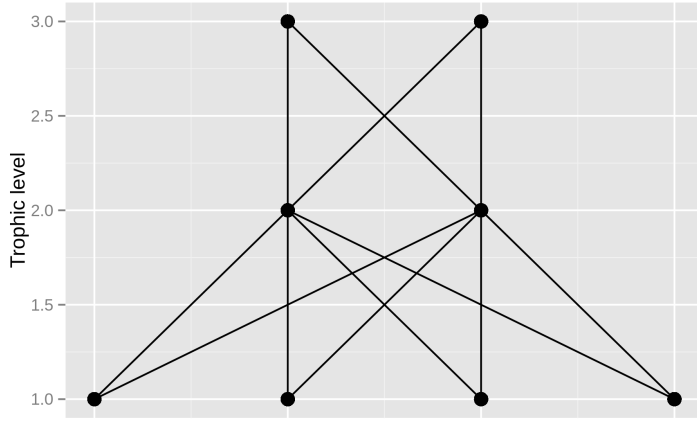


# Non-trophic interactions: consequences on secondary extinctions

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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:

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

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).

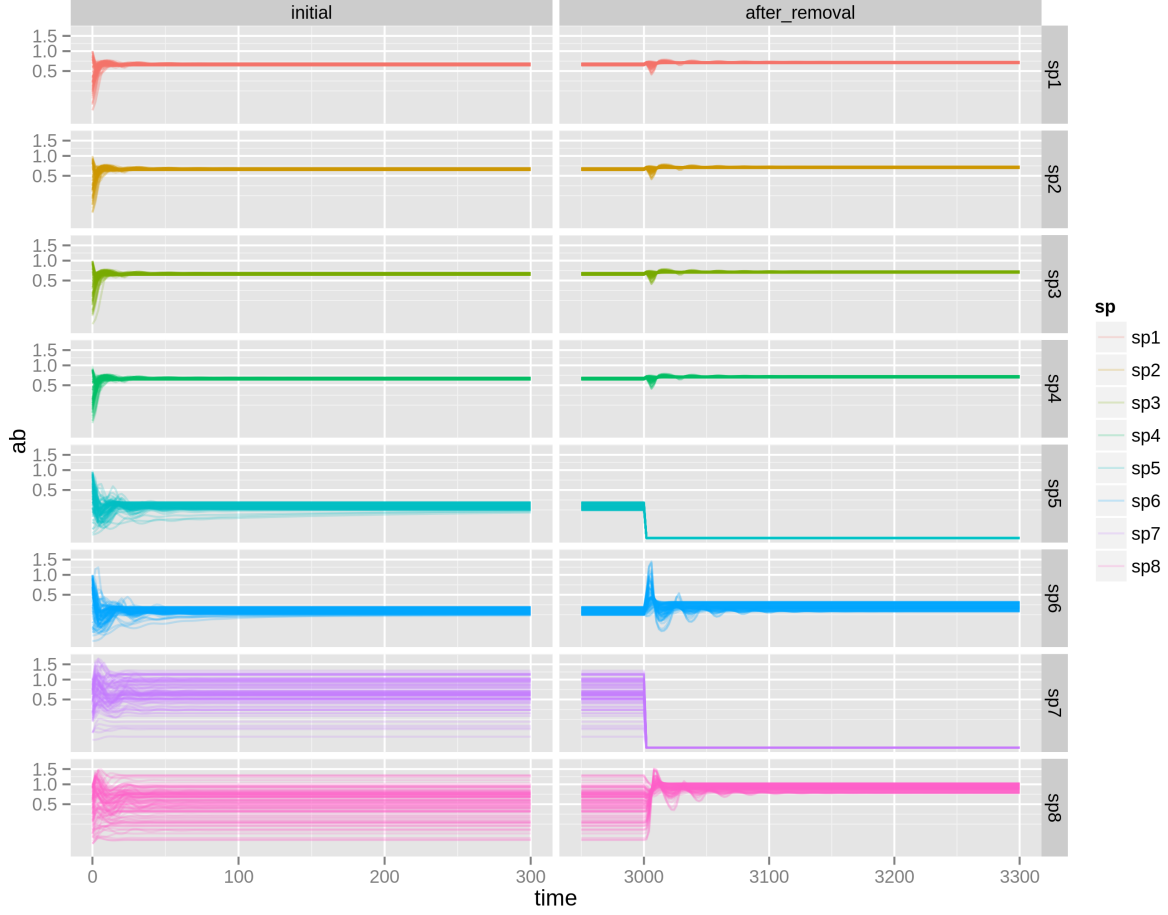
Many of these parameters can be chosen using metabolic scaling rules resulting in a plausible food web with few free parameters. Details on the default parameter values can be found in Table 1. The trophic topology (values for which  $a_{ij} > 0$ ) is held constant.

### 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 Generalization of NTIs

The introduction of a *generic* non-trophic interaction can be done by adding a term to the equation of a node (Eq. 1).

$$\frac{dB_i}{dt} = rB_i\left(1 - \frac{B_i}{K_i}\right) + \sum_{k=1}^N B_i w_{ik} F_{ik} - \sum_{j=1}^N B_j w_{ji} F_{ji} / e_{ji} - x_i B_i + \underbrace{\sum_{j=1}^N N_{ij}^t B_j}_{\text{non-trophic interactions}} \quad (3)$$

Note that the non-trophic interaction is constrained to be always below the “mortality” rate ( $-x_i B_i$ ) so that there is no creation of biomass from non-trophic interactions.

## 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 $j$
$b_i$	<b>Body mass of species <math>i</math></b>	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).