

# The ecological interpretation of probabilistic networks

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The stochastic nature of ecological interactions has led biologists to adopt a probabilistic view of ecological networks. Representing species interactions probabilistically (how likely are they occurring?) as opposed to deterministically (are they occurring?) allows a better assessment of their spatiotemporal variability and accounts for inherent uncertainties in both observations and predictions. However, despite this growing interest in probabilistic networks, guidelines for the estimation and documentation of probabilistic interaction data are still lacking. This is concerning given that our biological understanding of probabilistic interactions and their appropriate analyses depend on the often elusive methods and variables used for their estimation. We review how probabilistic interactions are defined at different spatial scales, from local interactions to regional networks (metawebs), with a strong emphasis on trophic interactions. These definitions are based on the distinction between the observation of an interaction at a specific time and space and its biological feasibility. We show that different network representations have different statistical properties 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 in metawebs remaining constant across spatial and temporal scales. This is in contrast with the taxonomic scaling of interactions, which does not qualitatively differ between both types of networks. We suggest two approaches to inferring 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 build a spatiotemporally explicit model of probabilistic interactions and develop different case studies using empirical data on host-parasite interactions in Europe. Overall, our results underscore the importance of clear metadata for

probabilistic ecological networks, both at the local and regional scales, to inform the appropriate reuse of interaction data.

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## **1 Introduction**

2 Cataloging ecological interactions is a substantial challenge. There are methodological and biological  
3 constraints that hinder our ability to observe all interactions, such as the spatial and temporal uncoupling of  
4 species (Jordano (1987)) and the large number of possible 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 difficult when accounting for the spatiotemporal variability of ecological networks (Poisot *et al.* (2012), Poisot  
7 *et al.* (2015)). Indeed, knowing the biological capacity of two species to interact is necessary but not sufficient  
8 for inferring their interaction at a specific time and space. For example, Golubski & Abrams (2011) presented  
9 many cases where trophic interactions in food webs depend on the presence or abundance of a third species  
10 (e.g., of a more profitable prey species). More generally, a handful of conditions must be satisfied for an  
11 interaction to be observed locally. First, both species must have overlapping geographic ranges, i.e. they must  
12 co-occur within the region of interest (Blanchet *et al.* (2020)). Then, they must encounter locally. Probabilities  
13 of interspecific encounters are typically low, especially for rare species with low relative abundances (Canard *et*  
14 *al.* (2012)). Finally, their traits must be locally compatible (Poisot *et al.* (2015)). This includes their phenology  
15 (Olesen *et al.* (2010), Singer & McBride (2012)), behavioral choices (Pulliam (1974), Choh *et al.* (2012)) and  
16 phenotypes (Bolnick *et al.* (2011), Stouffer *et al.* (2011), Gravel *et al.* (2013)). Environmental factors, such as  
17 temperature (Angilletta *et al.* (2004)), drought (Woodward *et al.* (2012)), climate change (Gilman *et al.* (2010),  
18 Woodward *et al.* (2010), Araujo *et al.* (2011)), and habitat modifications (Tylianakis *et al.* (2007)), contribute  
19 to this spatiotemporal variability of interactions by impacting species abundance and traits. In this context, it is  
20 unsurprising that our knowledge of ecological interactions remains limited (Hortal *et al.* (2015)) despite  
21 extensive biodiversity data 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 regarded as either occurring or not,  
25 probabilistic networks represent our degree of belief about the realization or feasibility of pairwise interactions  
26 at the local or regional scale, respectively. In other words, representing interactions probabilistically takes into  
27 account inherent uncertainties and variability associated with ecological data. In the broadest sense, binary  
28 networks are also a type of probabilistic network, in which the numerical value of an interaction is restrained to  
29 0 (non-occurring) or 1 (occurring). In probabilistic networks, only forbidden interactions (i.e., interactions

prohibited by biological traits, Jordano *et al.* (2003), Olesen *et al.* (2010)) have a probability value of zero, provided that intraspecific trait variability is considered (Gonzalez-Varo & Traveset (2016)). However, *neutrally* forbidden interactions (i.e., improbable interactions between rare species, Canard *et al.* (2012)) could have low probability values in local networks 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 network structure (i.e. community-level properties), which is a major driver of the functioning, dynamics, and resilience of ecosystems worldwide (Proulx *et al.* (2005), McCann (2007), McCann (2011), Rooney & McCann (2012)). Moreover, the application and development of computational methods in network ecology, often based on a probabilistic representation of interactions, can alleviate the 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 could inform the identification of priority sampling locations of ecological networks where data collection would yield the most valuable information, thereby reducing errors. Optimization models for sampling locations have mostly found applications in biological systems that are not networked, such as identifying priority sampling sites for disease hotspots (Andrade-Pacheco *et al.* (2020)), but there is substantial promise in applying them to probabilistic ecological interactions. Statistical models can also be used to generate network predictions without prior knowledge of pairwise interactions, for instance using body size (Petchey *et al.* (2008), Gravel *et al.* (2013)), phylogeny (Elmasri *et al.* (2020), Strydom *et al.* (2022)), or a combination of niche and neutral processes (Bartomeus *et al.* (2016), Pomeranz *et al.* (2019)) for inference. Topological null models (e.g., Bascompte *et al.* (2003), 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 (Ohlmann *et al.* (2019), 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)).

The lack of clear guidelines on the use of probabilistic interaction data is worrisome (Brimacombe *et al.*

60 (2023)), both for data producers and re-users who generate and manipulate these numbers. Besides  
61 methodological difficulties that may arise when assessing probabilistic interactions, a precise definition of  
62 probabilistic interactions appears to be lacking, making the estimation and use of these data more difficult. We  
63 aim to take a step back by outlining different ways in which probabilistic interactions are defined and used in  
64 network ecology. We distinguish two broad categories of probabilistic networks that necessitate distinct  
65 approaches when applied to key ecological questions: local networks of realized interactions, and regional  
66 networks (metawebs) of potential interactions. We highlight the distinctions in the ecological meaning of these  
67 two representations and show that they yield different statistical outcomes regarding e.g. the spatial and  
68 temporal scaling of interactions and the prediction of binary networks across space. Moreover, there is currently  
69 no metadata standard that could guide the documentation of all types of probabilistic interactions (Salim *et al.*  
70 (2022) discuss data standards for deterministic mutualistic networks). Well-defined metadata for probabilistic  
71 networks would support more adequate manipulation and integration of interaction data from different sources  
72 and guard against the potential misinterpretations arising from ambiguous definitions of probabilistic networks.  
73 These metadata should outline the nature (i.e., potential or local) and type (e.g., predatory or pollination) of the  
74 interactions, provide information regarding the taxonomic level, identities, and characteristics (e.g., life stages)  
75 of the individuals involved in an interaction, present the mathematical formulation of probabilities, including  
76 clearly identified conditional variables, and describe the methods and contexts (e.g., location, time,  
77 environmental conditions) in which interactions were estimated. Inadequately documented probabilistic  
78 interaction data should be used with caution when analyzing ecological networks. Although our contribution  
79 focuses on food webs, our observations and advice can be applied to other types of ecological networks, from  
80 plant-pollinator to host-virus networks. Indeed, excluding networks of indirect interactions such as competition  
81 and facilitation networks (Kéfi *et al.* (2015), Kéfi *et al.* (2016)), most ecological networks describe probabilities  
82 of direct interactions, which are conceptually and mathematically analogous regardless of their biological type  
83 (e.g., trophic and mutualistic interactions).

## 84 **Probabilistic representations of interactions**

85 One of the first aspects to take into consideration when estimating or interpreting probabilities of interactions is  
86 knowing if they describe potential or realized interactions. A potential interaction is defined as the biological  
87 capacity of two taxa to interact (i.e., the probability that they *can* theoretically interact) whereas a realized

interaction is the materialization or observation of this interaction in a well-defined space and time (i.e., the probability that they interact locally). Here, we use the terms *metaweb* (Dunne (2006)) to designate networks of potential interactions and *local networks* (Poisot *et al.* (2012)) for those of realized interactions. Metawebs are the network analogues of the species pool, where local networks originate from a subset of both species (nodes) and interactions (edges) of the regional metaweb (Saravia *et al.* (2022)). Without clear documentation, it can be challenging to know if published probabilistic networks describe potential or realized interactions, or if so-called probabilities are in reality *interaction scores* (i.e., non-probabilistic quantitative interactions). When probabilistic potential interactions are used and interpreted as local interactions (and conversely), this may generate misleading findings during data analysis. We believe that a better understanding of the differences, similarities, and relationships between these two probabilistic representations of ecological networks would alleviate interpretation errors and facilitate a more adequate utilization of interaction data.

## 99 Pairwise interactions: the building blocks of ecological networks

Local ecological networks and metawebs, like any type of network, are made of nodes and edges that can be represented at different levels of organization and precision. The basic unit of food webs and other ecological networks are individuals that interact with each other (e.g., by predation, Elton (2001)), forming individual-based networks (Melián *et al.* (2011)). The aggregation of these individuals into more or less homogeneous groups (e.g., populations, species, trophic species, families) allows us to represent nodes at broader taxonomic scales, which affects our interpretation of the properties of these systems (Guimarães (2020)). Moreover, edges linking these nodes can describe a variety of interaction measures. Ecologists have traditionally represented interactions as binary objects that were considered realized after observing at least one individual from group  $i$  interact with at least another individual from group  $j$ . Boolean interactions can be viewed as the result of a Bernoulli 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 characterizes our limited knowledge of the system and its intrinsic spatiotemporal variability. Depending on the type of networks (local or metaweb), the mathematical formulation and interpretation of stochastic parameters like  $P(i \rightarrow j)$  can be linked to environmental and biological factors such as species relative abundance, traits, area, and time (tbl. 1), for example using logistic regression with a logit link function with continuous explanatory variables. In these probabilistic network representations in which  $P(i \rightarrow j)$  are edge values, the only two possible outcomes are the presence ( $A_{i,j} = 1$ ) or absence ( $A_{i,j} = 0$ ) of an interaction between each pair of nodes. When considering uncertainties around the

117 estimation of  $P(i \rightarrow j)$ , a Beta distribution  $\text{Beta}(\alpha, \beta)$  can also be used to encompass all possible probability  
118 values. Observing an interaction between two taxa at a given location and time provides important information  
119 that can be used to update previous estimates of  $P(i \rightarrow j)$ , informing us on the biological capacity of both taxa  
120 to interact and the environmental conditions that enabled them to interact locally.

121 Even though binary networks constitute a highly valuable source of ecological information (Pascual *et al.*  
122 (2006)), they overlook important factors regarding interaction strengths. These are represented using  
123 quantitative interactions, which better describe the energy flows, demographic impacts or frequencies of  
124 interactions between nodes (Berlow *et al.* (2004), Borrett & Scharler (2019)), with  $A_{i,j}$  being a natural number  
125  $\mathbb{N}$  or a real number  $\mathbb{R}$  depending on the measure. For example, they may represent local interaction rates  
126 between pairs of taxa (e.g., the flower visiting rates of pollinators in a mutualistic network, Herrera (1989)).  
127 Because quantitative interactions can also describe predation pressure on prey taxa in food webs, they can be  
128 good estimators of the parameters describing species interactions in a Lotka-Volterra model (e.g., Emmerson &  
129 Raffaelli (2004)). The extra amount of ecological information in quantitative networks typically comes at a cost  
130 of greater sampling effort and data volume in predictive models (Strydom *et al.* (2021)), which can lead to  
131 relatively high levels of uncertainties when inferring quantitative networks with limited data. Just like binary  
132 networks, the uncertainty and spatiotemporal variability of quantitative interactions can be represented  
133 probabilistically. However, the need to estimate the probability distribution of all possible value of interaction  
134 strengths can make the inference of probabilities more challenging in quantitative networks compared to binary  
135 networks, which require only one probability estimate for each interaction. Quantitative interactions can follow  
136 various probability distributions depending on the measure used, the event's outcome being the value of  
137 interaction strength. For instance, quantitative interactions can follow a Poisson distribution  
138  $A_{i,j} \sim \text{Poisson}(\lambda_{i \rightarrow j})$  when predicting frequencies of interactions between pairs of nodes, with  $\lambda_{i \rightarrow j}$  being the  
139 expected rate at which individuals of taxa  $i$  and  $j$  interact (e.g., the average number of prey  $j$  consumed by all  
140 predators  $i$  in a given time period). The Poisson distribution can also be 0-inflated after initially modeling  
141 non-interacting taxa (e.g., Boulangeat *et al.* (2012) employ a 0-inflated model to analyze species abundance  
142 following the modeling of species presence and absence), which constitute the majority of taxa pairs in most  
143 local networks due to their typically high sparseness (Jordano (2016)). Because of the methodological  
144 difficulties typically encountered when building deterministic quantitative networks, binary networks, which are  
145 easier to sample (Jordano (2016)) and predict (Strydom *et al.* (2021)), are much more documented and modeled  
146 in the literature. Moreover, most published probabilistic networks and methods describe Bernoulli interactions

147 (whether interaction probabilities are regarded as constant or variable, e.g. represented by Beta distributions),  
148 which underlines the need for better guidelines regarding the interpretation and manipulation of these types of  
149 networks. For these reasons, our primary focus in this contribution will be on addressing the challenges in  
150 interpreting and using Bernoulli interactions, in both probabilistic local networks and metawebs.

151 **Local networks: communities interacting in space and time**

152 Probabilistic local networks describe how likely taxa are to interact at a given location and time period (i.e.,  
153 interactions are contingent upon the environmental and biological conditions of the community). In local  
154 networks, edges commonly represent our degree of belief that two taxa interact in nature, but can also represent  
155 the probability of *observing* this interaction (Catchen *et al.* (2023)). For example, Kopelke *et al.* (2017)  
156 assembled a dataset of binary local European food webs of willow-galling sawflies and their natural enemies,  
157 clearly referencing each food web in space and time. Gravel *et al.* (2019) used this dataset to infer the  
158 probabilities of locally observing interactions between co-occurring species, with the added aspect of situating  
159 local networks within the context of environmental variables. This was achieved by including temperature and  
160 precipitation as conditional variables in some of their models.

161 We define space as the set of geographic coordinates ( $x, y, z$ ) of the spatial boundaries delineating the system,  
162 whether sampled or targeted. Ecological interactions may exhibit variations spatially and along altitudinal  
163 gradients, as evidenced by changes in hummingbird-plant interactions (Weinstein & Graham (2017b) and  
164 Weinstein & Graham (2017a)) and mosquitoes biting rates (e.g., Kulkarni *et al.* (2006)) at different elevations.  
165 In contrast, time is defined as the specific time period within which interactions were either observed or  
166 predicted. With these definitions in mind, space and time can be conceptualized as distinct patches or time  
167 segments. Treating them as discrete dimensions aligns with the common sampling methods of ecological  
168 networks and provides actual probabilities of interactions across space and time. This differs from the approach  
169 of treating them as continuous variables, where edge values represent probability densities (i.e., relative  
170 likelihoods of interactions occurring at infinitesimal locations and instants in time) rather than discrete  
171 probability values (which can be obtained by integrating probability densities). By employing discrete locations  
172 and time periods, we can quantify both an area  $A$  and a duration  $t$ , which can be readily used in spatiotemporal  
173 analyses of ecological networks. For example, when studying network-area relationships (NAR, Galiana *et al.*  
174 (2018)), we anticipate that local probabilities of interactions scale positively with area and duration because  
175 taxa have more opportunities to interact as these dimensions expand.

176 The probability that two taxa  $i$  and  $j$  interact locally can be conditional on many environmental and biological  
 177 factors. One of these is their co-occurrence  $C_{i,j}$ , which is usually a Boolean describing if the geographic  
 178 distributions of both taxa overlap within the study area. Co-occurrence can be modeled probabilistically, in  
 179 which case it may conform to a Bernoulli distribution  $C_{i,j} \sim \text{Bernoulli}(P_{i,j}(x, y, z))$ , where the probability of  
 180 co-occurrence  $P_{i,j}(x, y, z)$  can be estimated through the application of joint species distribution models (e.g.,  
 181 Pollock *et al.* (2014)). Considering that the probability that two non co-occurring taxa interact locally is zero  
 182 (i.e.,  $P_N(i \rightarrow j|C = 0) = 0$ ), the probability of local interaction can be obtained by multiplying the probability of  
 183 interaction given co-occurrence with the probability of co-occurrence:

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

184 Other important factors that can impact our estimation of interaction probabilities at the local scale are taxa  
 185 relative abundance (Canard *et al.* (2012)) and traits (Poisot *et al.* (2015)), as well as environmental factors such  
 186 as temperature (Angilletta *et al.* (2004)), precipitation (Woodward *et al.* (2012)), habitat structure (Klecka &  
 187 Boukal (2014)), and presence of other interacting taxa in the network (Pilosof *et al.* (2017), Kéfi *et al.* (2012)).  
 188 Here, we use the variable  $\Omega$  to describe the biological and ecological context in which interaction probabilities  
 189 were estimated. For example, if a research team conducts a mesocosm experiment to estimate interaction  
 190 probabilities between predators and prey with and without shelters,  $\Omega$  would represent the presence or absence  
 191 of these shelters. Like co-occurrence,  $\Omega$  can also be modeled probabilistically when the stochasticity or  
 192 uncertainty of environmental and biological factors is considered. In sum,  $\Omega$  represents all ecological and  
 193 biological variables that were taken into consideration when measuring interaction probabilities and is,  
 194 therefore, a subset of all factors actually impacting ecological interactions.

195 The probability that two taxa  $i$  and  $j$  interact in a local network  $N$  can thus be conditional on the area  $A$ , the time  
 196 interval  $t$ , their co-occurrence  $C$  and chosen environmental and biological conditions  $\Omega$ . This gives us the  
 197 following equation when all of these conditions are included in the estimation of interaction probabilities:

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

198 The representation of the local context in which probabilities are estimated and the variables that should be  
 199 taken into consideration depend on the study system, the objectives of the study, and the resources available to

the researchers. In other words, these variables do not systematically need to be accounted for. For example, in Gravel *et al.* (2019), for the purpose of model comparison, some models incorporated environmental variables as conditional factors to estimate interaction probabilities, while others did not. When accounted for, these variables should be clearly described in the documentation of the data (Brimacombe *et al.* (2023)), preferentially in mathematical terms to avoid any confusion in their interpretation and to limit manipulation errors during their re-use. For instance, ecologists should be explicit about their consideration of co-occurrence in their estimation of local interaction probabilities. Indeed, it is 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 since this can significantly impact the interpretation and analysis of the data. In [tbl. 1](#), we present examples of studies that used these diverse formulations of probabilistic interactions and conditional variables.

**Table 1: Notation of probabilistic interactions.** The probability of interaction between two taxa  $i$  and  $j$  is interpreted differently in a metaweb  $M$  of potential interactions and a local network  $N$  of realized interactions. Each notation includes a different conditional variable, when applicable. An example of a study employing each of these notations and conditional variables is provided, with the specific variables used indicated in parentheses. The study marked with an asterisk has been carried out on binary networks. Note that interaction probabilities can be contingent upon multiple conditional variables, or none at all. Additionally, local interaction probabilities might represent the probability of observing an interaction, not necessarily its actual occurrence.

Notation	Type	Description	Reference
$P_M(i \rightarrow j)$	potential	biological feasibility of the interaction	Strydom <i>et al.</i> (2022)
$P_N(i \rightarrow j)$	local	realization of the interaction	Fortuna & Bascompte (2006) (null model)
$P_N(i \rightarrow j A)$	local	realization of the interaction in a given area	Galiana <i>et al.</i> (2018) *
$P_N(i \rightarrow j t)$	local	realization of the interaction during a given time period	Weinstein & Graham (2017a)
$P_N(i \rightarrow j C)$	local	realization of the interaction given that the taxa co-occur	Gravel <i>et al.</i> (2019)
$P_N(i \rightarrow j \Omega)$	local	realization of the interaction given environmental conditions	Gravel <i>et al.</i> (2019) (temperature and precipitation)

210 **Metawebs: regional catalogs of interactions**

211 Metawebs are networks of potential interactions that have been designed for broad spatial, temporal, and  
212 taxonomic scales (e.g., species food webs at the continental scale). They represent the probability that taxa can  
213 biologically interact regardless of their co-occurrence and local environmental conditions. Potential interactions  
214 are by definition context-independent, i.e. they are not measured at a specific location and time. In contrast with  
215 probabilistic local networks, which represent the stochasticity of interactions occurring in nature, probabilistic  
216 metawebs measure our degree of belief in the capacity of two taxa to interact (i.e., the probability that their  
217 traits could support an interaction in the right conditions). In other words, potential interactions describe the  
218 probability that there exists at least one combination of phenotypes of taxa  $i$  and  $j$  that can interact with each  
219 other if they were to encounter. To reduce any biases in our calculation of this probability, it is crucial to ensure  
220 that the set of traits sampled or considered accurately reflects the overall trait distribution in both taxa. This  
221 enhances our confidence in concluding that the taxa cannot interact when no positive observation has been  
222 made and increases our capacity to detect an interaction when it is biologically feasible. In addition to  
223 one-on-one interactions, the extent of sampling effort also contributes to shaping our assessment of metaweb  
224 properties, as sampling a larger number of local networks allows us to capture more potential interactions  
225 (McLeod *et al.* (2021a)). A probability of potential interaction in a metaweb  $M$  can be expressed as

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

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

227 Starting from a selected set of taxa, which are usually distributed within a broad region of interest, probabilistic  
228 metawebs can be built using different data sources, including literature review, fieldwork, and predictive models  
229 (e.g., the metaweb of trophic interactions between Canadian mammals inferred by Strydom *et al.* (2022)).  
230 Every pair of taxa that have confidently been observed to interact at least once can be given a probability of 1  
231 (i.e.,  $P_M(i \rightarrow j) = 1$ ) since we know that they *can* interact. This is not the case in local probabilistic networks,  
232 in which interaction events usually remain stochastic (i.e.,  $P_N(i \rightarrow j) < 1$ ) after empirically observing  
233 interactions because of their intrinsic spatiotemporal variability. Similarly, although rare interactions typically  
234 have low probabilities in local networks, they can have high probabilities in metawebs when the traits of both  
235 taxa are congruent. On the other hand, interactions that were never observed can have low probability values in  
236 both metawebs and local networks, going as low as 0 for forbidden links. However, because of observation

237 errors due to taxonomic misidentifications and ecological misinterpretations (e.g., due to cryptic species and  
238 interactions, Pringle & Hutchinson (2020)), many observations of interactions are in reality false positives.  
239 Likewise, forbidden interactions can be false negatives in metawebs, e.g. if they have been assessed for specific  
240 phenotypes, locations or time. Employing Bayesian models, whether they are mechanistic or  
241 phenomenological, has the potential to enhance the accuracy of our estimation of interaction probabilities  
242 within both local and potential networks (e.g., Bartomeus *et al.* (2016), Cirtwill *et al.* (2019)). This  
243 improvement is achieved in potential networks by leveraging prior information regarding the feasibility of  
244 interactions along with the empirical data on observed interactions.

## 245 Properties of probabilistic networks

246 Probabilistic local networks and metawebs differ in their type of interactions (i.e., local or potential) and in the  
247 conditional variables upon which interaction values depend. These differences are significant as they influence  
248 the characteristics of probabilistic networks. Neglecting to consider them may result in misleading results and  
249 interpretation errors when analyzing the properties of probabilistic networks, which could be particularly  
250 problematic when addressing crucial ecological questions about networks. Here we compare the characteristics  
251 of local networks and metawebs through the presentation of four common applications of probabilistic  
252 interactions.

### 253 Host-parasite network data

254 We use the collection of tripartite host-parasite networks sampled across Europe, created by Kopelke *et al.*  
255 (2017), in most of our case studies. This dataset contains well-resolved binary local interactions between  
256 willows (52 species), willow-galling sawflies (96 species), and their parasitoids (126 species). Given its  
257 replicated networks spanning large spatiotemporal scales, this dataset is well-suited for analyzing a variety of  
258 ecological hypotheses and processes. Out of a total of 374 local networks, we retained those containing at least  
259 5 species, resulting in a set of 233 georeferenced local networks. We built a binary metaweb by aggregating all  
260 local interactions, which gave us a regional metaweb composed of 274 species and 1080 interactions. In the first  
261 two panels of fig. 1, we show how the dissimilarity of interactions between common species ( $\beta_{OS}$ ) and the  
262 dissimilarity in species composition ( $\beta_S$ ) between the metaweb and aggregated local networks (Poisot *et al.*  
263 (2012)) vary with the number of sampled local networks. This shows that networks of local interactions are

264 highly dissimilar from the metaweb, both in terms of species and interactions, especially when only a limited  
265 number of sites has been sampled.

266 [Figure 1 about here.]

267 We converted these binary networks into probabilistic ones using models based on simple assumptions. Our  
268 models do not aim to precisely estimate the actual values of probabilistic interactions but rather to offer  
269 simplified networks as illustrative examples to underscore the differences between probabilistic local networks  
270 and metawebs. We created two probabilistic metawebs by employing constant false positive and false negative  
271 rates for all potential interactions. In the first metaweb, we set both false positive and false negative rates to zero  
272 to prevent artificially inflating the total number of links, enabling a more accurate comparison with binary  
273 networks. This gave us a probability of potential interaction of 1 when at least one interaction has been observed  
274 and of 0 in the absence of any observed interaction between a given pair of species. In the second metaweb, we  
275 introduced a 5% false positive rate to account for spurious interactions and a 10% false negative rate to capture  
276 the elevated occurrence of false negatives in ecological networks (Catchen *et al.* (2023)). Observed potential  
277 interactions were thus given a probability of 95%, whereas unobserved ones were assigned a probability of 10%.

278 To build probabilistic local networks, we first recognize that local interactions must initially be biologically  
279 feasible before occurring at a specific time and space. A local probability of interaction  $P_N(i \rightarrow j)$  can be  
280 expressed as the product of the probability of local interaction given that the two taxa can potentially interact  
281  $P_N(i \rightarrow j|M_{i \rightarrow j} = 1)$ , which we denote as  $p$  for the sake of simplicity, with their probability of potential  
282 interaction  $P_M(i \rightarrow j)$ :

$$P_N(i \rightarrow j) = P_N(i \rightarrow j|M_{i \rightarrow j} = 1) \times P_M(i \rightarrow j). \quad (4)$$

283 We built the probabilistic local networks from the binary ones by using the probabilistic metawebs and a  
284 constant value of  $p$  across interactions. Lower values of  $p$  indicate that feasible interactions rarely occur locally,  
285 intermediate values around 50% suggest considerable spatiotemporal variability, while higher values indicate  
286 that potential interactions are nearly always realized. Following eq. 4, the local probabilities of interaction  
287 between a given pair of taxa consistently remained equal to or below their probability of potential interaction.

288 In the last two panels of fig. 1, we show how the aggregated number of links and connectance (i.e., the  
289 proportion of all of the  $S^2$  possible links that are realized, where  $S$  represents species richness) scale with the

290 number of sampled local probabilistic networks, according to different values of  $p$ . When aggregating local  
291 probabilistic networks, the constancy of the probability of potential interaction across the entire study area  
292 means that any rise in the probability of local interaction is solely attributable to an increase in  $p$ . The  
293 probability  $p_{1,2}$  of local interaction among potentially interacting species in an aggregated network  $N_{1,2}$  is  
294 obtained by:

$$p_{1,2} = 1 - (1 - p_1) \times (1 - p_2), \quad (5)$$

295 where  $p_1$  and  $p_2$  are the probabilities of local interaction among two potentially interacting species in the  
296 subnetworks  $N_1$  and  $N_2$ , respectively.

297 By comparing the scaling relationships observed in binary and probabilistic networks, fig. 1 illustrates that high  
298 values of  $p$  lead to systematic overestimations in the number of links and connectance, especially when  $p = 1$   
299 (corresponding to the scenario where local probabilities of interactions are equivalent to the probabilities of  
300 potential interactions). However, these biases tend to diminish as the number of sampled networks increases.

### 301 Taxonomic scaling of interactions

302 Probabilistic networks offer a versatile approach to tackle a broad array of ecological questions, depending on  
303 their level of organization. For instance, the assemblage of interactions across ecological scales can be explored  
304 through species-based networks, while clade-based networks provide insights into macroevolutionary processes  
305 (e.g., Gomez *et al.* (2010)). Given that our interpretation of the properties and dynamics of ecological networks  
306 depends on their taxonomic scale (Guimarães (2020)), investigating the phylogenetic scaling of network  
307 structure emerges as a promising research avenue. Examining the same system at various taxonomic scales can  
308 yield meaningful and complementary ecological information, and, in our perspective, employing probabilistic  
309 networks is an effective approach for such analyses.

310 There are no inherent differences in the taxonomic scaling between local networks and metawebs, as only the  
311 nodes are defined taxonomically. In other words, the probability values of edges in both local networks (eq. 2)  
312 and metawebs (eq. 3) are not conditional on any taxonomic scale. The phylogenetic scale is tied to the definition  
313 of the event itself (i.e., the interaction between two taxa), not to the conditional variables. In both types of  
314 networks, transitioning to a broader level of organization can be accomplished directly by using probabilities  
315 from finer scales. For example, in a network with  $n_A$  species from genus A and  $n_B$  species from genus B, one

316 can compute the probability that at least one species from genus  $A$  interacts with at least one species from genus  
317  $B$  as follows:

$$P(A \rightarrow B) = 1 - \prod_{i=1}^{n_A} \prod_{j=1}^{n_B} (1 - P(A_i \rightarrow B_j)), \quad (6)$$

318 where  $A_i$  and  $B_j$  are the species of the corresponding genus. If it is known that at least two of these species  
319 interact (i.e.,  $P(A_i \rightarrow B_j) = 1$  for at least one pair of  $i,j$ ), it implies a probability of genus interaction equal to 1.  
320 Canard *et al.* (2012) built a species-based network following a similar approach, by using simulated interactions  
321 between individuals derived from a neutral model (i.e., a model that assumed ecological equivalence among  
322 individuals). In contrast, a more sophisticated approach is necessary when transitioning from a broader to a  
323 finer level of organization. This is because knowledge of an interaction between two genera does not guarantee  
324 that all possible pairwise combinations of their species will also interact. One possible method is to build a  
325 finer-scale network by generating probabilities of interactions through random sampling from a beta  
326 distribution, parameterized by the broader-scale network.

327 Ideally, our biological interpretation of probabilistic interactions should remain consistent across a network  
328 even if it incorporates heterogenous levels of organization (e.g., a network whose nodes are composed of both  
329 species and trophic species). This is common in ecological networks where taxonomic resolution is typically  
330 low (Hemprich-Bennett *et al.* (2021), Vázquez *et al.* (2022)). Interaction probabilities at broader taxonomic  
331 scales should be based on probabilities of interactions between individuals, for both local networks and  
332 metawebs. For instance, in local individual-based food webs, the probability that two individuals interact  
333 reflects our degree of belief that one individual will consume the other. Similarly, in local species-based food  
334 webs, the probability that two species interact represents our degree of belief that at least one individual from  
335 the predator species consumes at least another individual from the prey species. Furthermore, in local  
336 clade-based food webs, the probability that two clades interact represents our degree of belief that at least two  
337 species from these clades interact with each other or, equivalently, that at least two individuals from these clades  
338 interact with each other. Fundamentally, the taxonomic scaling of interactions involves aggregating interactions  
339 between individuals into larger groups, which may exhibit varying degrees of homogeneity based on the  
340 organisms and the study system. In that regard, taxonomic scaling is analogous to the spatial and temporal  
341 scaling of interactions, as they all represent different ways to aggregate individuals into broader groups (either  
342 spatially, temporally, or taxonomically).

343 **Spatial and temporal scaling of interactions**

344 The investigation of network-area relationships (NARs) and interaction accumulation curves (IACs) is an  
345 important area of research in network ecology. First, NARs elucidate the scaling of network properties (such as  
346 modularity and trophic chain lengths) with spatial scale (e.g., Wood *et al.* (2015), Galiana *et al.* (2018)). The  
347 variations in network structure across spatial scales may stem from the scaling of species richness (species-area  
348 relationships, SARs) and the number of interactions (Brose *et al.* (2004)) with the sampled area. Additionally,  
349 ecological processes unfolding at distinct spatial scales, such as the spatial variability in local community  
350 composition resulting from different sequences of extinction and colonization events, can also contribute to this  
351 variation (Galiana *et al.* (2018)). Next, IACs describe the scaling of the number of observed interactions with  
352 sampling effort (Jordano (2016)), which can also impact various measures of network structure such as  
353 connectance (McLeod *et al.* (2021b)). Apart from sampling effort, the temporal scaling of interactions  
354 elucidates how network structure changes with the duration of the network (Poisot *et al.* (2012)),  
355 acknowledging that distinct interactions take place over time. Given that probabilistic local networks can  
356 quantify the spatiotemporal variability of interactions (eq. 2), they serve as valuable tools for developing and  
357 testing equations describing the scaling of network structure with space and time.

358 Metawebs and local networks exhibit distinct relationships with spatial and temporal scales. On one hand,  
359 probabilistic metawebs, being independent of any local context, feature potential interactions that do not scale  
360 with space and time. This is because potential interactions depend solely on the biological capacity of two taxa  
361 to interact, regardless of their co-occurrence and specific environmental conditions. This implies that the  
362 probability of two taxa potentially interacting should theoretically be the same in all metawebs in which they are  
363 present, provided that the data and methods used for estimation are consistent. As a result, if a smaller metaweb  
364  $M_1$  is derived from subsampling a regional metaweb  $M_0$  to represent potential interactions among a subset of  
365 taxa in a smaller region, their probabilities of interaction should be identical regardless of scale,  
366 i.e.  $P_{M_1}(i \rightarrow j) = P_{M_0}(i \rightarrow j)$ . However, because the number of taxa may be higher in the larger metaweb, it is  
367 expected that the overall number of interactions would be higher in the larger network, despite pairwise  
368 probabilities being identical.

369 On the other hand, local interactions scale both spatially and temporally, given that they have more opportunities  
370 to be realized and observed in larger areas and longer durations. This is attributed to factors such as a higher  
371 number of individuals, greater trait variations, and increased opportunities for encounters, as highlighted by

372 McLeod *et al.* (2020). For example, if a local probabilistic network  $N_1$  with an area  $A_1$  is derived from a larger  
373 network  $N_0$  with an area  $A_0$ , and  $A_1$  is entirely nested within  $A_0$ , interaction probabilities should be lower in the  
374 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  
375 probabilities could potentially be higher in the smaller area, contingent upon their environmental and biological  
376 conditions. Likewise, interaction probabilities are expected to be lower in networks with shorter durations when  
377 time intervals are nested. In fig. 2, we show how the expected number of local host-parasite interactions scales  
378 with area, represented as an expanding latitudinal window, in comparison with potential interactions. Even  
379 though we employed local probabilities of interactions equal to potential interactions for the purpose of  
380 comparison (i.e., using  $p = 1$  here), we notice that the total number of potential interactions scales more rapidly  
381 than local interactions. This is due to the fact that numerous potential interactions involve species that never  
382 co-occur, and as a result, these interactions are not captured in local networks.

383 [Figure 2 about here.]

#### 384 **Box 1: A spatiotemporally explicit model of interactions**

385 Predicting local networks across time and space is an important goal of network ecology (Strydom *et al.*  
386 (2021)). Indeed, in a context of scarcity of interaction data (Jordano (2016)), ecologists must rely on predictive  
387 models to reconstruct networks at fine spatial and temporal scales. For example, local ecological networks  
388 could be reconstructed using real-time biomonitoring data and adequate numerical models (Bohan *et al.*  
389 (2017)), which could pave the way for fine-scale studies of ecosystem functioning and dynamics. Besides  
390 predictive models, statistical models can also be built to describe parameters of interest, such as probabilities of  
391 interactions. In that case, parameter values provide valuable ecological information in their own rights.  
392 Different types of models (e.g., Bayesian and machine learning models) of ecological interactions have been  
393 built for predictive and descriptive purposes (Strydom *et al.* (2021)). Representing interactions probabilistically  
394 reflects the uncertainty of these models, which is usually represented in terms of probability distributions. Here  
395 we show how to build a simple generative mechanistic model of probabilistic interactions that takes into account  
396 their inherent spatiotemporal variability, i.e. a spatiotemporally-explicit model. Our model is not suitable for  
397 potential interactions, which are scale-independent. Rather, it could prove useful for predicting local  
398 interactions across time and space by generating new interaction data after parameter inference.

399 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

400 of their probability of interaction given co-occurrence and their probability of co-occurrence. First, their  
 401 probability of co-occurrence is given by their respective probabilities of occurrence  $P_i(x, y)$  and  $P_j(x, y)$  and the  
 402 strength of association  $\gamma$  between their occurrence and co-occurrence (Cazelles *et al.* (2016)):

$$P_{i,j}(x, y) = P_i(x, y)P_j(x, y)\gamma. \quad (7)$$

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

$$C \sim \text{Bernoulli}(P_{i,j}(x, y)). \quad (8)$$

406 Second, the probability of interaction given co-occurrence can be made temporally explicit by modeling it as a  
 407 Poisson process with rate  $\lambda$ . This parameter corresponds to the expected frequency of interaction between both  
 408 taxa in a given time period and its value can be estimated using prior data on interaction strengths, if available.  
 409 Specifically, the probability that two co-occurring taxa interact during a time period  $t_0$  is:

$$P_N(i \rightarrow j|C = 1) = 1 - e^{-\lambda t_0}, \quad (9)$$

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

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

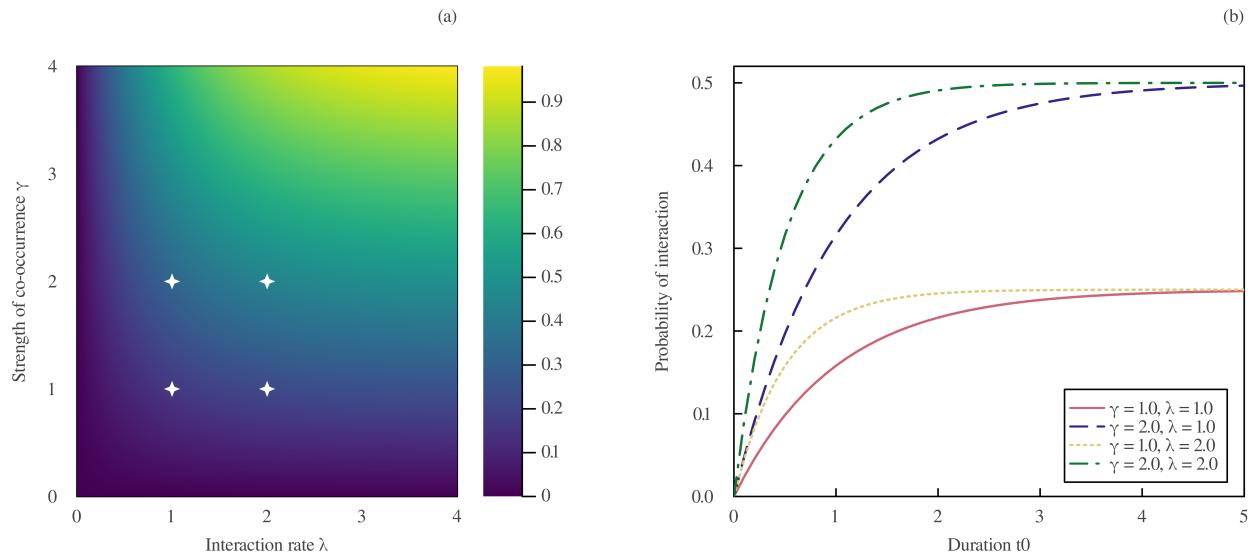
$$I \sim \text{Bernoulli}(P_N(i \rightarrow j)) \quad (10)$$

$$P_N(i \rightarrow j) = P_i(x, y)P_j(x, y)\gamma(1 - e^{-\lambda t_0}) \quad (11)$$

$$\gamma \sim \text{Gamma}(2, 0.5) \quad (12)$$

$$\lambda \sim \text{Exponential}(2) \quad (13)$$

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



419

## 420 Sampling binary networks

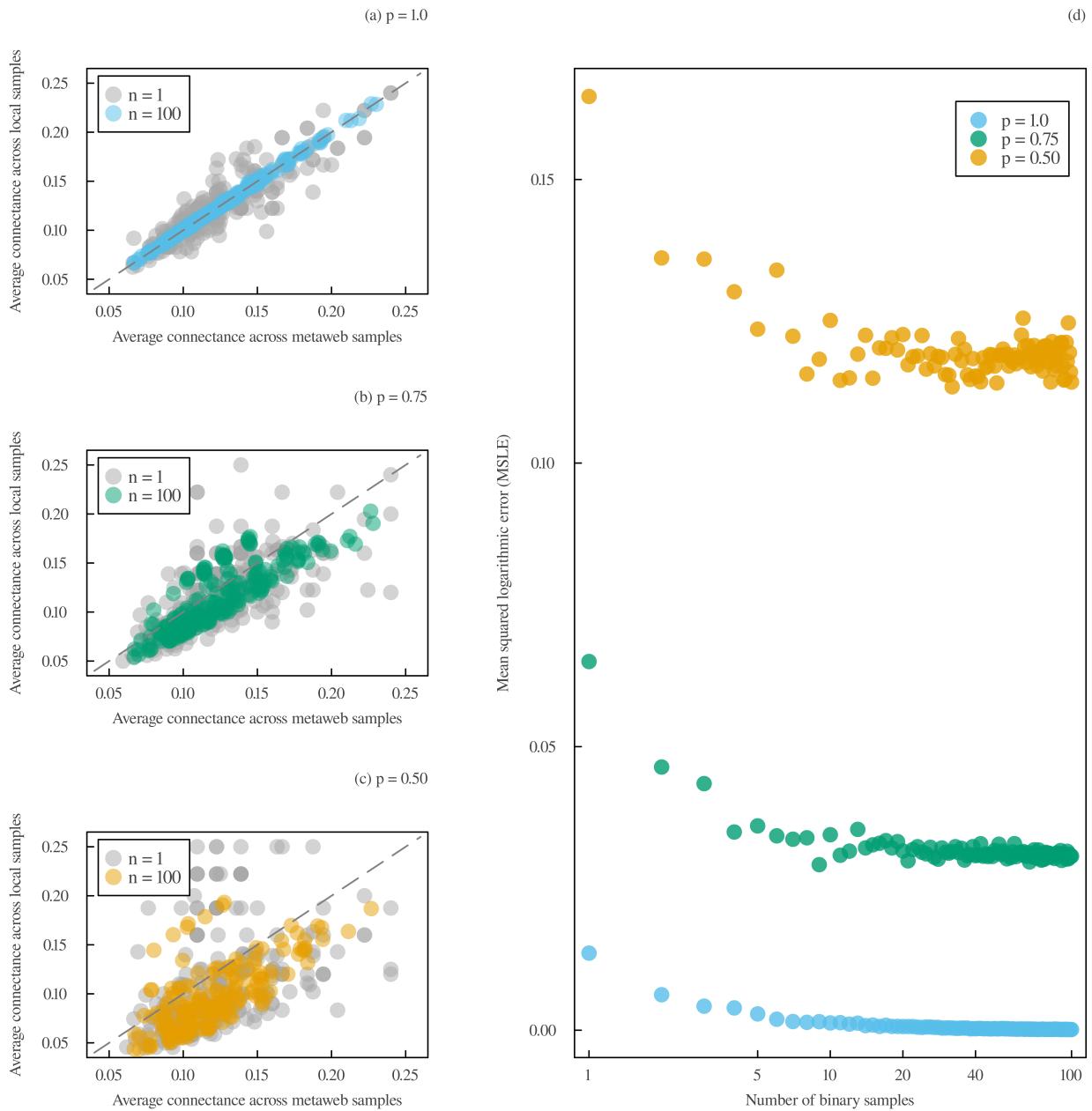
421 Probabilistic networks can be used to predict binary interactions through random draws. This can be useful  
 422 when analyzing the structure of a probabilistic network when analytical probabilistic measures are lacking. A  
 423 binary network can be generated from independent Bernoulli trials for each interaction. The distribution of a  
 424 network's property can then be obtained after measuring the structure of all randomly generated networks  
 425 (Poisot *et al.* (2016)). Doing so allows us to represent the variability of network structure, although possibly  
 426 with biases when connectance is low (Poisot & Gravel (2014), Chagnon (2015)). When binary networks are  
 427 generated under a null model, this method can be used for null hypothesis significance testing, in which case the  
 428 observed measure is compared to a null distribution (e.g., Bascompte *et al.* (2003)). Furthermore, randomly  
 429 generating binary networks across space and time can help us visualize the spatiotemporal variability of  
 430 network structure and test ecological hypotheses on interactions across large spatial and temporal scales.

431 There are at least two different approaches when sampling binary networks from probabilistic webs across  
 432 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  
 433 single Bernoulli trial for each pair of taxa found in the region of interest based on their regional probability of  
 434 interaction. As a result, each pair of taxa that are predicted to interact in the regional network realization will  
 435 interact in all of the  $n^2$  networks in which they co-occur. This sampling technique is best used with potential  
 436 interactions that have no spatial variation. The second approach is to independently sample each of the  $n^2$

437 networks. In practice, this can be done by generating a different probabilistic network for each grid cell.  
438 Depending on how they were obtained, these networks can differ in their taxa composition (nodes) and/or  
439 interaction probabilities (edges). Then, binary networks can be independently sampled for each grid cell.  
440 Because this method generates spatial variation in binary interactions, it is best used with local interactions.  
441 The choice of sampling approach has an impact on the selection of grid cell size. In the first approach,  
442 interactions will be the same regardless of cell size because interactions are sampled only once from the  
443 regional network. However, in the second approach, local interaction probabilities depend on the network area.  
444 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  
445 contiguous cells that form  $N_0$ . If  $N_1$  and  $N_2$  are independent (which is rarely the case in reality because of  
446 spatial auto-correlation), the probability that two taxa  $i$  and  $j$  interact in  $N_0$  is given by:

$$P_{N_0}(i \rightarrow j) = 1 - (1 - P_{N_1}(i \rightarrow j)) \times (1 - P_{N_2}(i \rightarrow j)). \quad (14)$$

447 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  
448 sampling binary interactions from local networks, it is thus important to sample at the same spatial scale as the  
449 one for which probabilities were estimated. Otherwise, interaction probabilities must be adjusted to correspond  
450 to the targeted cell size and avoid systematic biases in prediction.



451

## 452 Prediction of local networks from metawebs

453 Metawebs are an important source of ecological information that can be leveraged for predicting local networks.  
 454 Indeed, binary local networks can be reconstructed by selecting a subset of both taxa and interactions from the  
 455 metaweb (Dunne (2006)). This implies that there are always more interactions in a metaweb compared to its  
 456 corresponding local networks. In practice, because a community's composition is arguably easier to sample or  
 457 predict than its interactions, the list of taxa to select can be known empirically or obtained using range maps or

458 species distribution models. The challenge is rather to choose which interactions to select from the metaweb,  
459 which could require more sophisticated statistical models and ecological knowledge. Because the structure of  
460 local networks is constrained by the one of the metaweb (Saravia *et al.* (2022)), inferring their structure from  
461 the metaweb before predicting local pairwise interactions could prove promising (Strydom *et al.* (2021)).

462 When building probabilistic local networks from a probabilistic metaweb, interaction probabilities decrease.  
463 This is because two taxa must first have the capacity to interact (i.e.,  $M_{i,j}^* = 1$  in the binary metaweb  $M^*$ ) before  
464 interacting locally:

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

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

$$P_N(i \rightarrow j | A, t, C, \Omega) \leq P_M(i \rightarrow j). \quad (15)$$

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

$$\int_{\Omega} \int_A \int_t P_N(i \rightarrow j | A, t, \Omega) dt dA d\Omega \leq P_M(i \rightarrow j). \quad (16)$$

## 475 Conclusion

476 In this contribution, we underline the importance of network metadata for adequately interpreting and  
477 manipulating probabilistic interaction data. The mathematical representation of probabilities and their statistical

478 properties depend on the type of interactions (local or potential) and the conditions in which they were  
479 estimated. We showed that probabilistic local networks and metawebs differ in their relationship to spatial and  
480 temporal scales, with potential interactions remaining consistent across scales. In contrast with metawebs, local  
481 interactions are measured in a specific context (e.g., in a given area, time, and biological and environmental  
482 conditions) and depend on taxa co-occurrence. These important conceptual differences bring to light the need  
483 to use probabilistic data with caution, for instance when generating binary network realizations across space and  
484 predicting local networks from metawebs. Clear metadata describing the type of interaction and the variables  
485 used in their estimation are required to ensure adequate data manipulation. Better data practices and  
486 foundations for probabilistic thinking in network ecology could enable more reliable assessments of the  
487 spatiotemporal variability and uncertainty of biotic interactions.

488 It is essential to enhance our comprehension of both potential and local interactions, especially considering the  
489 current scarcity of interaction data. However, while sampling biological communities does decrease the  
490 uncertainty of interactions by accumulating evidence for their feasibility and local realization, there is a limit to  
491 how much we can diminish their inherent randomness. In metawebs, probabilities reflect our limited knowledge  
492 of interactions (i.e., our degree of belief that interactions are feasible), which is expected to improve with a  
493 larger volume of data. We should anticipate that potential interactions will become more definitive (with  
494 probabilities approaching 0 or 1) as we investigate various conditions, including different combinations of  
495 species traits. Conversely, in the case of local networks, which can be seen as random instances of metawebs,  
496 randomness cannot be as reduced. In local interactions, probabilities can be divided into a component  
497 representing uncertainty and another representing spatiotemporal variability. Owing to environmental  
498 heterogeneity, there will invariably be instances in which an interaction occurs and others in which it does not,  
499 across different times and locations, irrespective of the extent to which we can improve our knowledge of its  
500 biological feasibility and the local conditions that facilitate its occurrence. When local networks depict  
501 probabilities of observing interactions rather than just their actual occurrence, we must also consider the  
502 observation variability as an additional source of randomness. Every ecological process is stochastic but there is  
503 also a possibility that a phenomenon goes undetected. Quantifying and partitioning this stochasticity will enable  
504 us to make more accurate predictions about ecological interactions at various spatial and temporal scales.

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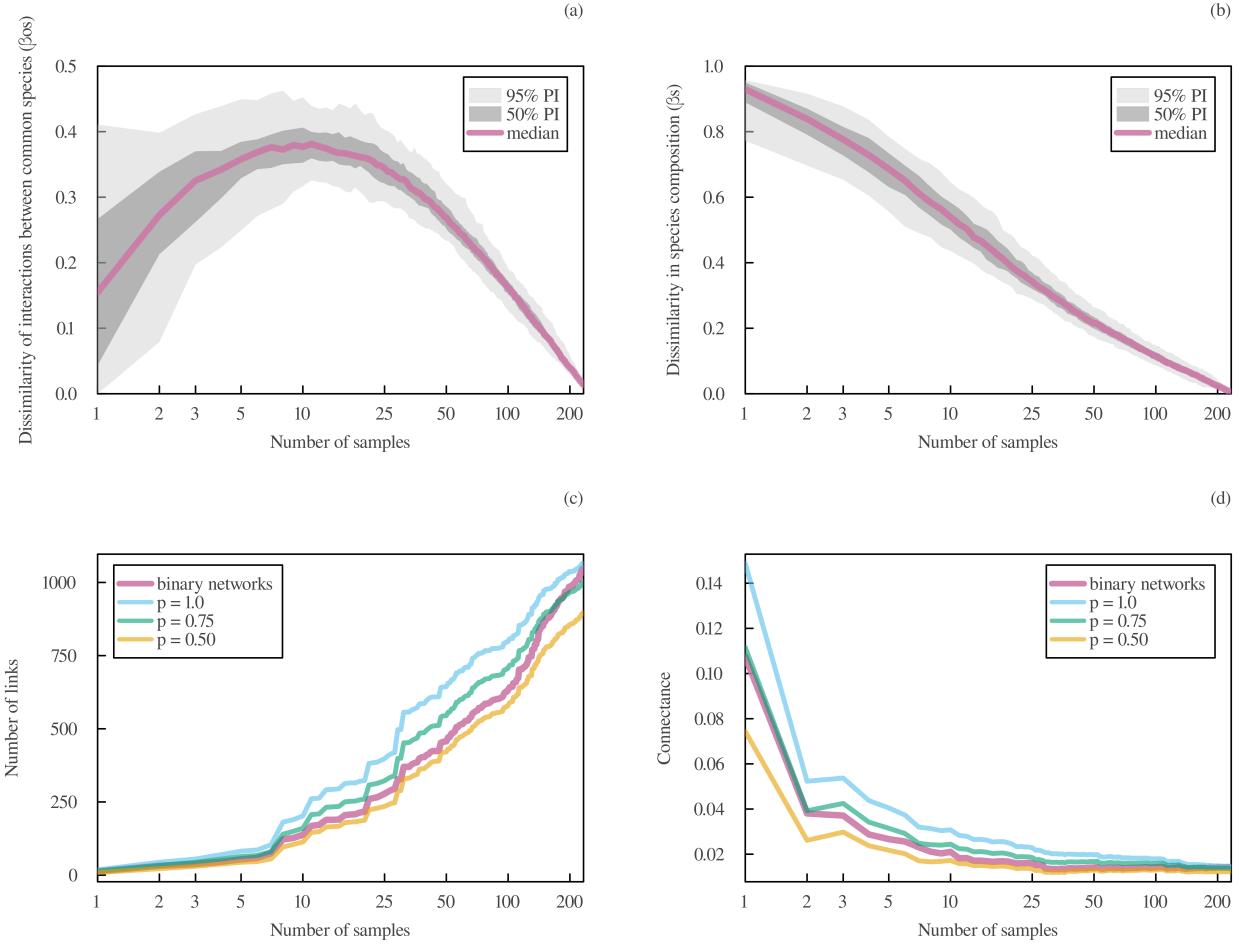
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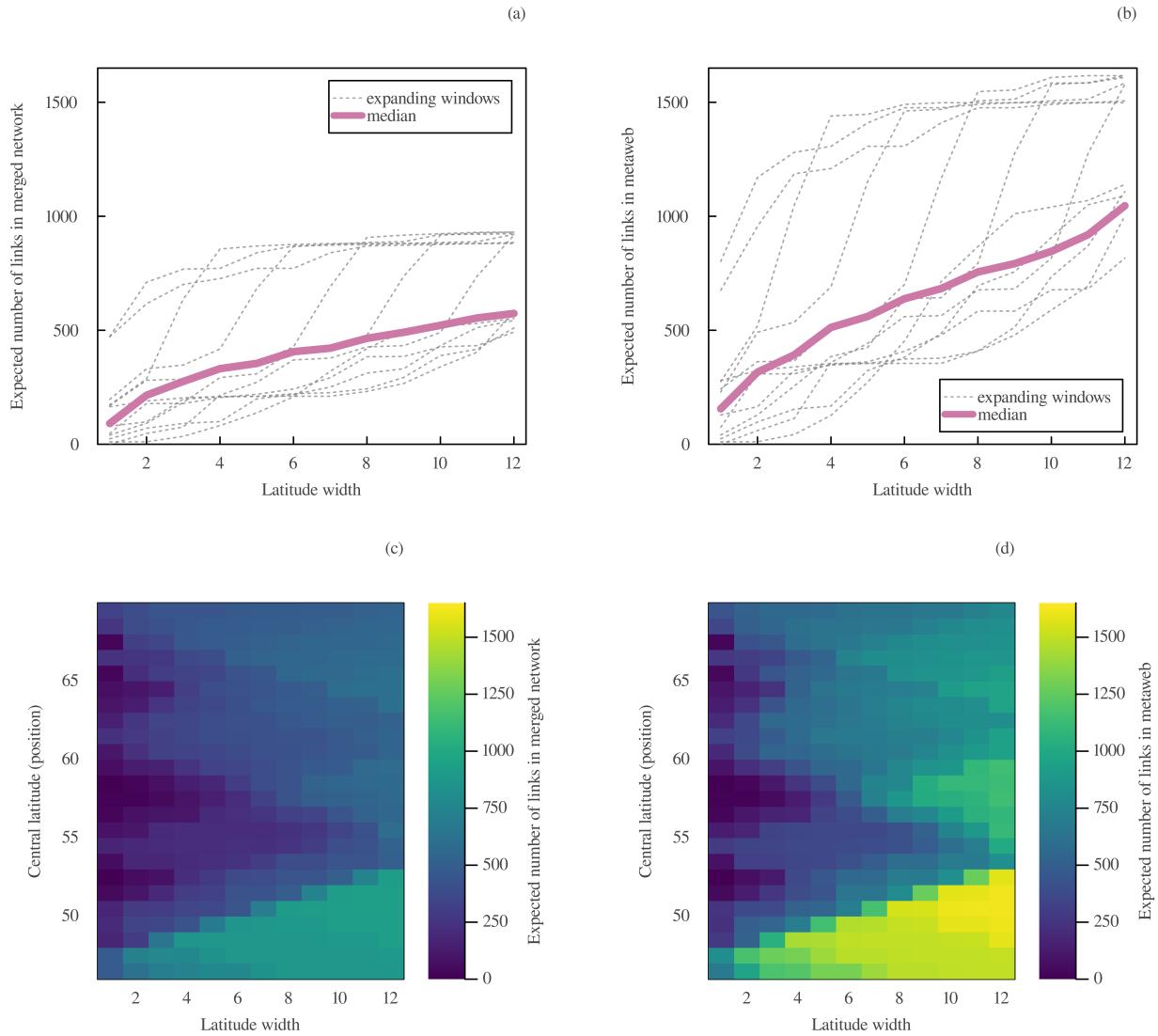
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**Figure 1: Network accumulation curves.** (a) Dissimilarity of interactions between common species and (b) dissimilarity in species composition between aggregated local networks and the binary metaweb of host-parasite interactions. Aggregated local networks were obtained by sequentially and randomly selecting a number of binary local networks and aggregating both their species and interactions. In both panels, the colored line represents the median dissimilarity across simulations and the grey areas cover the 50% and 95% percentile intervals. (c) Scaling of the number of links and (d) scaling of connectance with the number of sampled binary and probabilistic local networks. For a better comparison with binary networks, local probabilistic networks were derived from the probabilistic metaweb with a false positive and false negative rates of zero. A specific value of  $p$  (the local probability of interaction among potentially interacting species) was used for all local networks within a particular curve. Aggregated probabilistic local networks were obtained by sequentially and randomly selecting a number of probabilistic local networks and aggregating both their species and interactions (with the value of  $p$  adjusting according to eq. 5).



**Figure 2: Spatial scaling of interactions.** Expected number of host-parasite interactions in a network aggregating all probabilistic (a) local and (b) potential interactions within a latitudinal window of a given length. Every dashed curve corresponds to a different expanding window characterized by a different central latitude, with the colored solid line representing the median number of interactions. Heatmaps of the expected number of (c) local and (d) potential interactions found in windows of specified length and central latitudes. Probabilities of potential interactions were obtained with a false positive rate of 5% and a false negative rate of 10%. Local probabilistic interactions were derived from the probabilistic metaweb by setting the value of  $p$  (the local probability of interaction among potentially interacting species) to 1, ensuring a conservative comparison between aggregated local networks and metawebs. Aggregated local networks were obtained by aggregating both the species and interactions found within a particular latitudinal window, with the values of  $p$  remaining at their maximum value of 1 following eq. 5.