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Evolving eco-system: a network of networks

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Abstract

Ecology and evolution are inseparable. Motivated by some recent experiments, we have developed models of evolutionary ecology from the perspective of dynamic networks. In these models, in addition to the intra-node dynamics, which corresponds to an individual-based population dynamics of species, the entire network itself changes slowly with time to capture evolutionary processes. After a brief summary of our recent published works on these network models of eco-systems, we extend the most recent version of the model incorporating predators that wander into neighbouring spatial patches for food.

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Keywords: Food web; Monte Carlo simulation; Self organization

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1. Introduction

An eco-system may be viewed as a functional network of species; the food web [1] corresponding to the eco-system consists of nodes and links where each node corresponds to a species and the (directed) links represent the prey–predator interactions such that the direction of the link indicates the direction of flow of nutrient (i.e., *from* a prey *to* one of its predators) [2,3]. For convenience, most of the earlier ecological models that describe population dynamics, usually ignored

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macro-evolutionary changes in the eco-system and, therefore, assumed the food web to be independent of time. On the other hand, most of the macro-evolutionary models [4,5] of speciation and extinction of species did not explicitly explore the ageing and age distributions of the populations of various species in the system. The models of ageing, usually, focus on only one single species.

But, recent experimental evidences [6–8] have established that significant evolutionary changes can occur over ecologically relevant time scales. Motivated by these experiments, we have developed models [9–13] of evolutionary ecology from the perspective of dynamic networks. In these models, in addition to the intra-node dynamics, which corresponds to population dynamics of species, the entire network itself changes slowly with time to capture evolutionary processes. The aim of these models is to provide insight into the mechanisms that give rise to the generic features of the biological evolution of real eco-systems.

In this paper, after a brief review of the earlier network models, including our own [9–12], we extend the most recent version [13] of our model by allowing predators to prey on species in the neighbouring spatial patches as well.

2. Earlier network models

A network model of ecosystems was developed by Sole and Manrubia [14]. The state of the ith species ($i = 1, 2, \ldots, N$) is represented by a two-state variable S_i; $S_i = 0$ or 1 depending on whether it is extinct or alive, respectively. The inter-species interactions are captured by the interaction matrix $\mathbf{J}$; the element J_{ij} denotes the influence *of* the species j *on* the species i. If $J_{ij} > 0$ while, simultaneously, $J_{ji} < 0$ then i is the predator and j is the prey. On the other hand, if both J_{ij} and J_{ji} are positive (negative) they the two species cooperate (compete). The food web in the Sole–Manrubia model [14] has a random architecture.

The dynamics of the system consists in updating the states of the system in three steps. At the first step, one of the input connections J_{ij} for each species i is picked up randomly and assigned a new value drawn from the uniform distribution in the interval $[-1, 1]$, irrespective of its previous magnitude and sign. At the second step, the new state of each of the species is decided by the equation

$$S_i(t+1) = \Theta\left(\sum_{j=1}^{N} J_{ij} S_j(t) - \theta_i\right), \tag{1}$$

where θ_i is a threshold parameter for the species i and $\Theta(x)$ is the standard step function. If $S(t+1)$ becomes zero for m species, then an extinction of size m is said to have taken place. (This criterion for extinction is different from those formulated in terms of the eigenvalue spectrum of the interaction matrix corresponding to the given ecological networks [15].) Finally, at the third step, all the niches left vacant by the extinct species are refilled by copies of one of the randomly selected non-extinct species. Sole and Manrubia [14] observed that the distributions of the sizes of these extinctions could be fitted to a power law of the form $N(m) \sim m^{-\alpha}$ with an exponent $\alpha \simeq 2.3$.