

# The biological interpretation of probabilistic food webs

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Community ecologists are increasingly thinking probabilistically when it comes to food webs and other ecological networks. Assuredly, the benefits of representing ecological interactions as probabilistic events (e.g., how likely are species to interact?) instead of binary objects (e.g., do species interact?) are numerous, from a better assessment of the spatiotemporal variation of trophic interactions to an increase capacity to reconstruct networks from sparse data. However, probabilities need to be used with caution when working with species interactions. Indeed, depending on the system at hand and the method used to build probabilistic networks, probabilities can have different interpretations that imply different ways to manipulate them. At the core of these differences lie the distinction between assessing the likelihood that two groups of individuals *can* interact and the likelihood that they *will* interact. This impacts the spatial, temporal, and taxonomic scaling of interaction probabilities, thus enlightening the need to properly define them in their ecological context. Published data on probabilistic species interactions are poorly documented in the literature, which impedes our ability to use them appropriately. With these challenges in mind, we propose a general approach to thinking about probabilities in regards to ecological interactions, with a strong focus on food webs, and call for better definitions and conceptualizations of probabilistic ecological networks, both at the local and regional scales.

# 1 Introduction

2 Cataloging species interactions across space is a gargantuan task. At the core of this challenge lies the  
3 spatiotemporal variability of ecological networks (Poisot *et al.* 2012, 2015), which makes documenting the  
4 location and timing of interactions difficult. Indeed, it is not sufficient to know that two species have the  
5 biological capacity to interact to infer the realization of their interaction at a specific time and space  
6 (Dunne 2006). Taking food webs as an example, a predator species and its potential prey must first  
7 co-occur in order for a trophic interaction to take place (Blanchet *et al.* 2020). They must then encounter,  
8 which is conditional on their relative abundances in the ecosystem and the matching of their phenology  
9 (Poisot *et al.* 2015). Finally, the interaction occurs only if the predators have a desire to consume their prey  
10 and are able to capture and ingest them (Pulliam 1974). Environmental (e.g. temperature and presence of  
11 shelters) and biological (e.g. physiological state of both species and availability of other prey species)  
12 factors contribute to this variability by impacting species co-occurrence (**Araujo2011UsiSpe?**) and the  
13 realization of their interactions (Poisot *et al.* 2015). In this context, the development of computational  
14 methods in ecology can help alleviate the colossal sampling efforts required to document species  
15 interactions across time and space (Strydom *et al.* 2021). Having a better portrait of species interactions  
16 and the emerging structure of their food webs is important since it lays the groundwork for understanding  
17 the functioning, dynamics, and resilience of ecosystems worldwide (e.g., **Proulx2005NetThi?**;  
18 **Pascual2006EcoNet?**; **Delmas2019AnaEco?**).

19 The recognition of the intrinsic variability of species interactions and the emergence of numerical  
20 methods have led ecologists to rethink their representation of ecological networks, slowly moving from a  
21 binary to a probabilistic view of species interactions (Poisot *et al.* 2016). This has several benefits. For  
22 example, probabilities represent the limit of our knowledge about species interactions and can inform us  
23 about the expected number of interactions and emerging network properties despite this limited  
24 knowledge (Poisot *et al.* 2016). They are also very helpful in predicting the spatial distribution of species  
25 within networks (Cazelles *et al.* 2016) and the temporal variability of interactions (Poisot *et al.* 2015),  
26 generating new ecological data (e.g., Strydom *et al.* 2022), and identifying priority sampling locations of  
27 species interactions (see Andrade-Pacheco *et al.* 2020 for an ecological example of a sampling optimization  
28 problem). Moreover, the high rate of false negatives in ecological network data, resulting from the  
29 difficulty of witnessing interactions between rare species, makes it hard to interpret non-observations of

species interactions ecologically (Catchen *et al.* 2023). Using probabilities instead of yes-no interactions accounts for these observation errors; in that case, only forbidden interactions (Jordano *et al.* 2003; Olesen *et al.* 2010) would have a probability value of zero (but see Gonzalez-Varo & Traveset 2016). Many measures have been developed to describe the structure (Poisot *et al.* 2016) and diversity (Ohlmann2019DivInd?; Godsoe2022SpeInt?) of probabilistic interactions, which shows the potential of this framework in the study of a variety of ecological phenomena.

However, representing species interactions probabilistically can also be challenging. Beyond methodological difficulties in estimating these numbers, there are important conceptual challenges in defining what we mean by “probability of interactions.” To the best of our knowledge, because the building blocks of this mathematical representation of food webs are still being laid, there is no clear definition found in the literature. This is worrisome, since working with probabilistic species interactions without clear guidelines could be misleading as much for field ecologists as for computational ecologists who use and generate these data. In this contribution, we outline different ways to define and interpret interactions probabilities in network ecology and propose an approach to thinking about them. These definitions mostly depend on the study system (e.g. local network or metaweb) and on the method used to generate them. We show that different definitions can have different ecological implications, especially regarding spatial, temporal, and taxonomic scaling. Although we will focus on food webs, our observations and advice can be applied to all types of ecological networks, from plant-pollinator to host-parasite networks. Specifically, we argue that probabilities should be better documented, defined mathematically, and used with caution when describing species interactions.

## Definitions and interpretations

### Food-web representations

The basic unit of food webs and other ecological networks are individuals that interact with each others (e.g., by predation; Elton2001AniEco?), forming individual-based networks. The aggregation of these individuals into more or less homogeneous groups (e.g., populations, species, trophic species, families) allows us to represent networks at broader scales, which impacts the properties and behaviour of these systems (Guimaraes2020StrEco?). A network’s nodes can thus designate distinct levels of organization, whereas the edges linking these nodes can describe a variety of interaction measures. When using a

58 Boolean (yes-no) representation of biotic interactions, the observation that one individual from group (or  
 59 node)  $i$  interacts with another individual from group  $j$  is enough to set the interaction  $A_{i,j}$  to 1. This  
 60 simplified representation of food webs is a highly valuable source of ecological information  
 61 (**Pascual2006EcoNet?**) even though it overlooks important factors regarding interaction strengths.  
 62 These, in turn, can be represented using weighted interactions, which better describe the energy flows,  
 63 demographic impacts or frequencies of interactions between nodes (**Berlow2004IntStr?**;  
 64 **Borrett2019WalPar?**), with  $A_{i,j} \in \mathbb{N}$  or  $\mathbb{R}$  depending on the measure. For example, they can be used to  
 65 estimate the average number of prey individuals consumed by the predators in a given time period. This  
 66 extra amount of ecological information typically comes at a cost of greater sampling effort or data  
 67 requirement in predictive models (Strydom *et al.* 2021), which can lead to high uncertainties when  
 68 building these types of networks. Therefore, important methodological and conceptual decisions must be  
 69 made when sampling and building food webs.

70 The uncertainty and spatiotemporal variability of both types of trophic interactions (Boolean and  
 71 weighted) can be represented probabilistically. On one hand, Boolean interactions follow a Bernoulli  
 72 distribution  $A_{i,j} \sim \text{Bernoulli}(p)$ , with  $p$  being the probability of interactions. The only two possible  
 73 outcomes are the presence ( $A_{i,j} = 1$ ) or absence ( $A_{i,j} = 0$ ) of an interaction between the two nodes.  
 74 Weighted interactions, on the other hand, can follow various probability distributions depending on the  
 75 measure used. In this case, the event's outcome is the value of interaction strength. For instance, weights  
 76 can follow a Poisson distribution  $A_{i,j} \sim \text{Poisson}(\lambda)$  when predicting frequencies of interactions between  
 77 pairs of nodes, with  $\lambda$  being the expected rate of interaction. The definition and interpretation of  
 78 parameters like  $p$  and  $\lambda$  are inextricably linked to environmental and biological factors such as species  
 79 relative abundance, traits, area, and time, depending on the type of interaction. Because Boolean species  
 80 interactions are much more documented in the literature, our primary focus in this contribution will be on  
 81 addressing the challenges in defining and interpreting  $p$  for pairwise species interactions.

82 The first aspect to take into consideration when estimating or interpreting probabilities of interactions is  
 83 knowing if they describe the likelihood of potential or realized interactions. A potential interaction is  
 84 defined as the biological capacity of two species to interact (i.e., the probability that they *can* interact)  
 85 whereas a realized interaction refers to the materialization or observation of this interaction in a delineated  
 86 space and time period (i.e., the probability that they interact). Here, we will use the terms *metaweb* to  
 87 designate networks of potential interactions and *local networks* for those of realized interactions. Frequent

88 confusion arises among ecologists over the use of these two terms, especially in a probabilistic context.  
89 Indeed, in many studies of probabilistic ecological networks, it remains unclear when authors describe  
90 potential or realized interactions, or when so-called probabilities are actually *interaction scores*. Likewise,  
91 probabilistic potential interactions are often used as realized interactions (and conversely), even when the  
92 type of interaction is clearly indicated. We believe that a better understanding of these differences and  
93 concepts would alleviate interpretation errors and help ecologists use these numbers more appropriately.

## 94 **Probabilistic metawebs**

95 Metawebs are networks of potential interactions, representing the probability that two taxa can interact  
96 regardless of biological plasticity, environmental variability or co-occurrence. They are the network  
97 analogue to the species pool, where local networks originate from a subset of both species (nodes) and  
98 interactions (edges). For this reason, they have been initially designed for broad spatial, temporal, and  
99 taxonomic scales (e.g. species food webs at the continental scale). However, in the next section, we argue  
100 that this concept can also be used at smaller scales, with similar ecological meaning.

101 We can express the probability that two taxa  $i$  and  $j$  can interact in a metaweb  $M$  as

$$P_M(i \rightarrow j), \quad (1)$$

102 which is context independent. In other words, the probability that two species can interact is not  
103 contingent on location, time, and environmental factors. Nevertheless, one aspect of a metaweb that could  
104 be conditional on these factors is the list of species (or taxa) it is built from when assembled for a specific  
105 region.

106 Starting from a selected set of species, metawebs can be built using different data sources, including  
107 literature review, field work, and predictive models (e.g., the metaweb of Canadian mammals inferred by  
108 Strydom *et al.* 2022). Every pair of species that has been observed to interact at least once can be given a  
109 probability of interaction of 1; we know that they *can* interact. This means that rare interactions can  
110 technically be given high probabilities in the metaweb. Unobserved interactions, on the other hand, are  
111 given lower probabilities, going as low as 0 for forbidden links. Two important nuances must however be  
112 made here. Because of observation errors due to taxonomic misidentifications and ecological

misinterpretations (e.g., due to cryptic species and interactions; **Pringle2020ResFoo?**), many observations of interactions are actually false positives. Similarly, forbidden interactions can be false negatives if e.g. they have been assessed for specific phenotypes, locations or time. Implementing a Bayesian framework, which updates prior probabilities of interactions with empirical data, could lessen these errors.

## Probabilistic local networks

As opposed to metawebs, probabilistic local food webs represent the likelihood that two species will interact at a specific location and within a given time period; in other words, they are context dependant. To be specific, space is defined here as the geographic coordinates  $(x, y)$  of the spatial boundaries delineating the system, whereas time is the time interval  $t$  during which interactions were sampled or for which they were predicted. We want to point out that they are not single values, but rather continued dimensions that could be outlined differently depending on the study system. Regardless of how they were defined, they always delineate a specific area  $A$  and duration  $t$ . These could refer to the sampled area and duration or to the targeted location and time period.

Many factors could be taken into consideration when estimating the probability that a predator species  $i$  interacts with a given prey species  $j$  locally. One of the most important is species co-occurrence  $C$ , which is a Boolean describing if both species can be found at location and time  $(x, y, t)$ . Surely, the probability that the interaction is realized must be 0 when species do not co-occur ( $C = 0$ ). Interaction probabilities can also be conditional on other biological and environmental variables, such as temperature, precipitation, presence of shelters, phenotypic plasticity, phenology, and presence of other interacting species in the network. These conditions can affect species traits, which greatly impact the capacity of species to interact (Poisot *et al.* 2015). Similarly, species relative abundance is another important predictor of the probability of interaction, because it impacts the probability that species will randomly encounter (Poisot *et al.* 2015; **Canard2012EmeStr?**; **Canard2014EmpEva?**). Here, we will use the variable  $\Omega$  as a substitute for the biological and ecological context in which interaction probabilities were estimated. This gives us the following equation for the probability of realized interaction between species (or taxa)  $i$  and  $j$  in a local network  $N$ :

$$P_N(i \rightarrow j|A, t, C, \Omega), \quad (2)$$

139 which can be read as the probability of local interaction between the two species in an area  $A$  and time  
140 interval  $t$ , given their co-occurrence  $C$  and specific environmental and biological conditions  $\Omega$ .

141 Multiple difficulties of interpretation arise when the conditions are not clearly specified, which we found  
142 is often the case in the literature. For example, if  $P_N(i \rightarrow j|C = 1)$  represents the probability that two  
143 co-occurring species interact (i.e., the edge's probability value),  $P_N(i \rightarrow j)$  denotes instead the probability  
144 of interaction without knowing if they co-occur (i.e., the product of the nodes and edge's probability  
145 values). For practical reasons, probabilistic ecological networks are generally represented as matrices of  
146 probabilities (i.e., matrices of edges without node values), whose elements are thus hard to interpret  
147 without clear indications about  $C$ . Overall, when probabilities of interactions are estimated using specific  
148 values of  $A$ ,  $t$ ,  $C$ , and  $\Omega$ , ecologists should make them explicit in their metadata, preferably using  
149 mathematical equations to avoid any ambiguity. Below, we will see examples of why this matters when it  
150 comes to spatial, temporal, and taxonomic scaling of biotic interactions.

151 [Table 1 about here]. Articles using probabilistic interactions and the definitions and variables they  
152 considered.

### 153 **From potential to realized interactions**

154 Even though the spatiotemporal variability of interactions is not considered in metawebs, they can still be  
155 useful to reconstruct local networks of realized interactions. Indeed, local networks are formed from  
156 subsets of their metaweb (called subnetworks), which are obtained by selecting a subset of both species  
157 and interactions (Dunne 2006). Because a community's composition is arguably easier to sample (or  
158 predict) than its interactions, the biggest challenge is to sample links from the metaweb. This becomes a  
159 conceptual issue when we consider how potential and realized interactions differ. Despite these concerns,  
160 metawebs remain an important source of ecological information that can be leveraged for realistically  
161 predicting spatially explicit networks. First, metawebs set the upper limit of species interactions (McLeod  
162 *et al.* 2021), i.e. the probability that two species interact at a specific location is always lower or equal to  
163 the probability of their potential interaction:

$$P_N(i \rightarrow j|A, t, C, \Omega) \leq P_M(i \rightarrow j). \quad (3)$$



Therefore, inferring local networks from their metaweb keeping the same values of interaction probability would generate systematic biases in the prediction. In that case, these networks would instead be called *spatially explicit* or *local* metawebs (i.e., smaller-scale networks of potential interactions). Second, the structure of local networks is constrained by the one of their metaweb (Saravia2022EcoNet?). This suggests that a metaweb not only constrains the pairwise interactions of its corresponding local networks, but also their emerging properties. Inferring the structure of local networks from the metaweb could thus help estimate more realistically the likelihood that potential interactions are realized and observed locally (Strydom *et al.* 2021).

[Figure 1 about here]. Empirical example of the association between the number of interactions in realized local food webs and the number of interactions in the corresponding subnetworks of their regional metaweb. We should expect the association to be linear below the 1:1 line, illustrating eq. 3.

## Scaling

### Spatial and temporal scales

Metawebs and local networks intrinsically differ in their relation to scale. On one hand, as mentioned above, probabilistic metawebs are context independent, i.e., probabilistic pairwise interactions do not scale with space and time because they depend solely on the biological capacity of the two taxa to interact. This implies that the estimated likelihood that two species can potentially interact should be the same among all metawebs in which they are present. In practice, this is rarely the case because ecologists use different methods and data to estimate these probabilities of interactions. However, in the case where local metawebs  $M_{x,y}$  are subsampled from their regional counterpart  $M_0$ , we should expect edge values to be identical among all networks, regardless of their spatial scale, i.e.  $P_{M_{x,y}}(i \rightarrow j) = P_{M_0}(i \rightarrow j)$ . On the other hand, local probabilistic networks are indissociable from their spatial and temporal contexts because there are more opportunities of interactions (e.g., more individuals, more trait variations, more chance of encounter) in a larger area and longer time period (McLeod *et al.* 2020). Let  $N_0$  be a local probabilistic food web delineated in an area  $A_0$  and  $N_1$  a network of area  $A_1 < A_0$  within  $A_0$ . We should expect the probability that  $i$  and  $j$  interacts to scale spatially, i.e.  $P_{N_1}(i \rightarrow j | A < A_0) \leq P_{N_0}(i \rightarrow j | A = A_0)$ . Similarly, the temporal scaling of probabilistic local food webs could be manifested through the effect of sampling effort on the observation of interactions (McLeod *et al.* 2021; Jordano2016Samplinga?) or of time itself

on their realization (Poisot *et al.* 2012). There are many network-area relationships (e.g., Wood *et al.* 2015; Galiana *et al.* 2018) and interaction accumulation curves (e.g., Jordano2016Samplinga?) explored in the literature. These could inspire the development and testing of different equations describing the spatiotemporal scaling of probabilistic pairwise interactions in local networks, which are over the scope of this manuscript.

Another conceptual challenge encountered when using probabilistic food webs is the prediction of Boolean networks across space. Lets take  $n \times n$  grid cells each representing a probabilistic food web. If they contain potential interactions, a single random trial must be conducted for each pairwise interaction across the region (i.e., we should have only one random realization of the regional metaweb). On the contrary, if they represent probabilities of realized interactions, each food web must be independently sampled (i.e.,  $n^2$  independent random draws). This has direct implications on the spatial scaling of interactions. For example, let  $N_2$  be another network of area  $A_2 < A_0$  within  $A_0$  and disjoint from  $N_1$ , such as  $N_1$  and  $N_2$  form  $N_0$  (think of two contiguous cells that together delineate  $N_0$ ). All other things being equal, we should expect the probability that  $i$  and  $j$  interacts in  $A_0$  to be  $P_{N_0}(i \rightarrow j) = 1 - (1 - P_{N_1}(i \rightarrow j)) \times (1 - P_{N_2}(i \rightarrow j))$  if  $N_1$  and  $N_2$  are independently sampled. This also implies that we should expect interactions to be realized in a certain number of local networks depending on the probability value, which is not the case with metawebs. Note that spatial auto-correlation and the concept of meta-network (i.e., networks of networks) could invalidate the statistical assumption of independence. Nevertheless, the fundamental difference in sampling metawebs and local networks stands even when considering these factors. This difference in sampling further sheds light on the importance of clearly defining interaction probabilities. What we consider as a *Bernoulli trial*, when randomly drawing deterministic networks from probabilistic food webs, depends on our biological interpretation of these probabilities.

- Making interaction probabilities spatiotemporally explicit

[Figure 2 about here]. Conceptual figure showing (1) the spatiotemporal scaling of probabilistic metawebs and local food webs and (2) the spatial sampling of metawebs and local food webs into Boolean networks.

## Taxonomic scale

How do interaction probabilities scale taxonomically?

- There are different biological interpretations of probabilities in food webs at the individual level and at higher taxonomic levels.
- How does the scaling up of the nodes from an individual to population to any higher taxonomic group change our interpretation of interaction probabilities? How does the aggregation change our interpretation?
- How is it similar and different to spatial and temporal scaling? Basically, all kinds of scaling are just different ways to aggregate individuals or nodes.

[Figure 3 about here]. Conceptual figure of how a scale up of the nodes from an individual to a population to any higher taxonomic group change our interpretation of the probability of interaction.

## Conclusion

The emergence of probabilistic thinking in network ecology has paved the way to a better assessment of the spatiotemporal variability and uncertainty of biotic interactions. However, we showed that network metadata are perhaps as important as interaction data themselves when it comes to interpreting probabilistic food webs in ecological terms. First, the type of probabilistic interaction (potential or realized) impacts the importance of scale, with interactions in metawebs being scale independent, both spatially and temporally. Second, the conditions in which local networks were estimated (e.g., area, time, biological and environmental factors) and the attributes of the interacting species that were considered (e.g., species co-occurrence) are essential contextual factors that impact the mathematical representation of probabilities and their resulting behaviour. Third, the biological interpretation of probabilities changes with the level of organization of the network due to the aggregation of individuals into broader groups. All these information should be available as clear metadata so that ecologists can use probabilistic network data appropriately.

Moreover, many statistical models in ecology that yield accurate predictions of biotic interactions are black boxes difficult to interpret. Ecologists should be careful before using the output of these models as probabilistic objects, since there is often a thin line between a real probability and a non-probabilistic predictive number (or score). Probabilities are numbers between 0 and 1 that sum to 1 and either represent the expected frequency of a phenomenon or the degree of belief that it will be realized. Non-probabilistic

247 scores, which are more akin to interaction weights, have different mathematical properties, which impacts  
248 how we should handle these numbers in a spatially or temporally explicit context. Therefore, researchers  
249 should use their expertise to assess if their interaction data are actually probabilities or scores. This should  
250 also be added to the metadata before sharing them, as well as the methods used to build the networks.

251 Better metadata documentation would allow researchers to use and manipulate probabilistic ecological  
252 interactions according to how they were actually defined and obtained. This would support better  
253 scientific practices, in particular when these data are used for ecological prediction and forecasting. For  
254 instance, we showed that building a rigorous workflow to predict local networks from a probabilistic  
255 metaweb requires a good understanding of the data at hand. Similarly, explicitly stating the context in  
256 which probabilistic data were estimated would help using forecasting food-web models more rigorously  
257 under specific climate change and habitat use scenarios. Regardless of the method and application,  
258 fostering a better foundation for probabilistic reasonings in network ecology, from the very nature of  
259 probabilities and biotic interactions, is essential.

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