A phenomenological model of metacommunity coevolution

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Abstract

We outline the basic ingredients for a phenomenological model of coevolution in spatial interaction networks. This model relies on developments from the insular biogeography theory and the metacommunity theory. We show how it can be used to derive simple predictions about the relative consequences of spatial structure, interaction type, and evolutionary pace, on the evolutionary biogeography of interactive metacommunities.

1   Introduction

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Despite this, Urban et al. [2] emphasize that the current theories leaves us poorly prepared to handle the evolution of complex metacommunity over large spatial extents.

2   Ingredients of the model

The metapopulation framework is ....

Building on these previous results, TTIB built a trophic model of island biogeography. This model achieves the overlap between ecological network theory and biogeography, but lacks an evolutionary component. It is the goal of this paper to descibe how the TTIB model can be coupled to simple evolutionary rules, to obtain a phenomenological model of evolution in spatialized networks.

3   Rules for evolution

3.1   Populations and species delineation

Our model assumes that each population i occupies a position $\mathbf{n}_i$ in the hyperdimensional niche space. Given the position of all its populations, the center of mass of a species can be taken by averaging the position of each population allong each niche axis. This center of mass, for species s, is called $\mathbf{m}_s$. Everytime a species colonizes a new patch, it creates a new population in the model.

3.2   Speciation

The model assumes a fixed treshold σ, for which every population whose $d\left(\mathbf{m}_s, \mathbf{n}_i\right) \geq \sigma$, where d is any distance function, undergoes speciation. This process is illustrated in Fig. 1. As the center of mass of each species, and consequently the criteria for speciation, is calculated at the regional scale, our model does not allow sympatric speciation.
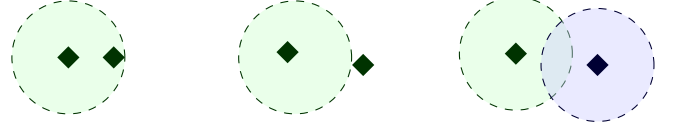

Figure 1: Conceptual model of speciation. Each species is defined by the center of mass of all its populations on the niche space, and a fixed distance. When one population falls outside of this distance, as in the case in the second step, it forms a new species. Note that, as the position of each population on the niche space changes randomly to simulate the effect of drift, the center of mass of the species will move through time.

3.3   Genetic drift

4   Rules for interaction

The existence of an interaction follows the same rules as in the niche model of Williams and Martinez [3]. Each population is identified by its position n on a niche space, which can be composed of as many arbitrary continuous quantitative niche axes as needed. On each axis, each population has a centroïd c, and a range r, meaning that each species will interact with any other species whose trait value falls within $n + c \pm r$. This relationship holds for each axis of the niche space, meaning that, for a k dimensional niche space, a species i is represented by the arrays $\mathbf{n}_i = \left\{n_{i1}, n_{i2}, ..., n_{ik}\right\}$, $\mathbf{c}_i = \left\{c_{i1}, c_{i2}, ..., c_{ik}\right\}$, and $\mathbf{r}_i = \left\{r_{i1}, r_{i2}, ..., r_{ik}\right\}$.

We assume that, for two populations i and j to interact, their niche positions need to be compatible on all axes. This allows an adjancency matrix of all potential interactions among existing populations to be calculated by

$$\mathbf{A}_{ij} = \prod_{a=0}^{k} \delta\left(n_{ia} + r_{ia} - c_{ia} \leq n_{ja} \leq n_{ia} + r_{ia} + c_{ia}\right) \quad (1)$$

, in which δ is Kronecker's delta function, taking a value of one when the condition is satisfied, and zero otherwise. This formulation lends itself nicely to simplifications. Intra-specific interactions can be easily forbidden. In addition, if one designs two or more sets of species (so as to simulate bipartite or tripartite networks), and fixes as a an evolutionary rule that speciation can never switch a population from one set to the other (a reasonnable assumption over micro-evolutionary times), all within-set interactions can be set to zero. A general expression of the metaweb adjacency matrix is therefore given by

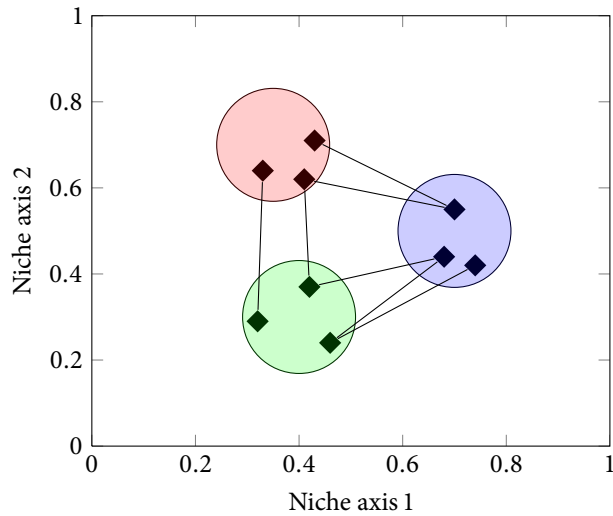$$\mathbf{M}_{ij} = \delta_{\text{sp}} \times \delta_{\text{set}} \times \mathbf{A}_{ij} \quad (2)$$

Figure 2: Example of three species, each made of several populations, on a two-axes niche represented in the unit square. Each circle correspond to the limits of one species, and each diamond on the niche space is a population. Populations which are close enough are connected.

, in which δ_{sp} is the existence of intra-specific interactions, and δ_{set} is the existence of intra-set interactions.

Note that because different populations are representing each species locally, there will be a turnover in the existence of interactions at the species level, which is a realistic feature of natural interacting metacommunities [1]. Two species are interacting if they have at least one interaction between their populations.

5   Metacommunity dynamics

6   Conclusion

References

[1] Timothée Poisot et al. "The dissimilarity of species interaction networks". In: *Ecology Letters* (2012).

[2] Mark C Urban et al. "The evolutionary ecology of metacommunities". In: *Trends in Ecology & Evolution* 23.6 (2008), pp. 311–317.

[3] Richard J Williams and Néo D Martinez. "Simple rules yield complex food webs". In: *Nature* 404.6774 (2000), pp. 180–183.