Omnomnomnivores

Tanya Strydom[1], Timothée Poisot[2,3]

[1]Curvenote,
[2]Université de Montreal,
[3]Québec Centre for Biodiversity Sciences,

Corresponding author: Timothée Poisot, `timothee.poisot@umontreal.ca`

Abstract

In September 2021, a significant jump in seismic activity on the island of La Palma (Canary Islands, Spain) signaled the start of a volcanic crisis that still continues at the time of writing. Earthquake data is continually collected and published by the Instituto Geográphico Nacional (IGN). ...

Plain Language Summary

Earthquake data for the island of La Palma from the September 2021 eruption is found ...

1 Introduction
2 Data & Methods
2.1 Metacommunity model

The metacommunity model developed by (**Thompson2017Dispersala?**) is a good starting point to use for this 'case study' as it allows us some flexibility with how we want to parameterise the system. The model (Equation 1) itself is based on a tritrophic community ('plants', 'herbivores', and 'carnivores') and is a collection of modified Lotka–Volterra equations and (broadly) models species abundance as a function of interaction strength, environmental effect, immigration, and emigration. The metacommunity consists of S species with M environmental patches and looks as follows:

$$X_{ij}(t+1) = X_{ij}(t)exp\left[C_i + \sum_{k=1}^{S} B_{ik}X_{kj}(t) + A_{ij}(t)\right] + I_{ij}(t) - X_{ij}(t)a_i \quad (1)$$

Where $X_{ij}(t)$ is the abundance of species i in patch j at time t. C_i is its intrinsic rate of increase (which we have set to 0.1 for 'plants' and -0.01 for 'herbivores' and 'carnivores'). B_{ik} is the per capita effect of species k on species i. The exact interaction strength for each species pair is drawn from a uniform distribution with the parameters for the interaction pairs listed in Table 1, the values drawn from the uniform distribution are scaled by dividing by $0.33S$ to yield the final interaction strength for each interacting pair.

Table 1: Intervals used for the uniform distribution from which interaction strengths values are drawn from for the different types of species pair interactions. Note this is represent the effect of species type 1 on species type 2 *i.e.,* herbivore-plant represents the effect of a herbivore species on a plant species

Interacting pair	Range of uniform distribution
Plant-plant	-1.0 – 0.00
Plant-herbivore	0.0 – 0.10
Plant-carnivore	0.0
Herbivore-plant	-0.3 – 0.00
Herbivore-herbivore	-0.2– -0.15
Herbivore-carnivore	0.0 – 0.08
Carnivore-plant	0.0
Carnivore-herbivore	-0.1 – 0.00
Carnivore-carnivore	-0.1 – 0.00

$A_{ij}(t)$ is the effect of the environment in patch j on species i at time t and can be further expanded as follows:

$$\hat{A}_{ij}(t) = h \times \frac{1}{\sigma\sqrt{2\pi}} \exp -\frac{1}{2}\left(\frac{E_j(t) - H_i}{\sigma}\right)^2$$

$$A_{ij}(t) = \hat{A}_{ij}(t) - max(\hat{A}) \tag{2}$$

Species environmental optima (H_i) are evenly distributed across the entire range of environmental conditions for each trophic level, meaning that species from different trophic levels will be at, or near the same environmental optima. h is a scaling parameter (set to 300), $E_j(t)$ is the environment in patch j at time t and σ is the standard deviation (set to 50).

$I_{ij}(t)$ is the abundance of species i immigrating to patch j at time t and can be expanded as follows:

$$I_{ij}(t) = \sum_{l=j}^{M} a_i X_{il}(t) exp(-Ld_{jl}) \tag{3}$$

Where ai is the proportion of the population of species i that disperses at each time step, the dispersal rate is drawn from a normal distribution ($\mu = 0.1$, $\sigma = 0.025$) for each species. The abundance of immigrants to patch j from all other patches is governed by where d_{jl} is the geographic distance between patches j and l, and L (the strength of the exponential decrease in dispersal with distance), which is also drawn from a normal distribution for each species. The parameters used for L are trophic level dependant and are show in Table 2

Table 2: Parameters for the normal distributions used to determine the dispersal decay (L) for each species depending on its trophic level.

Trophic level	μ	σ
Plant	0.3	0.075
Herbivore	0.2	0.050
Carnivore	0.1	0.025

2.2 Generating networks

More info on the baking process and the various connectivity stuff and whatnot

2.3 Spatial wombling

Broadly speaking spatial wombling is an edge-detection algorithm which traverses a geographic area and defines this area in terms of the rate (m) and corresponding direction (θ) of change. This is done by using first-order partial derivative (∂) of the 'curvature' of the landscape as described by $f(x,y)$ (see Equation 4). This essentially gives an indiaction how steep the gradient (m) is between neighbouring cells as well as the direction (θ) of the slope.

$$m = \sqrt{\frac{\partial f(x,y)}{\partial x}^2 + \frac{\partial f(x,y)}{\partial y}^2} \tag{4}$$

The spatial wombling analyses were done using `SpatialBoundaries.jl` (**Strydom2023Spatialboundariesa?**). The docuemntation provides a more detailed breakdown of the underlying methodology.

3 Conclusion

References

Source: [Article Notebook](#)