toolkit to model social dynamics in interaction with natural resource dynamics. It provides the framework for building models of interactions between individuals and groups sharing natural resources. Its main purpose is to provide the possibility to manipulate and to incorporate into the same model spatial entities defined at different hierarchical levels. VLS is a software and an API which supports multi-modelling, simulation and analysis of natural complex systems from environmental sciences like physics, biology, ecology and economy for the integration of heterogeneous models.

The previous frameworks are originals and can be used to simulate environmental issues. Nevertheless, the BioMASS model proposed in this paper is built on a strong theoretical basis and it does not aim to be a general ecological ABS tool as the ones cited above, instead it is a domain-oriented easily customizable open tool that provides ecologists with a modeling and simulation tool that leverage the potential of MAS methodologies and architectures to enforce the implementation of true individual models.

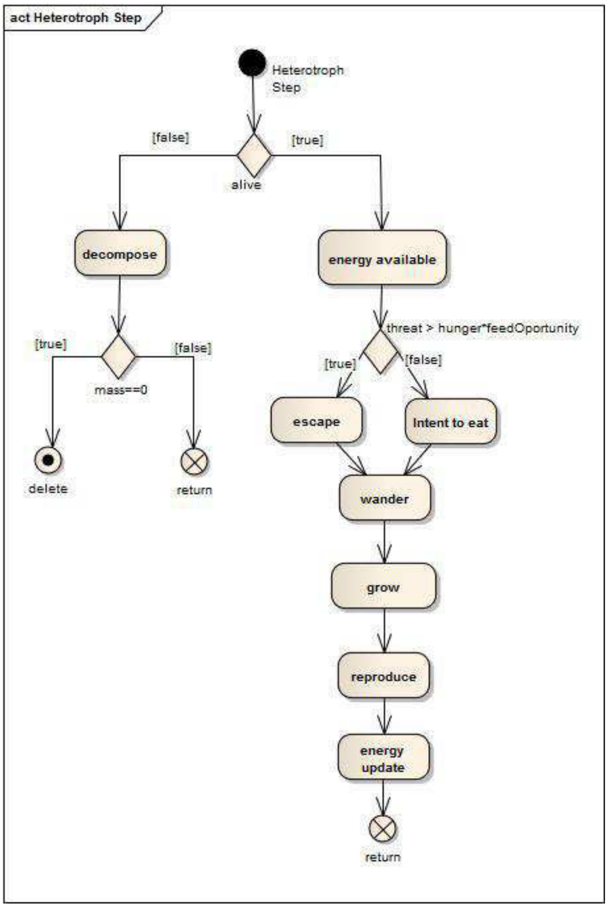


Fig. 2. Individual activities performed at each step of simulation

A. Agents Resource Dynamics

The main purpose of the model is to analyse material and mass flows in the trophic chain. Therefore, simulation of agent resource dynamics becomes a relevant part of the model.

The physical resources employed by a population of living organisms in their interaction with the environment are ultimately defined by the local and independent relationship between each individual and its surroundings. The local resource utilization is a very important factor for diversity among organisms of the same class and age and the only way for energy and mass transfer between the living populations and the physical environment.

Under this approach, the cumulative biomass is the most important distinguishing feature of each individual since it determines the amount of energy available for the organism functions as well as the amount of resources to be taken from the environment. As the individual grows gaining biomass, other attributes such as energy consumption, strength and speed of displacement might be automatically modified according to a predefined relationship for this kind of organism. In BioMASS, and with the aim of adding realism to the model graphical representation, density and volume spatial attributes are also included in each individual because they are essential for its graphical representation and for the definition of the physical interactions among the individuals or between them and the environment structure.

Following Parrott and Kok's ideas [13], each organism is modelled as being composed of lean mass and fatty mass both of which increase through the ingestion of another organism with similar composition. The fatty mass, composed of lipids and water, is susceptible of being transformed into energy through metabolism and for that reason might increase or decrease according to the rate of biomass ingestion and energy usage. In contrast, the lean mass never decreases because at this stage does not exist any process for protein conversion into lipids, carbohydrates or energy (as it happens in nature).

Every organims may eat as much food as the physical volume of its stomach and the availability of food allows it. Then, under a periodical basis the ingested biomass, or a portion of it, is incorporated to the animal own biomass, but only enough to satisfy both, the requirements imposed by a programmed growth rate function specific for the functional group, and the fatty mass deficit caused by energy consumption. The excess of biomass ingested is expelled as waste. The proportion of fatty mass to lean mass is kept under certain limits that are specific for each functional group, but being subject to conversion into energy and thus consumed, the fatty mass might decrease beyond a critical limit and the animal starve to death. The system incorporates a mechanism to collect the biomass of death organisms and digestive waste transfering that biomass to the software object that represents the environment for further quantification and decomposition.

B. Growing as a differential trait (life cycle)

In nature, the organisms go through different development stages or phases as they complete their life cycle. It is common that starting as larvae, organisms evolve into juvenile, mature and senile individuals presenting at each phase important and distinctive physical attributes, like size and form, and physiological characteristics such as their capability to reproduce or their feeding habits. Therefore, an IBM should be able to reflect these changes.

In this case, the differential characteristics related to the individual life cycle involve two aspects: feeding habits (some animals, specially in marine ecosystems, are herbivores during larval stage and carnivores there after) and growth rate (usually younger organisms grow faster). The growth rate, r_t, for every individual in age t, is modeled using the proposal of [13]:

$$r_t = k_2 m_t e^{-k_1 t} e^{k_3(mp_t - m_t)} \; . \tag{1}$$

Under this model, the growth rate is directly proportional to the lean mass, m_t, and due to the term $e^{-k_1 t}$ younger individuals grow faster than older ones. When the lean mass is below its potential value mp_t the growth rate is multiplied by the factor $e^{k_3(mp_t - m_t)}$ in order to reduce the difference. The constant values k_1, k_2 and k_3 are positive and species-specific.

Once the growth rate is evaluated the lean mass is actualized with the next discrete approximation

$$m_{t+1} = m_t + c_t r_t \Delta t \; , \tag{2}$$

where coefficient $c_t \in [0,\ 1]$ mesures food availability.

The potential lean mass is obtained setting $c = 1$, $\forall t$ (food is completely available at every instant). Determination of the constants k_1, k_2, k_3 on the base of the growth function for this model is neither straightforward nor intuitive. It is more natural to establish restrictions on the lean mass in order to deduce the values of the constants. Indeed, k_1 and k_2 can be easily evaluated if the growth function is stated as a differential equation of the potential lean mass

$$\frac{d(mp)}{dt} = k_2 m_t e^{-k_1 t} \; , \tag{3}$$

with solution

$$mp(t) = C e^{-\frac{k_2}{k_1} e^{-k_1 t}} \; , \tag{4}$$

where C is a new and arbitrary constant.

Applying the restriction $mp(t = 0) = m_0$ (lean mass at birth), C is determined and the lean mass function can be rewritten as

$$mp(t) = m_0 e^{\frac{k_2}{k_1}(1 - e^{-k_1 t})} \; . \tag{5}$$

Considering that the lean mass attains its maximum value, m_f, asimptotically

$$\lim_{t \to \infty} mp(t) = m_f = m_0 e^{\frac{k_2}{k_1}} \tag{6}$$

the next equation is obtained

$$k_2 = k_1 \log \left(\frac{m_f}{m_0} \right) \tag{7}$$

A further restriction of the lean mass at adult age, $mp(t = A) = \epsilon m_f$, yields

$$k_1 = \frac{1}{A} \log \left[\frac{\log \left(\frac{m_0}{m_f} \right)}{\log \epsilon} \right] \tag{8}$$

In the simulation every individual computes its growing rate periodically basing this computation on its present mass and age and then depending on the available resources (ingested biomass) increases its size.

C. Population Dynamics as Emergence

Section II has discussed the importance for an IBM to be able to produce the population dynamics and statistics as emergent products of the generational succession of individuals. However, in practice it is almost impossible to reach equilibrium for a population in such a way that its age distribution is sustainable through several generations if we do not start with an already adequate population. For this, an initial population must be carefully constructed. One way to do this is to assume a constant death rate to obtain an exponential age distribution (details can be found in the 9th chapter of [17])

$$N_i = Me^{\delta(i\Delta t)} \tag{9}$$

where N_i is the expected population for age group i ($i \in \{0,\ 1,\ 2,\ \ldots\}$), Δt is the lapse of time separating two consecutive generations, M is the expected number of individuals incorporated in a new generation and δ is the constant death rate. On future developments BioMASS will incorporate not only this but other tools to produce the initial populations for the different functional groups.

IV. SIMULATION CONFIGURATION

BioMASS tool allows biologists to define and simulate ecological models following a set of steps, which are guided by an assistant. These steps are essentially the following:

1) Define the functional groups to be incorporated into the model. It is possible to identify an already defined funcional group that is close in properties and behavior to the new class.
2) Fill in the parameters that characterize the functional group.
3) Define the environment. This is a 3D grid with a set of parameters to configure as well.
4) Define the population parameters for each functional group.
5) Define simulation execution parameters such as number of iterations, files to keep monitoring data, etc.

Some of the steps are expected to be improved in the future, for instance, to allow defining new behavioral rules for the different functional groups.

V. EXPERIMENTATION

BioMASS has been tested with a simulation model of an hypothetical marine ecosystem. In this simulation model a new generation of aquatic pelagic individuals (fish) belonging to two different functional groups, herbivores and carnivores, are instantiated periodically as if they were born from randomly dispersed eggs. The herbivores feed on plankton which is uniformly distributed over the space. However the density of plankton is dynamically updated by following the logistic differential equation and considering the total amount of compsumption by herbivores:

$$\frac{dP}{dt} = k\left(1 - \frac{P(t)}{M}\right)P(t) - C(t)\ . \tag{10}$$

In this differential equation, $P(t)$ is the total amount of plankton biomass at time t, k is a proportionality constant, M is the maximum plankton biomass that the environment can support and $C(t)$ is the consumption rate by herbivores.

Herbivores gain biomass rigorously following their potential growing function and the plankton availability. Carnivores predate on herbivores whenever they get close enough, they also gain biomass following their potential growing function, but unlike herbivores, their growing function depends on the herbivores availability. Both carnivores and herbivores move randomly (at this development phase there are not hunting or evasion functions) and the result of close encounters among them may be carnivores eating the herbivores (if the size difference allows it), or simply a direction change for collision avoidance.

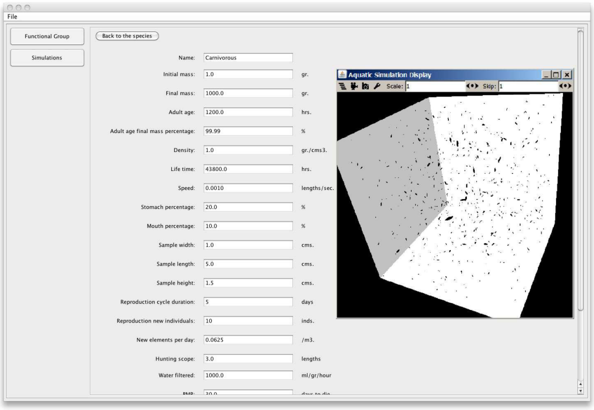
Organisms incorporate biomass as they feed following the growth function described above. They also spend biomass (fatty mass) converted to energy as they live and move but might replenish their reserves. If they do not do it, after some time they might starve to death. Fig. 3 shows a screenshot of the running simulation system illustrating the interface used to define new species and their attributes. It also shows a rendering of the simulated world with organisms represented by means of ellipsoids with different size, position and orientation. Fig. 4 depicts the evolution of the amount of biomass of the system and Fig. 5 shows the population distribution by age classes for one moment of the simulation.

Under this preliminary configuration with only two functional groups participating on the simulation, the system showed a tendency to instability either by extinction or explosion of the populations. The determining factors for either of these results were the number of new organisms spawned on each generation and the rate at which they grow. The exploding scenario was preferable since it could be contained by controlling the amount of new biomass introduced into the system in the form of environment's plankton.

Thanks to the user graphical interface of the simulation tool it was easy to manipulate the parameters of the simulation so the experimental cycle of setting, running and feedback could be effortlessly and quickly repeated.

VI. CONCLUSIONS

Biomass tool offers ecologists the ability to design computational simulation experiments about natural ecosystems using a user-friendly graphical interface and concepts familiar to them. With this interface the researcher describes one or more functional groups which are classes of individuals with common characteristics, then populations from these functional groups and finally the parameters of the simulation itself. Among the adjustable parameters for the definition of the functional groups are those that distinguish a set of individuals such as diet, minimum and maximum size, growth rate, etc. Some of these features are related to the behavior of the individuals of a functional group enabling BioMASS to be used to model relationships among organisms that go beyond the predator-prey relationship.



Name: Carnivorous
Initial mass: 1.0 gr.
Final mass: 1000.0 gr.
Adult age: 1200.0 hrs.
Adult age final mass percentage: 99.99 %
Density: 1.0 gr./cms3.
Life time: 43800.0 hrs.
Speed: 0.0010 lengths/sec.
Stomach percentage: 20.0 %
Mouth percentage: 10.0 %
Sample width: 1.0 cms.
Sample length: 5.0 cms.
Sample height: 1.5 cms.
Reproduction cycle duration: 5 days
Reproduction new individuals: 10 inds.
New elements per day: 0.0625 /m3.
Hunting scope: 3.0 lengths
Water filtered: 1000.0 ml/gr/hour

Fig. 3. Graphical user interface

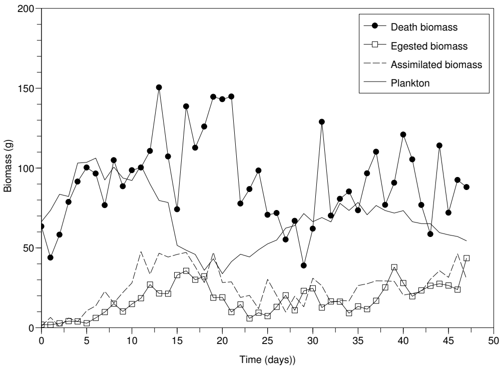


Fig. 4. Biomass dynamics in a simulation run

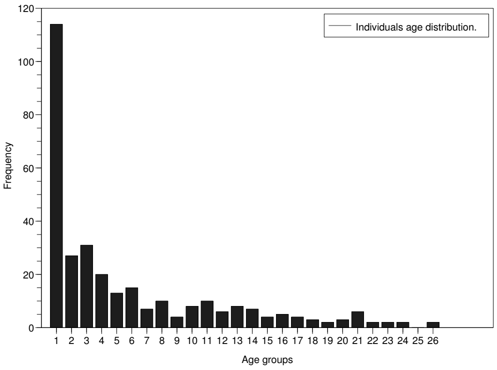


Fig. 5. Population age distribution at a given day

The selection of adjustable parameters for the definition of functional groups is sufficiently broad to permit the configuration of great diversity of simulation scenarios using the GUI provided. If necessary, Biomass provides the ecologist with programming skills and object-oriented architecture that can be extended to incorporate new properties or modify the existing ones.

Based on the preliminary results of the experimentation phase, and as future work we envisage to extend the tool to consider a spatial distribution of primary production of biomass resources (such as plankton). Also, we intend to incorporate some simple hunting and evading functions as well as a more realistic energy consumption model for individuals. An open issue to be addressed is the computing power necessary to simulate the great amount of individuals of some of the most interesting and complex ecosystems such as the tropical reefs.

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