

# The ecological interpretation of probabilistic networks

Francis Banville<sup>1,2,3,‡</sup> Tanya Strydom<sup>1,3,‡</sup> Timothée Poisot<sup>1,3</sup>

<sup>1</sup> Université de Montréal <sup>2</sup> Université de Sherbrooke <sup>3</sup> Quebec Centre for Biodiversity Science

‡ Equal contributions

## Correspondance to:

Francis Banville — [francis.banville@umontreal.ca](mailto:francis.banville@umontreal.ca)

The stochastic nature of ecological interactions has led many biologists to adopt a probabilistic view of ecological networks. Representing species interactions probabilistically (how likely are they to interact?) as opposed to deterministically (do they interact?) allows a better assessment of their spatiotemporal variability and accounts for inherent uncertainties in observations and predictions. However, despite this growing interest in probabilistic networks, general guidelines regarding the estimation and documentation of probabilistic interaction data are still lacking. This is concerning given that their biological interpretation and statistical manipulation are contingent upon the methods and variables used to estimate them. In this contribution, we review how probabilistic interactions are defined in the literature at different spatial scales, from local interactions to regional networks (metawebs), with a strong emphasis on food webs. These definitions are based on the distinction between the realization of an interaction at a specific time and space and its biological feasibility. We show that different network representations have different statistical behaviours when it comes to common ecological applications. Specifically, we argue that local probabilistic networks and metawebs differ in their spatial and temporal scaling of interactions, with potential interactions being scale-independent. This is in contrast with the taxonomic scaling of interactions, which does not qualitatively differ between both types of networks. Moreover, we suggest two approaches to sampling deterministic networks from probabilistic webs that account for these differences and argue that systematic biases arise when directly inferring local networks from subsets of metawebs. To support our arguments, we built a spatiotemporally explicit model of probabilistic interactions and developed different case studies using empirical and simulated data. Overall, our results emphasize the need for better documentation of probabilistic ecological networks, both at the local and regional scales, to inform the appropriate reuse of these data.

Last revision: *September 5, 2023*

# 1 Introduction

2 Cataloging ecological interactions is a gargantuan task. Regardless of sampling effort, there are practical and  
3 biological constraints that hinder our ability to observe all interactions in nature, such as the spatial and  
4 temporal uncoupling of species and the large number of potential interactions in a community, of which the vast  
5 majority are rare (Jordano 2016). Documenting the location and timing of interactions becomes even more  
6 challenging when accounting for the spatiotemporal variability of ecological networks (Poisot *et al.* (2012),  
7 Poisot *et al.* (2015)). Indeed, it is now recognized that knowing the biological capacity of two species to interact  
8 is necessary but not sufficient for inferring their interaction at a specific time and space. For example, Golubski  
9 & Abrams (2011) presented many cases where trophic interactions in food webs depend on the presence or  
10 abundance of a third species (e.g., of a more profitable prey species). More generally, a handful of conditions  
11 must be satisfied for an interaction to be observed locally. First, both species must have overlapping geographic  
12 ranges, i.e. they must co-occur within the region of interest (Blanchet *et al.* 2020). Then, they must encounter  
13 locally. Probabilities of interspecific encounters are typically low, especially for rare species with low relative  
14 abundances (Canard *et al.* 2012). Finally, their traits must be locally compatible (Poisot *et al.* 2015). This  
15 includes their phenology (Olesen *et al.* (2010), Singer & McBride (2012)), behavioral choices (Pulliam (1974),  
16 Choh *et al.* (2012)) and phenotypes (Bolnick *et al.* (2011), Stouffer *et al.* (2011), Gravel *et al.* (2013)).  
17 Environmental factors, such as temperature (Angilletta *et al.* 2004), drought (Woodward *et al.* 2012), climate  
18 change Araujo *et al.* (2011), and habitat modifications (Tylianakis *et al.* 2007), contribute to this spatiotemporal  
19 variability of interactions by impacting species abundance and traits. In this context, it is unsurprising that our  
20 knowledge of ecological interactions remains limited (Hortal *et al.* 2015) despite extensive biodiversity data  
21 collection (Schmeller *et al.* 2015).

22 The recognition of the intrinsic variability of species interactions has led ecologists to expand their  
23 representation of ecological networks to include a probabilistic view of interactions (Poisot *et al.* 2016). As  
24 opposed to binary deterministic networks, in which interactions are either observed or not, probabilistic  
25 networks represent our degree of belief about the realization or feasibility of pairwise interactions at the local or  
26 regional scale, respectively. In other words, representing interactions probabilistically considers inherent  
27 uncertainties and observation errors associated with ecological data. In the broadest sense, binary networks are  
28 also a type of probabilistic network, in which the value of interactions is restrained to 0 (non-observed) or 1  
29 (observed). In probabilistic networks, only forbidden interactions Olesen *et al.* (2010) have a probability value

of zero (but see Gonzalez-Varo & Traveset 2016). However, *neutral* forbidden interactions (i.e., improbable interactions between rare species, Canard *et al.* 2012) could have low probability values in a local network but high probability in a regional network (metaweb) describing the biological capacity of species to interact.

By accounting for the uncertainty of interactions, probabilistic networks provide a more realistic portrait of species interactions and their emerging structure. This is important given that network structure is one of the major drivers of the functioning, dynamics, and resilience of ecosystems worldwide Rooney & McCann (2012). Moreover, the application and development of computational methods in network ecology, which are often based on a probabilistic representation of interactions, can help alleviate the colossal sampling efforts required to document species interactions (Strydom *et al.* 2021). For example, statistical models can be used to estimate the uncertainty of pairwise interactions (Cirtwill *et al.* 2019) and the probability of missing (false negatives) and spurious (false positives) interactions (Guimerà & Sales-Pardo 2009). Considering the high rate of false negatives in species interaction data due to the difficulty of witnessing rare interactions (Catchen *et al.* 2023), these models can inform the identification of priority sampling locations of ecological networks (e.g., Andrade-Pacheco *et al.* 2020 present an approach to identify priority sampling locations of disease hotspots). Statistical models can also be used to generate network predictions without prior knowledge of pairwise interactions, for instance using body size Gravel *et al.* (2013), phylogeny Strydom *et al.* (2022), or a combination of niche and neutral processes Pomeranz *et al.* (2019) for inference. Topological null models Fortuna & Bascompte (2006), which can be used to generate underlying distributions of network measures for null hypothesis significance testing, are other examples of common probabilistic network models. Many measures have been developed to describe the structure (Poisot *et al.* 2016) and diversity Godsoe *et al.* (2022) of probabilistic networks. These models and measures support the use of this approach for the study of a wide range of ecological questions, from making better predictions of species distribution (Cazelles *et al.* 2016) to forecasting the impact of climate change on ecological networks (Gilman *et al.* 2010).

Despite these advances and opportunities, the lack of clear guidelines on the use of probabilistic interaction data is worrisome, especially for field and computational ecologists who manipulate and generate these numbers. Indeed, beyond methodological challenges encountered when evaluating them, there are important and perhaps more fundamental conceptual challenges when it comes to defining them. To the best of our knowledge, there is currently no data standard that could guide the estimation and documentation of interaction probabilities (Salim *et al.* 2022 discuss data standards for deterministic mutualistic networks). General guidelines could support more adequate manipulation and integration of interaction data from different sources and prevent ecologists

60 from being misled by ambiguous and often diverging interpretations of probabilistic networks. In this  
61 contribution, we aim to take a step back by outlining different ways in which they were defined and used in  
62 network ecology and propose an approach to thinking about them. We distinguish two broad categories of  
63 probabilistic networks that have different statistical behaviors when applied to key ecological questions: local  
64 networks of realized interactions and regional networks (metawebs) of potential interactions. We show that  
65 these representations have different ecological and statistical implications, especially regarding the spatial and  
66 temporal scaling of interactions and the prediction of binary networks across space. Although we focus on food  
67 webs, our observations and advice can be applied to most types of ecological networks, from plant-pollinator to  
68 host-parasite networks. Indeed, excepting networks of indirect interactions such as competition and facilitation  
69 networks Kéfi *et al.* (2016), most ecological networks describe probabilities of direct interactions, which are  
70 conceptually and mathematically analogous to each other regardless of their biological type (e.g., trophic and  
71 parasitic interactions). Overall, we argue that probabilistic networks should be better documented, clearly  
72 defined in mathematical terms, and used with caution when analyzing ecological interactions.

## 73 **Probabilistic representations of interactions**

74 One of the first aspects to take into consideration when estimating or interpreting probabilities of interactions is  
75 knowing if they describe potential or realized interactions. A potential interaction is defined as the biological  
76 capacity of two taxa to interact (i.e., the probability that they *can* theoretically interact) whereas a realized  
77 interaction refers to the materialization or observation of this interaction in a delineated space and time (i.e., the  
78 probability that they interact locally). Here, we use the terms *metaweb* to designate networks of potential  
79 interactions and *local networks* for those of realized interactions. Metawebs are the network analog of the  
80 species pool, where local networks originate from a subset of both species (nodes) and interactions (edges) of  
81 the regional metaweb (Saravia *et al.* 2022). Frequent confusion arises among ecologists over the use of these  
82 two terms, especially in a probabilistic context. Indeed, it can be difficult to know when published probabilistic  
83 networks describe potential or realized interactions, or when so-called probabilities are in reality *interaction*  
84 *scores* (i.e., a type of non-probabilistic quantitative interactions). Likewise, probabilistic potential interactions  
85 are often used and interpreted as realized interactions (and conversely), which may generate misleading findings  
86 when analyzing these data. We believe that a better understanding of the differences, similarities, and  
87 relationships between these two probabilistic representations of ecological networks would alleviate

88 interpretation errors and help ecologists use these numbers more appropriately.

## 89 **Pairwise interactions: the building blocks of ecological networks**

90 Local ecological networks and metawebs, like any type of network, are made of nodes and edges that can be  
91 represented at different levels of organization and precision. The basic unit of food webs and other ecological  
92 networks are individuals that interact with each other (e.g., by predation, Elton (2001)), forming  
93 individual-based networks. The aggregation of these individuals into more or less homogeneous groups (e.g.,  
94 populations, species, trophic species, families) allows us to represent nodes at broader taxonomic scales, which  
95 impacts our interpretation of the properties and behavior of these systems (Guimarães 2020). Moreover, edges  
96 linking these nodes can describe a variety of interaction measures. Ecologists have traditionally represented  
97 interactions as binary objects that were considered realized after observing at least one individual from group  $i$   
98 interact with at least another individual from group  $j$ . Boolean interactions are actually the result of a Bernoulli  
99 process  $A_{i,j} \sim \text{Bernoulli}(P(i \rightarrow j))$ , with  $P(i \rightarrow j)$  being the probability of interaction between  $i$  and  $j$  that  
100 characterizes our limited knowledge of the system and its intrinsic spatiotemporal variability. Depending on the  
101 type of networks (local or metaweb), the mathematical formulation and interpretation of stochastic parameters  
102 like  $P(i \rightarrow j)$  can be linked to environmental and biological factors such as species relative abundance, traits,  
103 area, and time (tbl. 1). In these probabilistic network representations in which  $P(i \rightarrow j)$  are edge values, the only  
104 two possible outcomes are the presence ( $A_{i,j} = 1$ ) or absence ( $A_{i,j} = 0$ ) of an interaction between each pair of  
105 nodes. Observing an interaction between two taxa at a given location and time provides important information  
106 that can be used to update previous estimates of  $P(i \rightarrow j)$ , informing us on the biological capacity of both taxa  
107 to interact and the environmental conditions that enabled them to interact locally.

108 Even though binary networks constitute a highly valuable source of ecological information (Pascual *et al.*  
109 2006), they overlook important factors regarding interaction strengths. These are represented using quantitative  
110 interactions, which better describe the energy flows, demographic impacts or frequencies of interactions  
111 between nodes Borrett & Scharler (2019), with  $A_{i,j}$  being a natural number  $\mathbb{N}$  or a real number  $\mathbb{R}$  depending on  
112 the measure. For example, they can represent the average number of prey individuals consumed by a predator in  
113 a given time period (e.g., the average number of fish in the stomach of a piscivorous species). Because  
114 quantitative interactions can describe predation pressure on prey taxa, they can be good estimators of the  
115 parameters describing species interactions in a Lotka-Volterra model (e.g., Emmerson & Raffaelli 2004).  
116 However, this extra amount of ecological information typically comes at a cost of greater sampling effort or data

117 requirement in predictive models (Strydom *et al.* 2021), which can lead to relatively high levels of uncertainties  
 118 when inferring quantitative networks with limited data. Just like binary networks, the uncertainty and  
 119 spatiotemporal variability of quantitative interactions can be represented probabilistically, with the difference  
 120 that quantitative interactions can follow various probability distributions depending on the measure used, the  
 121 event's outcome being the value of interaction strength. For instance, quantitative interactions can follow a  
 122 Poisson distribution  $A_{i,j} \sim \text{Poisson}(\lambda_{i \rightarrow j})$  when predicting frequencies of interactions between pairs of nodes,  
 123 with  $\lambda_{i \rightarrow j}$  being the expected rate at which individuals of taxa  $i$  and  $j$  interact (e.g., the average number of prey  $j$   
 124 consumed by all predators  $i$ ). The Poisson distribution can also be 0-inflated when considering non-interacting  
 125 taxa, which constitute the majority of taxa pairs in most local networks due to their typically high sparseness  
 126 (Jordano 2016). Because of the methodological difficulties typically encountered when building deterministic  
 127 quantitative networks, binary networks, which are easier to sample (Jordano 2016) and predict (Strydom *et al.*  
 128 2021), are much more documented and modeled in the literature. Moreover, most published probabilistic  
 129 networks and methods describe Bernoulli interactions, which underlines the need for better guidelines regarding  
 130 the interpretation and manipulation of these types of networks. For these reasons, our primary focus in this  
 131 contribution will be on addressing the challenges in estimating and using Bernoulli interactions, in both  
 132 probabilistic local networks and metawebs.

### 133 **Local networks: communities interacting in space and time**

134 As opposed to metawebs, probabilistic local networks describe how likely taxa are to interact at a given location  
 135 and time period (i.e., they are context-dependent). In local networks, edges commonly represent our degree of  
 136 belief that two taxa interact in nature, but can also document the probability of *observing* this interaction  
 137 (Catchen *et al.* 2023). For example, Kopelke *et al.* (2017) assembled a dataset of binary local European food  
 138 webs of willow-galling sawflies and their natural enemies, clearly referencing each food web in space and time.  
 139 Because of its large number of replicated samples, this dataset can be used to infer the probability of locally  
 140 observing an interaction between any pair of taxa by measuring the proportion of sites where an interaction was  
 141 observed (Gravel *et al.* 2019). More generally, we define space as the geographic coordinates  $(x, y)$  of the  
 142 spatial boundaries delineating the system (sampled or targeted) and time as the time interval during which  
 143 interactions were sampled or for which they were predicted. Given that space and time are in reality continuous  
 144 variables, the probability that an interaction occurs within a particular spatial and temporal setting is given by  
 145 the integral of the probability density function describing the relative likelihood that this interaction is realized

146 at any specific and infinitely small location and time. Therefore, the edge value could represent a probability  
 147 density or a probability mass depending on how space and time are measured. For simplicity reasons, we will  
 148 consider space and time as discrete dimensions that provide actual probabilities of interactions, which is  
 149 conform to how ecological interactions are usually sampled. Using space and time intervals allows us to  
 150 measure an area  $A$  and duration  $t$ , which can be directly used in spatiotemporal analyses of ecological networks.  
 151 For example, when studying network-area relationships (NAR, Galiana *et al.* 2018), we should expect local  
 152 probabilities of interactions to scale with area and duration because taxa have more opportunities to interact.  
 153 The probability that two taxa  $i$  and  $j$  interact locally can also be conditional on many environmental and  
 154 biological factors. One of these is their co-occurrence  $C_{i,j}$ , which is usually a Boolean describing if the  
 155 geographic distribution of both taxa overlaps within the study area. In local networks, the probability that the  
 156 interaction is realized must be 0 when taxa do not co-occur, i.e.  $P_N(i \rightarrow j|C = 0) = 0$ . Co-occurrence can also  
 157 be modeled probabilistically. In that case, it follows a Bernoulli distribution  $C_{i,j} \sim \text{Bernoulli}(P_{i,j}(x, y))$ , where  
 158 the probability of co-occurrence  $P_{i,j}(x, y)$  can be estimated using species distribution models (e.g., Pollock *et*  
 159 *al.* 2014). More generally, the probability that two taxa interact locally can be obtained by the product of their  
 160 probability of interaction given co-occurrence with their probability of co-occurrence:

$$P_N(i \rightarrow j) = P_N(i \rightarrow j|C = 1) \times P_{i,j}(x, y). \quad (1)$$

161 Other important factors that can impact our estimation of interaction probabilities at the local scale are taxa  
 162 relative abundance (Canard *et al.* 2012) and traits (Poisot *et al.* 2015), as well as environmental factors such as  
 163 temperature (Angilletta *et al.* 2004), precipitation (Woodward *et al.* 2012), habitat structure (Klecka & Boukal  
 164 2014), and presence of other interacting taxa in the network Kéfi *et al.* (2012). Here, we will use the variable  $\Omega$   
 165 to describe the biological and ecological context in which interaction probabilities were estimated. For example,  
 166 if a research team conducts a mesocosm experiment to estimate interaction probabilities between predators and  
 167 prey with and without shelters,  $\Omega$  would represent the presence or absence of these shelters. Like  
 168 co-occurrence,  $\Omega$  can also be modeled probabilistically when the stochasticity or uncertainty of environmental  
 169 and biological factors is considered. In sum,  $\Omega$  represents all ecological and biological variables that were taken  
 170 into consideration when measuring interaction probabilities and is, therefore, a subset of all factors actually  
 171 impacting ecological interactions.

172 The probability that two taxa  $i$  and  $j$  interact in a local network  $N$  can thus be conditional on the area  $A$ , the time



173 interval  $t$ , their co-occurrence  $C$  and chosen environmental and biological conditions  $\Omega$ . This gives us the  
 174 following equation when all these conditions are included in the estimation of interaction probabilities:

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

175 The local context in which probabilities are estimated and the variables that should be taken into consideration  
 176 depend on the study system, the objective of the study, and the resources available to the researchers. In other  
 177 words, these variables do not systematically need to be accounted for. However, when they are, they should be  
 178 specified in the documentation of the data, preferentially in mathematical terms to avoid any confusion in their  
 179 interpretation and to limit manipulation errors during their re-use. For example, ecologists should be explicit  
 180 about their consideration of co-occurrence in their estimation of local interaction probabilities. Indeed, it is  
 181 important to specify if probability values are conditional  $P_N(i \rightarrow j|C = 1)$  or not  $P_N(i \rightarrow j)$  on co-occurrence  
 182 since this can significantly impact the interpretation and analysis of the data. In tbl. 1, we present a handful of  
 183 studies of probabilistic ecological networks and their formulation of probabilistic interactions. This table  
 184 illustrates the variety of definitions of probabilistic interactions found in the literature and emphasizes the need  
 185 to carefully describe interaction data before integrating and analyzing them.

Table 1: Interaction probabilities are interpreted differently in metawebs and local networks. Each formula includes different conditional variables and is described in plain text. A non-exhaustive list of studies using these formulas is included, with the variables used specified in parentheses.

Formula	Description	Studies
$P_M(i \rightarrow j)$	probability that the interaction is biologically feasible	
$P_N(i \rightarrow j)$	probability that the interaction is realized locally	
$P_N(i \rightarrow j A)$	probability that the interaction is realized locally given network area	
$P_N(i \rightarrow j t)$	probability that the interaction is realized locally given duration	
$P_N(i \rightarrow j C)$	probability that the interaction is realized locally given co-occurrence	
$P_N(i \rightarrow j \Omega)$	probability that the interaction is realized locally given chosen environmental and biological factors	

Formula	Description	Studies
$P_N(i \rightarrow j A, t, C, \Omega)$	probability that the interaction is realized locally given many conditional factors	

## Metawebs: regional catalogs of interactions

Metawebs are networks of potential interactions that have been designed for broad spatial, temporal, and taxonomic scales (e.g., species food webs at the continental scale). They represent the probability that two taxa can biologically interact regardless of their co-occurrence and local environmental conditions. Indeed, potential interactions are by definition context-independent, i.e. they are not measured at a specific location and time. In contrast with probabilistic local networks, which represent the stochasticity of interactions occurring in nature, probabilistic metawebs measure our degree of belief in the capacity of two taxa to interact (i.e., the probability that their traits could support an interaction in the right conditions). In other words, potential interactions describe the probability that there exists at least one combination of phenotypes of taxa  $i$  and  $j$  that can interact with each other if they were to encounter. This probability of interaction, in a metaweb  $M$ , can be expressed as

$$P_M(i \rightarrow j), \quad (3)$$

which, in contrast with eq. 2, is not conditional on any spatial, temporal, or environmental variables (tbl. 1).

Starting from a selected set of taxa, which are usually distributed within a broad region of interest, metawebs can be built using different data sources, including literature review, fieldwork, and predictive models (e.g., the metaweb of Canadian mammals inferred by Strydom *et al.* 2022). Every pair of taxa that have confidently been observed to interact at least once can be given a probability of 1 (i.e.,  $P_M(i \rightarrow j) = 1$ ) since we know that they *can* interact. This is usually not the case in local probabilistic networks, in which probabilities usually remain stochastic (i.e.,  $P_N(i \rightarrow j) < 1$ ) after empirically observing interactions because of their intrinsic spatiotemporal variability. Similarly, although rare interactions typically have low probabilities in local networks, they can have high probabilities in metawebs if the traits of both taxa match. On the other hand, interactions that were never observed can have low probability values in both metawebs and local networks, going as low as 0 for forbidden links. However, because of observation errors due to taxonomic misidentifications and ecological misinterpretations (e.g., due to cryptic species and interactions, Pringle & Hutchinson (2020)), many

208 observations of interactions are actually false positives. Similarly, forbidden interactions can be false negatives  
209 in metawebs, e.g. if they have been assessed for specific phenotypes, locations or time. Implementing a  
210 Bayesian framework, which updates prior probabilities with empirical data (e.g., Bartomeus *et al.* (2016),  
211 Cirtwill *et al.* (2019)), could improve our estimation of interaction probabilities in both systems.

## 212 **Statistical behaviors of probabilistic networks**

213 The differences in the mathematical formulations of local and potential interactions can affect their statistical  
214 behaviors when applied to key ecological questions. These disparities must therefore be taken into account  
215 when analyzing probabilistic interaction data to prevent misleading results and minimize interpretation errors.  
216 Here we show four common applications of probabilistic interactions and compare the characteristics of local  
217 networks and metawebs using simulated and empirical data.

## 218 **Taxonomic scaling of interactions**

219 Probabilistic networks can be used to address a wide range of ecological questions based on their level of  
220 organization. For example, the assemblage of interactions across ecological scales can be studied using  
221 species-based networks, whereas clade-based networks can be used to study macroevolutionary processes (e.g.,  
222 Gomez *et al.* 2010). Because our interpretation of the properties and dynamics of ecological networks depends  
223 on their taxonomic scale (Guimarães 2020), examining the phylogenetic scaling of network structure is also a  
224 promising research avenue. Analyzing the same system at different taxonomic scales can thus provide  
225 meaningful and complementary ecological information and is, in our perspective, best conducted using  
226 probabilistic networks.

227 There is no qualitative difference in the taxonomic scaling of local networks compared to metawebs because  
228 only the nodes are defined taxonomically. In other words, the edge probability values of local networks (eq. 2)  
229 and metawebs (eq. 3) are not conditional on any taxonomic scale. It is the definition of the event itself (i.e., the  
230 interaction of the two taxa) that has a given phylogenetic scale, not their conditional variables. In both types of  
231 networks, shifting to a broader level of organization can be directly done using probabilities at finer scales. For  
232 example, if we have a network of  $n_A$  species from genus  $A$  and  $n_B$  species from genus  $B$ , we can calculate the  
233 probability that at least one species from genus  $A$  interact with at least one species from genus  $B$  as follows:

$$P(A \rightarrow B) = 1 - \prod_{i=1}^{n_A} \prod_{j=1}^{n_B} (1 - P(A_i \rightarrow B_j)), \quad (4)$$

where  $A_i$  and  $B_j$  are the species of the corresponding genus. Knowing that two species interact (i.e.,  $P(A_i \rightarrow B_j) = 1$ ) gives a probability of genus interaction of 1. Canard *et al.* (2012) built a species-based network from neutrally simulated interactions between individuals using a similar approach. In contrast, more sophisticated models need to be built when shifting to a finer level of organization. Indeed, knowing that two genera interact does not imply that all of their pairwise species combinations can also interact. One could, for example, build a finer-scale network by generating probabilities of species interactions by randomly sampling them from a beta distribution parametrized by the broader-scale network.

Ideally, the biological interpretation of probabilistic interactions should not differ across a network even if it has heterogenous levels of organization, i.e. if different nodes are represented at different taxonomic scales (e.g., a network composed of species and trophic species). This is frequent in ecological networks where taxonomic resolution is typically low Vázquez *et al.* (2022). Broader-scale interactions should be based on probabilities of interactions between individuals, either at the local or regional scale. For example, in local individual-based food webs, the probability that two individuals interact represents the degree of belief that one individual will actually consume the other. Similarly, in local species-based food webs, the probability that two species interact represents the degree of belief that at least one individual from the predator species consumes at least another individual from the prey species. Moreover, in local clade-based food webs, the probability that two clades interact represents the degree of belief that at least two species from these clades interact with each other or, equivalently, that at least two individuals from these clades interact with each other. Fundamentally, the taxonomic scaling of interactions is an aggregation of interactions between individuals into larger groups, which could be more or less homogeneous depending on the organisms and the study system. This type of scaling is analogous to the spatial and temporal scaling of interactions to the extent that they represent different ways to aggregate individuals into broader groups, either spatially, temporally, or taxonomically.

## **Spatial and temporal scaling of interactions**

The study of network-area relationships (NARs) and interaction accumulation curves (IACs) are important realms of research in network ecology. Firstly, NARs describe the scaling of network properties (such as modularity and trophic chain lengths) with spatial scale Galiana *et al.* (2018). The variation of network

structure across spatial scales can be the result of the scaling of species richness (species-area relationships, SARs) and the number of interactions (Brose *et al.* 2004) with the area sampled, but can also be due to ecological processes (e.g., spatial variability in community composition and extinction and colonization events) occurring at different scales (Galiana *et al.* 2018). Secondly, IACs describe the scaling of the number of interactions observed with sampling effort (Jordano 2016), which can impact many measures of network structure such as connectance (McLeod *et al.* 2021). Beyond sampling effort, the temporal scaling of interactions describes how network structure changes with the duration of the network (Poisot *et al.* 2012) given that different interactions are occurring through time. Because probabilistic local networks can assess the spatiotemporal variability of interactions (eq. 2), they are useful tools to develop and test different equations of the scaling of network structure with space and time.

Metawebs and local networks intrinsically differ in their relationship to spatial and temporal scales. On one hand, because probabilistic metawebs are context-independent, potential interactions do not scale with space and time since they depend solely on the biological capacity of the two taxa to interact, regardless of any particular environmental conditions. This suggests that the probability that two taxa can potentially interact should theoretically be the same in all metawebs in which they are present, provided that the data and methods used to estimate them are the same. As a result, if a potential network  $M_1$  is subsampled from a regional metaweb  $M_0$  to represent the potential interactions between a subset of taxa found in a smaller region, their probabilities of interaction should be identical regardless of scale, i.e.  $P_{M_1}(i \rightarrow j) = P_{M_0}(i \rightarrow j)$ . On the other hand, local ecological networks scale both spatially and temporally since interactions have more opportunities to be realized and observed in a larger area and duration (e.g., more individuals, more trait variations, more chance of an encounter, McLeod *et al.* (2020)). For example, if a local probabilistic network  $N_1$  of area  $A_1$  is obtained from a larger network  $N_0$  of area  $A_0$ , with  $A_1$  being completely nested within  $A_0$ , interaction probabilities should be smaller in the smaller network, i.e.  $P_{N_1}(i \rightarrow j|A_1 < A_0) \leq P_{N_0}(i \rightarrow j|A_0)$ . However, if  $A_1$  and  $A_0$  are disjoint, interaction probabilities could be incidentally higher in the smaller area depending on their environmental and biological conditions. Similarly, interaction probabilities should be smaller in networks of shorter durations if time intervals are nested. Statistical models, such as network-area relationships and interaction accumulation curves, can be used to generate estimates of local probabilities of interactions across spatial and temporal scales.

## 287 **A spatiotemporally explicit model of interactions**

288 Predicting local networks across time and space is an important goal of network ecology (Strydom *et al.* 2021).  
289 Indeed, in a context of scarcity of interaction data (Jordano 2016), ecologists must rely on predictive models to  
290 reconstruct networks at fine spatial and temporal scales. For example, local ecological networks could be  
291 reconstructed using real-time biomonitoring data and adequate numerical models (Bohan *et al.* 2017), which  
292 could pave the way for fine-scale studies of ecosystem functioning and dynamics. Besides predictive models,  
293 statistical models can also be built to describe parameters of interest, such as probabilities of interactions. In  
294 that case, parameter values provide valuable ecological information in their own rights. Different types of  
295 models (e.g., Bayesian and machine learning models) of ecological interactions have been built for predictive  
296 and descriptive purposes (Strydom *et al.* 2021). Representing interactions probabilistically reflects the  
297 uncertainty of these models, which is usually represented in terms of probability distributions. Here we show  
298 how to build a simple generative mechanistic model of probabilistic interactions that takes into account their  
299 inherent spatiotemporal variability, i.e. a spatiotemporally-explicit model. Our model is not suitable for  
300 potential interactions, which are scale-independent. Rather, it could prove useful for predicting local  
301 interactions across time and space by generating new interaction data after parameter inference.

302 As stated by eq. 1, the probability that two taxa  $i$  and  $j$  interact at a given location  $(x, y)$  is given by the product  
303 of their probability of interaction given co-occurrence and their probability of co-occurrence. First, their  
304 probability of co-occurrence is given by their respective probabilities of occurrence  $P_i(x, y)$  and  $P_j(x, y)$  and the  
305 strength of association  $\gamma$  between their occurrence and co-occurrence (Cazelles *et al.* 2016):

$$P_{i,j}(x, y) = P_i(x, y)P_j(x, y)\gamma. \quad (5)$$

306 When  $\gamma > 1$ , the geographic distributions of both taxa are positively associated, which implies that the  
307 occurrence of one taxon increases the probability of occurrence of the other. In empirical networks,  $\gamma > 1$  for  
308 most species pairs (Catchen *et al.* 2023). The co-occurrence of both taxa is the result of a Bernoulli trial

$$C \sim \text{Bernoulli}(P_{i,j}(x, y)). \quad (6)$$

309 Second, the probability of interaction given co-occurrence can be made temporally explicit by modeling it as a  
310 Poisson process with rate  $\lambda$ . This parameter corresponds to the expected frequency of interaction between both

311 taxa in a given time period and its value can be estimated using prior data on interaction strengths, if available.  
 312 Specifically, the probability that two co-occurring taxa interact during a time period  $t_0$  is:

$$P_N(i \rightarrow j | C = 1) = 1 - e^{-\lambda t_0}, \quad (7)$$

313 which approaches 1 when  $t_0 \rightarrow \infty$ .

314 The realization of the interaction between  $i$  and  $j$  is the result of a Bernoulli trial with probability  $P_N(i \rightarrow j)$ . A  
 315 Bayesian inference model can thus be built from the previous equations to estimate the value of the  $\lambda$  parameter  
 316 and generate new interaction data:

$$I \sim \text{Bernoulli}(P_N(i \rightarrow j)) \quad (8)$$

$$P_N(i \rightarrow j) = P_i(x, y)P_j(x, y)\gamma(1 - e^{-\lambda t_0}) \quad (9)$$

$$\gamma \sim \text{Gamma}(2, 0.5) \quad (10)$$

$$\lambda \sim \text{Exponential}(2) \quad (11)$$

320 This simple model can be customized in many ways, e.g. by linking  $\lambda$  with given environmental variables or by  
 321 explicitly modeling observation errors (i.e., the probability of false negatives and false positives).

## 322 Sampling binary networks

323 Probabilistic networks can be used to predict binary interactions through random draws. This can be useful  
 324 when analyzing the structure of a probabilistic network when analytical probabilistic measures are lacking. A  
 325 binary network can be generated from independent Bernoulli trials for each interaction. The distribution of a  
 326 network's property can then be obtained after measuring the structure of all randomly generated networks  
 327 (Poisot *et al.* 2016). Doing so allows us to represent the variability of network structure, although possibly with  
 328 biases when connectance is low (Poisot & Gravel 2014; Chagnon 2015). When binary networks are generated  
 329 under a null model, this method can be used for null hypothesis significance testing, in which case the observed  
 330 measure is compared to a null distribution (e.g., Bascompte *et al.* 2003). Furthermore, randomly generating  
 331 binary networks across space and time can help us visualize the spatiotemporal variability of network structure

and test ecological hypotheses on interactions across large spatial and temporal scales.

There are at least two different approaches when sampling binary networks from probabilistic webs across space, e.g. if we want to predict a binary network for each of  $n \times n$  grid cells. The first approach is to conduct a single Bernoulli trial for each pair of taxa found in the region of interest based on their regional probability of interaction. As a result, each pair of taxa that are predicted to interact in the regional network realization will interact in all of the  $n^2$  networks in which they co-occur. This sampling technique is best used with potential interactions that have no spatial variation. The second approach is to independently sample each of the  $n^2$  networks. In practice, this can be done by generating a different probabilistic network for each grid cell. Depending on how they were obtained, these networks can differ in their taxa composition (nodes) and/or interaction probabilities (edges). Then, binary networks can be independently sampled for each grid cell. Because this method generates spatial variation in binary interactions, it is best used with local interactions. The choice of sampling approach has an impact on the selection of grid cell size. In the first approach, interactions will be the same regardless of cell size because interactions are sampled only once from the regional network. However, in the second approach, local interaction probabilities depend on the network area. For example, let  $N_1$  and  $N_2$  be networks of area  $\frac{1}{2}A_0$  nested within  $A_0$  and disjoint from each other, i.e. two contiguous cells that form  $N_0$ . If  $N_1$  and  $N_2$  are independent (which is rarely the case in reality because of spatial auto-correlation), the probability that two taxa  $i$  and  $j$  interact in  $N_0$  is given by:

$$P_{N_0}(i \rightarrow j) = 1 - (1 - P_{N_1}(i \rightarrow j)) \times (1 - P_{N_2}(i \rightarrow j)). \quad (12)$$

Because of its larger area, the probability that the two taxa interact in  $N_0$  is higher than in  $N_1$  and  $N_2$ . When sampling binary interactions from local networks, it is thus important to sample at the same spatial scale as the one for which probabilities were estimated. Otherwise, interaction probabilities must be adjusted to correspond to the targeted cell size and avoid systematic biases in prediction.

### **Prediction of local networks from metawebs**

Metawebs are an important source of ecological information that can be leveraged for predicting local networks. Indeed, binary local networks can be reconstructed by selecting a subset of both taxa and interactions from the metaweb (Dunne 2006). This implies that there are always more interactions in a metaweb compared to its corresponding local networks. In practice, because a community's composition is arguably easier to sample or



358 predict than its interactions, the list of taxa to select can be known empirically or obtained using range maps or  
 359 species distribution models. The challenge is rather to choose which interactions to select from the metaweb,  
 360 which could require more sophisticated statistical models and ecological knowledge. Because the structure of  
 361 local networks is constrained by the one of the metaweb (Saravia *et al.* 2022), inferring their structure from the  
 362 metaweb before predicting local pairwise interactions could prove promising (Strydom *et al.* 2021).  
 363 When building probabilistic local networks from a probabilistic metaweb, interaction probabilities decrease.  
 364 This is because two taxa must first have the capacity to interact (i.e.,  $M_{i,j}^* = 1$  in the binary metaweb  $M^*$ ) before  
 365 interacting locally:

$$P_N(i \rightarrow j) = P_M(i \rightarrow j) \times P_N(i \rightarrow j | M_{i,j}^* = 1).$$

366 Therefore, inferring local networks from their metaweb keeping the same values of interaction probability  
 367 would generate systematic biases in the prediction. In that case, these networks would instead represent  
 368 smaller-scale metawebs of potential interactions, which could be misinterpreted as local interactions. As  
 369 suggested by McLeod *et al.* (2021), even though metawebs do not capture the spatiotemporal variability of  
 370 interactions, they set the upper limit of local interactions. In other words, the probability that two taxa interact at  
 371 a given location and time is always lower or equal to the probability of their potential interaction:

$$P_N(i \rightarrow j | A, t, C, \Omega) \leq P_M(i \rightarrow j). \quad (13)$$

372 Moreover, the probability that two taxa have the biological capacity to interact must be higher than the  
 373 probability that they will ever interact because they might never co-occur or encounter locally. More precisely,  
 374 the accumulated probability of realized interactions across all spatial, temporal, and environmental conditions  
 375 must be lower than the probability of potential interaction, i.e.

$$\int_{\Omega} \int_A \int_t P_N(i \rightarrow j | A, t, \Omega) dt dA d\Omega \leq P_M(i \rightarrow j). \quad (14)$$

## 376 Conclusion

377 In this contribution, we underlined the importance of network metadata for adequately interpreting and  
378 manipulating probabilistic interaction data. Indeed, the mathematical representation of probabilities and their  
379 statistical behaviors depend on the type of interactions (local or potential) and the conditions in which they were  
380 estimated. We showed that probabilistic local networks and metawebs differ in their relationship to spatial and  
381 temporal scales, with potential interactions being scale-independent. In contrast, local interactions are measured  
382 in a specific context (e.g., in a given area, time, and biological and environmental conditions) and are  
383 conditional on taxa co-occurrence. These important conceptual differences bring to light the need to use  
384 probabilistic data with caution, for instance when generating binary network realizations across space and  
385 predicting local networks from metawebs. Clear metadata describing the type of interaction and the variables  
386 used in their estimation are required to ensure adequate data manipulation. Better data practices and rigorous  
387 foundations for probabilistic thinking in network ecology could enable more reliable assessments of the  
388 spatiotemporal variability and measurement uncertainty of biotic interactions.

## 389 Acknowledgment

390 We acknowledge that this study was conducted on land within the traditional unceded territory of the Saint  
391 Lawrence Iroquoian, Anishinabewaki, Mohawk, Huron-Wendat, and Omàmiwininiwak nations. This work was  
392 supported by the Institute for Data Valorisation (IVADO) and the Natural Sciences and Engineering Research  
393 Council of Canada (NSERC) Collaborative Research and Training Experience (CREATE) program, through the  
394 Computational Biodiversity Science and Services (BIOS<sup>2</sup>) program. A special thanks to all members of the  
395 Black Holes and Revelations working group (organized by BIOS<sup>2</sup>) for their insightful discussions and valuable  
396 feedback on this manuscript.

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