

EcoSim: an individual-based platform for studying evolution

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Abstract

To study the evolutionary process and the emergence of species, we have conceived an individual-based evolving predator-prey ecosystem simulation presented in (Gras, 2009). One major and unique contribution of this simulation is that it combines a behavioral, an evolutionary and a speciation mechanism. This is the only simulation modeling the fact that individual behaviors affect evolution and speciation. We have already obtained some very interesting and promising results from our simulation on species abundance distribution, study of chaotic patterns or population spatial distribution.

Introduction

Since the last decade, the individual-based modeling approach became more common as machine capable of running time-consuming simulations appeared (DeAngelis, 2005). However, few attempts have been made to simulate a complete and complex ecosystem. The first one is Echo (Hraber, 1997), which includes an evolutionary mechanism. However, the organisms are very simple, and have no behavior model. Another system studying long term evolution is Avida (Lenski, 1999). It has nevertheless limitations such as: the individuals do not move, are quite limited in number, and there is a fix fitness function which means that the system is mostly an optimization process. Other models, such as PolyWorld (Yaeger, 1992), Bubbleworld.Evo (schmickl, 2006) or Framsticks (Comosinski, 2000), have been proposed including more complex agents and behavioral models. They use Artificial Neural Networks or system of learned rules to evolve the agent's behavioral model during their life and by an evolutionary process. However, these approaches are highly computational expensive and only allows small population (few hundred) of agents. They are therefore more dedicated to investigate evolution of learning capacities than high scale mechanisms involving populations and species dynamics. To investigate several open theoretic ecological questions we have designed, Ecosim¹ (Gras, 2009), a large scale simulation platform. Our general purpose is to study how individuals and local events can affect high level mechanisms such as community formation, speciation or evolution.

¹ <http://sites.google.com/site/ecosimgroup/research/ecosystem-simulation>

Our model

To observe phenomena at the evolutionary scale that affect the individual behaviors, several constraints need to be fulfill: (1) every individual should possess genomic information that will be the subject of the evolutionary process; (2) this genetic material should affect the individual behavior and consequently its fitness; (3) it has also to be transmitted and modified from generation to generation; (4) a sufficiently high number of individuals should coexist and their behavioral model should be sophisticated enough in order that complex interactions and organizations could emerge; (5) a model for species representation and an speciation mechanism, leaning on the genomic and behavioral model, has to be defined; (6) for speciation events to occur and new co-adapted behavioral models to emerge and in turn affect the whole system, a large number of time steps need to be performed. We therefore face a computational challenge for both memory management and computational power. We need a model which allies the compactness and easiness of computation with a high potential of complex representation.

We have used a modified version of the Fuzzy Cognitive Map (FCM) model (Kosko, 1986) and adapted it to our problem. This model is used at the same time as the behavioral model of our agents (our individuals) and as the vector of transmission of the evolutionary information. It allows a combination of compactness with a very low computational requirement while having the capacity to represent complex high level notions. Therefore, each agent can possess its unique proper FCM, which is an inherited modified combination of the ones of its two parents. The system can still manage several hundreds of thousands of agents simultaneously with reasonable computational requirements. The FCM contains sensitive concepts such as: predatorClose, foodClose, mateClose, energyLow; internal concepts such as: fear, hunger, sexualNeed, curiosity, satisfaction; and motor concepts such as: escape, searchForFood, socialize, eat, breed. It includes also weighted links representing the mutual influences of these concepts. Our simulation implements a speciation mechanism related to the genotypic cluster definition (Mallet, 1995). A species is a set of individuals associated with the average of the genetic characteristics of its members. A species split if the difference between the FCMs

of the two most dissimilar agents is greater than a threshold (Aspinall, 2010) leading to two sister species that rapidly diverge to become genetically isolated with no more interbreeding events. Since species membership is evaluated at each time step, a species can emerge or extinct at any time. A typical run last several tens of thousands of time steps, each time step being the time needed for each agent to perceive its environment, to use its behavioral model to make a decision, perform its action, to update the species and the world parameters. In total, more than one billion of agents will be born and several thousands of species will be generated, which allows the evolutionary process to take place and new behaviors to emerge reacting to a constantly changing environment. In addition, a food chain consisting of three levels, primary producers, predators and preys, has been implemented allowing complex interactions between agents and co-evolution to occur.

Results

Species abundance distribution

To validate EcoSim, we have compared the ecological patterns it generates with those observed in natural ecosystems (Devaurs, 2010). We have focused on species abundance patterns as they are a key component of ecological theories. To analyze them, we used Fisher's logseries, since it is one of the most classical models of species abundance distribution. The following results, well established in the ecological literature, are also observed in the communities generated by our simulation: the logseries presents a good fit to the distributions of small samples; it fails to do so for large samples and complete community; the logseries performs better on species-rich communities. Even though the logseries does not provide a good fit for large samples, the distribution patterns observed in our communities are very similar to those observed in nature. Thus, at any level, our simulation gives coherent results in terms of relative species abundance.

Chaotic behavior

Any attempt to model a real system needs to have the capacity to generate patterns as complex as the ones of the real system. We have studied the properties of the time series representing the variation of the number of: preys, prey species, predators and predator species (Golestani, 2010). We examined whether a chaotic behavior exists in these signals. To enforce our results, we use four different methods: Higuchi fractal dimension, correlation dimension, largest Lyapunov exponent, P&H method. To obtain a statistically significant evaluation, we apply the surrogate test method on 24 samplings of these data. All of them providing clear predictions that the behavior of simulation is deterministic chaotic.

Population spatial distribution

We have conceived a measure to compute the spatial center of a population in a torus world (Sina, 2011). Computing spatial distribution in an ecosystem simulation is important for analyzing various aspects of species or group of individuals.

One of the applications is prediction of extinction of a population. When individuals of a population are dying, their spatial distribution either globally or locally, starts to decrease; since it has a relationship with number of living individuals of the population. Also it was shown, as expected in the parapatric model of speciation that genetically similar individuals in a population tend to live closer to each other.

Conclusion

This project is at its early stage but we have already many interesting results. We have submitted several papers: diffusion and mitigations of diseases in an ecosystem, a machine learning approach for modeling species abundance distribution, the natural selection effect on the variation of the ecosystem's complexity, and the multifractal properties of the individuals' spatial distribution. We are currently working on: the effect of reduction of gene flow on the rate of speciation, the emergence of new complex behaviors and their effect on fitness, applying machine learning techniques to predict species extinction and speciation events, the effect of choice of mating partner on variation of the population's fitness and the effect of multiple food resources on emergence of species.

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