Self-organized predation and migration model

Abstract

[1]

Author Summary

1 Introduction

Understanding the structure and dynamics of ecological networks has become critical for understanding the persistence and stability of ecosystems [2]. Robustness studies based on the simulation of sequential extinction of species have revealed aspects about the response of ecosystems to ecological disturbances at species level [1]. Such structural analyses are relatively fast and easy but their utility in capturing important information about functions and processes is often questioned [3], especially when considered the variability of the effects of ecological disturbances among individuals of the same species. Dynamical models in contrast provide essential information especially if one needs to understand changes in abundances, with the structure of the food web being almost constant [3].

2 Results

Steady State

Space of Parameters

Metabolic Theory of Ecology

3 Discussion

4 Materials and Methods

Here we describe a dynamic model that represents dynamics of predation and migration considering biological and geographical conditions defined by ecological networks. The biological conditions are the trophic relationships among species living in a same region, and the geographical conditions is the connectivity among different regions.

We use a Monte Carlo (MC) approach to simulate the dynamics of predation and migration in an ecosystem for different timeline. Different patches are represented as nodes of a geographical neighborhood network and the connectivity of those patches are represented as edges of this network. At each patch i there are N_i^k individuals of each k species. The trophic relationships among these species are represented by a directed network in which each node represents a species and each edge represents a trophic relationship between a pair of species in which the origin of the edge represents a prey species and its target represents a predator species. This network is called food-web and it is the basis for running the predation dynamic simulation.

4.1 Predation dynamics

At each time of the MC simulation we leave all the individuals of each patch i to be choosen by a *Multinomial Distribution* [4]. The chosen individual k can have three different behaviors:

1. it can die for natural reasons;

2. it can eat one individual among its prey;

3. if k have eaten an individual among its prey, so it can give an offspring.

If k individual is not a predator (if it is a basal species) the model assumes it has infinity food suply and the only possible behaviors are 1. and 2.. For each MC time-step mc, this simulation is repeated for all individuals of each patch of the landscape. The births will occur only if there is free space in the patch i, that means, if the number of individuals alive at i is lower than its carrying capacity (cc). For each time t in which one individual of species k gives an offspring in a patch i, its number of individuals in this patch will be increased by 1; for each time t in which one individual of species k dies naturally or by predation in a patch i, its number of individuals will be decreased by 1. In Figure 1 we show a fluxogram that summarizes the running of the predation dynamic of the model.

4.1.1 Predation Equations

- **General Equation**

$$\left\{ [1 - NDp\,(k)] \left[\sum_{b \in H(k)} \rho\,(b)\,Dp\,(b) \right] [Bp\,(k)] - \left[\sum_{c \in P(k)} \rho\,(c)\,(1 - NDp\,(c)) \frac{\rho\,(k)}{\sum_{d \in H(c)} \rho\,(d)} Dp\,(k) \right] - [NDp\,(k)] \right\} \tag{1}$$

- **Self-Organized Parameters: Birth Probability**

$$Bp\,(k) = [1 - \rho\,(k)] \times \left[\sum_{b \in H(k)} \rho\,(b) \left(1 - \sum_{c \in P(b)} \rho\,(c) \right) \right]$$
$$\times \left[1 - \sum_{c \in P(k)} \rho\,(c) \right]$$

Where: Availability of Resources of Basal Species is 1.0

- **Self-Organized Parameters: Death Probability**

$$Dp\,(k) = [\rho\,(k)] \times \left[\sum_{b \in H(k)} (1 - \rho\,(b)) \left(\sum_{c \in P(b)} \rho\,(c) \right) \right]$$
$$\times \left[1 - \sum_{c \in P(k)} \rho\,(c) \right]$$

Where: Death Probability of Basal Species is 1.0

- **Self-Organized Parameters: Natural Death Probability**

$$NDp\,(k) = \left[\rho\,(k)\right] \times \left[\sum_{b\in H(k)}\left(1 - \rho\,(b)\right)\left(\sum_{c\in P(b)}\rho\,(c)\right)\right]$$
$$\times \left[1 - \sum_{c\in P(k)}\rho\,(c)\right]$$

- **Self-Organized Parameters: Carrying Capacity (for each species in each site)**

$$CC\,(k) = \left[\sum_{b\in H(k)}\frac{(\rho(b))}{\left(\sum_{c\in P(b)}\rho(c)\right)}\right]$$

4.2   Dispersal Migration

The model allows the Dispersal Migration of individuals living in any patche i to each patch in its neighborhood. The i-neighborhood is given by the topology of the neighborhood network, here we consider a neighborhood defined by a regular 2-dimensional toroidal lattice. Is assumed that, for each time step, each species in the landscape has a level of preference to each patch. The preference of a species k for a patch i in time t ($Pref_i^k(t)$) is defined as the difference between the number of individuals of species that are prey and species that are predators of k in that patch. The migration of a species k from a patch i to a neighborhood patch j will occur only if $Pref_j^k(t) > Pref_i^k(t)$. The number of individuals of species k that move from i to j must respect the threshold imposed by the carrying capacity of the target patch ($cc_j^k(t)$) and is defined as seen below:

4.2.1   Migration Equations

- **Mobility of species *sp* from site *i* to *j***

$$\Delta N_{sp}\,(i) = \sum_{j\in Neigh(i)}\left(\left(N_{sp}(j)\,M_{sp}(j,i) \;-\; N_{sp}(i)\,M_{sp}(i,j)\right)\right)$$

$$M(i,j) = \overbrace{\left[\lambda^i\,\frac{\Delta_{ij}\,f\,\Theta\,(\Delta_{ij}\,f\,)}{\sum_{k\in Neigh(i)}\Delta_{ik}\,f\,\Theta\,(\Delta_{ik}\,f\,)}\right]}^{Biotic}\overbrace{\left[w_{ij}\,\frac{\Delta_{ij}\,f_\eta\,\Theta\,(\Delta_{ij}\,f_\eta\,)}{\sum_{k\in Neigh(i)}\Delta_{ik}\,f_\eta\,\Theta\,(\Delta_{ik}\,f_\eta\,)}\right]}^{Abiotic}$$

$$\Delta_{ij}\,f = f^{i,j} - f^{j,i}\left\{\begin{array}{l} f^{i,j} = \rho_H(j) + \rho_P(i) \\ f^{j,i} = \rho_H(i) + \rho_P(j) \end{array}\right.$$

$$\lambda^i = \tfrac{1}{2}\left(1 - RE^i\right)$$

$$RE^i = \frac{New^t}{N^t}$$

$$\Delta_{ij} f_\eta = f_\eta^j - f_\eta^i \left\{ \begin{array}{l} f_\eta^i = \eta_{sp}^* - \eta_{sp}^i \\ f_\eta^j = \eta_{sp}^* - \eta_{sp}^i \end{array} \right.$$

$$w_{ij} = Connectivity\ between\ sites\ i and\ j$$

Acknowledgments

References

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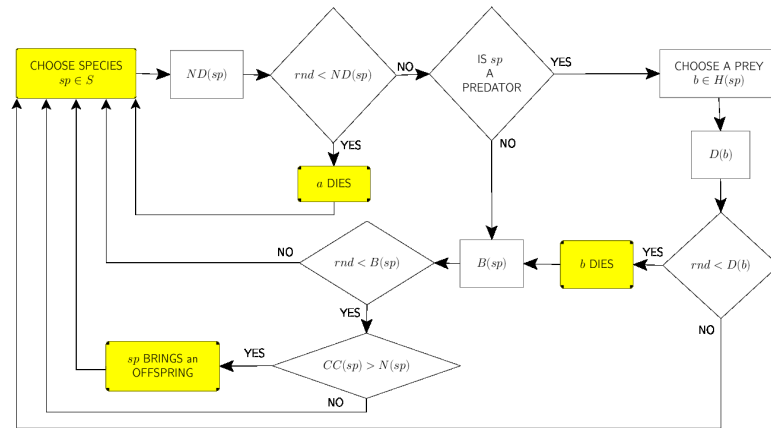
Figures

Figure 1. Fluxogram. Fluxogram of the model.

Tables