

1 **Supplementary Material to:**  
2 **Does structural sensitivity alter complexity-stability**  
3 **relationships?**

4 C. Aldebert<sup>a,\*</sup>, D. Nerini<sup>a</sup>, M. Gauduchon<sup>a</sup>, JC. Poggiale<sup>a</sup>

5 **a** Mediterranean Institute of Oceanography, Aix-Marseille University, Toulon University, CNRS/INSU,  
6 IRD, MIO, UM 110, 13288, Marseille, Cedex 09, France.

7 \* corresponding author, +33 (0)4 860 90 640

8 E-mails:

- 9 • clement.aldebert@univ-amu.fr,
- 10 • david.nerini@univ-amu.fr,
- 11 • mathias.gauduchon@univ-amu.fr,
- 12 • jean-christophe.poggiale@univ-amu.fr

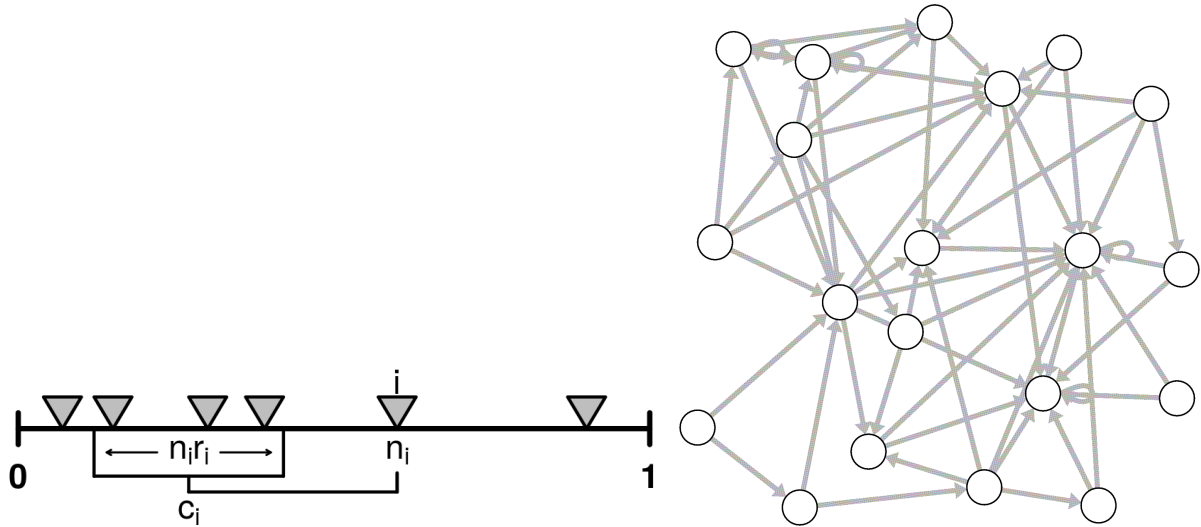
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## 1 Niche model, primary producers and cannibal species

Food webs are composed by  $S$  species (*sensu* trophic species) and one resource. Species are linked by  $L$  trophic interactions, so that food web connectance is  $C = L/S^2$  (directed connectance, as defined by Martinez, 1991). In order to statistically investigate the effect of trophic complexity, we need to produce millions of different food webs. We use the niche model (Williams & Martinez, 2000) to randomly build food webs with the desired number of species and an *a priori* fixed connectance. This stochastic model generates quickly numerous food webs with patterns that are roughly empirically consistent (Allesina *et al.*, 2008; Cattin *et al.*, 2004; Williams & Martinez, 2000). It is based on the principle of ecological niche (Hutchinson, 1957). A species  $i$  is characterized by a niche value  $n_i$ , that indicate its position on the segment  $[0, 1]$ , the niche axis (figure 1). Each species is also characterized by a continuous feeding range, a sub-interval of this axis. Species  $i$  feeds on all species whose niche value belongs to this range. It is defined by its center  $c_i$  and its relative width  $r_i$ . So this feeding range is  $[c_i \pm n_i r_i / 2]$ . The niche value  $n_i$  is uniformly drawn in the interval  $[0, 1]$ . The relative width of the feeding range  $r_i$  is drawn from a beta distribution  $\mathcal{B}(1, \frac{1}{2C} - 1)$ , where  $C$  is the desired food web connectance. If  $C$  is high (low), the expected width of the feeding range is also high (low), and thus the expected number of prey species is high (low) too. The center of the feeding range  $c_i$  is uniformly drawn in the interval  $[n_i r_i / 2, \min(n_i, 1 - n_i r_i / 2)]$  so that the feeding range is always a sub-interval of  $[0, 1]$  (Williams & Martinez, 2004). Species whose feeding range does not contain any other species niche value do not feed on any prey species and define primary producers. Other species are called predators. Species whose niche value does not belong to any other species feeding range define top predators. Construction of the feeding range intervals allows the possibility that the feeding range of a species contains its own niche value, so that it becomes its own prey (this is cannibalism). A predator may even feed on prey of higher niche value than itself, what may generate trophic loops in resulting food webs. In order to have at least one primary producer in the food web, the species with the lowest  $n_i$  has always  $r_i = 0$ .

The construction method in the niche model is such that the average connectance among numerous generated food webs is equal to the desired *a priori* connectance (through the second parameter of the beta distribution). Nevertheless, due to the variability of random draws, all food webs do not have exactly this desired connectance. Beside that, some generated food webs present unrealistic patterns. So we added a rejection step after food webs construction. We only studied food webs with a connectance

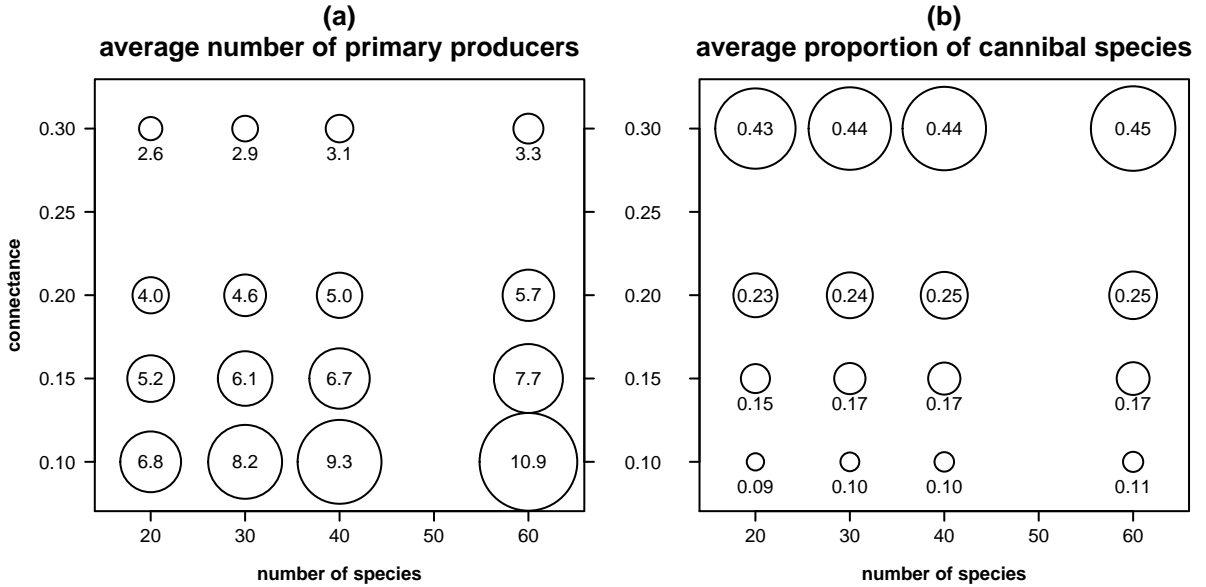


**Figure 1.** Scheme of the principle of the niche model (left, redrawn from Williams & Martinez, 2000, 2004) and an example of a 20 species food web generated by this model (right). This model is used to build all food webs studied in the remaining of the paper. The left scheme represents a food web with  $S = 6$  species. The set of all possible ecological niches is summarized by the segment  $[0, 1]$ . The ecological niche of each species  $i$  is summarized by a niche value  $n_i \in [0, 1]$ . Each species feeds on a continuous range of prey species defined by its center  $c_i$  and its relative width  $r_i$ . Species which do not have any prey species in their feeding range are defined as primary producers. See section 2.1 for details on how the parameters values are randomly drawn.

49 that deviated at most by 0.01 of the desired one, that are connected (no disconnected parts), and in which  
 50 all predators feed (as a prey or through a food chain) upon at least one primary producer. The average  
 51 number of primary producers and the average proportion of cannibal species in food webs generated by  
 52 the niche model are shown in figure 2.

## 53 2 Algorithm to classify asymptotic dynamics

54 In order to characterize the asymptotic dynamics of the numerous food webs studied, we built the following  
 55 automatized classification algorithm. The algorithm starts by a time  $T_{ini}$  of initial simulation in order  
 56 to limit transient effects due to the arbitrary initial condition. After that, the asymptotic dynamics is  
 57 considered as associated to extinction(s) if at least one species has a biomass that becomes lower than  
 58 an arbitrary extinction threshold  $B_{min}$ . Else, if the system converges to a point in the phase space  
 59 (criterion  $\sum_{i \in S} |dB_i/B_i dt| < \varepsilon_{cv}$ ) where all eigenvalues of the jacobian matrix have negative real parts,  
 60 the asymptotic dynamics is a positive equilibrium. As long as no criterion is reached, the simulation



**Figure 2. Average number of primary producers and proportion of cannibal species in the food webs studied.** These numbers vary with trophic complexity (number of species and connectance). Estimations are realized on 10 000 food webs generated using the niche model proposed by Williams & Martinez (2000, 2004) for each trophic complexity.

61 continues. The whole simulation is divided in subparts of length  $T_{sub}$ . After each subpart, jacobian's  
62 eigenvalues at the temporal average of the dynamic during the current subpart are computed. If all  
63 eigenvalues have a negative real part the simulation continues, and finally an equilibrium is reached in all  
64 our simulations ending before  $T_{max}$  (see below). If at least one eigenvalue has a positive real part and if  
65 fluctuations do not change significantly between subparts of the simulation ( $\sum_{i \in S} |\bar{B}_i^m - \bar{B}_i^{m-1}| < \varepsilon_{mean}$ ,  
66 with  $\bar{B}_i^m$  being the average of  $B_i(t)$  for  $t \in [T_{ini}, T_{ini} + mT_{sub}]$ ), the asymptotic dynamics will be  
67 considered as a fluctuating dynamic without any extinction. This is done because the multiple estimations  
68 of the jacobian matrix indicate that the flow is divergent at the average of the fluctuating dynamics. This  
69 means that the presence of a stable equilibrium around this average is very unlikely. Sometimes, reaching  
70 one of the criteria needs a long time of simulation. So we fixed a maximal time of simulation  $T_{max}$ . If  
71 the algorithm fails to classify a food web dynamics in one of the three classes before the simulation end,  
72 the dynamics is consider as unknown.

73 The algorithm used to solve ODEs is a Runge-Kutta-Fehlberg-4,5 numerical scheme, with absolute  
74 and relative error tolerances set to  $10^{-6}$ . Preliminary tests showed that the choice of a specific numerical  
75 scheme among those tested does not affect the results. Tests were also done to choose the values of absolute

76 and relative error tolerance. The parameter values used for our algorithm were tuned after preliminary  
77 tests to improve the algorithm efficiency. We set  $T_{ini} = 500$ ,  $T_{sub} = 5\,000$ ,  $T_{max} = 50T_{sub} + T_{ini}$ ,  
78  $B_{min} = 10^{-6}$ ,  $\varepsilon_{cv} = 10^{-6}$  and  $\varepsilon_{mean} = 0.01$ . Results are the same if a lower  $B_{min}$  value is used to define  
79 extinctions. All simulations start with the arbitrary initial condition  $B_i(0) = 1 \forall i$ . We used only one  
80 initial condition. Tests with 10 random initial conditions on 20-species food webs (connectance equals to  
81 0.15) indicate that a small fraction of these food webs ( $< 1\%$ ) can reach significantly different asymptotic  
82 dynamics depending on the initial condition. For computational reasons, we choose to use only one initial  
83 condition per food web.

84 The algorithm failed to classify food web dynamics before reaching  $T_{max}$  in 0.2 % of the food webs  
85 with Holling's FR and 2 % with Ivlev. However, a study of the calculus made by the algorithm along the  
86 simulation allows to determine which asymptotic dynamics the system is likely to reach is the simulation  
87 continues. The proportion of these food webs which will likely reach a positive equilibrium is close to  
88 the proportion observed in food webs for which the algorithm determines the dynamics before  $T_{max}$   
89 is reached. For example, among the 2 % of unknown dynamics with Ivlev, 98.5 % are likely to reach  
90 a positive equilibrium ( $\varepsilon_{cv} < \sum_{i \in S} |dB_i/B_i dt| < 10^{-5}$ ) on average within the tested range of trophic  
91 complexity. This proportion is roughly equal to that observed in food webs for which dynamics have  
92 been determined (figure 2 in the article). So using a greater  $T_{max}$  will not significantly affect our results.

93 For some food webs which dynamics seems to converge on a positive equilibrium, the point reached  
94 is unstable. We found for some of these food webs that in fact the dynamics converges on a limit cycle  
95 which size is such that the algorithm considers it as an equilibrium. This happens when the food web is  
96 closed to a Hopf bifurcation (i.e. a pair of complex conjugated eigenvalues have small positive real parts).  
97 For some other food webs, we supposed that the dynamics fluctuates around one (or more) saddle(s)  
98 connected by an homoclinic or an heteroclinic loop (one eigenvalue is real and slightly positive), but  
99 stays bounded in a set of the phase space which size is again such that the algorithm considers it as an  
100 equilibrium. This phenomenon is negligible with Holling's FR, with less than 10 cases observed among  
101 the hundreds thousands positive equilibria studied. With Ivlev's functional response, it concerns up to  
102 4.5 % of the food webs with a positive equilibrium. This proportion decreases with trophic complexity,  
103 mainly with connectance. When functional response fit at low prey densities is improved (see section 3.3  
104 in the article), it concerns up to 30 % of the food webs with a positive equilibrium. We consider these  
105 food webs as food webs which reach a positive equilibrium, because the ecological meaning of such small

106 fluctuating dynamics is the same as an equilibrium. Considering these food webs as food webs with  
107 fluctuating dynamics, or neglecting them, do not affect our qualitative results and conclusions.

### 108 **3 Different parameter sets for Ivlev’s functional response**

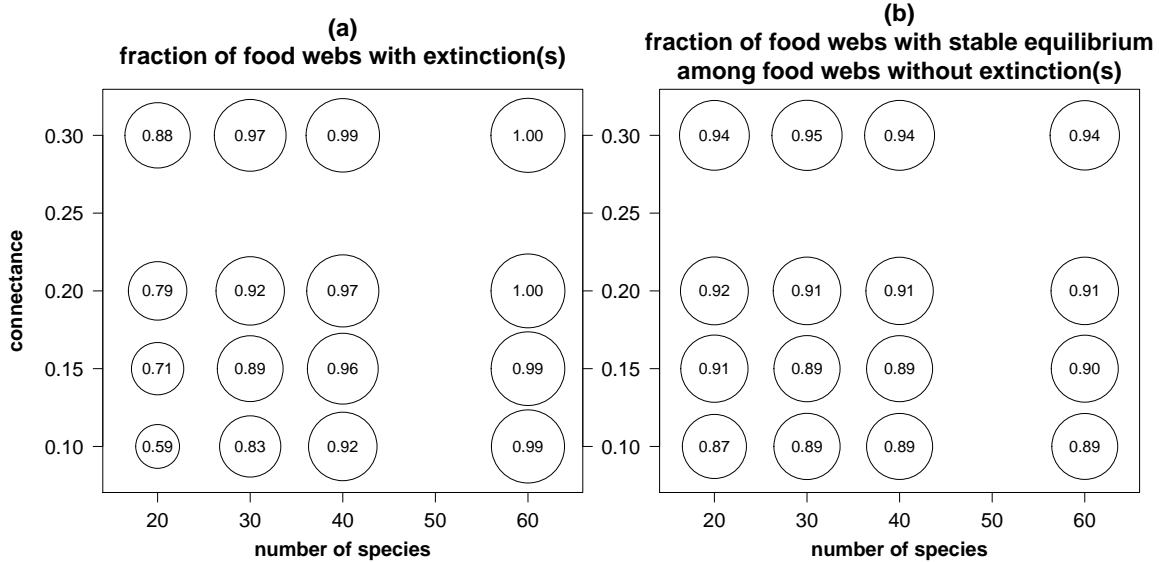
109 Table 2 in the article presents the dynamics of 30 species food webs (with a connectance of 0.15) predicted  
110 by different parameter sets for Ivlev’s FR. These parameter sets come from different ways to fit the  
111 functional responses. To test the robustness of our main conclusions to the method of fit, some of  
112 these parameter sets are used to predict complexity-stability relationships with Ivlev’s FR. We used the  
113 parameter sets obtained with a fitting range  $T_i \in [0, 3.5]$  with both weight functions (uniform  $\omega_U$  and  $\omega_P$   
114 presented in figure 1b of the article), as well as the parameter set obtained using the empirical distribution  
115 of total prey biomass available predicted by Holling’s FR (figure 3b in the article).

116 The three parameter sets predict the same qualitative complexity-stability relationships as the ones  
117 presented in figure 2 in the article (figures 3-5). The two parameter sets obtained with the more classical  
118 methods (see discussion in section 3.6 in the article) predict a higher frequency of equilibrium dynamics  
119 than Holling’s FR ( $\times 2.1$  for the uniform weight function, figure 3, and  $\times 1.9$  for the empirical distribution,  
120 figure 5). A higher frequency of equilibrium dynamics is also predicted by the parameter set derived using  
121  $\omega_P$  over  $T_i \in [0, 3.5]$ , despite the difference is quantitatively lower ( $\times 1.2$ , figure 4).

### 122 **4 Changes in model assumptions**

123 We tested the influence of three assumptions on food web dynamics: fixing the number of primary  
124 producer species in food webs, deleting cannibalistic links, setting the body mass of primary producers  
125 equals to 1. Some of these assumptions are made in some previous studies about complexity-stability  
126 relationships in food webs, but the same combination is not always use. So we tested their influence in  
127 order to get the widest picture as possible. These results are used in section 3.5 in the article to explain  
128 the complexity-stability relationships predicted by the model. Here, we present the dynamics obtained  
129 within the tested range of trophic complexity for different combinations of assumptions, as well as a short  
130 description of their trends.

131 When food webs with a fixed number of five primary producer species are considered (figure 6),

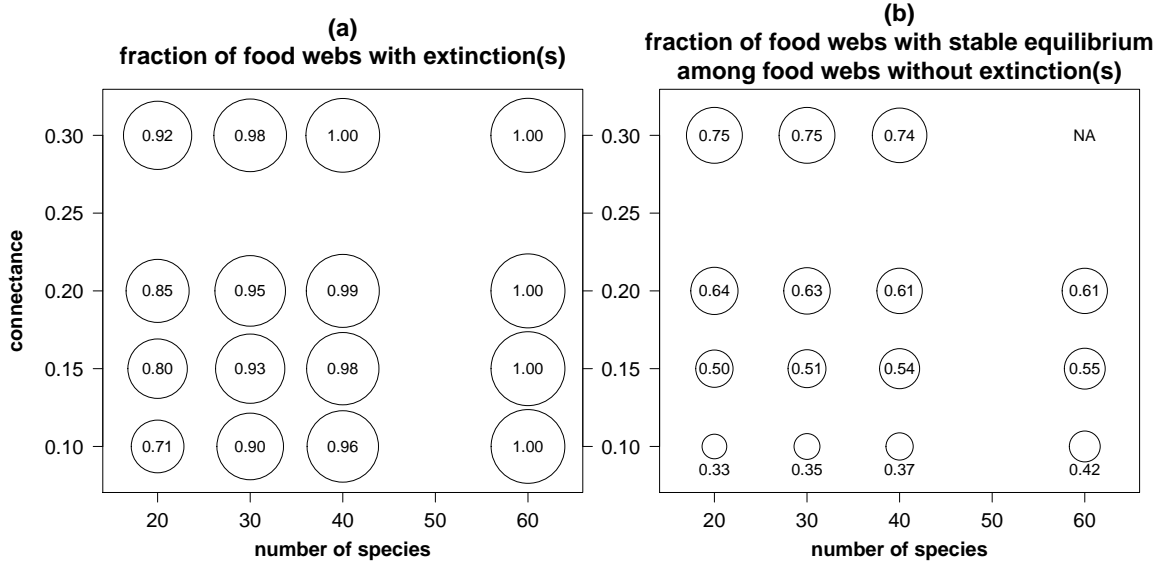


**Figure 3. Food web dynamics as a function of trophic complexity predicted by Ivlev’s functional response, fitted using a uniform weight function over  $T_i \in [0, 3.5]$ .** a: fraction of food webs with at least one species extinction. b: fraction of persistent food webs with a stable positive equilibrium. The number of food webs studied for each pair of parameters is enough to obtain 1 000 food webs with a stable positive equilibrium.

132 Ivlev’s FR predicts on average less extinctions than Holling’s FR (from  $-10\%$  to  $+3\%$ ). Their frequency  
 133 increases with the number of species (on average  $\times 1.6$  with Holling’s FR and  $\times 1.7$  with Ivlev’ FR) and  
 134 decreases with connectance ( $\times 0.8$  and  $\times 0.9$ ). On average, there are 2.6 times more equilibrium dynamics  
 135 with Ivlev’s FR (from  $92\%$  to  $99\%$ ) than with Holling’s FR (from  $15\%$  to  $78\%$ ). The frequency of  
 136 equilibrium dynamics increases with connectance ( $\times 4.3$  with Holling’s FR and  $+3\%$  with Ivlev’s FR).  
 137 We do not discuss any effect of the number of species as the number of food webs studied is lower for  
 138 food webs with 40 and 60 species.

139 When body mass is set to 1 for primary producers (figures 7a,b and 8a,b), Ivlev’s FR predicts on  
 140 average less extinctions than Holling’s FR (from  $-5\%$  to  $+2\%$ ). Their frequency increases more with the  
 141 number of species ( $\times 1.6$  with Holling’s FR and  $\times 1.7$  with Ivlev’s FR) than with connectance ( $\times 1.2$  with  
 142 Holling’s FR and  $\times 1.3$  with Ivlev’s FR). Within the tested range of trophic complexity, the proportion  
 143 of persistent food webs reaching an equilibrium is always  $100\%$  with Ivlev’s FR and ranges from  $38\%$   
 144 to  $86\%$  with Holling’s FR. With the latter, this proportion increases with connectance ( $\times 2.2$ ) and does  
 145 not show a clear trend with the number of species (from  $-3\%$  to  $+4\%$  depending on connectance).

146 When cannibalistic link are deleted and body mass is set to 1 for primary producers (figures 7c,d



**Figure 4. Food web dynamics as a function of trophic complexity predicted by Ivlev’s functional response, fitted using the weight function  $\omega_{\mathcal{P}}$  over  $T_i \in [0, 3.5]$ .** a: fraction of food webs with at least one species extinction. b: fraction of persistent food webs with a stable positive equilibrium. NA means that the precise data has not been acquired for computational reasons (fraction of food webs with extinction(s) close to 1). The number of food webs studied for each pair of parameters is enough to obtain 1 000 food webs with a stable positive equilibrium.

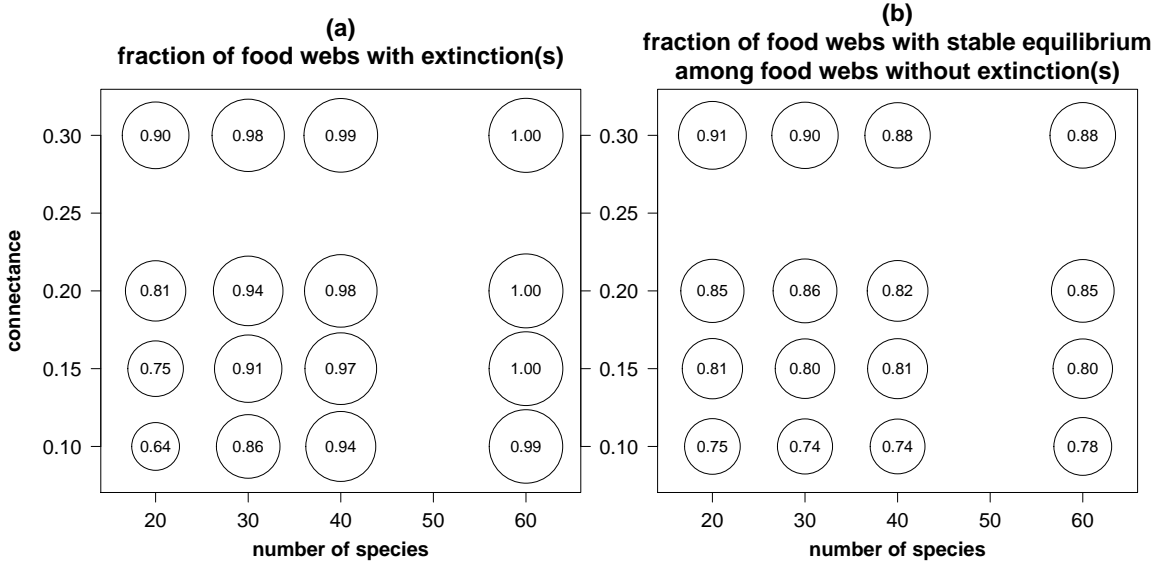
147 and 8c,d), Ivlev’s FR predicts less extinction(s) than Holling’s FR (from  $-9\%$  to no difference). Their  
 148 frequency increases more with the number of species ( $\times 1.4$  with Holling’s FR and  $\times 1.5$  with Ivlev’s FR)  
 149 than with connectance ( $\times 1.2$  and  $\times 1.3$ ). Within the tested range of trophic complexity, the proportion  
 150 of persistent food webs reaching an equilibrium is always  $100\%$  with Ivlev’s FR and ranges from  $35\%$   
 151 to  $81\%$  with Holling’s FR. With the latter, this proportion increases more with connectance ( $\times 2.2$ ) than  
 152 with the number of species (from  $-2\%$  to  $+7\%$  depending on connectance).

## 153 5 Different metrics to quantify food web persistence and vari- 154 ability

155 We tested different metrics to quantify food web persistence and variability. Their estimation is based on  
 156 the analysis of species biomass after a simulation of 100 000 time steps. Mean and variation coefficient  
 157 were computed for each species over the last 10 000 time steps of the simulation.

158 Relationships between these metrics and those used in the article are presented in figures 9 and 10

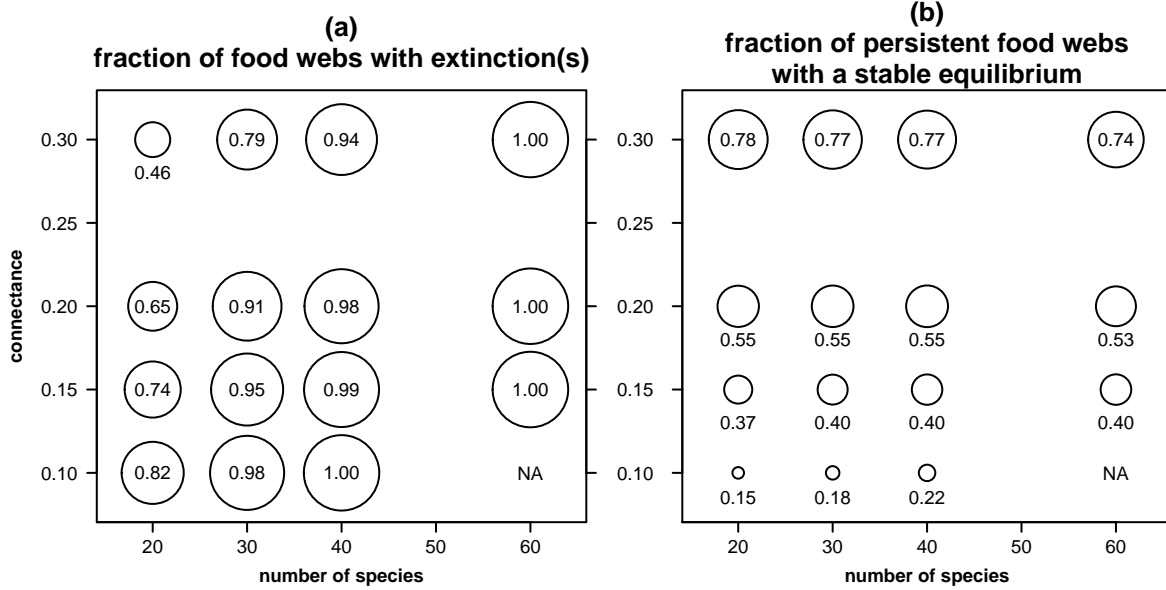




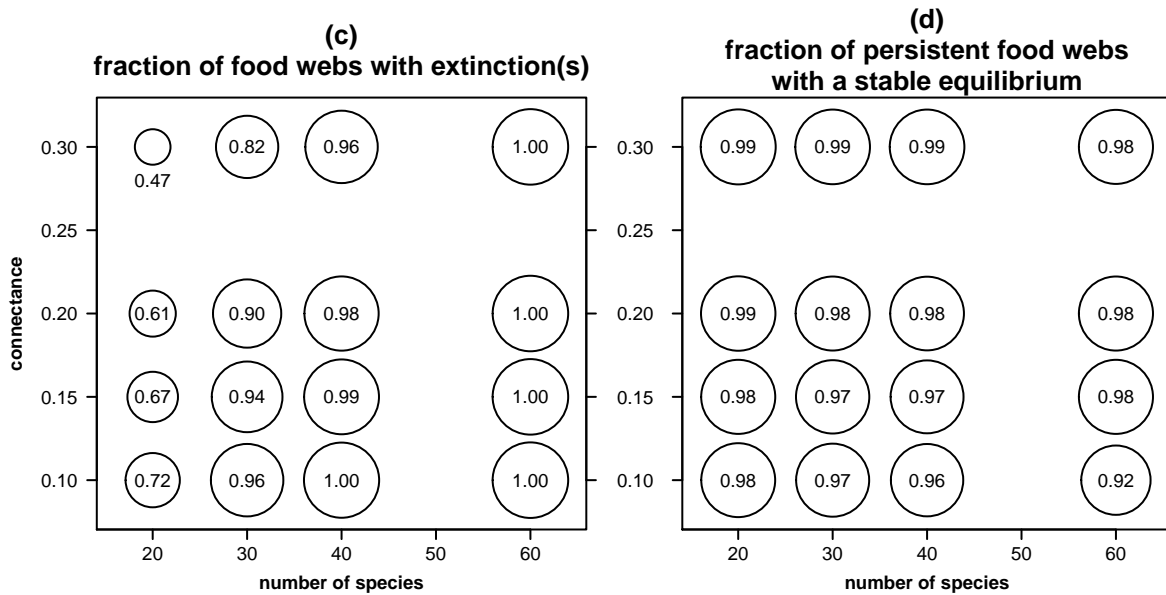
**Figure 5. Food web dynamics as a function of trophic complexity predicted by Ivlev’s functional response, fitted using the empirical distribution of prey biomass observed with Holling’s disc equation (figure 3b in the article).** a: fraction of food webs with at least one species extinction. b: fraction of persistent food webs with a stable positive equilibrium. The number of food webs studied for each pair of parameters is enough to obtain 1 000 food webs with a stable positive equilibrium.

159 for Holling’s FR and Ivlev’s FR respectively. Both functional responses again predict similar food web  
 160 persistence if it is quantified using the average proportion of extincted species in networks (mean species  
 161 biomass below  $10^{-6}$ , panel a in both figures). Using this metrics, food web persistence also decreases  
 162 more with the number of species than with connectance. Food web variability is again significantly  
 163 lower with Ivlev’s FR (non-overlapping ranges of values between formulations) when different metrics  
 164 are used. Metrics based on the variation coefficient predict different complexity-stability relationships  
 165 between formulations (panels c and d). However, we will not discuss relationships obtained with Ivlev as  
 166 the estimated values are close to 0 and within a small range of variations. Opposite complexity-stability  
 167 relationships are also obtained if we focus on the fraction of food webs with fluctuating dynamics, whatever  
 168 the number of species extinctions that occurred (panel b). However, the predicted food web variability  
 169 is still lower with Ivlev. Furthermore, considering food webs with extinctions, as for all these metrics,  
 170 introduces a bias as the number of species and connectance are changed during simulation.

Holling's disc equation

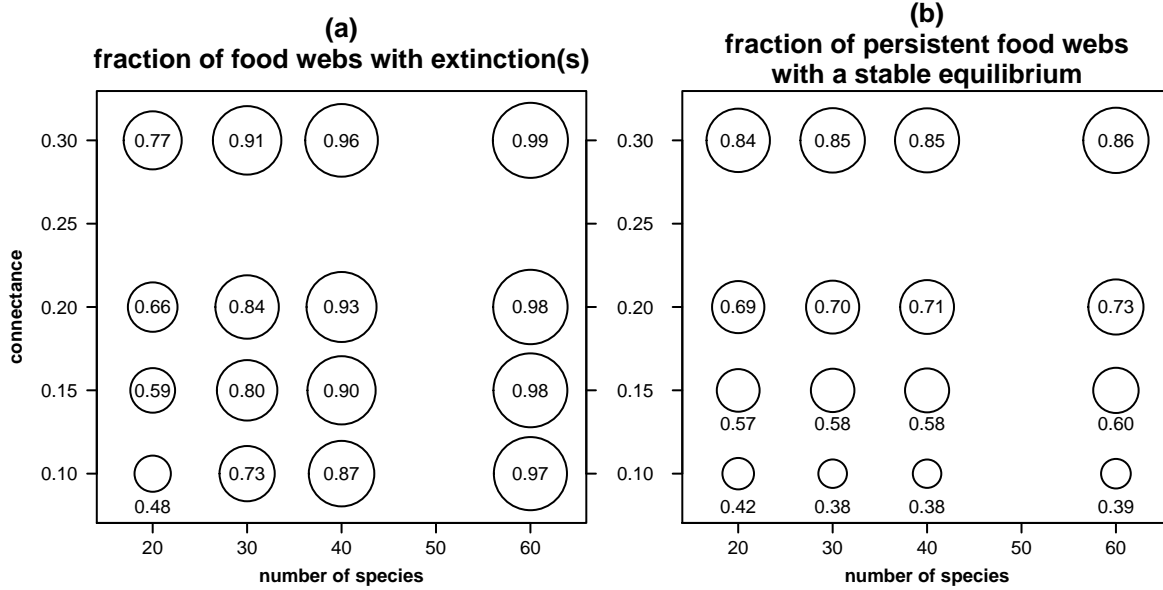


Ivlev's functional response

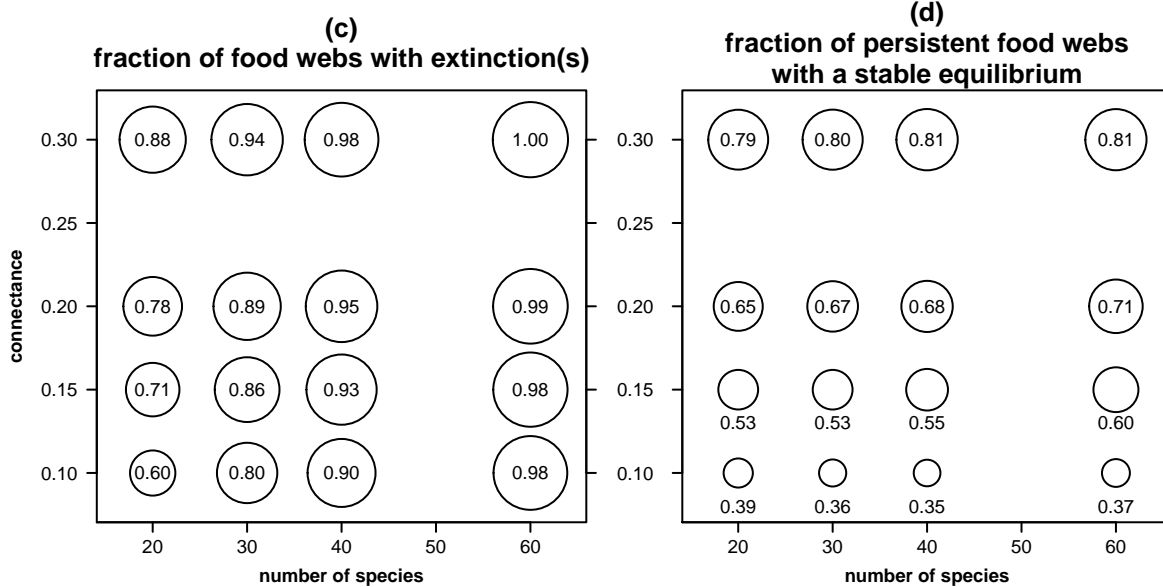


**Figure 6. Food web dynamics as a function of trophic complexity predicted by Holling's (a, b) and Ivlev's functional responses (c, d) for food webs with a fixed number of five primary producer species.** a, c: fraction of food webs with at least one species extinction. b, d: fraction of persistent food webs with a stable positive equilibrium. NA means that the precise data has not been acquired for computational reasons (fraction of food webs with extinction(s) close to 1). The number of food webs studied for each pair of parameters is enough to obtain  $N$  food webs with a stable positive equilibrium. For computational reasons, the value of  $N$  depends on the number of species ( $S$ ),  $N = 100$  if  $S = 60$ ,  $N = 1\ 000$  if  $S = 40$  and  $N = 10\ 000$  otherwise.

$M_i = 1$  for primary producers

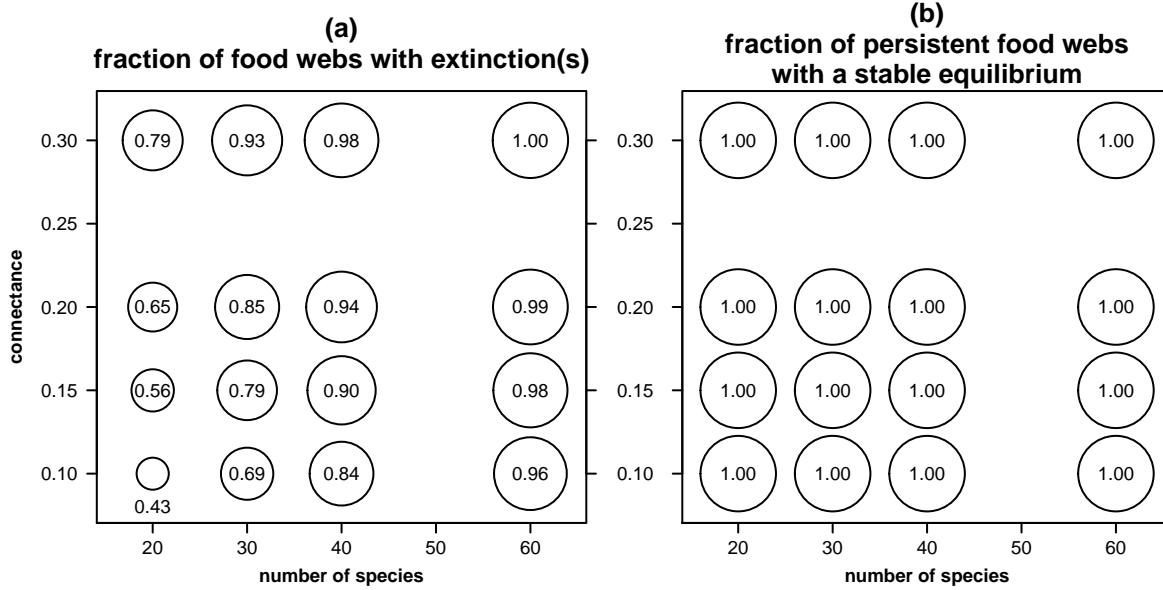


$M_i = 1$  for primary producers and absence of cannibalism

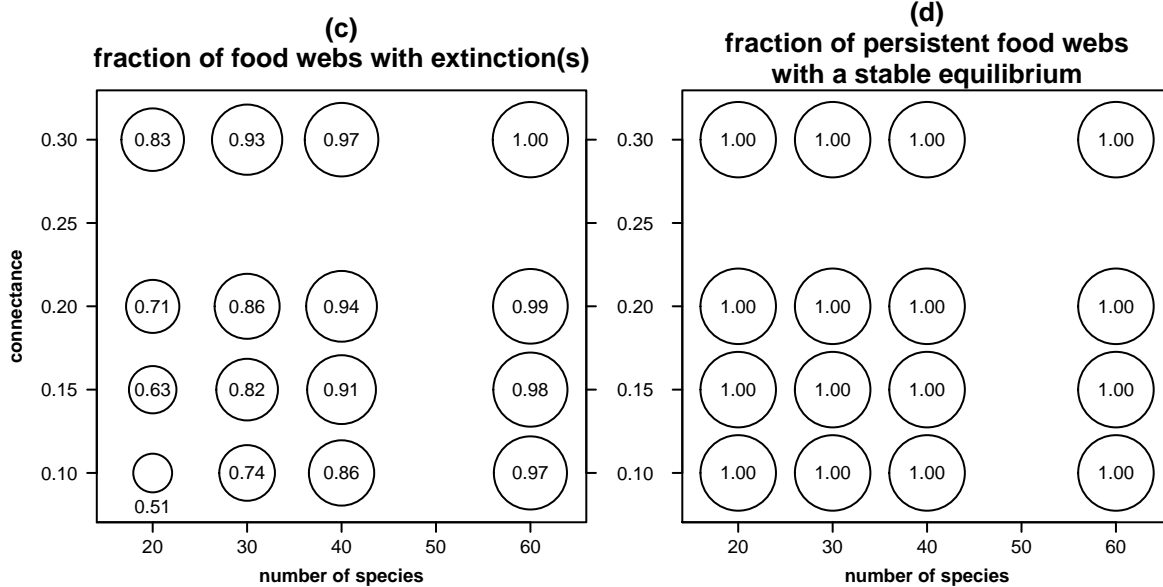


**Figure 7.** Food web dynamics as a function of trophic complexity predicted by Holling's disc equation, if the body mass  $M_i$  of all primary producer species is set to 1, for food webs in which cannibalistic links are kept (a, b) or removed (c, d). a, c: fraction of food webs with at least one species extinction. b, d: fraction of persistent food webs with a stable positive equilibrium. The number of food webs studied for each pair of parameters is enough to obtain 10 000 food webs with a stable positive equilibrium.

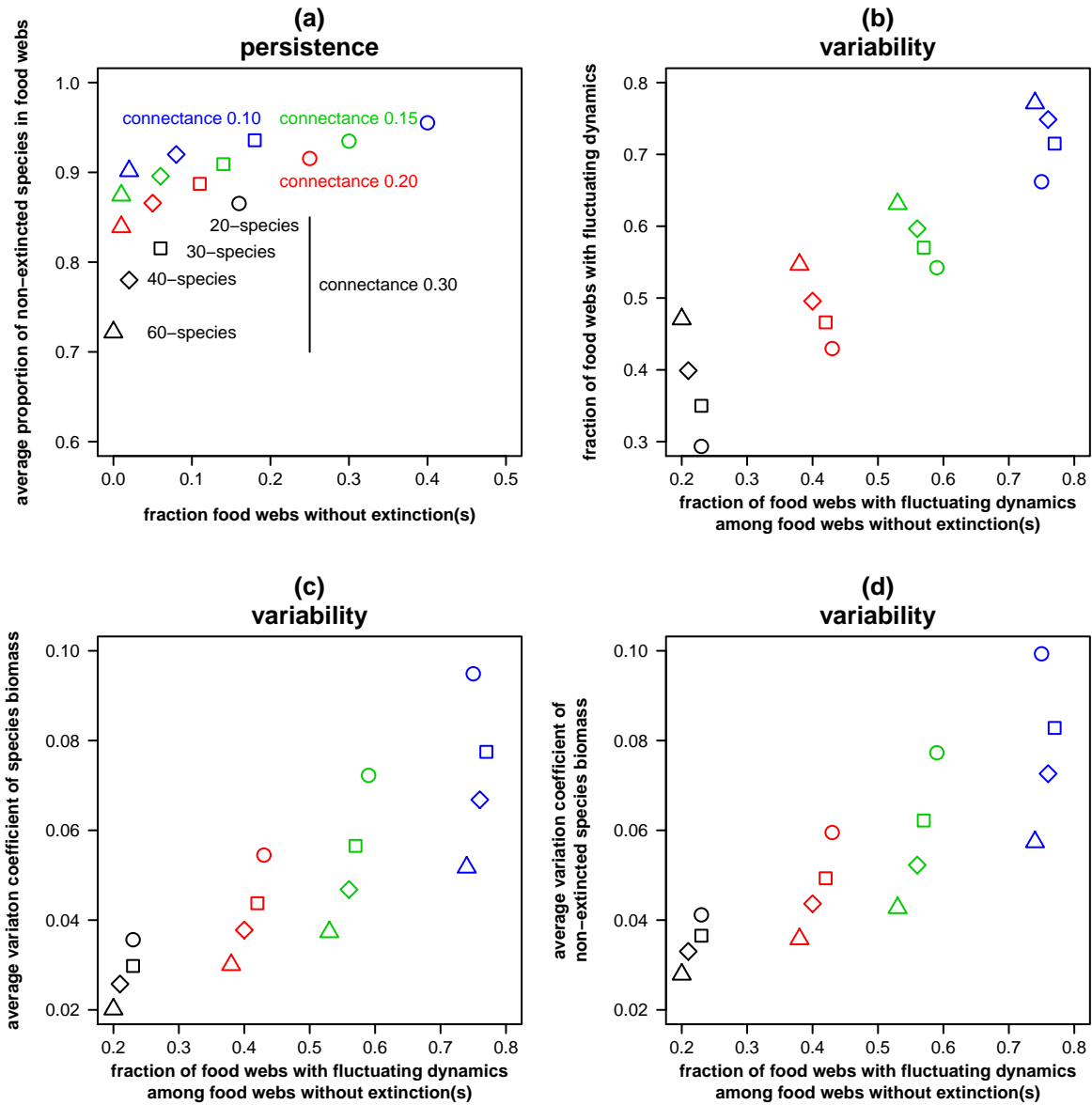
$M_i = 1$  for primary producers



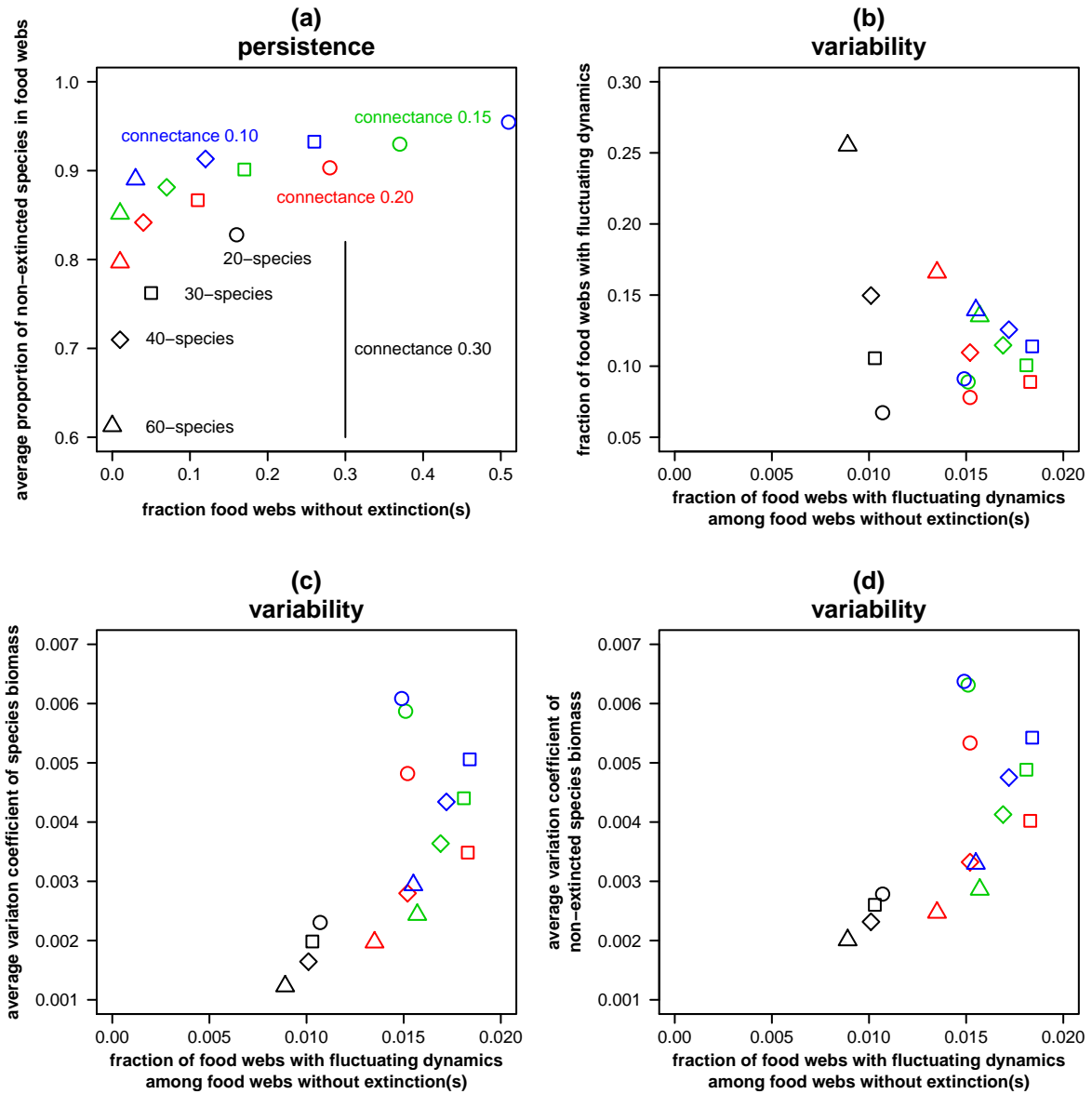
$M_i = 1$  for primary producers and absence of cannibalism



**Figure 8.** Food web dynamics as a function of trophic complexity predicted by Ivlev's functional response, if the body mass  $M_i$  of all primary producer species is set to 1, for food webs in which cannibalistic links are kept (a, b) or removed (c, d). a, c: fraction of food webs with at least one species extinction. b, d: fraction of persistent food webs with a stable positive equilibrium. The number of food webs studied for each pair of parameters is enough to obtain 10 000 food webs with a stable positive equilibrium.



**Figure 9. Relationships between different measures of the persistence (a) and the variability (b-d) of the food webs modeled using Holling’s disc equation.** The x-axis corresponds to the measure used in our study whereas the y-axis corresponds to another one. Each point indicates the values obtained for 10 000 food webs with the same number of species and connectance. Sixteen pairs of values are studied: four number of species (20: circle, 30: square, 40: diamond, 60: triangle) times four connectance levels (0.10: blue, 0.15: green, 0.20: red, 0.30: black). Simulations of 100 000 time units were performed to estimate the measures which are not used in the remaining of our study. The average and the standard deviation of species biomass were calculated across the 10 000 last time units. Extinct species are those with an average biomass below  $10^{-6}$ .



**Figure 10. Relationships between different measures of the persistence (a) and the variability (b-d) of the food webs modeled using Ivlev’s functional response.** The x-axis corresponds to the measure used in our study whereas the y-axis corresponds to another one. Each point indicates the values obtained for 10 000 food webs with the same number of species and connectance. Sixteen pairs of values are studied: four number of species (20: circle, 30: square, 40: diamond, 60: triangle) times four connectance levels (0.10: blue, 0.15: green, 0.20: red, 0.30: black). Simulations of 100 000 time units were performed to estimate the measures which are not used in the remaining of our study. The average and the standard deviation of species biomass were calculated across the 10 000 last time units. Extinct species are those with an average biomass below  $10^{-6}$ .

## 6 Identification of stabilizing factors through Generalized Modelling

We want to identify the stabilizing factors in the food web model for any type-II functional response and use them to explain our results from dynamical simulations. Here, we start by explaining how we derived the generalized model use to identify these factors expressed in terms of generalized parameters. Then we summarize the key results about the role of generalized parameters in equilibria stability. Finally, these generalized parameters are calculated in food webs at equilibrium in our dynamical simulations to explain why more equilibrium dynamics are predicted by Ivlev's FR.

To build the generalized model, we first consider the differential system made of  $S$  equations corresponding to  $S$  species (1) (see section 2.2 of the article for details):

$$\frac{dB_i}{dt} = \lambda q_i^\phi B_i + \lambda \sum_{j \in R_i} G_{i,j}^\phi B_i - \sum_{j \in C_i} G_{j,i}^\phi B_j - \alpha_i B_i - \beta_i B_i^2 \quad i = 1, \dots, S \quad (1)$$

without specifying the functional response  $G_{i,j}^\phi$  and the parameter values. We only claim that the functional response assumes no prey switching with constant fractional foraging effort, fulfills properties):

$$G_i^{\phi,tot} \in \mathcal{C}^2, G_i^{\phi,tot}(0) = 0, G_i^{\phi,tot} \geq 0, G_i^{\phi,tot}'(T_i) > 0, G_i^{\phi,tot}''(T_i) < 0, \lim_{T_i \rightarrow +\infty} G_i^{\phi,tot}(T_i) < +\infty. \quad (2)$$

So we consider in fact a family of models. Generalized modelling supposes that some models in this family have positive equilibria. The qualitative stability of a positive equilibrium is then studied using the Jacobian matrix:

$$\begin{cases} J_{i,i}^\phi = \lambda \left[ q_i^\phi + G_i^{\phi,tot*} + B_i^* \frac{\partial G_i^{\phi,tot}}{\partial B_i} \right]_{\mathbf{B}^*} - G_{i,i}^{\phi*} - \sum_{k \in C_i} B_k^* \frac{\partial G_{k,i}^\phi}{\partial B_i} \Big|_{\mathbf{B}^*} - \alpha_i - 2\beta_i B_i^* & i = 1, \dots, S \\ J_{i,j}^\phi = \lambda B_i^* \frac{\partial G_i^{\phi,tot}}{\partial B_j} \Big|_{\mathbf{B}^*} - G_{j,i}^{\phi*} + \sum_{k \in C_i} \frac{\partial G_{k,i}^\phi}{\partial B_j} \Big|_{\mathbf{B}^*} & i, j = 1, \dots, S, j \neq i \end{cases} \quad (3)$$

evaluated at a positive equilibrium  $\mathbf{B}^* = (\dots, B_i^*, \dots)$ . Then we re-write this matrix using generalized

187 parameters that describe the system close to this equilibrium (table 1):

$$\begin{cases} J_{i,i} &= \tau_i \left[ 1 - (1 - \delta_i)\mu_i - \delta_i \left( \rho_{i,i}(1 - \lambda\gamma_i) + \sum_{k \in C_i} \rho_{k,i}[(\gamma_k - 1)\chi_{k,i} + 1] \right) \right] & \forall i, j \in \{1, \dots, S\} \\ J_{i,j} &= \tau_i \nu_{i,j} \left[ \theta_i \gamma_i \chi_{i,j} - \delta_i \left( \rho_{j,i} + \sum_{k \in C_i} \rho_{k,i}(\gamma_k - 1)\chi_{k,j} \right) \right] & j \neq i \end{cases} \quad (4)$$

188 Details on the derivation procedure to define generalized parameters are presented in Gross & Feudel  
 189 (2006) and Yeakel *et al.* (2011). Then, equilibrium stability is studied as a function of the generalized  
 190 parameter values without specific assumptions on the functions and original parameter (such as  $a^\phi$  or  
 191  $h^\phi$ ) values behind them.

192 This generalized model is an extension of a model proposed by Plitzko *et al.* (2012). First, we correct a  
 193 mistake in Plitzko *et al.* (2012)'s calculus by adding the parameter  $\nu_{i,j}$  (a biomass ratio) to non-diagonal  
 194 terms. We checked that this mistake does not affect results presented by Plitzko *et al.* (2012) under  
 195 the assumptions they made for their numerical study. Second, we also complete the diagonal terms to  
 196 take cannibalism into account. Finally, we provide a generalized parameter formulation independent of  
 197 a specific functional response.

198 For food webs made with  $S$  species, there are  $5S(S + 1)/2$  degrees of freedom in the parameter set  
 199 of the generalized model (4) if no special assumption is made. It is not possible to realize a bifurcation  
 200 analysis like for a predator-prey model (Aldebert *et al.*, 2016). Furthermore, results depend on the trophic  
 201 complexity and food web structure. So, numerous food webs have to be studied to obtain statistical  
 202 results. To avoid unreasonable computing costs, we need to make some assumptions to decrease the  
 203 number of degrees of freedom and study only some parameters of interest. As in all this study, we first  
 204 assume that a species is either a primary producer ( $\theta_i = 0$ ) or a predator ( $\theta_i = 1$ ), the selection being  
 205 done during food web construction by the niche model (see section 2.1 in the article for details). Since  
 206 Gross *et al.* (2009) reported that the time scale  $\tau_i$  does not significantly affect equilibria stability, it is  
 207 arbitrarily set to 1 for all species. Then, as the mean biomass ratio is  $\bar{\nu} = 1$  by definition, we assume  
 208  $\nu_{i,j} = 1 \forall i, j$ . It implies that  $B_i^* = B_j^* \forall i, j$  and so that  $\chi_{i,j} = 1/|R_i|$  if  $j \in R_i$  (0 otherwise). Note that  
 209  $1/|R_i|$  is also by definition the mean fraction of total prey biomass represented by each prey of species  $i$ .  
 210 Similarly,  $1/|C_i|$  is by definition the mean fraction of total predative losses represented by each predator  
 211 of species  $i$ . We assume  $\rho_{j,i} = 1/|C_i|$  if  $j \in C_i$  (0 otherwise). Values of other parameters are assumed



**Table 1. Formulation and ecological meaning of the generalized parameters used to build the generalized model.** Generalized parameters are used in the generalized model to describe the local dynamics of the system close to an equilibrium. Their value are independent of the specific formulation of the functional response because they only describe a local dynamics. So the stability of an equilibrium depends only of their value at these equilibrium. The scale parameters describe the time scale of species dynamics (for  $\tau_i$ ) and the relative contribution of the different processes to this dynamics. Elasticities (called exponent parameters by some authors) measure the non-linearity of processes.

generalized parameter formulation	ecological meaning
<i>scale parameters</i>	
$\begin{aligned} \tau_i &= \lambda (q_i^\phi + G_i^{\phi, tot*}) \\ &= \sum_{j \in C_i} G_{j,i}^{\phi*} \frac{B_j^*}{B_i^*} + (\alpha + \beta B_i^*) M_i^{-0.25} \end{aligned}$	time scale of species $i$ 's dynamics
$\theta_i = \frac{1}{\tau_i} \lambda G_i^{\phi, tot*}$	fraction of gains of species $i$ obtained by predation
$1 - \theta_i = \frac{1}{\tau_i} \lambda q_i^\phi$	fraction of gains of species $i$ obtained by primary production
$\delta_i = \frac{1}{\tau_i} \sum_{j \in C_i} G_{j,i}^{\phi*} \frac{B_j^*}{B_i^*}$	fraction of losses of species $i$ due to predation
$1 - \delta_i = \frac{1}{\tau_i} (\alpha + \beta B_i^*) M_i^{-0.25}$	fraction of losses of species $i$ due to intrinsic dynamics
$\chi_{i,j} = \begin{cases} \frac{B_j^*}{T_i^*} & \text{if } j \in R_i \\ 0 & \text{otherwise} \end{cases}$	fraction of gains by predation of species $i$ from species $j$
$\rho_{i,j} = \begin{cases} \frac{1}{\tau_i} \frac{1}{\delta_i} G_{j,i}^{\phi*} \frac{B_j^*}{B_i^*} & \text{if } i \in R_j \\ 0 & \text{otherwise} \end{cases}$	fraction of losses by predation of species $i$ due to species $j$
$\nu_{i,j} = B_i^*/B_j^*$	biomass ratio between species $i$ and $j$
<i>elasticities (also called exponent parameters)</i>	
$\mu_i = 1 + \frac{\beta B_i^*}{\alpha + \beta B_i^*} \in [1, 2]$	non-linearity of intrinsic mortality for species $i$
$\begin{aligned} \gamma_i &= g_i^{\phi'}(1) \in [0, 1] \\ &\text{with } t_i = \frac{T_i}{T_i^*} \text{ and } g_i^\phi(t_i) := \frac{G_i^{\phi, tot}(t_i T_i^*)}{G_i^{\phi, tot}(T_i^*)} \end{aligned}$	slope of the normalized functional response of species $i$

212 to be constant across a food web. Numerical simulations were realized with  $\mu_i = \mu \in \{4/3, 3/2, 5/3\}$ ,  
213  $\delta_i = \delta \in \{1/3, 1/2, 2/3\}$  if species  $i$  has predators and  $\delta_i = 0$  if species  $i$  is a top-predator,  $\gamma_i = \gamma \in [0, 1]$   
214 (discretized by step of 0.01) and  $\lambda \in \{0, 1/4, 1/2, 3/4, 1\}$ . We studied food webs of varying number of  
215 species  $S \in \{20, 30, 40, 60\}$  and connectance  $C \in \{0.10, 0.15, 0.20, 0.30\}$  as in the rest of this study.

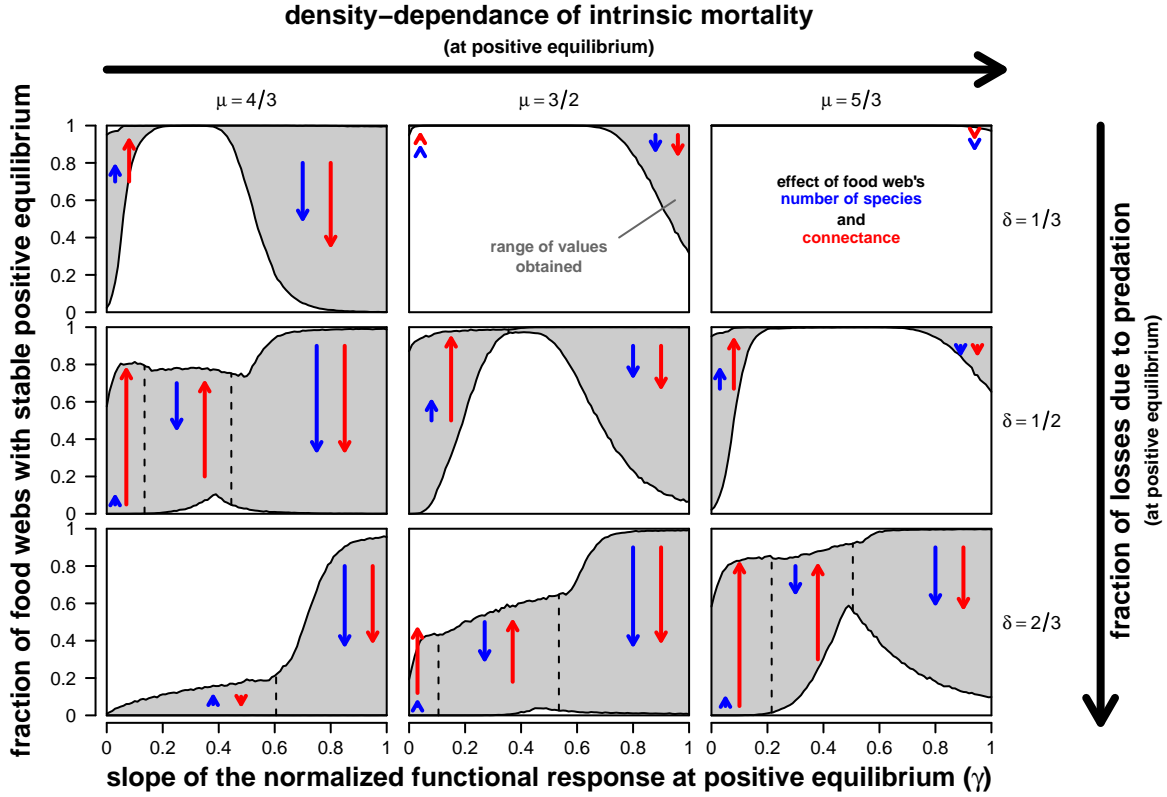
216 According to the jacobian matrix of the generalized model (4), the proportion of food webs with a  
217 stable positive equilibrium is higher if density-dependent mortality is high (high value of  $\mu$ ) and/or if  
218 there is a small fraction of losses due to predation (low value of  $\delta$ , figure 11). This corresponds to a high  
219 value of  $(1 - \delta)\mu$ , which plays a negative role in the diagonal elements of the jacobian matrix. Negative  
220 terms in diagonal elements of the jacobian matrix are known to increase local stability of equilibria in

221 some food web models (Takeuchi, 1996). If  $(1 - \delta)\mu$  is high, more food webs have a stable equilibrium  
222 for intermediate values of  $\gamma$ , whatever the trophic complexity. Otherwise, the proportion of all the food  
223 webs with a stable equilibrium increases on average with  $\gamma$  values.

224 For each set of generalized parameter valued, we use a statistical linear model to quantify the effect of  
225 the number of species and connectance on the proportion of food webs with a stable positive equilibrium  
226 (arrows in figure 11). For low values of  $\gamma$  (high prey biomass), there is a positive complexity-stability  
227 relationship. It is mainly due to connectance, which affect more the fraction of food webs with a stable  
228 equilibrium than the number of species. For intermediate values of  $\gamma$ , the fraction of food webs with a  
229 stable equilibrium is increased by connectance and decreased by the number of species. For high values  
230 of  $\gamma$  (low prey biomass), there is a negative complexity-stability relationship, with a similar impact of the  
231 number of species and connectance. The assimilation efficiency  $\lambda$  slightly affects the quantitative results,  
232 but not the qualitative trends (figures 12 and 13). The highest proportions of food webs with a stable  
233 equilibrium are obtained in the limit case of  $\lambda = 0$ , and the lowest in the opposite limit case  $\lambda = 1$ . On  
234 average, deleting cannibalistic links decreases the proportion of food webs with a stable equilibrium but  
235 do not affect the qualitative results on complexity-stability relationships (figure 14). Considering only  
236 food webs with a fixed number of primary producers has only a little quantitative impact on the results  
237 (figures 15 and 16) as the positive equilibrium is assumed to exist.

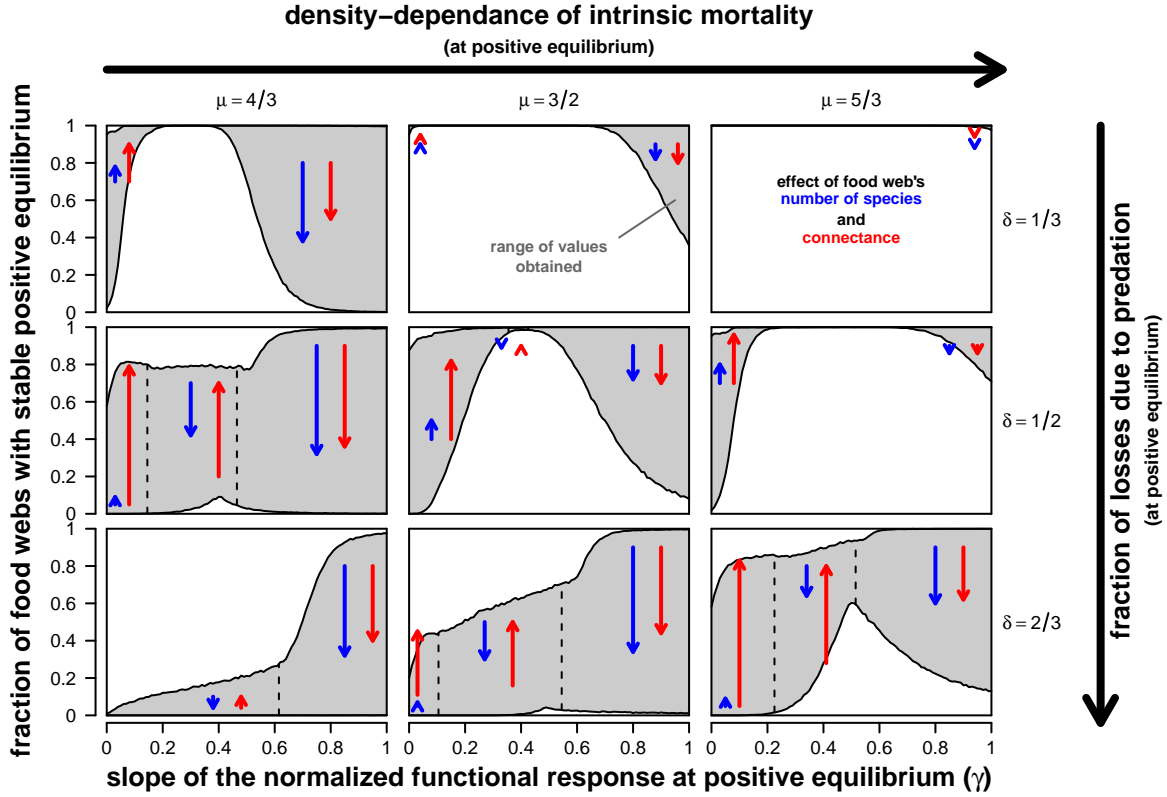
238 To summarize, the stabilizing factors of positive equilibria found in a predator-prey model (Aldebert  
239 *et al.*, 2016) are also observed at the food web scale. Nevertheless they are less straightforward, because  
240 of the interplay with trophic complexity. For example, highest stability is found for a high or intermediate  
241 slope of the functional response  $\gamma$ , depending on other parameter values and trophic complexity.

242 We calculated generalized parameters for food webs at positive equilibrium simulated in figure 3 of  
243 the article. Generalized parameters can be viewed as indicators of the food web functioning close to this  
244 equilibrium. Because the statistical distributions of species biomass at equilibrium are similar between  
245 functional responses (figure 17a), similar distributions for the parameters (such as  $\delta_i$ ) and for the non-  
246 linearity of species mortality  $\mu_i$  are also observed (figure 17c,d). At the opposite, different distributions are  
247 observed for the normalized slope of the functional response  $\gamma_i$  (figure 17b). The average value obtained  
248 with Ivlev's FR ( $\bar{\gamma} = 0.60$ ) is 1.6 times higher than the average obtained with Holling's functional response  
249 ( $\bar{\gamma} = 0.37$ ).



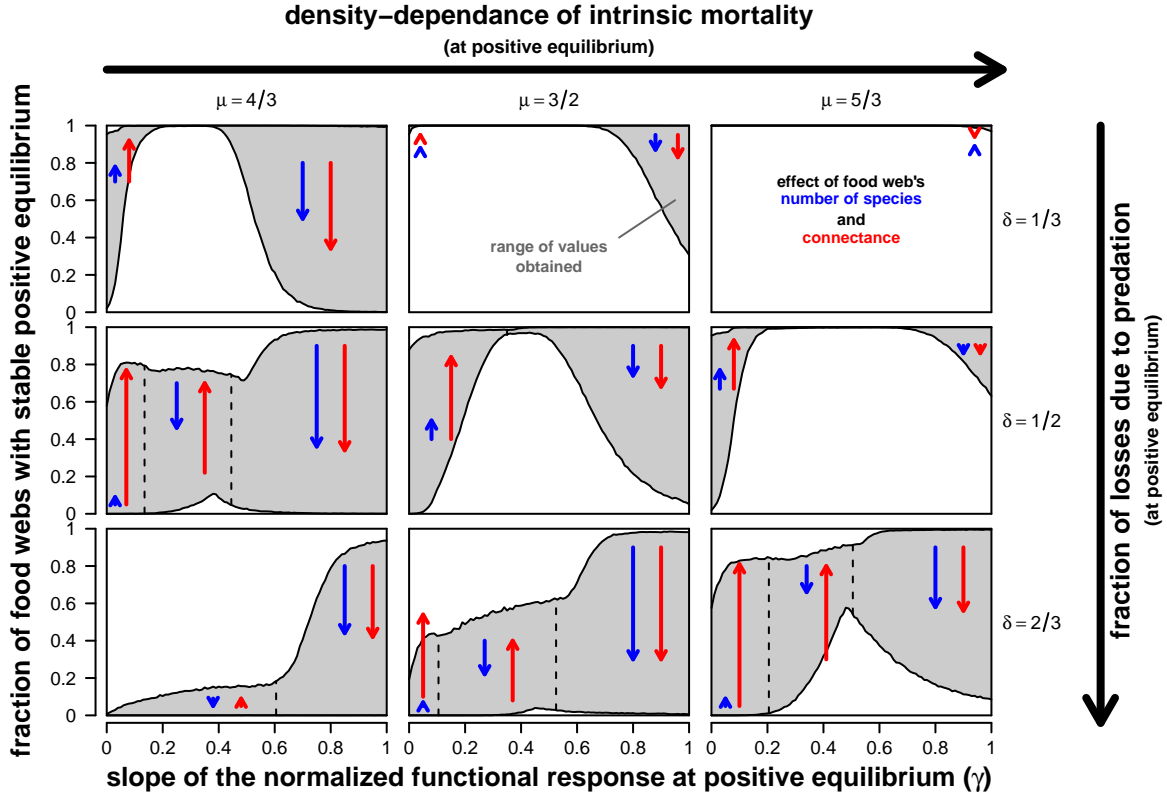
**Figure 11.** Fraction of food webs with a stable positive equilibrium for the generalized model, as a function of generalized parameters values and trophic complexity (number of species and connectance). Food web topology is generated using niche model (Williams & Martinez, 2000, 2004). For each set of parameters, 10000 food webs are studied. Assimilation efficiency  $\lambda$  is set to 0.75 (the value has a little impact on the results).

Results are presented for 9 pairs of density-dependence of mortality ( $\mu$ , varying across columns) and fraction of losses due to predation ( $\delta$ , varying across rows). In each panel, the fraction of food webs with a stable positive equilibrium is presented as a function of the slope of the normalized functional response ( $\gamma$ , discretized by step of 0.01). Results were estimated for 16 pairs of connectance ( $C \in \{0.10, 0.15, 0.20, 0.30\}$ ) and number of species ( $S \in \{20, 30, 40, 60\}$ ). The grey area on each graph indicates the range of values obtained. For each value of  $\gamma$ , a linear model  $y = z_1 + z_2 S + z_3 C + \varepsilon$  (with  $y$  the fraction of stable food webs,  $z = {}^t(z_1, z_2, z_3) \in \mathbb{R}^3$  the vector of parameters and  $\varepsilon$  the error of prediction) is used to estimate the respective effect of the number of species and connectance on the proportion of food webs with a stable positive equilibrium. Changes in the sign of  $z_2$  and/or  $z_3$  occur at values of  $\gamma$  corresponding to vertical dashed lines. Blue and red arrows represent respectively the average  $z_1$  and  $z_2$  between two vertical dashed lines. The length of the arrow's tail is equal to the average value of its associated parameter (normalized value of the parameter readable on the left axis with a  $\pm 0.01$  precision).



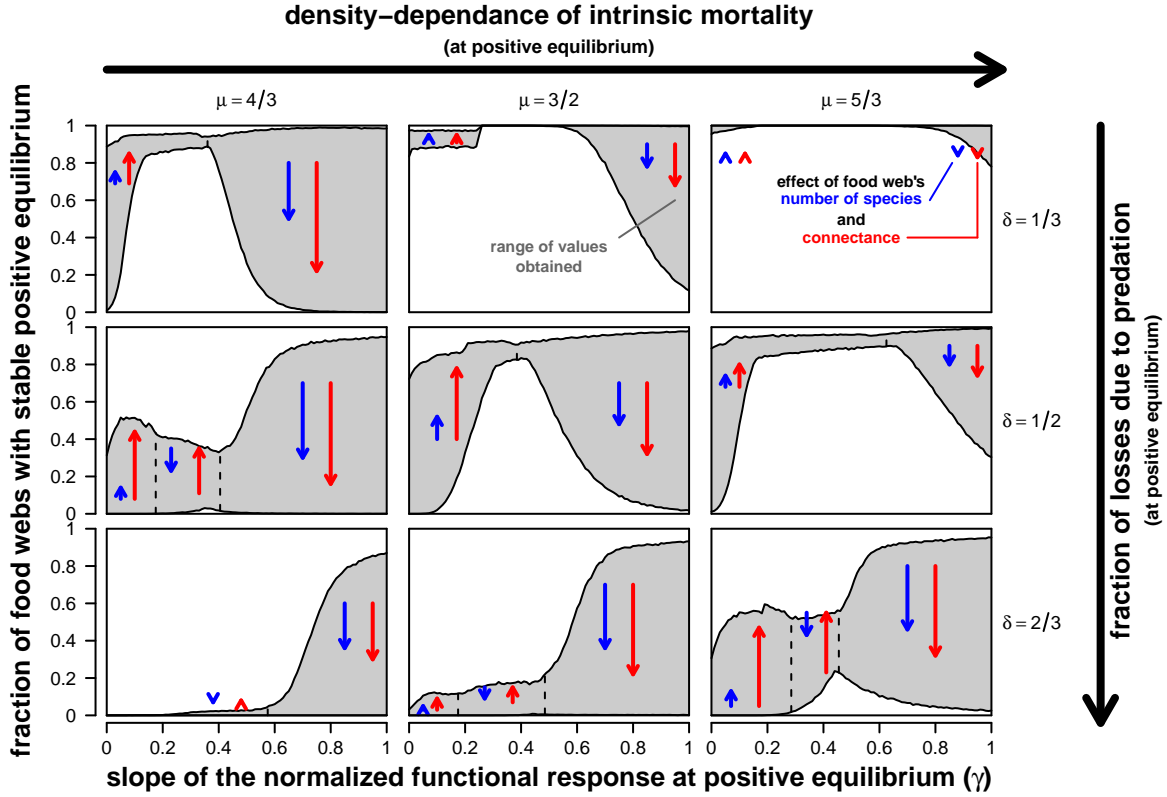
**Figure 12.** Fraction of food webs with a stable positive equilibrium for the generalized model, as a function of generalized parameters values and trophic complexity (number of species and connectance) when assimilation efficiency  $\lambda$  is set to 0. Food web topology is generated using niche model (Williams & Martinez, 2000, 2004). For each set of parameters, 10000 food webs are studied.

Results are presented for 9 pairs of density-dependence of mortality ( $\mu$ , varying across columns) and fraction of losses due to predation ( $\delta$ , varying across rows). In each panel, the fraction of food webs with a stable positive equilibrium is presented as a function of the slope of the normalized functional response ( $\gamma$ , discretized by step of 0.01). Results were estimated for 16 pairs of connectance ( $C \in \{0.10, 0.15, 0.20, 0.30\}$ ) and number of species ( $S \in \{20, 30, 40, 60\}$ ). The grey area on each graph indicates the range of values obtained. For each value of  $\gamma$ , a linear model  $y = z_1 + z_2 S + z_3 C + \varepsilon$  (with  $y$  the fraction of stable food webs,  $z = {}^t(z_1, z_2, z_3) \in \mathbb{R}^3$  the vector of parameters and  $\varepsilon$  the error of prediction) is used to estimate the respective effect of the number of species and connectance on the proportion of food webs with a stable positive equilibrium. Changes in the sign of  $z_2$  and/or  $z_3$  occur at values of  $\gamma$  corresponding to vertical dashed lines. Blue and red arrows represent respectively the average  $z_1$  and  $z_2$  between two vertical dashed lines. The length of the arrow's tail is equal to the average value of its associated parameter (normalized value of the parameter readable on the left axis with a  $\pm 0.01$  precision).



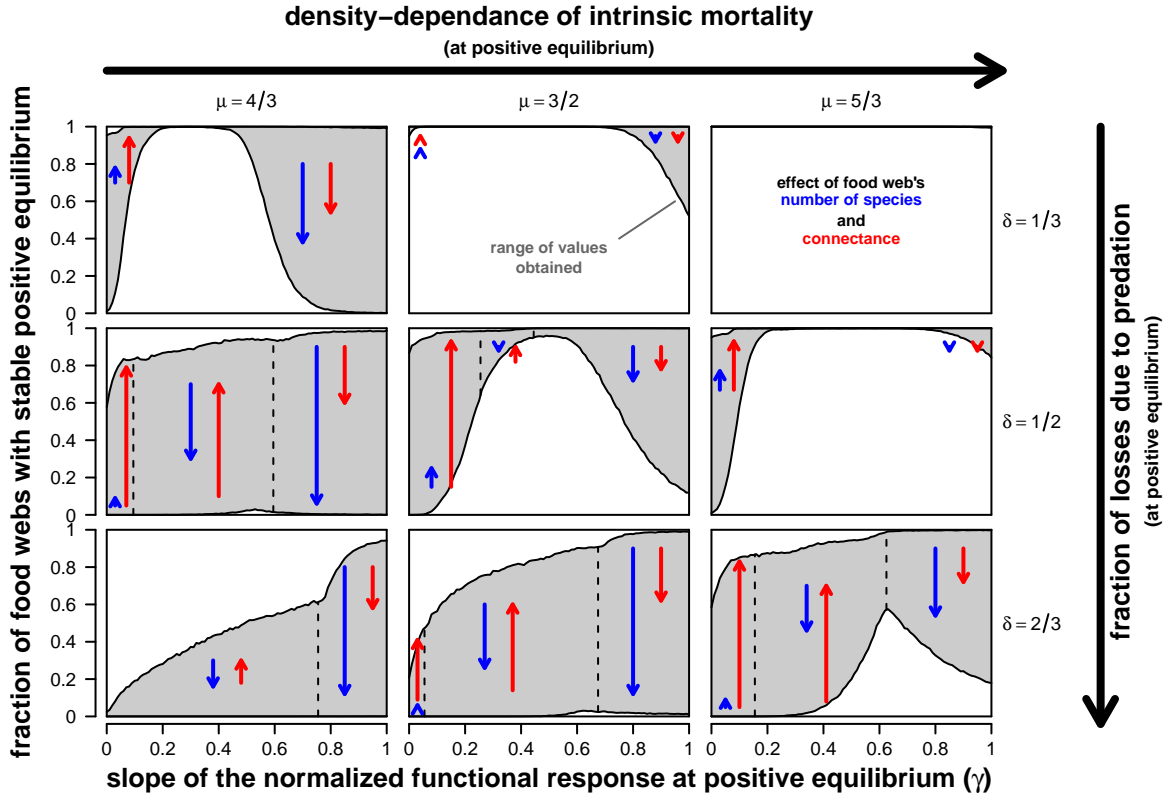
**Figure 13.** Fraction of food webs with a stable positive equilibrium for the generalized model, as a function of generalized parameters values and trophic complexity (number of species and connectance) when assimilation efficiency  $\lambda$  is set to 1. Food web topology is generated using niche model (Williams & Martinez, 2000, 2004). For each set of parameters, 10000 food webs are studied.

Results are presented for 9 pairs of density-dependence of mortality ( $\mu$ , varying across columns) and fraction of losses due to predation ( $\delta$ , varying across rows). In each panel, the fraction of food webs with a stable positive equilibrium is presented as a function of the slope of the normalized functional response ( $\gamma$ , discretized by step of 0.01). Results were estimated for 16 pairs of connectance ( $C \in \{0.10, 0.15, 0.20, 0.30\}$ ) and number of species ( $S \in \{20, 30, 40, 60\}$ ). The grey area on each graph indicates the range of values obtained. For each value of  $\gamma$ , a linear model  $y = z_1 + z_2 S + z_3 C + \varepsilon$  (with  $y$  the fraction of stable food webs,  $z = {}^t(z_1, z_2, z_3) \in \mathbb{R}^3$  the vector of parameters and  $\varepsilon$  the error of prediction) is used to estimate the respective effect of the number of species and connectance on the proportion of food webs with a stable positive equilibrium. Changes in the sign of  $z_2$  and/or  $z_3$  occur at values of  $\gamma$  corresponding to vertical dashed lines. Blue and red arrows represent respectively the average  $z_1$  and  $z_2$  between two vertical dashed lines. The length of the arrow's tail is equal to the average value of its associated parameter (normalized value of the parameter readable on the left axis with a  $\pm 0.01$  precision).



**Figure 14.** Fraction of food webs with a stable positive equilibrium for the generalized model, as a function of generalized parameters values and trophic complexity (number of species and connectance) in absence of cannibalism. Food web topology is generated using niche model (Williams & Martinez, 2000, 2004). For each set of parameters, 10000 food webs in which cannibalistic links have been removed are studied.

Results are presented for 9 pairs of density-dependence of mortality ( $\mu$ , varying across columns) and fraction of losses due to predation ( $\delta$ , varying across rows). In each panel, the fraction of food webs with a stable positive equilibrium is presented as a function of the slope of the normalized functional response ( $\gamma$ , discretized by step of 0.01). Results were estimated for 16 pairs of connectance ( $C \in \{0.10, 0.15, 0.20, 0.30\}$ ) and number of species ( $S \in \{20, 30, 40, 60\}$ ). The grey area on each graph indicates the range of values obtained. For each value of  $\gamma$ , a linear model  $y = z_1 + z_2 S + z_3 C + \varepsilon$  (with  $y$  the fraction of stable food webs,  $z = {}^t(z_1, z_2, z_3) \in \mathbb{R}^3$  the vector of parameters and  $\varepsilon$  the error of prediction) is used to estimate the respective effect of the number of species and connectance on the proportion of food webs with a stable positive equilibrium. Changes in the sign of  $z_2$  and/or  $z_3$  occur at values of  $\gamma$  corresponding to vertical dashed lines. Blue and red arrows represent respectively the average  $z_1$  and  $z_2$  between two vertical dashed lines. The length of the arrow's tail is equal to the average value of its associated parameter (normalized value of the parameter readable on the left axis with a  $\pm 0.01$  precision).



**Figure 15.** Fraction of food webs with a stable positive equilibrium for the generalized model, as a function of generalized parameters values and trophic complexity (number of species and connectance) for food webs with a fixed number of primary producer species. Food web topology is generated using niche model (Williams & Martinez, 2000, 2004). For each set of parameters, 10000 food webs with five primary producers are studied. Assimilation efficiency  $\lambda$  is set to 0.75 (the value has a little impact on the results).

Results are presented for 9 pairs of density-dependence of mortality ( $\mu$ , varying across columns) and fraction of losses due to predation ( $\delta$ , varying across rows). In each panel, the fraction of food webs with a stable positive equilibrium is presented as a function of the slope of the normalized functional response ( $\gamma$ , discretized by step of 0.01). Results were estimated for 16 pairs of connectance ( $C \in \{0.10, 0.15, 0.20, 0.30\}$ ) and number of species ( $S \in \{20, 30, 40, 60\}$ ). The grey area on each graph indicates the range of values obtained. For each value of  $\gamma$ , a linear model  $y = z_1 + z_2 S + z_3 C + \varepsilon$  (with  $y$  the fraction of stable food webs,  $z = {}^t(z_1, z_2, z_3) \in \mathbb{R}^3$  the vector of parameters and  $\varepsilon$  the error of prediction) is used to estimate the respective effect of the number of species and connectance on the proportion of food webs with a stable positive equilibrium. Changes in the sign of  $z_2$  and/or  $z_3$  occur at values of  $\gamma$  corresponding to vertical dashed lines. Blue and red arrows represent respectively the average  $z_1$  and  $z_2$  between two vertical dashed lines. The length of the arrow's tail is equal to the average value of its associated parameter (normalized value of the parameter readable on the left axis with a  $\pm 0.01$  precision).

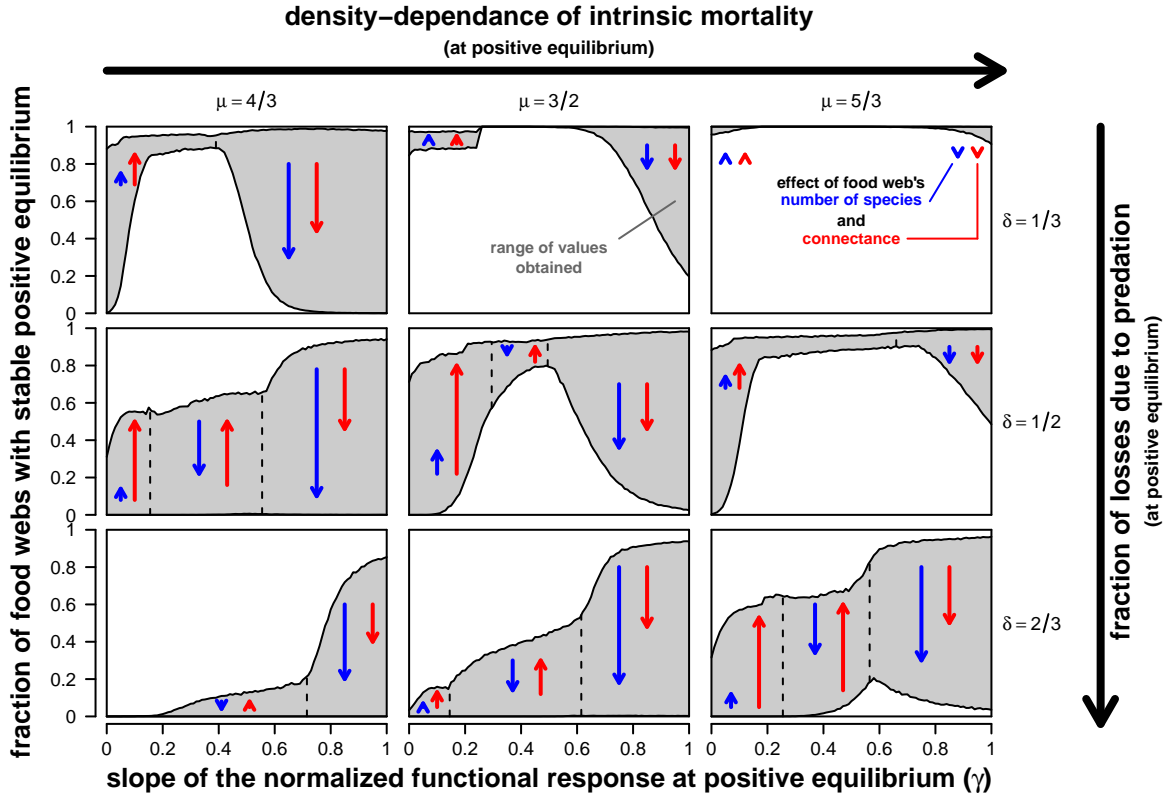
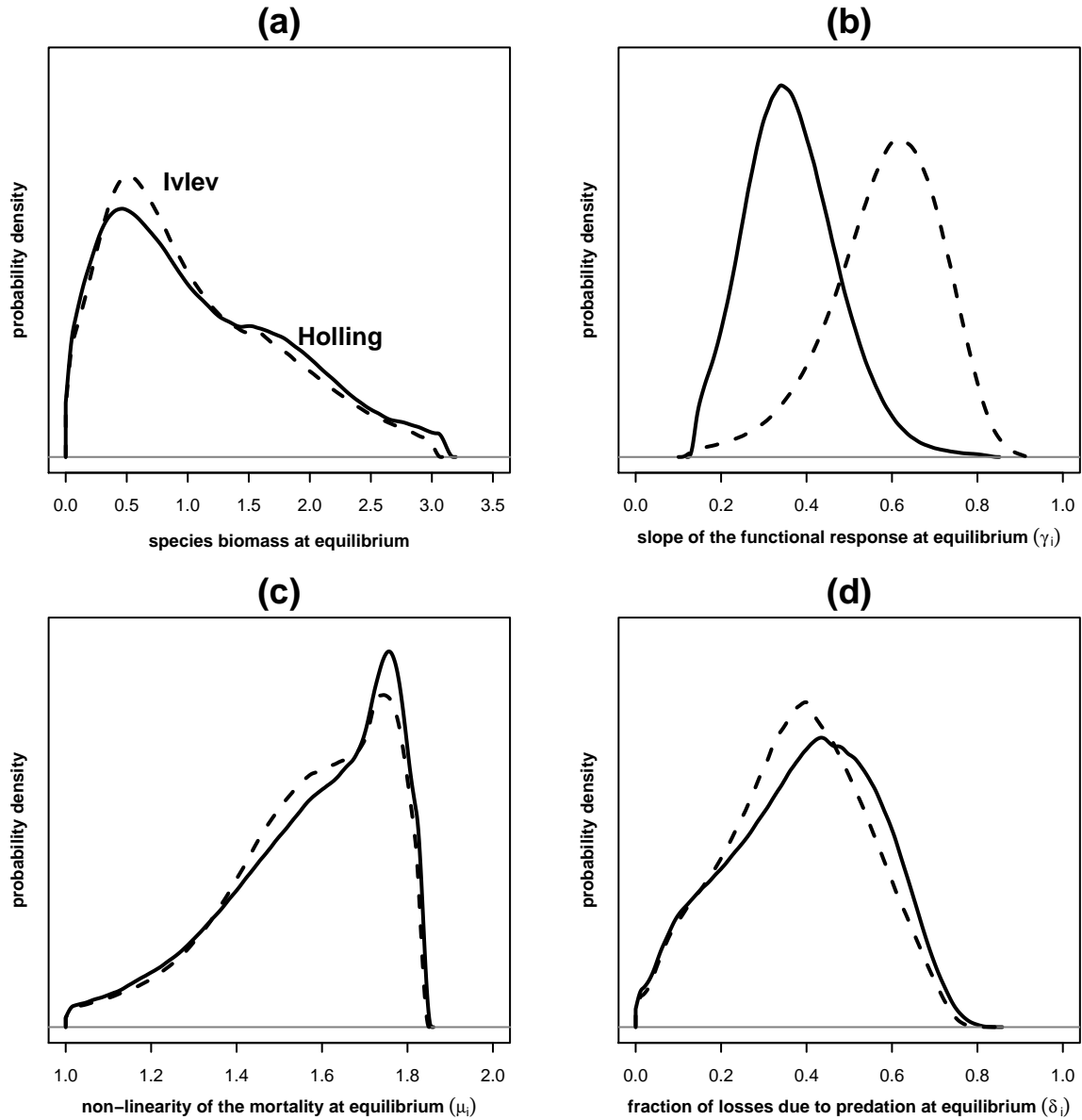


Figure 16. Fraction of food webs with a stable positive equilibrium for the generalized model, as a function of generalized parameters values and trophic complexity (number of species and connectance) for food webs with a fixed number of primary producer species and in absence of cannibalism. Food web topology is generated using niche model (Williams & Martinez, 2000, 2004). For each set of parameters, 10000 food webs with five primary producers and in which cannibalistic links have been removed are studied.

Results are presented for 9 pairs of density-dependence of mortality ( $\mu$ , varying across columns) and fraction of losses due to predation ( $\delta$ , varying across rows). In each panel, the fraction of food webs with a stable positive equilibrium is presented as a function of the slope of the normalized functional response ( $\gamma$ , discretized by step of 0.01). Results were estimated for 16 pairs of connectance ( $C \in \{0.10, 0.15, 0.20, 0.30\}$ ) and number of species ( $S \in \{20, 30, 40, 60\}$ ). The grey area on each graph indicates the range of values obtained. For each value of  $\gamma$ , a linear model  $y = z_1 + z_2 S + z_3 C + \varepsilon$  (with  $y$  the fraction of stable food webs,  $z = {}^t(z_1, z_2, z_3) \in \mathbb{R}^3$  the vector of parameters and  $\varepsilon$  the error of prediction) is used to estimate the respective effect of the number of species and connectance on the proportion of food webs with a stable positive equilibrium. Changes in the sign of  $z_2$  and/or  $z_3$  occur at values of  $\gamma$  corresponding to vertical dashed lines. Blue and red arrows represent respectively the average  $z_1$  and  $z_2$  between two vertical dashed lines. The length of the arrow's tail is equal to the average value of its associated parameter (normalized value of the parameter readable on the left axis with a  $\pm 0.01$  precision).





**Figure 17.** Estimated probability densities of the species biomass and 3 generalized parameters for food webs which reach a positive equilibrium at the end of the dynamical simulations for Holling’s disc equation (plain) and Ivlev’s functional response (dashed). Generalized parameters are here used as indicators to describe system dynamics close to equilibrium. Results are obtained from 160 000 food webs with 16 pairs of number of species and connectance values (10 000 food webs by pair of values). The null values ( $\gamma_i$  for primary producers and  $\delta_i$  for top-predators) are not taken into account. Density estimates are realized using non-parametric kernel methods (Simonoff, 1996) with the same weight for all simulated food webs.

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