

# **What constrains food webs? A maximum entropy framework for predicting their structure with minimal biases**

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**Abstract:** Food webs are complex ecological networks whose structure is both ecologically and statistically constrained, with many network properties being correlated with each other. Despite the recognition of these invariable relationships in food webs, the use of the principle of maximum entropy (MaxEnt) in network ecology is still rare. This is surprising considering that MaxEnt is a renowned and rigorous statistical tool precisely designed for understanding and predicting many different types of constrained systems. Precisely, this principle asserts that the least-biased probability distribution of a system's property, constrained by prior knowledge about that system, is the one with maximum information entropy. MaxEnt has been proven useful in many ecological modelling problems, but its application in food webs and other ecological networks is limited. Here we show how MaxEnt can be used to derive many food-web properties both analytically and heuristically. First, we show how the joint degree distribution (the joint probability distribution of the numbers of prey and predators for each species in the network) can be derived analytically using the number of species and the number of interactions in food webs. Second, we present a heuristic and flexible approach of finding a network's adjacency matrix (the network's representation in matrix format) based on simulated annealing and SVD entropy. We built two heuristic models using the connectance and the joint degree sequence as statistical constraints, respectively. We compared both models' predictions against corresponding null and neutral models commonly used in network ecology using open access data of terrestrial and aquatic food webs sampled globally ( $N = 257$ ). We found that the heuristic model constrained by the joint degree sequence was a good predictor of many measures of food-web structure, especially the nestedness and motifs distribution. Specifically, our results suggest that the structure of terrestrial and aquatic food webs is mainly driven by their joint degree distribution.

## **1 Introduction**

### **2 The constrained structure of ecological networks**

3 A variety of measures of the structure of ecological networks have been used to describe the  
4 organization of species interactions in a biological community (Delmas et al. 2019). These  
5 measures provide valuable information on the functioning of ecosystems and their responses  
6 to environmental change (e.g., Pascual and Dunne 2006; Gómez, Perfectti, and Jordano 2011).  
7 For instance, Bascompte et al. (2003) suggest that plant–pollinator and seed-disperser networks  
8 have a highly nested structure that can promote species persistence. Another example, in food  
9 webs, shows that a high connectance can promote the robustness of the system to species lost  
10 (Dunne, Williams, and Martinez 2002). However, despite the growing literature on the ecologi-  
11 cal implications of network structure, the association between many of these measures impedes  
12 our ability to fully understand what drives the structure and behavior of ecological networks. In  
13 particular, nestedness and modularity are strongly associated in ecological networks (Fortuna et  
14 al. 2010), and network connectance has been shown to be an important driver of many other  
15 emerging network properties (Timothée Poisot and Gravel 2014). In light of these observations,  
16 it is difficult to assess whether attributed effects of given properties are the artifacts of other,  
17 perhaps simpler, measures.

18 One way to tackle this issue is first to recognize that food webs and other ecological networks  
19 are constrained systems. In other words, the space of possible network configurations shrinks  
20 as we know more about a network structure. For example, there is a finite number of networks  
21 with specified numbers of nodes and edges. Indeed, the structure of ecological networks is first  
22 and above all constrained by the number of species, or nodes, present. Food webs with high  
23 species richness typically have a lower connectance (MacDonald, Banville, and Poisot 2020)  
24 than smaller networks. This is because the number of realized interactions in empirical food  
25 webs scales slower than the number of possible species pairs (MacDonald, Banville, and Poisot  
26 2020). As shown by Timothée Poisot and Gravel (2014), connectance itself can constrain differ-  
27 ent aspects of network structure such as the degree distribution (i.e. the probability distribution  
28 of the number of interspecific interactions realized by a species). Other measures, such as the

29 maximum trophic level, can also constrain the space of feasible networks.

30 Prior knowledge on the structure of ecological networks is thus especially useful in the current  
31 context of data scarcity about species interactions (Jordano 2016). Indeed, this Eltonian shortfall  
32 (Hortal et al. 2015) can be partially alleviated using known information about an ecological  
33 network. As suggested by Strydom et al. (2021), network structure can be used to improve the  
34 prediction of pairwise species interactions when data is lacking by constraining the space of  
35 feasible networks. Similarly, partial knowledge on the structure of an ecological network can  
36 also be used to predict others of its properties by constraining their range of possible values.  
37 This is important given that many aspects of network structure cannot be measured empirically  
38 without data on pairwise species interactions, a prevailing situation worldwide (Timothée Poisot  
39 et al. 2021).

40 Understanding the ecological constraints that shape species interactions networks and predicting  
41 their emerging structure are thus two complementary aims of network ecology. This distinction  
42 between understanding and predicting is essential when using statistical and mathematical mod-  
43 els in network ecology and interpreting them. On one hand, null models help us identify potential  
44 ecological mechanisms that drive species interactions and constrain ecological networks. Null  
45 models generate a distribution for a target measure using a set of rules that exclude the mecha-  
46 nism of interest (Fortuna and Bascompte 2006; Delmas et al. 2019). The deviation between the  
47 model and empirical data helps us evaluate the effect of this ecological process in nature. On  
48 the other hand, predictive models can help fill many gaps on species interactions data. A variety  
49 of such models have recently been developed using machine learning and other statistical tools,  
50 most of which are presented in Strydom et al. (2021). However, given the constrained nature of  
51 ecological networks, it is surprising that the principle of maximum entropy, a rigorous mathe-  
52 matical method designed for both the analysis and prediction of constrained systems, has been  
53 barely used in network ecology.

#### 54 **The principle of maximum entropy: A primer for ecologists**

55 The principle of maximum entropy (MaxEnt) is a mathematical method of finding probabil-  
56 ity distributions, strongly rooted in statistical mechanics and information theory (Jaynes 1957a,

57 1957b; Harremoës and Topsøe 2001). Starting from a set of constraints given by prior knowl-  
58 edge of a system (i.e. what we call state variables), this method helps us find least-biased prob-  
59 ability distributions subject to the constraints. These probability distributions are guaranteed to  
60 be unique given our prior knowledge and represent the most we can say about a system without  
61 making more assumptions. For example, if the only thing we know about a biological commu-  
62 nity is its average number of individuals per species, the least-biased inference we could make on  
63 its species abundance distribution is the exponential distribution (Frank and Smith 2011; Harte  
64 and Newman 2014). However, this does not imply that this distribution will be the best fit to  
65 empirical data. The challenge is to find the right set of constraints that would best reproduce  
66 distributions found in nature.

67 MaxEnt states that the least-biased probability distribution given the constraints used is the one  
68 with the highest entropy among all probability distributions that satisfy these constraints. En-  
69 tropy is a measure of the average amount of information given by the outcome of a random  
70 variable. Many measures of entropy have been developed in physics (Beck 2009), but only  
71 a fraction of them could be used as an optimization measure with the principle of maximum  
72 entropy. According to Beck (2009) and Khinchin (2013), a measure of entropy  $H$  should sat-  
73 isfy four properties in the discrete case: (1) it should be a function of a probability distribution  
74  $p(n)$  only; (2) it should be maximized when  $p(n)$  is uniform; (3) it should not be influenced by  
75 outcomes with a null probability; and (4) it should be independent of the order of information  
76 acquisition. The Shannon's entropy (Shannon 1948)

$$H = - \sum_n p(n) \log p(n) \quad (1)$$

77 satisfies all of these properties. Finding the probability distribution  $p(n)$  that maximizes  $H$  under  
78 a set of  $m$  constraints  $g$  can be done using the method of Lagrange multipliers. These constraints  
79 could include one or many properties of the probability distribution (e.g., its mean, variance, and  
80 range). However, the normalization constraint always need to be included in  $g$  in order to make  
81 sure that  $p(n)$  sums to 1. The objective is then to find the values of the Lagrange multipliers  $\lambda_i$   
82 that optimize a function  $F$ :

$$F = H - \sum_{i=1}^m \lambda_i(g_i - c_i), \quad (2)$$

83 where  $g_i$  is the mathematical formulation of the constraint  $i$  and  $c_i$ , its value. Note that  $F$  is just  
 84 Shannon's entropy to which we added terms that each sums to zero ( $g_i = c_i$ ).  $F$  is maximized  
 85 by setting to 0 its partial derivative with respect to  $p(n)$ .

86 The principle of maximum entropy has been used in a wide range of disciplines, from thermo-  
 87 dynamics, chemistry and biology (Martyushev and Seleznev 2006) to graph and network theory  
 88 (e.g., Park and Newman 2004; van der Hoorn, Lippner, and Krioukov 2018). It has also been  
 89 proven useful in ecology, e.g. in species distribution models (Phillips, Anderson, and Schapire  
 90 2006) and macroecological models (Harte et al. 2008; Harte and Newman 2014). In network  
 91 ecology, MaxEnt has been used to predict the degree distribution of bipartite networks from the  
 92 number of species and the number of interactions (Williams 2011) and to predict interaction  
 93 strengths between species pairs using their relative abundances within an optimal transportation  
 94 theory regularized with information entropy (Stock, Poisot, and De Baets 2021). However, to  
 95 the best of our knowledge, MaxEnt has never been used to predict food-web structure directly,  
 96 even though food webs are among the most documented and widespread ecological networks  
 97 (Ings et al. 2009).

98 Food-web properties that can be derived using MaxEnt are varied and pertain to different ele-  
 99 ments of the network (i.e. at the species (node), the interaction (edge) or the community (net-  
 100 work) levels). Because MaxEnt is a method of finding least-biased probability distributions  
 101 given partial knowledge about a system, these properties need to be represented probabilistically.  
 102 For example, at the species level, MaxEnt can be used to predict the distribution of trophic levels  
 103 among species, as well as the distribution of species' vulnerability (number of predators) and  
 104 generality (number of prey). By contrast, at the interaction level, predictions can be made on  
 105 the distribution of interaction strengths in weighted food webs. At the community level, it can  
 106 generate probability distributions of many measures of their emerging structure and of networks  
 107 themselves (i.e. a probability distribution that specific network configurations are realized given  
 108 the model and constraints). Overall, the potential of this method in the study of food webs is  
 109 broad. The applicability and performance of MaxEnt mostly depend on the ecological infor-

110 mation available and on our capacity to find the right set of state variables that best represent  
111 natural systems and to translate them into appropriate statistical constraints. Having a validated  
112 maximum entropy model for the system at hand allows us to make least-biased predictions using  
113 a minimal amount of data, as well as identify the most important ecological processes shaping  
114 that system. In other words, MaxEnt is a valuable and underexploited tool in network ecology  
115 that allows us to better understand and predict the structure of ecological networks.

## 116 Analytical and heuristic approaches

117 In this contribution, we used two complementary approaches to predict the structure of food  
118 webs using the principle of maximum entropy. The first approach consists in deriving con-  
119 strained probability distributions of given network properties analytically, whereas the second  
120 approach consists in finding the adjacency matrix of maximum entropy heuristically, from which  
121 network properties can be measured. We compared our predictions against empirical data and  
122 null and neutral models commonly used in network ecology. We focus on deterministic and  
123 unweighted (Boolean) food webs in both approaches for data availability reasons. However, our  
124 framework can be applied to all types of ecological networks and a wide variety of measures.

125 For the first approach (analytic), we focus on species level properties. Specifically, we derived  
126 the joint degree distribution (i.e. the joint probability distribution that a species has a given  
127 number of prey and predators in its network) of maximum entropy using only the number of  
128 species  $S$  and the number of interactions  $L$  as state variables. Then, we predicted the degree  
129 distribution of maximum entropy directly from the joint degree distribution since the first is the  
130 sum of the marginal distributions of the second. Because of the scarcity of empirical data on  
131 the number of interactions in food webs, we present a method to predict  $L$  from  $S$  (Box 1), thus  
132 allowing the prediction of the joint degree distribution from  $S$  solely.

133 For the second approach (heuristic), we focus on network level properties. We used a flexible and  
134 heuristic model based on simulated annealing (an optimization algorithm) to find the network  
135 configuration *close* to maximum entropy and measured its structure. We developed this heuristic  
136 model because the analytical derivation of a maximum entropy graph model of food webs is  
137 difficult, and because this model is readily applicable to other types of ecological networks and

measures. Indeed, the mathematical representation of food webs (i.e. directed simple graphs frequently having self-loops) makes the optimization of maximum entropy graph models more complicated than with many other types of (non-ecological) networks. In other words, deriving a probability distribution on the graphs themselves is difficult when working with food webs.

We built two types of heuristic MaxEnt models depending on the constraint used. Our type I MaxEnt model uses the connectance of the network (i.e. the ratio  $L/S^2$ ) as a constraint, whereas our type II MaxEnt model uses the whole joint degree sequence as a constraint.

## 145 Data and code

We tested our analytical and heuristic MaxEnt models against open food-web data queried from three different sources and integrated into what we call our *complete dataset*. These sources include (1) terrestrial and aquatic food webs sampled globally and archived on the ecological interactions database Mangal; (2) freshwater stream food webs from New Zealand; and (3) aquatic food webs from Tuesday Lake (Michigan, United States). First, all food webs archived on `mangal.io` (Timothée Poisot et al. 2016; Banville, Vissault, and Poisot 2021) were directly queried from the database ( $N = 235$ ). Most ecological networks archived on Mangal are multi-layer networks, i.e. networks that describe different types of interactions. We kept all networks whose interactions were mainly of predation and herbivory types, and removed the largest network ( $S = 714$ ) for computational efficiency reasons. Then, to this set we added food webs from two different sources: the New Zealand dataset ( $N = 21$ ; J. P. Pomeranz et al. 2018) and the Tuesday Lake dataset ( $N = 2$ ; Cohen, Jonsson, and Carpenter 2003). Our complete dataset thus contained a total of 257 food webs. Of the New Zealand and Tuesday Lake datasets, 19 networks had data on species' relative abundances that were used in the neutral model (Box 2). These 19 food webs constitute our *abundance dataset*, which is a subset of our complete dataset.

All code and data to reproduce this article are available at the Open Science Framework. Data cleaning, simulations and analyses were conducted in Julia v1.6.1.

163 **Analytical maximum entropy models**

164 Our analytical approach is the most common way to use and develop maximum entropy models.  
165 As shown above, starting from a defined set of constraints, a mathematical expression for the  
166 target distribution is derived using the method of Lagrange multipliers. The derived distribution  
167 of maximum entropy is unique and least biased given the constraints used. Although we refer to  
168 this approach as analytic, finding the values of the Lagrange multipliers usually requires the use  
169 of numerical methods. Here we use MaxEnt to derive two species level properties in food webs:  
170 the joint degree distribution and the degree distribution. The degree distribution has driven the  
171 attention of ecologists because of its role in determining the assembly of ecological networks  
172 (Vázquez 2005), shaping their emerging structure (Fortuna et al. 2010), and understanding  
173 interaction mechanisms (Williams 2011). As noted above, although the degree distribution of  
174 maximum entropy has already been derived in bipartite networks (Williams 2011), we show  
175 in much greater details its mathematical derivation in food webs. But first, we derive the joint  
176 degree distribution, a related property that holds significantly more ecological information than  
177 the degree distribution.

178 **Joint degree distribution**

179 The joint degree distribution  $p(k_{in}, k_{out})$  of a food web with  $S$  species is a joint discrete proba-  
180 bility distribution describing the probability that a species has  $k_{in}$  predators and  $k_{out}$  prey, with  
181  $k_{in}$  and  $k_{out} \in [0, S]$ . Basal species (e.g., plants) have a  $k_{out}$  of 0, whereas top predators have  
182 a  $k_{in}$  of 0. In contrast, the maximum number of prey and predators a species can have is set  
183 by the number of species in the food web. Here we show how the joint degree distribution of  
184 maximum entropy can be obtained given knowledge of the number of species  $S$  and the number  
185 of interactions  $L$ .

186 We want to maximize Shannon's entropy

$$H = - \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S p(k_{in}, k_{out}) \log p(k_{in}, k_{out}) \quad (3)$$

<sup>187</sup> subject to the following constraints:

$$g_1 = \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S p(k_{in}, k_{out}) = 1; \quad (4)$$

$$g_2 = \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S k_{in} p(k_{in}, k_{out}) = \langle k_{in} \rangle = \frac{L}{S}; \quad (5)$$

$$g_3 = \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S k_{out} p(k_{in}, k_{out}) = \langle k_{out} \rangle = \frac{L}{S}. \quad (6)$$

<sup>188</sup> The first constraint  $g_1$  is our normalizing constraint, whereas the other two ( $g_2$  and  $g_3$ ) fix the  
<sup>189</sup> average of the marginal distributions of  $k_{in}$  and  $k_{out}$  to the linkage density  $L/S$ . It is important  
<sup>190</sup> to notice that  $\langle k_{in} \rangle = \langle k_{out} \rangle$  because every edge is associated to a predator and a prey. Therefore,  
<sup>191</sup> without using any further constraints, we would expect the joint degree distribution of maximum  
<sup>192</sup> entropy to be a symmetric probability distribution with regards to  $k_{in}$  and  $k_{out}$ . However, this  
<sup>193</sup> does not mean that the joint degree *sequence* will be symmetric, since the joint degree sequence  
<sup>194</sup> is essentially a random realization of its probabilistic counterpart.

<sup>195</sup> The joint probability distribution of maximum entropy given these constraints is found using the  
<sup>196</sup> method of Lagrange multipliers. To do so, we seek to maximize the following expression:

$$F = H - \lambda_1(g_1 - 1) - \lambda_2 \left( g_2 - \frac{L}{S} \right) - \lambda_3 \left( g_3 - \frac{L}{S} \right), \quad (7)$$

<sup>197</sup> where  $\lambda_1$ ,  $\lambda_2$ , and  $\lambda_3$  are the Lagrange multipliers. The probability distribution that maximizes  
<sup>198</sup> entropy is obtained by finding these values. As pointed out above,  $F$  is just Shannon's entropy  
<sup>199</sup> to which we added terms that each sums to zero (our constraints).  $F$  is maximized by setting to  
<sup>200</sup> 0 its partial derivative with respect to  $p(k_{in}, k_{out})$ . Because the derivative of a constant is zero,  
<sup>201</sup> this gives us:

$$\frac{\partial H}{\partial p(k_{in}, k_{out})} = \lambda_1 \frac{\partial g_1}{\partial p(k_{in}, k_{out})} + \lambda_2 \frac{\partial g_2}{\partial p(k_{in}, k_{out})} + \lambda_3 \frac{\partial g_3}{\partial p(k_{in}, k_{out})}. \quad (8)$$

202 Evaluating the partial derivatives with respect to  $p(k_{in}, k_{out})$ , we obtain:

$$-\log p(k_{in}, k_{out}) - 1 = \lambda_1 + \lambda_2 k_{in} + \lambda_3 k_{out}. \quad (9)$$

203 Then, solving eq. 9 for  $p(k_{in}, k_{out})$ , we obtain:

$$p(k_{in}, k_{out}) = \frac{e^{-\lambda_2 k_{in} - \lambda_3 k_{out}}}{Z}, \quad (10)$$

204 where  $Z = e^{1+\lambda_1}$  is called the partition function. The partition function ensures that probabilities  
205 sum to 1 (our normalization constraint). It can be expressed in terms of  $\lambda_2$  and  $\lambda_3$  as follows:

$$Z = \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S e^{-\lambda_2 k_{in} - \lambda_3 k_{out}}. \quad (11)$$

206 After substituting  $p(k_{in}, k_{out})$  in eq. 5 and eq. 6, we get a nonlinear system of two equations and  
207 two unknowns:

$$\frac{1}{Z} \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S k_{in} e^{-\lambda_2 k_{in} - \lambda_3 k_{out}} = \frac{L}{S}; \quad (12)$$

$$\frac{1}{Z} \sum_{k_{in}=0}^S \sum_{k_{out}=0}^S k_{out} e^{-\lambda_2 k_{in} - \lambda_3 k_{out}} = \frac{L}{S}. \quad (13)$$

208 We solved eq. 12 and eq. 13 numerically using the Julia library JuMP.jl v0.21.8 (Dunning,  
209 Huchette, and Lubin 2017). JuMP.jl supports nonlinear optimization problems by providing  
210 exact second derivatives that increase the accuracy and performance of its solvers. The estimated  
211 values of  $\lambda_2$  and  $\lambda_3$  can be substituted in eq. 10 to have a more workable expression for the joint  
212 degree distribution.

213 We assessed the empirical support of this expression using all food webs in our complete dataset.  
214 First, we predicted the joint degree distribution of maximum entropy for each of these food webs,  
215 i.e. using their number of species and number of interactions as state variables. Then, we sam-  
216 pled one realization of the joint degree sequence for each network using the probabilities given

217 by the joint degree distribution of maximum entropy, while fixing the total number of interac-  
218 tions. This gave us a random realization of the number of prey and predators for each species in  
219 each network. We standardized the predicted  $k_{out}$  and  $k_{in}$  of each species by the total number of  
220 species in their network to generate relative values, which can be compared across networks. In  
221 fig. 1 (left panels), we show the relationship between these relative  $k_{out}$  and  $k_{in}$  obtained from the  
222 joint degree distributions of maximum entropy (bottom panel) and this relationship using em-  
223 pirical values (top panel). We observe that our model predicts higher values of generality and  
224 vulnerability compared to empirical food webs (i.e. relative values of  $k_{out}$  and  $k_{in}$  both closer to  
225 1) for many species. In other words, our model predicts that species that have many predators  
226 also have more prey than what is observed empirically (and conversely). This is not surprising,  
227 given that our model did not include biological factors preventing generalist predators from hav-  
228 ing many prey. Nevertheless, with the exception of these generalist species, MaxEnt adequately  
229 predicts that most species have low generality and vulnerability values.

230 Examining the difference between predicted and empirical values for each species gives a slightly  
231 different perspective (right panel of fig. 1). To do so, we must first associate each of our predic-  
232 tions to a specific species in a network in order to make that comparison. Indeed, our predicted  
233 joint degree sequences have the same number of species (elements) as their empirical counter-  
234 parts, but they are species agnostic. In other words, instead of predicting a value for each species  
235 directly, we predicted the entire joint degree sequence without taking into account species' iden-  
236 tity. The challenge is thus to adequately associate predictions with empirical data. In fig. 1, we  
237 present these differences when species are ordered by their total degree in their respective net-  
238 works (i.e. by the sum of their in and out-degrees). This means that the species with the highest  
239 total degree in its network will be associated with the highest prediction, and so forth. Doing so,  
240 we see that species predicted to have a higher number of predators than what is observed gen-  
241 erally have a lower number of prey than what is observed (and conversely). This is because the  
242 difference in total degree ( $k_{out} + k_{in}$ ) between predictions and empirical data is minimized when  
243 species are ranked by their total degree (i.e. the average deviation of the sum of relative  $k_{out}$  and  
244  $k_{in}$  is close to 0 across all species). This result thus shows that the difference between predicted  
245 and empirical total degrees is low for most species when ordered by their total degrees. There

246 are no apparent biases towards in or out degrees. In fig. S1, we show how these differences  
247 change when species are instead ordered by their out-degrees (left panel) and in-degrees (right  
248 panel), respectively.

249 [Figure 1 about here.]

250 Another way to evaluate the empirical support of the predicted joint degree sequences is to com-  
251 pare their shape with the ones of empirical food webs. We can describe the shape of a joint degree  
252 sequence by comparing its marginal distributions with one another. To do so, we calculated the  
253 Kullback–Leibler (KL) divergence between the in and out-degree sequences sampled from the  
254 joint degree distribution of maximum entropy. Similarly, we calculated the divergence between  
255 the in and out-degree sequences obtained empirically. This allows us to compare the symmetry  
256 of empirical and predicted joint degree sequences (left panel of fig. 2). As we expected, our  
257 model predicts more similar in-degree and out-degree sequences than empirical data (shown  
258 by lower KL divergence values). However, this difference decreases with connectance (right  
259 panel of fig. 2). This might be due to the fact that food webs with a low connectance are harder  
260 to predict than food webs with a high connectance. Indeed, in low connectance systems, what  
261 makes two species interact might be more important for prediction than in high connectance  
262 systems, in which what prevents species from interacting might be more meaningful. This im-  
263 plies that more ecological information might be needed in food webs with a low connectance  
264 because more ecological processes determine interactions compared to non-interactions. There-  
265 fore, other ecological constraints might be needed to account for the asymmetry of the joint  
266 degree distribution, especially for networks with a lower connectance. However, our MaxEnt  
267 model was able to capture quite well the shape of the joint degree sequence for networks having  
268 a high connectance.

269 [Figure 2 about here.]

270 **Degree distribution**

271 The joint degree distribution derived using MaxEnt (eq. 10) can be used to obtain the degree  
272 distribution of maximum entropy. Indeed, the degree distribution  $p(k)$  represents the probability

273 that a species has  $k$  interactions in its food web, with  $k = k_{in} + k_{out}$ . It can thus be obtained  
 274 from the joint degree distribution as follows:

$$p(k) = \sum_{i=0}^k p(k_{in} = k - i, k_{out} = i).$$

275 The degree distribution could have also been obtained directly using the principle of maximum  
 276 entropy, as discussed in Williams (2011). This gives the following distribution:

$$p(k) = \frac{e^{-\lambda_2 k}}{Z}, \quad (14)$$

277 with  $Z = \sum_{k=0}^S e^{-\lambda_2 k}$ .

278 This can be solved numerically using the constraint of the average degree  $\langle k \rangle = \frac{2L}{S}$  of a species,  
 279 yielding an identical solution to the one obtained using the joint degree distribution as an inter-  
 280 mediate. Note that the mean degree is twice the value of the linkage density, because every link  
 281 must be counted twice when we add in and out-degrees together.

$$\frac{1}{Z} \sum_{k=0}^S k e^{-\lambda_2 k} = \frac{2L}{S} \quad (15)$$

282 One aspect of the degree distribution that informs us of its ecological realism is the number of  
 283 isolated species it predicts. As MacDonald, Banville, and Poisot (2020) pointed out, the size of  
 284 food webs should at least be of  $S - 1$  interactions, since a lower number would yield isolated  
 285 species, i.e. species without any predators or prey. Because non-basal species must eat to survive,  
 286 isolated species could indicate that other species are missing or they could simply be removed  
 287 from the food web. In fig. S2, we show that the degree distribution of maximum entropy, given  
 288  $S$  and  $L$ , gives very low probabilities that a species will be isolated in its food web (i.e. having  
 289  $k = 0$ ) above the  $S - 1$  threshold. However, under our purely information-theoretic model,  
 290 the probability that a species is isolated is quite high when the total number of interactions is  
 291 below  $S - 1$ . Moreover, the expected proportion of isolated species rapidly declines by orders  
 292 of magnitude with increasing numbers of species and interactions. This supports the ecological  
 293 realism of the degree distribution of maximum entropy derived above. Nevertheless, ecologists

294 wanting to model a system without allowing isolated species could simply change the lower limit  
295 of  $k$  to 1 in eq. 15 and solve the resulting equation numerically.

## 296 Box 1 - Working with predicted numbers of interactions

297 Our analytical MaxEnt models require information on the number of species and the number of  
298 interactions. However, since the later is rarely measured empirically, ecologists might need to  
299 use predictive models to estimate the total number of interactions in a food web before using  
300 MaxEnt. Here we illustrate how this can be done by combining both models sequentially.

301 We used the flexible links model of MacDonald, Banville, and Poisot (2020) to predict the  
302 number of interactions from the number of species. The flexible links model, in contrast to other  
303 predictive models of the number of interactions, incorporates meaningful ecological constraints  
304 into the prediction of  $L$ , namely the minimum  $S - 1$  and maximum  $S^2$  numbers of interactions  
305 in food webs. It estimates the proportion of the  $S^2 - (S - 1)$  *flexible links* that are realized.  
306 More precisely, this model states that the number of *realized* flexible links (or interactions)  
307  $L_{FL}$  in a food web represents the number of realized interactions above the minimum (i.e.  $L =$   
308  $L_{FL} + S - 1$ ) and is obtained from a beta-binomial distribution with  $S^2 - (S - 1)$  trials and  
309 parameters  $\alpha = \mu e^\phi$  and  $\beta = (1 - \mu) e^\phi$ :

$$L_{FL} \sim \text{BB}(S^2 - (S - 1), \mu e^\phi, (1 - \mu) e^\phi), \quad (16)$$

310 where  $\mu$  is the average probability across food webs that a flexible link is realized, and  $\phi$  is the  
311 concentration parameter around  $\mu$ .

312 We fitted the flexible links model on all food webs in our complete dataset, and estimated the  
313 parameters of eq. 16 using a Hamiltonian Monte Carlo sampler with static trajectory (1 chain  
314 and 3000 iterations):

$$[\mu, \phi | \mathbf{L}, \mathbf{S}] \propto \prod_{i=1}^m \text{BB}(L_i - (S_i - 1) | S_i^2 - (S_i - 1)), \mu e^\phi, (1 - \mu) e^\phi) \times \text{B}(\mu | 3, 7) \times \mathcal{N}(\phi | 3, 0.5), \quad (17)$$

315 where  $m$  is the number of food webs ( $m = 257$ ) and  $\mathbf{L}$  and  $\mathbf{S}$  are respectively the vectors of their  
 316 numbers of interactions and numbers of species. Our weakly-informative prior distributions  
 317 were chosen following MacDonald, Banville, and Poisot (2020), i.e. a beta distribution for  $\mu$   
 318 and a normal distribution for  $\phi$ . The Monte Carlo sampling of the posterior distribution was  
 319 conducted using the Julia library Turing v0.15.12.

320 The flexible links model is a generative model, i.e. it can generate plausible values of the pre-  
 321 dicted variable. We thus simulated 1000 values of  $L$  for different values of  $S$  using the joint  
 322 posterior distribution of our model parameters (eq. 17), and calculated the mean degree for each  
 323 simulated value. The resulting distributions are shown in the left panel of fig. 3 for three different  
 324 values of species richness. In the right panel of fig. 3, we show how the probability distribution  
 325 for the mean degree constraints can be used to generate a distribution of maximum entropy de-  
 326 gree distributions, since each simulated value of mean degree generates a different maximum  
 327 entropy degree distribution (eq. 14 and eq. 15).

328 [Figure 3 about here.]

## 329 **Box 2 - Corresponding null and neutral models**

### 330 **Null models (types I and II)**

331 The predictions of our heuristic maximum entropy models were compared against two topologi-  
 332 cal null models. These null models use the same ecological information as our heuristic models  
 333 and thus constitute an adequate baseline for comparison. The first is the type I null model of  
 334 Fortuna and Bascompte (2006), in which the probability that a species  $i$  predares on another  
 335 species  $j$  is given by

$$p(i \rightarrow j) = \frac{L}{S^2}. \quad (18)$$

336 The second is the type II null model of Bascompte et al. (2003), in which the probability of  
 337 interaction is instead given by

$$p(i \rightarrow j) = \frac{1}{2} \left( \frac{k_{in}(j)}{S} + \frac{k_{out}(i)}{S} \right), \quad (19)$$

338 where  $k_{in}(j)$  and  $k_{out}(i)$  are the in and out-degrees of species  $j$  and  $i$ , respectively. The type I  
 339 null model is based on connectance, whereas the type II null model is based on the joint degree  
 340 sequence. Therefore, the type I and II topological null models correspond to our type I and II  
 341 heuristic MaxEnt models, respectively, since they use similar constraints.

342 We generated probabilistic networks using both types of null models for all empirical food webs  
 343 in our complete dataset. Then, we converted these networks to adjacency matrices of Boolean  
 344 values by generating 100 random networks for each of these probabilistic webs, and kept the  $L$   
 345 entries that were sampled the most amount of times, with  $L$  given by the number of interactions  
 346 in each food web. This ensured that the resulting null networks had the same number of inter-  
 347 actions as their empirical counterparts. Thus, for each null model, we ended up with one null  
 348 adjacency matrix for each empirical network.

### 349 Neutral model

350 We also compared our heuristic MaxEnt models with a neutral model of relative abundances, in  
 351 which the probabilities of interaction are given by

$$p(i \rightarrow j) \propto \frac{n_i}{N} \times \frac{n_j}{N}, \quad (20)$$

352 where  $n_i$  and  $n_j$  are the abundances (or biomass) of both species, and  $N$  is the total abundance  
 353 (or biomass) of all species in the network. We generated neutral abundance matrices for all em-  
 354 pirical food webs in our abundance dataset, and converted these weighted networks to adjacency

355 matrices of Boolean values using the same method as the one we used for our null models.

## 356 **Heuristic maximum entropy models**

357 With the analytical approach, we showed how important measures of food-web structure (e.g.,  
358 the degree distribution and the joint degree distribution) can be derived with the principle of  
359 maximum entropy using minimal knowledge about a biological community. This type of mod-  
360 els, although useful to make least-biased predictions of many network properties, can be hard  
361 to apply for other measures. Indeed, there are dozens of measures of network structure (Del-  
362 mas et al. 2019) and many are not directly calculated with mathematical equations, but are  
363 instead estimated algorithmically. Moreover, the applicability of this method to empirical sys-  
364 tems is limited by the state variables we can actually measure and use. Here, we propose a more  
365 flexible method to predict many measures of network structure simultaneously, i.e. by finding  
366 heuristically the network configuration having maximum entropy given partial knowledge of its  
367 emerging structure.

## 368 **From Shannon's to SVD entropy**

369 The principle of maximum entropy can be applied on the network itself if we decompose its  
370 adjacency matrix into a non-zero vector of relative values. This is a necessary step when work-  
371 ing with food webs, which are frequently expressed as a matrix  $A = [a_{ij}]$  of Boolean values  
372 representing the presence ( $a_{ij} = 1$ ) or absence ( $a_{ij} = 0$ ) of an interaction between two species  $i$   
373 and  $j$ . Knowing one or many properties of a food web of interest (e.g., its number of species and  
374 number of interactions), we can simulate its adjacency matrix randomly by using these known  
375 ecological information to constrain the space of potential networks. The entropy of this hypo-  
376 thetical matrix can then be measured after decomposing it into appropriate values. Simulating  
377 a series of networks until we find the one having the highest entropy allows us to search for the  
378 most complex food-web configuration given the ecological constraints used. This configuration  
379 is the least biased one considering the information available. In other words, the most we can  
380 say about a network's adjacency matrix, without making more assumptions than the ones given

381 by our incomplete knowledge of its structure, is the one of maximum entropy. Generating the  
382 most complex network that corresponds to this structure allows us to explore more easily other  
383 properties of food webs under MaxEnt.

384 Shannon's entropy can only be calculated on conventional probability distributions such as the  
385 joint degree distribution. This is an issue when working with the adjacency matrix of ecological  
386 networks. For this reason, we need to use another measure of entropy if we want to predict a  
387 network's configuration directly using MaxEnt. We used the SVD entropy as our measure of  
388 entropy, which is an application of Shannon's entropy to the relative non-zero singular values  
389 of a truncated singular value decomposition (t-SVD; Strydom, Dalla Riva, and Poisot 2021) of  
390 a food web's Boolean adjacency matrix. We measured SVD entropy as follows:

$$J = - \sum_{i=1}^R s_i \log s_i, \quad (21)$$

391 where  $s_i$  are the relative singular values of the adjacency matrix ( $s_i = \sigma_i / \sum_{i=1}^R \sigma_i$ , where  $\sigma_i$   
392 are the singular values). Note that the distribution of relative singular values is analogous to  
393 a probability distribution, with  $0 < s_i < 1$  and  $\sum s_i = 1$ . This measure also satisfies all four  
394 properties of an appropriate entropy measure above-mentioned, while being a proper measure of  
395 the internal complexity of food webs (Strydom, Dalla Riva, and Poisot 2021). Following Stry-  
396 dom, Dalla Riva, and Poisot (2021), we standardized this measure with the rank  $R$  of the matrix  
397 (i.e.  $J / \ln(R)$ ) to account for the difference in dimensions between networks (*sensu* Pielou's  
398 evenness; Pielou 1975).

### 399 **Types I and II heuristic MaxEnt models**

400 We used SVD entropy to predict the network configuration of maximum entropy (i.e. of max-  
401 imum complexity) heuristically given different constraints for all food webs in our complete  
402 dataset. We built two types of heuristic MaxEnt models that differ on the constraint used. The  
403 type I heuristic MaxEnt model is based on connectance, whereas the type II heuristic MaxEnt  
404 model is based on the joint degree sequence. These models are thus based on the same con-  
405 straints as the types I (Fortuna and Bascompte 2006) and II (Bascompte et al. 2003) null models

406 (Box 2) frequently used to generate random networks topologically. This allows direct com-  
407 parison of the performance of null and heuristic MaxEnt models in reproducing the emerging  
408 structure of empirical food webs.

409 For each network in our complete dataset, we estimated their configuration of maximum entropy  
410 given each of these constraints. For both types of heuristic MaxEnt models, we used a simulated  
411 annealing algorithm with 4 chains, 2000 steps and an initial temperature of 0.2. For each food  
412 web, we first generated one random Boolean matrix per chain while fixing the number of species.  
413 We also maintained the total number of interactions (i.e. the sum of all elements in the matrix) in  
414 the type I MaxEnt model and the joint degree sequence (i.e. the rows and columns sums) in the  
415 type II MaxEnt model. These were our initial configurations. Then, we swapped interactions se-  
416 quentially while maintaining the original connectance or joint degree sequence. Configurations  
417 with a higher SVD entropy than the previous one in the chain were always accepted, whereas  
418 they were accepted with a probability conditional to a decreasing temperature when lower. The  
419 final configuration with the highest SVD entropy among the four chains constitute the estimated  
420 maximum entropy configuration of a food web given the constraint used.

## 421 **Structure of MaxEnt food webs**

422 We measured various properties of these configurations of maximum entropy to evaluate how  
423 well they reproduce the structure of sampled food webs. Specifically, we evaluated their nest-  
424 edness  $\rho$ , their maximum trophic level  $maxtl$ , their network diameter  $diam$ , their average maxi-  
425 mum similarity between species pairs  $MxSim$  (Williams and Martinez 2000), their proportion  
426 of cannibal species  $Cannib$ , their proportion of omnivorous species  $Omniv$ , their SVD entropy,  
427 and their motifs profile. Nestedness indicates how much the diet of specialist species is a subset  
428 of the one of generalists (Delmas et al. 2019) and was measured using the spectral radius of  
429 the adjacency matrix (Staniczenko, Kopp, and Allesina 2013). In turn, the network diameter  
430 represents the longest of the shortest paths between all species pair (Albert and Barabasi 2002).  
431 Further, cannibal species are species that can eat members of their own species (i.e. species  
432 having self loops), whereas omnivorous species can prey on different trophic levels (Williams  
433 and Martinez 2000). Finally, a motifs profile represents the proportion of three-species motifs

434 (subnetworks), which can be considered as simple building blocks of ecological networks (Milo  
435 et al. 2002; Stouffer et al. 2007). All of these properties are relatively easy to measure and were  
436 chosen based on their ecological importance and prevalent use in network ecology (McCann  
437 2011; Delmas et al. 2019).

438 We compared the performance of both heuristic MaxEnt models in predicting these measures to  
439 the one of the null (tbl. 1) and neutral models (tbl. 2). Overall, we found that the models based  
440 on the joint degree sequence (i.e. the type II null and heuristic MaxEnt models) reproduced the  
441 structure of empirical food webs much better than the ones based on connectance (i.e. the type I  
442 null and heuristic MaxEnt models). This suggests that the predictive power of connectance might  
443 be more limited than what was previously suggested (Timothée Poisot and Gravel 2014). On  
444 the other hand, the neutral model of relative abundances was surprisingly good at predicting the  
445 maximum trophic level and the network diameter. However, with the exception of the network  
446 diameter, the type II heuristic MaxEnt model was better at predicting network structure than the  
447 neutral model for all measures considered. This might be because, although neutral processes are  
448 important, they act in concert with niche processes in determining species interactions Canard et  
449 al. (2014). The joint degree sequence encodes information on both neutral and niche processes  
450 because the number of prey and predators a species has is determined by its relative abundance  
451 and biological traits. Therefore, these results show that having information on the number of  
452 prey and predators for each species substantially improves the prediction of food-web structure,  
453 both compared to models solely based on connectance and the ones solely based on species  
454 relative abundances.

455 Next, the predictions of the type II heuristic MaxEnt model can be compared to its null model  
456 counterpart. On average, the type II heuristic MaxEnt model was better at predicting nestedness  
457 ( $0.62 \pm 0.08$ ) than its corresponding null model ( $0.73 \pm 0.05$ ; empirical networks:  $0.63 \pm 0.09$ ) for  
458 all networks in our complete dataset (tbl. 1). This might in part be due to the fact that nestedness  
459 was calculated using the spectral radius of the adjacency matrix, which directly leverages infor-  
460 mation on the network itself just like the heuristic MaxEnt models. The proportion of self-loops  
461 (cannibal species) was also better predicted by the type II heuristic MaxEnt model in comparison  
462 to the type II null model. However, the type II null model was better at predicting network diam-

463 eter and average maximum similarity between species pairs, and predictions of the maximum  
 464 trophic level and the proportion of omnivorous species were similar between both types of mod-  
 465 els. This suggests that, although the joint degree sequence is an important driver of food-web  
 466 structure, other ecological constraints might need to be added to our MaxEnt model to account  
 467 for some emerging food-web properties, especially the ones regarding food-chain lengths.

Table 1: Standardized mean difference between predicted network measures and empirical data for all food webs in our complete dataset ( $N = 257$ ). Positive (negative) values indicate that the measure is overestimated (underestimated) on average. Empirical networks include most food webs archived on Mangal, as well as the New Zealand and Tuesday Lake food webs. Null 1: Type I null model based on connectance. MaxEnt 1: Type I heuristic MaxEnt model based on connectance. Null 2: Type II null model based on the joint degree sequence. MaxEnt 2: Type II heuristic MaxEnt model based on the joint degree sequence.  $\rho$ : nestedness measured by the spectral radius of the adjacency matrix. *maxtl*: maximum trophic level. *diam*: network diameter. *MxSim*: average maximum similarity between species pairs. *Cannib*: proportion of cannibal species (self loops). *Omniv*: proportion of omnivorous species. *entropy*: SVD entropy.

model	rho	maxtl	diam	MxSim	Cannib	Omniv	entropy
null 1	-0.167	0.980	1.428	-0.502	2.007	1.493	0.056
MaxEnt 1	-0.226	0.831	1.274	-0.524	1.982	1.863	0.106
null 2	0.160	-0.125	0.016	0.007	1.078	0.559	-0.023
MaxEnt 2	-0.015	0.178	0.565	-0.282	0.698	0.589	0.058

Table 2: Standardized mean difference between predicted network measures and empirical data for all food webs in our abundance dataset ( $N = 19$ ). Positive (negative) values indicate that the measure is overestimated (underestimated) on average. Empirical networks include the New Zealand and Tuesday Lake food webs having abundance data. Neutral: Neutral model of relative abundances. Null 1: Type I null model based on connectance. MaxEnt 1: Type I heuristic MaxEnt model based on connectance. Null 2: Type II null model based on the joint degree sequence. MaxEnt 2: Type II heuristic MaxEnt model based on the joint degree sequence.  $\rho$ : nestedness measured by the spectral radius of the adjacency matrix. *maxtl*: maximum trophic level. *diam*: network diameter. *MxSim*: average maximum similarity between species pairs. *Cannib*: proportion of cannibal species (self loops). *Omniv*: proportion of omnivorous species. *entropy*: SVD entropy.

model	rho	maxtl	diam	MxSim	Cannib	Omniv	entropy
neutral	0.367	-0.090	0.027	0.266	6.870	0.576	-0.083
null 1	-0.134	0.950	1.919	-0.369	2.077	0.614	0.068

model	rho	maxtl	diam	MxSim	Cannib	Omniv	entropy
MaxEnt 1	-0.229	1.020	1.946	-0.355	2.215	0.801	0.121
null 2	0.128	-0.115	-0.135	0.157	1.444	0.029	-0.021
MaxEnt 2	-0.010	0.054	0.243	-0.062	-0.038	0.083	0.038

468 Finally, in fig. 4 we also show how well empirical measures are predicted using the type II  
 469 MaxEnt network model. In accordance with our previous results, we found that nestedness was  
 470 very well predicted by our model. However, the type II MaxEnt network model overestimated  
 471 the maximum trophic level and network diameter, especially for networks with high empirical  
 472 values. In fig. S3, we show that the pairwise relationships between these four measures and  
 473 species richness in empirical food webs are similar (in magnitude and sign) to the ones in type  
 474 II MaxEnt networks.

475 [Figure 4 about here.]

476 Moreover, we found that empirical networks are close to their maximum entropy considering a  
 477 fixed joint degree sequence (fig. S4). Empirical networks had an SVD entropy of  $0.89 \pm 0.04$ ,  
 478 compared to type II MaxEnt networks which had values of  $0.94 \pm 0.03$ . The relationship between  
 479 the SVD entropy of empirical food webs and their maximum entropy configuration is plotted in  
 480 the last panel of fig. 4. We also found no relationship between the difference in SVD entropy  
 481 between empirical and type II MaxEnt networks and species richness, the number of interactions,  
 482 or connectance (fig. S5). Similarly, we found no correlation between the difference in SVD  
 483 entropy and the Jaccard distance of empirical and type II MaxEnt networks.

484 The picture slightly changes when we consider another important property of ecological net-  
 485 works, i.e. their motifs profile. We measured the proportion of three-species motifs, which can  
 486 be considered as simple building blocks of ecological networks (Milo et al. 2002; Stouffer et  
 487 al. 2007). Motifs are the backbone of complex ecological networks from which network struc-  
 488 ture is built upon and play a crucial role in community dynamics and assembly (Stouffer and  
 489 Bascompte 2011). In fig. 5, we show that the motifs profile of networks generated using the

490 type II MaxEnt network model was very close to the one of empirical data, and that they made  
491 better predictions than the type II null model. This is also shown in fig. 6, where we see that  
492 relationships between motifs pairs of empirical food webs are very similar to the ones of the  
493 type II MaxEnt networks. Overall, these results suggest that the type II MaxEnt network model  
494 can reproduce many aspects of network structure. This highlights the importance of the joint  
495 degree sequence in shaping ecological networks.

496 [Figure 5 about here.]

497 [Figure 6 about here.]

## 498 Discussion

499 The principle of maximum entropy is a robust mathematical method of finding least-biased  
500 probability distributions that have some desired properties given by prior knowledge on a sys-  
501 tem. We first used MaxEnt to predict the joint degree distribution and the degree distribution  
502 of maximum entropy given known numbers of species and of interactions. We found that the  
503 resulting joint degree distributions were more symmetric than the ones of empirical food webs,  
504 which suggests that other constraints might be needed to improve those predictions. We also  
505 used MaxEnt to predict networks of maximum entropy with a specified structure. These net-  
506 works are the most complex, or random, given the constraints used. Likewise, we found that  
507 knowledge of species richness and of the number of interactions were not sufficient to reproduce  
508 many aspects of network structure found in nature. However, a model based on the entire joint  
509 degree sequence, i.e. on the number of prey and predators for each species, gave more convinc-  
510 ing results. Our type II MaxEnt network model yielded better or similar predictions than the  
511 type II null model, also based on the joint degree sequence, for most measures considered in-  
512 cluding the motifs profile. This suggests that the joint degree sequence drives many aspects of  
513 network structure. Indeed, considering our findings that empirical networks are close to max-  
514 imum entropy for a given joint degree sequence, our results suggest that food-web topology is  
515 configured almost entirely randomly around these marginal numbers of predators and prey.

516 Our results bring to the forefront the role of the joint degree distribution in shaping food-web  
517 structure. This echoes the work of Williams (2011), which shows using MaxEnt how the degree  
518 distribution can drive the structure of bipartite networks. Fortuna et al. (2010) also found that  
519 the degree distribution of ecological networks is associated with some of their emerging prop-  
520 erties such as nestedness and modularity. Network ecologists tend to focus on several emerging  
521 properties of food webs (Delmas et al. 2019), although we show that food-web structure is very  
522 well predicted by the joint degree distribution. In the light of our results, there is a lot more  
523 ecological information in the difference between properties of empirical networks and MaxEnt  
524 predictions than in these properties themselves.

## 525 Alternative MaxEnt models

526 There are different ways to generate food webs using MaxEnt. In this contribution, we used a  
527 method based on simulated annealing to find the network configuration with the highest SVD  
528 entropy while fixing some aspects of its structure. Another technique, also based on simulated  
529 annealing, could start by generating a food web randomly with fixed numbers of species and  
530 interactions and calculating its joint degree distribution. Pairs of interactions could be swapped  
531 sequentially until we minimize the divergence between the calculated joint degree distribution  
532 and the one of maximum entropy obtained analytically. In that case, this is the entropy of the  
533 joint degree distribution that would be maximized, not the one of the network's topology. To a  
534 certain extent, this method would thus bridge the gap between the two approaches presented in  
535 this article (i.e. analytical and heuristic MaxEnt models). More research is needed to compare  
536 the quality of different methods generating adjacency matrices of food webs using MaxEnt.

537 Another method generating adjacency matrices are maximum entropy graph models, which pre-  
538 dict a probability distribution of networks under soft or hard constraints (e.g., Park and Newman  
539 2004; Cimini et al. 2019). Under hard constraints, every network with a non-zero probability  
540 exactly satisfies the constraints on its structure. This is in contrast with soft constraints, which  
541 require that networks satisfy them on average (i.e. many networks with a non-zero probability do  
542 not have the exact structure set by the constraints). Maximum entropy graph models are helpful  
543 because they can provide probability distributions for many network properties, by measuring

544 the structure of all adjacency matrices with a non-zero probability. However, we consider that  
545 our approach based on simulated annealing is more flexible and more computationally efficient.  
546 Indeed, many measures of food-web structure are hard to translate into mathematical constraints.  
547 Moreover, because food webs are directed networks with self-loops, it makes the mathematical  
548 derivation of maximum entropy graph models difficult. We believe that identifying heuristically  
549 what really constrains the topology of food webs is a useful first step before attempting to derive  
550 the mathematical formulation of a maximum entropy graph model adapted to food webs.  
551 Even though we decided to work with point estimates, it is possible to have a (non MaxEnt)  
552 probability distribution of networks when working with the entire chains (or part of the chains).

## 553 Applications

554 Our method and results could be used for different purposes. First, they could be used as first-  
555 order approximations of network structure when only state variables are known. This could  
556 prove useful when predicting network structure at large spatial scales, where few ecological in-  
557 formation is known at that scale. Second, they could be used as informative priors in Bayesian  
558 analyses of the structure of ecological networks (e.g., Cirtwill et al. 2019). Third, they could  
559 be used to make better predictions of pairwise species interactions by constraining the space of  
560 feasible networks, as discussed in Strydom et al. (2021). Finally, they could be used as alter-  
561 native null models of ecological networks to better understand ecological mechanisms driving  
562 food-web structure. In that case, our model might need to be slightly adapted to give a proba-  
563 bility distribution of Boolean networks (in contrast with point estimates of maximum entropy  
564 networks).

## 565 Conclusion

566 One of the biggest challenges in using the principle of maximum entropy is to identify the set  
567 of state variables that best reproduce empirical data. We found that the numbers of prey and  
568 predators for each species are important state variables for the prediction of maximum entropy  
569 networks. However, our predictions overestimated some measures of network structure, espe-

570 cially the maximum trophic level and network diameter. Therefore, we should continue playing  
571 the ecological detective to find these other topological constraints that would improve the pre-  
572 dictions of our MaxEnt network models.

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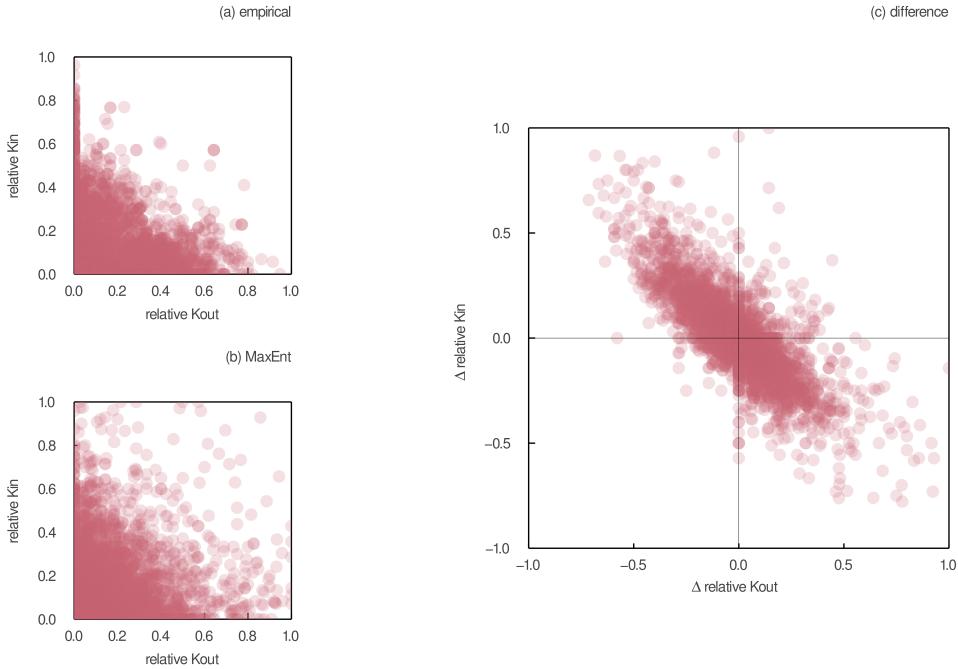


Figure 1: Relative number of predators ( $k_{in}$ ) as a function of their relative number of prey ( $k_{out}$ ) for each species in (a) empirical and (b) joint degree sequences obtained from the analytical MaxEnt model. Empirical networks include most food webs archived on Mangal, as well as the New Zealand and Tuesday Lake datasets (our complete dataset). The predicted joint degree sequences were obtained after sampling one realization of the joint degree distribution of maximum entropy for each network, while keeping the total number of interactions constant. (c) Difference between predicted and empirical values when species are ordered according to their total degrees. In each panel, each dot corresponds to a single species in one of the networks.

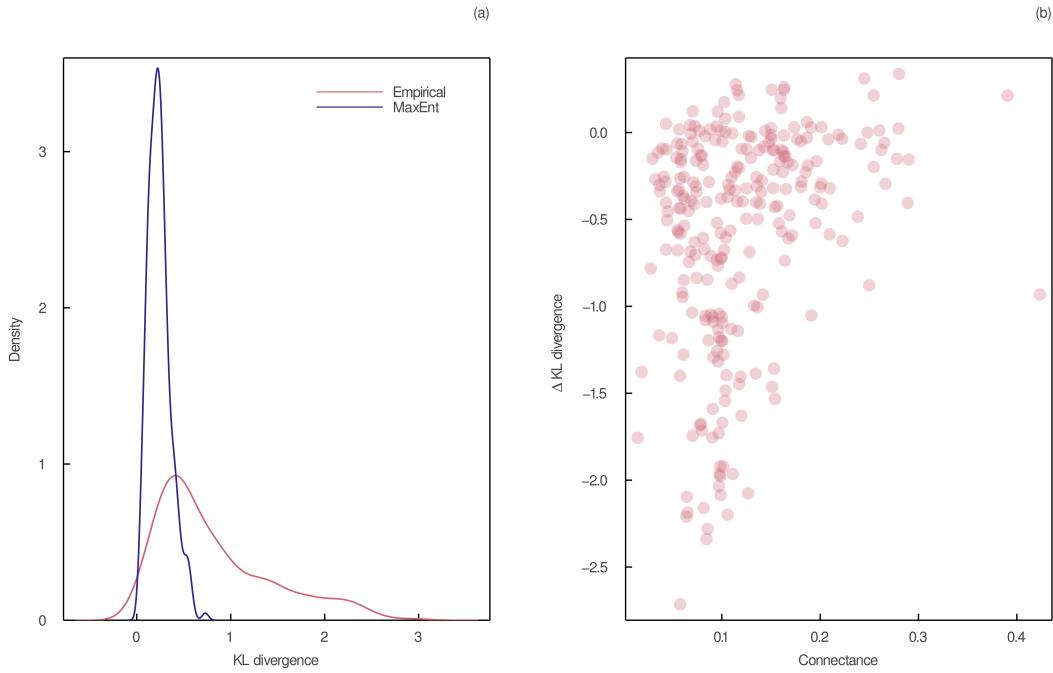


Figure 2: (a) Probability density of KL divergence between in and out-degree sequences of empirical and predicted joint degree sequences. (b) Difference between the KL divergence of empirical and predicted joint degree sequences as a function of connectance. In both panels, empirical networks include most food webs archived on Mangal, as well as the New Zealand and Tuesday Lake datasets (our complete dataset). The predicted joint degree sequences were obtained after sampling one realization of the joint degree distribution of maximum entropy for each network, while keeping the total number of interactions constant.

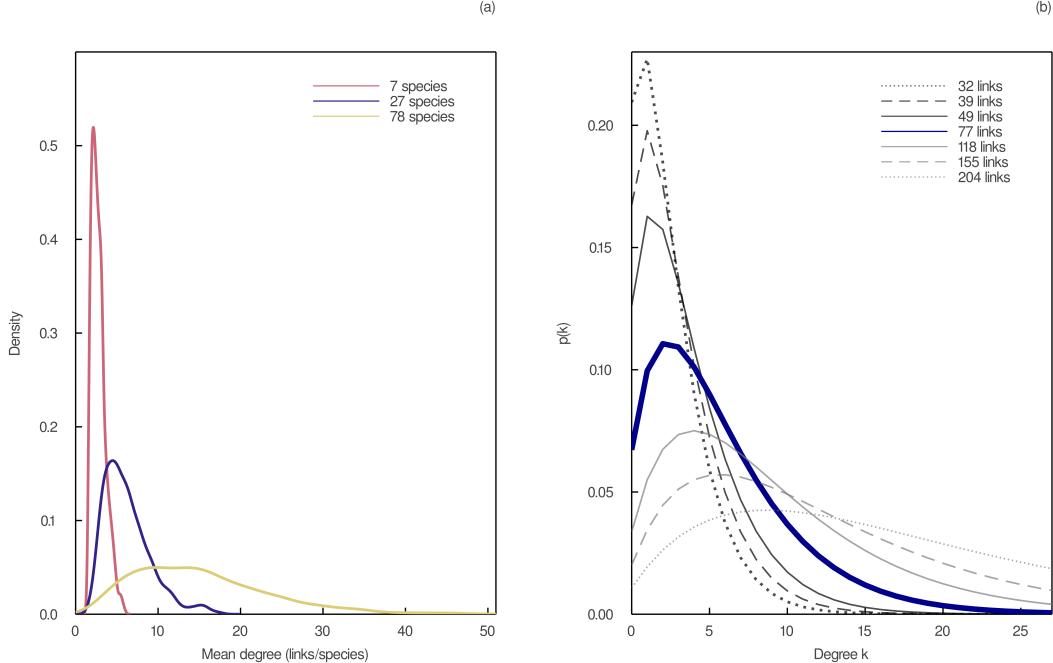


Figure 3: (a) Probability density of the mean degree of a food web obtained using different values of species richness  $S$ . The number of interactions  $L$  was simulated 1000 times using the flexible links model fitted to all empirical networks in our complete dataset (eq. 17). The mean degrees  $2L/S$  were then obtained from these simulated values. (b) Degree distributions of maximum entropy for a network of  $S = 27$  species and different numbers of interactions. The numbers of interactions correspond to the lower and upper bounds of the 67, 89, and 97 percentile intervals (PI), as well as the median (in blue), of the counterfactuals of the flexible links model. Each degree distribution of maximum entropy was obtained using eq. 14 after solving numerically eq. 15 using different values of the mean degree constraint.

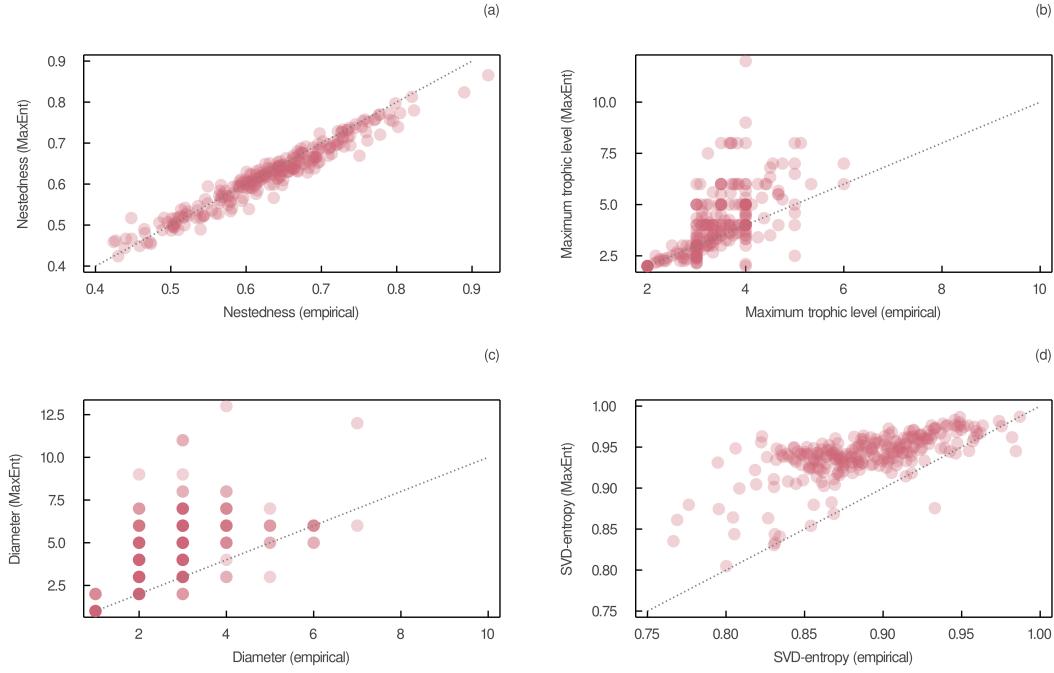


Figure 4: Relationship between the structure of empirical and maximum entropy food webs. Empirical networks include most food webs archived on Mangal, as well as the New Zealand and Tuesday Lake datasets (our complete dataset). Maximum entropy networks were estimated using a simulated annealing algorithm to find the network of maximum SVD entropy while maintaining the joint degree sequence (type II MaxEnt network model). (a) Nestedness (estimated using the spectral radius of the adjacency matrix), (b) the maximum trophic level, (c) the network diameter, and (d) the SVD entropy were measured on these empirical and maximum entropy food webs. The identity line is plotted in each panel.

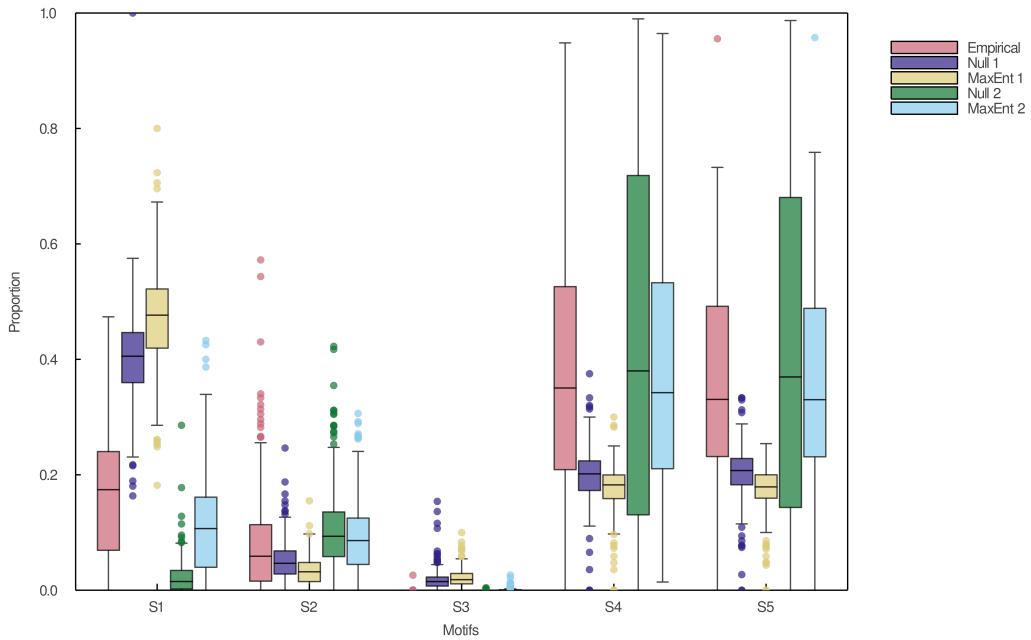


Figure 5: Motifs profile of empirical, maximum entropy, and null food webs. Empirical networks include most food webs archived on Mangal, as well as the New Zealand and Tuesday Lake datasets (our complete dataset). Maximum entropy networks were estimated using a simulated annealing algorithm to find the network of maximum SVD entropy while maintaining the connectance (type I MaxEnt network model) or the joint degree sequence (type II MaxEnt network model). The predictions of the types I and II null models are also plotted. Boxplots display the median proportions of each motif (middle horizontal lines), as well as the first (bottom horizontal lines) and third (top horizontal lines) quartiles. Vertical lines encompass all data points that fall within 1.5 times the interquartile range from both quartiles, and dots are data points that fall outside this range. Motifs names are from Stouffer et al. (2007).

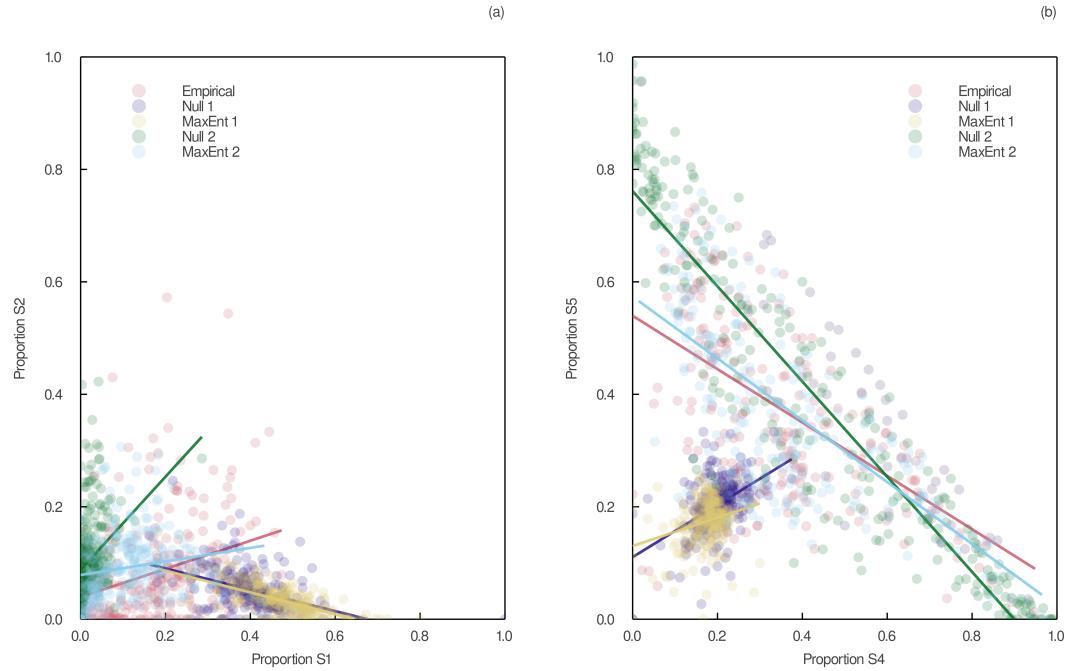


Figure 6: Relationship between motifs proportions of empirical, maximum entropy, and null food webs. Empirical networks include most food webs archived on Mangal, as well as the New Zealand and Tuesday Lake datasets (our complete dataset). Maximum entropy networks were estimated using a simulated annealing algorithm to find the network of maximum SVD entropy while maintaining the connectance (type I MaxEnt network model) or the joint degree sequence (type II MaxEnt network model). The predictions of the types I and II null models are also plotted. Regression lines are plotted in each panel. Motifs names are from Stouffer et al. (2007).