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# Modelling ecology and evolution of Foraminifera in the agent-oriented distributed platform



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#### ABSTRACT

We present a new software platform called eVolutus for simulating evolution of living organisms. We choose Foraminifera as model organisms that represent a group of single-cellular, mainly marine, organisms that construct well fossilisable protective shells. They have lived on Earth for more than 540 million years and have left an extraordinary fossil record that is excellent for testing palaeoecological and evolutionary hypotheses. We use the AgE platform, which is a lightweight agent-oriented platform supporting distributed computation. The paper presents the general architecture of this modelling environment as well as more detailed descriptions of the implemented rules and applied solutions. The utility of this software is demonstrated by presenting the configuration and results of sample experiments.

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#### 1. Introduction

Agent-based modelling (ABM) is a bottom-up computational methodology where autonomous agents interact with each other and their environment according to defined rules [6,23]. ABM is very convenient for modelling complex systems as, instead of implementing general rules that describe a whole system, it focuses on particular parts of the system that include behaviours and interactions with other agents and the environment. As a result, simulations are easy to design and implement, giving experiments expressive power.

Most biological studies deal with systems in which objects (molecules, cells, individuals) reveal some kind of an autonomic behaviour. Thus, ABM seems to constitute a perfect methodology for computer modelling of biological phenomena. In fact, a methodology that is very similar to ABM, namely "Individual Based Modelling" (IBM), has been used in ecology and biology for quite a long time. Uchmański and Grimm defined IBM as a methodology where the biological system is represented while preserving discreteness, uniqueness and a full life cycle of individuals [70].

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http://dx.doi.org/10.1016/j.jocs.2016.07.009 1877-7503/© 2016 Elsevier B.V. All rights reserved. Railsback [55] added autonomous and adaptive behaviour to this definition.

At the heart of Agent-Based Modelling lies the concept of an agent. Most acceptable definitions [71] include some features - therefore, an agent is:

- autonomous fully in control of itself;
- situated located in an environment, gathers information, stimuli and resources, makes decisions that influence the environment;
- responsive reacts to changes in the environment;
- goal-oriented acts in order to achieve particular goals;
- socially-oriented communicates with other agents;
- mobile moves within the environment;
- learning-oriented (adaptive) changes its behaviour according to environmental conditions;
- rational makes decisions that lead to a defined goal.

All these features can be assigned to many biological beings: from the subcellular level, through cells and organs, up to the individual level in multicellular organisms. In unicellulars, cells represent independent individuals. Moreover, some of them are similar to features that are promoted by IBM users. Thus, ABM is able to provide a conceptual framework that is able to cover IBM and express it as a computational model.

In biological applications, ABM can reveal many advantages. Agents' behaviour can be encoded in an elegant, intuitive way. Their

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rules can be easily changed, extended and replaced without changing the overall framework. Agents' heterogeneity can be easily implemented. Three-dimensional systems, as well as any irregular configuration, can also be realised. On the other hand, ABM, where each entity is individually tracked, can be expensive compared to the models that are based on solving continuous equations.

This paper presents eVolutus: an agent-based simulation platform of foraminifera and their habitat implemented using the agent paradigm [33,32] and agent-based software framework AgE [18,40]. Besides showing the actual correctness of the simulation, the experiments regarding the scalability of the framework are presented. The paper is structured as follows: first, a detailed motivation for the foraminifera-related research is given, then a detailed description of Foraminifera is presented and then principles of the agent-based framework AgE are sketched. A description of the eVolutus platform is given next followed by the details of its implementation using AgE. Finally, results demonstrating the validity of the simulation as well as scalability of the framework are shown, discussed, and conclusions are offered.

#### 2. Project motivations

Our main objective is to design and implement an agent-based simulator for testing ecological and evolutionary principles, as well as their consequences within defined environments. We choose Foraminifera, single-celled marine microorganisms, as a model group of organisms [26,46,45,49]. The decision was motivated by several facts:

- Foraminifera have lived on Earth for at least 540 million years. Their record is known from fossilized shells that serve as excellent archives of the past. Micropaleontology, based on morphological and biochemical studies, provides significant information about their evolution and palaeoecology [46,49].
- Living foraminifera are known from almost all marine habitats. Biological and oceanographic investigations provide extensive knowledge on their physiology, behaviour, ecological, and phylogenetic relationships [26,45,49].
- Foraminifera are single-celled organisms with relatively simple physiology and behaviour. On the other hand, they use quite complex life history strategies that are the subjects of extensive studies [46,49,22].
- There is a model of foraminiferal shell morphogenesis [65,69,67] that, despite its simplicity, is able to generate an extensive set of shapes. This model can be applied in further studies.

The simulator can be adapted to model ecology of other living organisms, if their physiology and morphology have a similar level of complexity. eVolutus is able to simulate population dynamics of any other organism whose life cycle is limited to gathering food, growing and reproducing, including unicellular and simple multicellular taxa. Due to the fact that we do not track the exact position of agents, we are not able to simulate microhabitats in which individuals directly interact with each other.

The simulator will be used to test various hypotheses related to ontogeny, physiology, habitat adaptation and evolution of foraminifera. Our aim is to provide a tool that allows, in a simple and efficient way, to introduce various rules of foraminiferal behaviour and to observe its impact on population dynamics end evolutionary adaptations. To fulfil this requirement, we have defined a software architecture that incorporates fundamental knowledge about some aspects of foraminiferal life in the form of partial models (e.g. motility model, reproduction model, morphogenesis model) and provides a user interface to create "ad hoc" models for those aspects that still remain unknown.



Fig. 1. Living benthic foraminifera dominated by *Ammonia* and *Elphidium*. Some individuals show extended reticulopodia (pseudopodial networks).



**Fig. 2.** Planktonic foraminifer *Orbulina universa*: a common ocean symbiotic species with attached ectosymbionts along thin radial spines. Symbionts are represented by Dinoflagellates (yellow spots). A trochospiral foraminifera shell is placed in the centre. Its diameter is 0.4 mm.

While there exist general-use artificial life software platforms [35], due to the biological complexity of foraminifera and their interactions with the environment, we decided to implement a dedicated simulation environment. To the best of our knowledge, a numerical framework for the simulation of evolutionary patterns derived from the fossil record of real organisms has not yet been developed. This objective is now feasible as computational resources are becoming sufficient. Versatile models of evolution of three-dimensional life forms have already been developed [35], although they are not dedicated to a single biological species and a specific biological genetic encoding [61,17,36,34,31,30,37].

As computer simulations can be helpful in understanding the foraminiferal evolution, our goal is to construct a model reflecting growth processes of foraminiferal individuals (ontogenesis) within a simplified virtual environment where they could move, eat, grow and reproduce, following rules that resemble their physiology and behaviour. The ultimate aim is to test micro- and macroevolutionary rules and interactions controlling the overall system which acts at various spatiotemporal scales necessary for the emergence of the complexity of life [35].

#### 3. Foraminifera

Foraminifera are single-celled eukaryotic organisms that mainly inhabit marine environments (Figs. 1 and 2). Most foraminifers produce protective shells (also called "tests") made either of Download English Version:

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