

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

4.1 Dispersal dynamics

Here we describe the dynamics of predation and migration in explicit landscapes. There can be several species at each trophic level and there are several spatially distinct sites. The trophic levels are resources (R), consumers (H), and predators (P), thus, we have three distinct metacommunities of resource, consumers, and predators/parasitoids. To model spatio-temporal changes in the abundance of these sites, we need to define dispersal and trophic interaction rules together with population dynamics. We consider two models of dispersal between sites. Model 1 assumes that dispersal between any two sites occurs only between the neighbors and it is density-independent in the sense that dispersal probabilities are a function of species abundance of the leaving site. Model 1 also assumes that resources, consumers and predators move independently of each other. This means individuals are not aware of the state of each site before the disperse (i.e., the number of prey or predators in each site). Dispersal to the neighbors is also occurring in the model 2, but now individuals have information of each site and they disperse with higher probabilities to the sites that have a low number of predators and a high number of resources available.

4.1.1 Model 1: Density-independent and non-informed dispersal dynamics

Our first model assumes the dispersal rates are density-independent and an individual that emigrates has the same preference for any other site within the neighborhood. Thus, individuals movement is independent of the state of each site. We consider a neighborhood as a regular 2-dimensional toroidal lattice (check other topologies to test the robustness of the results). This leads to the dispersal rate of species k_ϕ in metacommunity ϕ from site j to site i (where ϕ stands either for the resource (R), the consumer (H), or the predator metacommunity (P))

EQUATION NOT TRANSFORMED!

$$M(i, j) = \left[\overbrace{\lambda^i \frac{\Delta_{ij} f \Theta(\Delta_{ij} f)}{\sum_{k \in \text{Neigh}(i)} \Delta_{ik} f \Theta(\Delta_{ik} f)}}^{\text{Biotic}} \right] \left[\overbrace{w_{ij} \frac{\Delta_{ij} f_\eta \Theta(\Delta_{ij} f_\eta)}{\sum_{k \in \text{Neigh}(i)} \Delta_{ik} f_\eta \Theta(\Delta_{ik} f_\eta)}}^{\text{Abiotic}} \right] \quad (1)$$

where... is the ... between site i and j and m_ϕ is the metacommunity-specific background dispersal rate (we need here a figure with the landscape considered and we also need to simplify the flow chart and explain this model).

4.1.2 Model 2: Density-dependent predator-prey ratio dispersal dynamics

Our second model assumes the dispersal rates are density-dependent and an individual that emigrates has a preference that is a function of the state of each site. The state of each site is driven by the number of resources available and the number of predators in each site. Thus, the migration probability of a species k_ϕ in metacommunity ϕ from site j to site i is defined as the difference between the number of individuals of species that are prey and species that are predators of species k_ϕ in site i . This leads to the dispersal rate of species k_ϕ in metacommunity ϕ from site j to site i

EQUATION NOT TRANSFORMED!

$$M(i, j) = \left[\overbrace{\lambda^i \frac{\Delta_{ij} f \Theta(\Delta_{ij} f)}{\sum_{k \in \text{Neigh}(i)} \Delta_{ik} f \Theta(\Delta_{ik} f)}}^{\text{Biotic}} \right] \left[\overbrace{w_{ij} \frac{\Delta_{ij} f_\eta \Theta(\Delta_{ij} f_\eta)}{\sum_{k \in \text{Neigh}(i)} \Delta_{ik} f_\eta \Theta(\Delta_{ik} f_\eta)}}^{\text{Abiotic}} \right] \quad (2)$$

$$\Delta_{ij} f = f^{i,j} - f^{j,i} \begin{cases} f^{i,j} = \rho_H(j) + \rho_P(i) \\ f^{j,i} = \rho_H(i) + \rho_P(j) \end{cases}$$

$$\lambda^i = \frac{1}{2} (1 - RE^i)$$

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

$$\Delta_{ij} f_\eta = f_\eta^j - f_\eta^i \begin{cases} f_\eta^i = \eta_{sp}^* - \eta_{sp}^i \\ f_\eta^j = \eta_{sp}^* - \eta_{sp}^j \end{cases}$$

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

where... is the ... between site i and j and m_ϕ is the metacommunity-specific background dispersal rate (we need here a figure with the landscape considered and we also need to simplify the flow chart and explain this model). The migration of a species k_ϕ from site j to a neighborhood site i occurs only if $m_j^k(t) > m_i^k(t)$. 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 Demographic dynamics

In the previous section we have described the dispersal dynamics. Here we describe the birth and death probabilities associated with each model...

4.2.1 Model 1: Density-independent and non-informed dispersal dynamics

At each time (specify the MC rate) we leave all the individuals of each site i to be chosen 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 supply 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.

EQUATION NOT TRANSFORMED!

• 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
EQUATION NOT TRANSFORMED!

• 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
EQUATION NOT TRANSFORMED!

- **Natural Death Probability**

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

EQUATION NOT TRANSFORMED!

- **Carrying Capacity (for each species in each site)**

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

4.2.2 Model 2: Density-dependent predator-prey ratio dispersal dynamics

At each time (specify the MC rate) we leave all the individuals of each site 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.

EQUATION NOT TRANSFORMED!

- **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
EQUATION NOT TRANSFORMED!

- **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
EQUATION NOT TRANSFORMED!

- **Natural Death Probability**

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

EQUATION NOT TRANSFORMED!

- **Carrying Capacity (for each species in each site)**

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

4.3 Multi-trophic metacommunity dynamics

Here, we describe the equations that combine dispersal, trophic and population dynamics across multiple sites and trophic levels in a broad geographic region. We track demography and species abundances in each site by considering at each time step birth-death events across all the sites.

EQUATION NOT TRANSFORMED!

$$\left\{ [1 - NDp(k)] \left[\sum_{b \in H(k)} \rho(b) Dp(b) \right] [Bp(k)] - \left[\sum_{c \in P(k)} \rho(c) (1 - NDp(c)) \frac{\rho(k)}{\sum_{d \in H(c)} \rho(d)} Dp(k) \right] - [NDp(k)] \right\} \quad (3)$$

where ... describes the probability to choose...

4.4 Spatial patterns of ecological and spatial networks

4.4.1 Simulations

We use a Monte Carlo (MC) approach to simulate the dispersal and predation dynamics. Sites are represented as nodes of a geographical neighborhood network and the connectivity of those sites are represented as edges of this network (refs). Trophic relationships among species within each site are represented by a directed network in which each node represents a species and each directed link represents a trophic relationship between a pair of species.

Acknowledgments

References

1. de Santana CN, Rozenfeld AF, Marquet PA, Duarte CM (2013) Topological properties of polar food webs. Marine ecology Progress series 474: 15–26.
2. Dunne JA, Brose U, Williams RJ, Martinez ND (2005) Modeling food-web dynamics: complexity-stability implications. Aquatic food webs: an ecosystem approach : 117.
3. Jordán F, Gjata N, Mei S, Yule CM (2012) Simulating food web dynamics along a gradient: Quantifying human influence. PloS one 7: e40280.
4. Levin B (1981) A representation for multinomial cumulative distribution functions. The Annals of Statistics 9: 1123–1126.

Figures

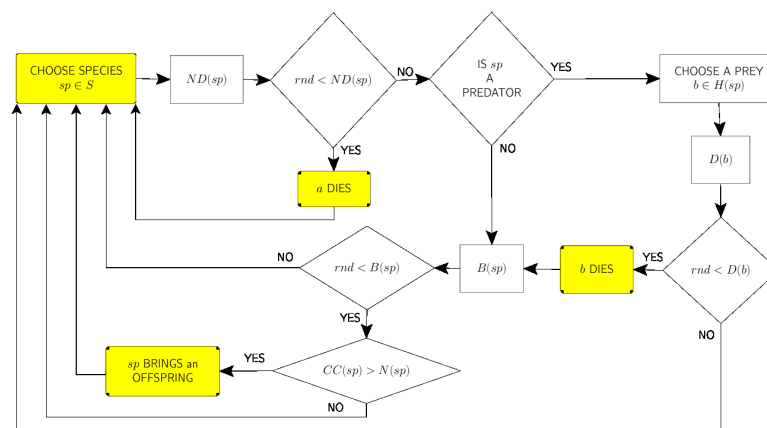


Figure 1. Fluxogram. Fluxogram of the model.

Tables