

Non-trophic interactions: consequences on secondary extinctions

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1 The trophic model

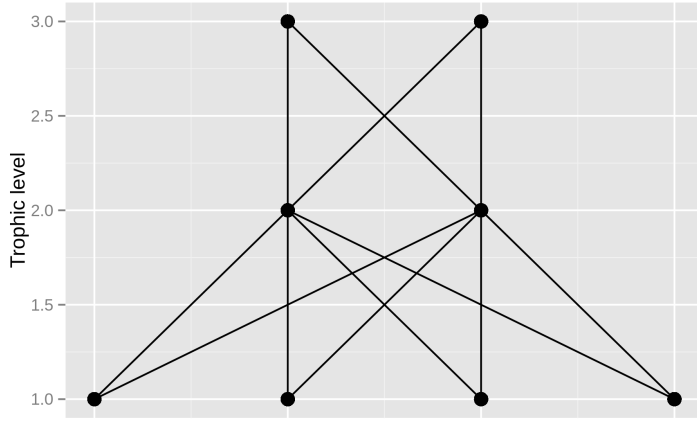


Figure 1

The fixed trophic topology: 4 basal producers, 2 grazers and 2 consumers. Species consume everyone on the lower trophic level. x-axis has no meaning.

The node dynamics model is inspired from [1]. It is given by its main equation that describes the dynamics of one species' biomass:

$$\frac{dB_i}{dt} = \underbrace{rB_i\left(1 - \frac{B_i}{K_i}\right)}_{\text{logistic growth}} + \underbrace{\sum_{k=1}^N B_i w_{ik} e_{ik} F_{ik}}_{i \text{ eats}} - \underbrace{\sum_{j=1}^N B_j w_{ji} F_{ji}}_{i \text{ gets eaten}} \underbrace{- x_i B_i}_{\text{mortality}} \quad (1)$$

where F_{ij} describes a generic functional response in which species i feeds on j as followed:

$$F_{ij} = \frac{a_{ij} w_{ij} B_j^{q+1}}{1 + h_i w_{ij} \sum_k a_{ik} B_k^{q+1}} \quad (2)$$

Parameters are described in Table 1. In the functional response, q is a coefficient taken randomly in the $[0, 1]$ range (a value of 0 yields a type-II functional and 1 a type-III functional response).

Many of these parameters can be chosen using metabolic scaling rules resulting in a plausible food web with few free parameters. Details on the default parameter values can be found in Table 1. The trophic topology (values for which $a_{ij} > 0$) is held constant.

1.1 Results

1.1.1 Example output

The simulation process is as follow:

- Species initial biomasses are chosen randomly in the range $]0; K_i]$, q is chosen randomly between 0 and 1.
- The simulation is run until $t = 3000$ is reached, when one or more species are removed. The run lasts until $t = 5000$ is reached.

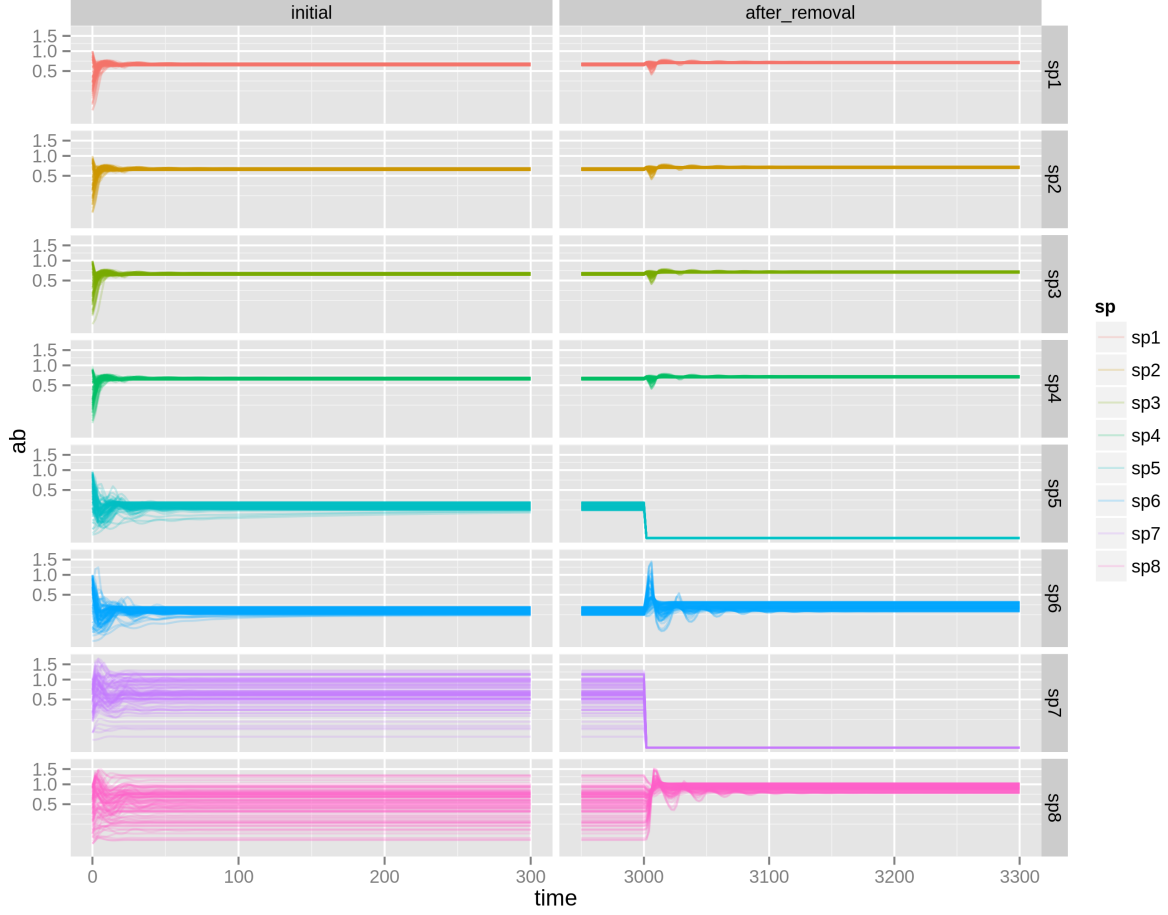


Figure 2

100 replicates. sp1-4 are producers, sp5-6 are intermediate consumers and sp7-8 are top predators. In this simulation, species 5 (grazer) is removed at time $t = 3000$. Mind the non-linear vertical scale

2 An example of non-trophic interaction

All the parameters of the model here are fixed beforehand and do not depend on the biomasses of species. Non-trophic interactions can be implemented by introducing that dependence on species abundances.

For example, let's consider species i , a producer: its logistic growth is controlled by its fixed carrying capacity K . However, let's consider that some species from upper trophic levels create new space for algae to grow on, thus increase its value (e.g. mussels/propagules).

Instead of a fixed value K in Eq. 1, we replace it by K_i that depends on interactions with other species:

$$K_i = \sum_{j=1| \delta K_{ij} \neq 0}^N \frac{K_0 B_0 + (K_0 + \delta K_{ij}) B_j}{B_0 + B_j} \quad (3)$$

δK_{ij} represents the bonus (if positive), or penalty (if negative) on parameter K that species i receives from species j .

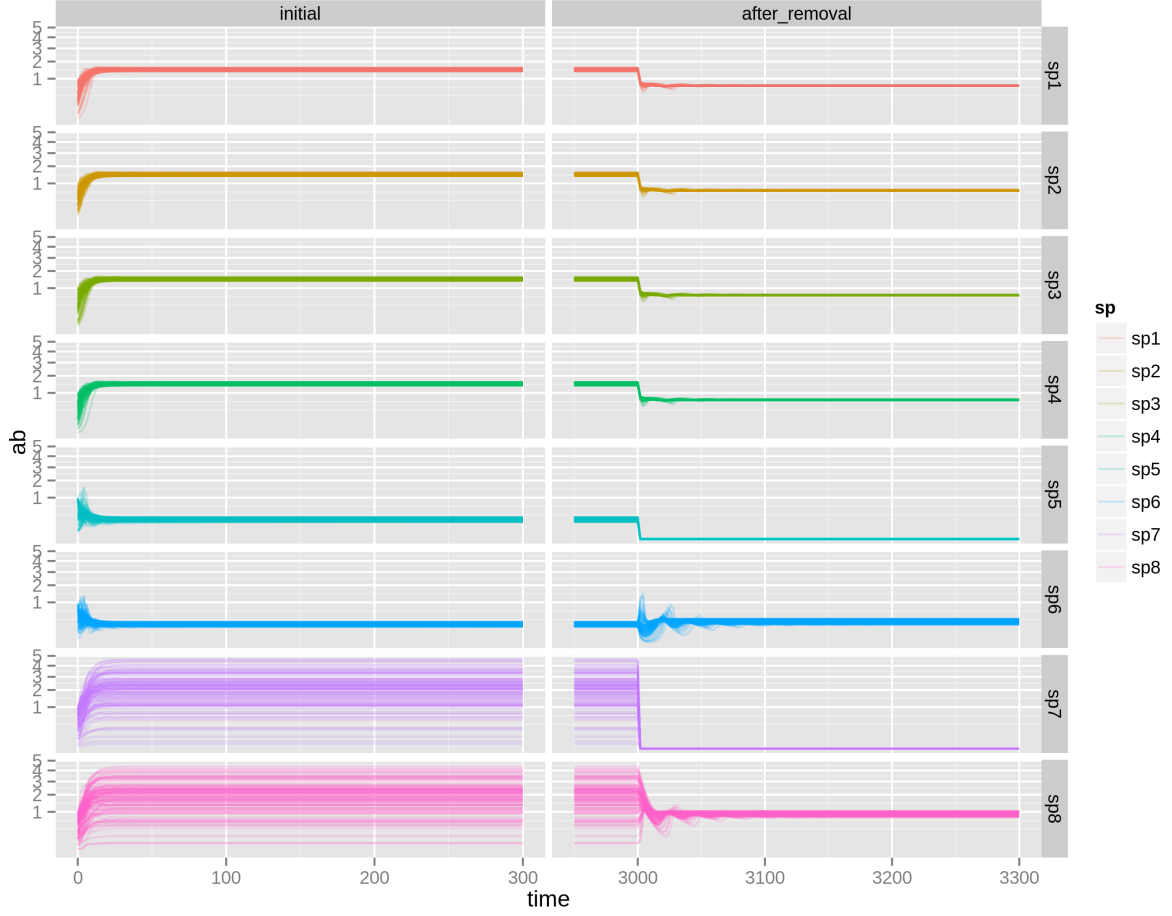


Figure 3

Example output for 100 simulations, where the carrying capacity K of producers (sp1-4) depend on the abundance of species 5 i.e. $\delta K_{5(1,2,3,4)}$ is set to 0.3. In this simulation, species 5 (grazer) is removed at time $t = 3000$.

Note that these two examples produce no secondary extinctions.

3 Generalization of NTIs

This approach can be used for any parameter. However, not all parameters can be altered in a way that makes sense. For example, the grazers and predators have no K thus the above example is not easily generalizable to any pair of species.

A possibility would be to introduce a generic coefficient of bonus/penalty in trophic interactions, on w_{ij} for instance, or add a new term N^t representing a “generic” non-trophic interaction to the main equation:

$$\frac{dB_i}{dt} = r_i B_i \left(1 - \frac{B_i}{K_i}\right) + \sum_{k=1}^N B_i w_{ik} e_{ik} F_{ik} - \sum_{j=1}^N B_j w_{ji} F_{ji} - x_i B_i + \sum_j N_{ij}^t B_j \quad (4)$$

TODO

- Why do top predators have different responses ?
- Think about how to set the body mass ratios between preys and predators.
- Check and think about metabolic relationships (ectoterm/endotherm, that paper about metabolism of plants)
- Think about which ones should be free and which ones should be fixed.

References

- [1] U Brose, RJ Williams, and ND Martinez. “Allometric scaling enhances stability in complex food webs”. In: *Ecology Letters* (2006), pp. 1228–1236.

Param.	Comment	Value
r_i	Reproductive rate of species i	1 for producers, 0 otherwise
K_i	The carrying capacity of species i	1 for all producers
w_{ij}	The consumption rate of species j by species i	equal between all preys (e.g. 0.25 for grazers (4 preys))
F_{ij}	The functional response of species i on j	
q	The “hill” coefficient in the functional response	random between 0 and 1
e_{ji}	The conversion efficiency of species i into j	0.85 for all i and j
b_i	Body mass of species i	producers: 1, grazers: 3 predators: 6
x_i	The metabolic (mortality) rate	scaling rule with body size $x_i = 0.223b_i^{-.25}$
a_{ij}	The attack rate of species i on j	for species i attacking j : $27.24 * x_i * \exp(0.01 * b_i / b_j)$
h_i	The handling time of species i	$1/(8 * x_i)$

Table 1

Default parameters and values used in the model. Some of them (e.g. x_i use metabolic scaling relationships).