

# Deciphering ecological networks of probabilistic interactions

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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 to occur?) as opposed to deterministically (are they occurring?) highlights uncertainties in our knowledge of interactions. The origin of the uncertainty captured by interaction probabilities differs depending on the method used to evaluate them. It may consist of the uncertainty of predictive models, the subjective assessment of experts, or even the empirical evaluation of interaction spatiotemporal variability. Despite this growing interest in probabilistic interactions, guidelines for the estimation and documentation of probabilistic interaction data are still lacking. This is concerning because our biological understanding of interaction probabilities and the decisions made during data analysis rely heavily on the often elusive definition of the probabilistic event. 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 (predatory, herbivory, and parasitic interactions). These definitions are based on the distinction between the realization of an interaction at a specific time and space (local) and its biological feasibility (regional). Through case studies using open data on host-parasite interactions in Europe, we show that these two network representations have different statistical properties when it comes to common ecological applications. Specifically, we found that local and metawebs differ in their spatial and temporal scaling of probabilistic interactions, but not in their taxonomic scaling. We suggest two approaches to inferring binary interactions from probabilistic ones that account for these differences and show that systematic biases arise when directly inferring local webs from subsets of metawebs. Our results underscore the importance of clear metadata for networks of probabilistic interactions that describe the type of interaction (local or regional)

and uncertainty sources. Comprehensive metadata are particularly useful for the identification of optimal sampling locations where data collection may provide the greatest amount of new information on interactions and minimize their uncertainty.

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## **1 Introduction**

2 As we try to navigate global biodiversity change, filling in knowledge gaps about biodiversity becomes  
3 instrumental to monitoring and mitigating those changes (Gonzalez & Londoño (2022), Abrego *et al.* (2021)).  
4 However, cataloging species, populations and, in particular, ecological interactions (e.g., predation, parasitism,  
5 and pollination) is a substantial challenge (Polis (1991), Pascual *et al.* (2006)). There are methodological and  
6 biological constraints that hinder our ability to observe all ecological interactions, leading to significant  
7 uncertainties in our understanding of these interactions. For example, the spatial and temporal uncoupling of  
8 species (e.g., nocturnal and diurnal species coexisting in the same space without interacting due to differences  
9 in the timing of their daily activities, Jordano (1987)) and the large number of rare and cryptic interactions in a  
10 community contribute to these uncertainties (Jordano (2016)). More generally, a handful of conditions must be  
11 satisfied for an interaction to be observed locally. First, both species must have overlapping geographic ranges,  
12 i.e. they must co-occur within the region of interest (Blanchet *et al.* (2020)). Second, they must have some  
13 probability of meeting. Probabilities of interspecific encounters are typically low, especially for rare species  
14 with low abundances. While species' absolute abundances may impact interaction frequencies (Vázquez *et al.*  
15 (2007)), encounter probabilities are determined by their relative abundances (Canard *et al.* (2012), Canard *et al.*  
16 (2012)). The probability that species meet each other also depends on their biological characteristics, such as  
17 the synchronization of their phenology (Olesen *et al.* (2010), Singer & McBride (2012)) and their  
18 discoverability (e.g., Broom & Ruxton (2005)). Finally, when species do come into contact, an interaction  
19 occurs only if their traits are locally compatible (Poisot *et al.* (2015)), including but not limited to their body  
20 phenotypes (Bolnick *et al.* (2011), Stouffer *et al.* (2011), Gravel *et al.* (2013)) and behavioral choices (Pulliam  
21 (1974), Choh *et al.* (2012)). Interactions may also be influenced by the presence or prevalence of a third species  
22 (e.g., of a more profitable prey species, Golubski & Abrams (2011), Sanders & van Veen (2012)). Documenting  
23 the location and timing of interactions becomes even more difficult when accounting for the spatiotemporal  
24 variability of ecological interactions (Poisot *et al.* (2012), Poisot *et al.* (2015)). Environmental factors, such as  
25 temperature (Angilletta *et al.* (2004)), drought (Woodward *et al.* (2012)), climate change (Gilman *et al.* (2010),  
26 Woodward *et al.* (2010), Araujo *et al.* (2011)), and habitat modifications (Tylianakis *et al.* (2007)), contribute  
27 to this spatiotemporal variability by impacting species abundance and traits. Even after satisfying all these  
28 conditions, there remains a possibility that the interaction does not occur locally, either due to the intricate  
29 nature of the system or simply by chance. If it does occur, it might still go unnoticed, particularly if it happens  
30 infrequently. In this context, it is unsurprising that our knowledge of ecological interactions remains limited

31 (Hortal *et al.* (2015)) despite extensive biodiversity data collection (Schmeller *et al.* (2015)).

32 Knowing the biological capacity of two species to interact directly (via e.g., trophic interactions) is necessary

33 but not sufficient for inferring their interaction at a specific time and space. The recognition of the intrinsic

34 variability of species interactions has led ecologists to expand their representation of ecological networks (also

35 known as ecological webs) to include a probabilistic view of interactions (Poisot *et al.* (2016), Dallas *et al.*

36 (2017), Fu *et al.* (2021)). This different perspective allows us to fill in the Eltonian shortfall (Hortal *et al.*

37 (2015)) by modeling the probability of occurrence of interactions, which can be an important tool for directing

38 efforts and taking action, especially in places where access and resources for research are scarce. The

39 probabilistic representation of interactions is thus far limited to direct interactions, which are conceptually and

40 mathematically analogous regardless of their biological type (e.g., predation and pollination). This is in contrast

41 with indirect interactions (e.g., interspecific competition), which arise from distinct ecological processes and are

42 often not directly observable (Kéfi *et al.* (2015), Kéfi *et al.* (2016)). Representing direct interactions

43 probabilistically enables us to capture the spatiotemporal variability of the aforementioned ecological processes

44 and the uncertainties associated with their occurrence. As opposed to webs of binary deterministic interactions,

45 in which interactions are regarded as either occurring or not, webs of probabilistic interactions, within a

46 Bayesian framework, express our degree of belief (or confidence) regarding the occurrence or observation of

47 interactions. Based on the scale at which they are estimated, probabilistic interactions may reflect our level of

48 confidence in whether interactions will be observed, realized locally, or biologically feasible. As an illustration,

49 we could outline a situation in which there is a 50% certainty that an interaction occurs 50% of the time, or that

50 there is a 50% certainty that it simply occurs. Our level of confidence should be more definitive (approaching

51 either 0 or 1) as we extend our sampling to a broader area and over a longer time period, thereby diminishing the

52 uncertainty of the interactions (but not necessarily the estimation of their variability). In the broadest sense,

53 binary interactions are also a type of probabilistic interaction, in which the numerical value of an interaction is

54 restrained to 0 (non-occurring) or 1 (occurring). Yet, for the sake of clarity, we omit binary interactions from

55 our discussion of probabilistic interactions in this contribution. In networks of probabilistic interactions, only

56 forbidden interactions (i.e., interactions prohibited by biological traits or species absence, Jordano *et al.* (2003),

57 Olesen *et al.* (2010)) have a probability value of zero, provided that intraspecific trait variability is considered

58 (Gonzalez-Varo & Traveset (2016)).

59 By accounting for the uncertainty of interactions, networks of probabilistic interactions may provide a more

60 realistic portrait of species interactions. However, how the uncertainty of pairwise interactions propagates to

network structure (i.e., community-level properties driving the functioning, dynamics, and resilience of ecosystems, Proulx *et al.* (2005), McCann (2007), McCann (2011), Rooney & McCann (2012)) remains to be elucidated. The application and development of computational methods in network ecology, often based on a probabilistic representation of interactions, can alleviate (and guide) 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 webs 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 networks, 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 predictions of ecological webs 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, which generate networks of probabilistic interactions by preserving chosen characteristics of the adjacency matrix of binary interactions while intentionally omitting others (Bascompte *et al.* (2003), Fortuna & Bascompte (2006)), serve as other examples of common probabilistic interaction models.

Null models can be used to produce underlying distributions of network measures for null hypothesis significance testing. 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 interaction webs. 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 webs (Gilman *et al.* (2010)).

The lack of clear guidelines on the use of probabilistic interaction data is worrisome, both for data producers and re-users who generate and manipulate these numbers. This is concerning because sampling strategies and decisions regarding network construction can affect our understanding of network properties (Brimacombe *et al.* (2023)). Besides methodological difficulties that may arise when assessing probabilistic interactions, a precise definition of probabilistic interactions appears to be lacking, making the estimation and use of these data

more difficult. We aim to take a step back by outlining different ways in which probabilistic interactions are defined and used in network ecology. We distinguish two broad categories of probabilistic interaction networks that necessitate distinct approaches when applied to key ecological questions: local webs describing probabilities of realized interactions, and regional webs (metawebs) describing probabilities of potential interactions. We highlight the distinctions in the ecological meaning of these two representations and examine some of their properties and relationships (particularly with space, time, and between each other) through empirical case studies. Moreover, there is currently no metadata standard that could guide the documentation of all types of probabilistic interactions (although see e.g., Salim *et al.* (2022) who discuss data standards for deterministic mutualistic webs). Well-defined metadata for probabilistic interactions would support more adequate manipulation and integration of interaction data from different sources and guard against possible misinterpretations arising from ambiguous definitions of probabilistic interaction networks. These metadata should outline the nature (i.e., local or regional) and type (e.g., predatory or pollination) of the interactions, provide information regarding the taxonomic level, identities, and characteristics (e.g., life stages) of the individuals involved in an interaction, present the mathematical formulation of probabilities, including clearly identified conditional variables (e.g., spatial and temporal scales), and describe the methods and contexts (e.g., location, time, environmental conditions) in which interactions were estimated. Inadequately documented probabilistic interaction data should be used with caution when analyzing ecological webs. Our observations and advice can be applied to most types of ecological networks representing direct interactions, from food webs to host-virus networks. Even though the measurement of interaction probabilities may differ between network types (e.g., estimations often based on frequencies of interactions in plant-pollinator networks), the broad principles underlying our findings remain relevant and applicable across diverse ecological contexts.

## Probabilistic representations of interactions

Consider a scenario where a species of avian predator has just established itself in a northern habitat home to a small rodent species. Suppose these species have never co-occurred before, and as a result, their interaction has not been previously observed. What is the probability that the rodent is part of the diet of the avian predator, or put differently, what is the probability that they interact? Answering this question requires some clarification, as there are multiple ways to interpret and calculate interaction probabilities. We may calculate the probability that the traits of these species match, i.e. that the avian predator possesses the biological attributes to capture and

119 consume the rodent. We may also calculate the probability that their traits support an interaction under the  
120 typical environmental conditions of the new habitat. For example, because avian predators hunt by sight,  
121 predation could be possible in the absence of snow but highly improbable when snow is present, as rodents may  
122 use it as a shelter to hide from predators. Finally, we may calculate the probability that the avian predator will  
123 consume the rodent at *that* particular location, for which the spatial and temporal boundaries need to be  
124 specified. The estimation of interaction probabilities, whether through predictive models or prior distributions,  
125 hinges on our comprehension of these probabilities and the specific ecological processes we aim to capture.

126 One of the first aspects to take into consideration when estimating or interpreting probabilities of interactions is  
127 knowing if they describe potential or realized interactions, as these two types of interactions have distinct  
128 conceptual underpinnings and sources of uncertainty. A potential (regional) interaction is defined as the  
129 biological capacity of two taxa to interact (i.e., the probability that they interact if they were to encounter each  
130 other and given sufficient time) whereas a realized (local) interaction is the occurrence or observation of this  
131 interaction in a well-defined space and time (i.e., the probability that they interact locally). For two co-occurring  
132 taxa and over infinite time, the probability of local interaction is equivalent to the probability of regional  
133 (potential) interaction. Our discussion of local interactions focuses on their occurrence rather than their direct  
134 empirical observation, as one of the primary goals of describing them probabilistically is to characterize our  
135 uncertainty regarding their actual realization. We use the terms *metaweb* (Dunne (2006)) to designate regional  
136 webs of potential interactions and *local webs* (Poisot *et al.* (2012)) for those of realized interactions. Metawebs  
137 are the network analogs of the species pool, where local webs originate from a subset of both species (nodes)  
138 and interactions (edges) of the regional metaweb (Saravia *et al.* (2022)). Without clear documentation, it can be  
139 challenging to know if published probabilistic interaction webs describe local or regional interactions (tbl. 1  
140 provides examples of studies employing both types of probabilistic interaction networks), or if so-called  
141 probabilities are in reality *interaction scores* (i.e., non-probabilistic quantitative interactions analogous to  
142 interaction strengths). When probabilistic regional interactions are used and interpreted incorrectly as local  
143 interactions (and conversely), this may generate misleading findings during data analysis. We believe that a  
144 better understanding of the differences, similarities, and interconnections between these two probabilistic  
145 representations of ecological interactions would alleviate interpretation errors (e.g., when studying network-area  
146 relationships) and facilitate a more adequate utilization of interaction data.

147 **Pairwise interactions: the building blocks of ecological networks**

148 Local and metawebs, like any type of network, are made of nodes and edges that may be represented at different  
149 levels of organization and precision. The basic units of ecological networks are individuals that interact with  
150 each other (e.g., by predation in food webs, Elton (2001)), forming individual-based networks (Melián *et al.*  
151 (2011)). The aggregation of these individuals into more or less homogeneous groups (e.g., populations, species,  
152 families, feeding guilds) allows us to represent nodes at broader taxonomic scales, which affects our  
153 interpretation of the properties of these systems (Guimarães (2020), Hemprich-Bennett *et al.* (2021)).  
  
154 Edges linking nodes may describe a variety of interaction measures. Ecologists have traditionally represented  
155 interactions as binary objects that were considered realized after observing at least one individual from group  $i$   
156 interact with at least another individual from group  $j$ . In an adjacency matrix  $B$  of binary interactions, the  
157 presence or absence of an interaction  $B_{i \rightarrow j}$  between two taxa can be viewed as the result of a Bernoulli trial  
158  $B_{i \rightarrow j} \sim \text{Bernoulli}(P(B_{i \rightarrow j}))$ , with  $P(B_{i \rightarrow j})$  being the probability of interaction. This interaction probability  
159 characterizes our limited ecological knowledge and/or the intrinsic spatiotemporal variability of interactions. It  
160 may be estimated through predictive models (e.g., those based on biological traits and species abundances) or  
161 expert (prior) knowledge about the interaction. In networks of probabilistic interactions,  $P(B_{i \rightarrow j})$  are edge  
162 values, and the only two possible outcomes are the presence ( $B_{i \rightarrow j} = 1$ ) or absence ( $B_{i \rightarrow j} = 0$ ) of an interaction  
163 between each pair of nodes. Depending on the type of probabilistic interaction network (local or metaweb), the  
164 mathematical formulation and interpretation of stochastic parameters like  $P(B_{i \rightarrow j})$  can be linked to  
165 environmental and biological factors such as species abundance, traits, area, and time (tbl. 1), for example using  
166 logistic regression with continuous explanatory variables. Predicting the number of local webs in which the  
167 interaction between two given taxa occurs can be achieved by using a Binomial distribution, assuming a constant  
168 interaction probability and independence between networks (trials). When considering uncertainties around the  
169 estimation of  $P(B_{i \rightarrow j})$  or its spatiotemporal variability, a Beta distribution may be used to represent the relative  
170 likelihood of different probability values. For example, when calculating the probability of interaction between  
171 two taxa based on their local abundances, any spatiotemporal fluctuations in their abundances would introduce  
172 variability in the interaction probability at the local scale. If we take into account the stochasticity of the  
173 interaction probability, a Beta-Binomial distribution can be used to predict the number of networks in which the  
174 interaction occurs. Empirically observing an interaction between two taxa at a given location and time provides  
175 important information that can be used to update previous estimates of  $P(B_{i \rightarrow j})$ , informing us on the biological  
176 capacity of both taxa to interact and the environmental conditions that enabled them to interact locally.

177 Even though binary interaction webs constitute a highly valuable source of ecological information (Pascual *et*  
178 *al.* (2006)), they overlook important factors regarding interaction strengths. Represented in a quantitative  
179 adjacency matrix  $W$  as numbers not confined to the  $[0, 1]$  range, interaction strengths better describe the energy  
180 flows, demographic impacts or frequencies of interactions between nodes (Berlow *et al.* (2004), Borrett &  
181 Scharler (2019)), with  $W_{i \rightarrow j}$  being a natural  $\mathbb{N}$  or real  $\mathbb{R}$  number depending on the measure. For example, they  
182 may represent local interaction rates between pairs of taxa (e.g., the flower-visiting rates of pollinators in a  
183 mutualistic network, Herrera (1989)). When interaction strengths characterize predation pressure on prey taxa  
184 in food webs, they can serve as good estimators of the parameters describing species interactions in a  
185 Lotka-Volterra model (e.g., Emmerson & Raffaelli (2004)). The extra amount of ecological information in  
186 quantitative networks typically comes at a cost of greater sampling effort and data volume in predictive models  
187 (Strydom *et al.* (2021)), which can lead to relatively high levels of uncertainties when inferring quantitative  
188 webs with limited data.

189 Just like binary interaction networks, the uncertainty and spatiotemporal variability of interaction strengths can  
190 be represented probabilistically. However, the need to estimate the probability distribution of all possible values  
191 of interaction strengths can make the inference of probabilities more challenging in quantitative webs compared  
192 to binary interaction webs, which require only one probability estimate for each interaction. Interaction  
193 strengths can follow various probability distributions depending on the measure used. For instance, they can  
194 follow a Poisson distribution  $W_{i \rightarrow j} \sim \text{Poisson}(\lambda_{i \rightarrow j})$  when predicting frequencies of interactions between pairs  
195 of nodes, with  $\lambda_{i \rightarrow j}$  being the expected rate at which individuals of taxa  $i$  and  $j$  interact (e.g., the average  
196 number of prey  $j$  consumed by all predators  $i$  in a given time period). The Poisson distribution can also be  
197 0-inflated after initially modeling non-interacting taxa (e.g., Boulangeat *et al.* (2012) employ a 0-inflated model  
198 to analyze species abundance following the modeling of species presence and absence), which constitute the  
199 majority of taxa pairs in most local webs due to their typically high sparseness (Jordano (2016)). Because of the  
200 methodological difficulties typically encountered when building deterministic quantitative webs (which are only  
201 partially mitigated by models such as Ecopath, Plagányi & Butterworth (2004)), binary interaction webs, which  
202 are easier to sample (Jordano (2016)) and predict (Strydom *et al.* (2021)), have been more frequently studied  
203 and modeled. Moreover, most published networks of probabilistic interactions and methods describe  
204 probabilistic interactions whose outcome is binary (whether interaction probabilities are regarded as constant or  
205 variable, e.g. represented by a Beta distribution), which underlines the need for better guidelines regarding the  
206 interpretation and manipulation of these types of webs first. For these reasons, our primary focus in this

207 contribution will be on addressing the challenges in interpreting and using interaction probabilities in Bernoulli  
208 distributions, in both local and metawebs.

## 209 Local webs: communities interacting in space and time

210 Local webs of probabilistic interactions describe how likely taxa are to interact at a given location and time  
211 period. Local interactions are contingent upon the environmental and biological conditions of the community.  
212 In local webs, edges commonly represent our degree of belief that two taxa interact in nature, but can also  
213 represent the probability of *observing* this interaction (Catchen *et al.* (2023)). For example, Gravel *et al.* (2019)  
214 analyzed local European trophic webs of willow-galling sawflies and their natural enemies depicting binary  
215 interactions, all referenced in space and time, to infer the probabilities of locally observing interactions between  
216 co-occurring species. This was achieved by situating local webs within the context of environmental variables,  
217 i.e. by including temperature and precipitation as conditional variables in some of their models.

218 We define space as the collection of geographic coordinates  $(x, y, z)$ , with  $(x, y)$  representing longitude and  
219 latitude coordinates, and  $z$  denoting either altitudes or depths. These point coordinates delineate the spatial  
220 boundaries of the system, which may be portrayed as a polyhedron. Ecological interactions may exhibit  
221 variations along latitudinal and altitudinal gradients, as evidenced by changes in hummingbird-plant interactions  
222 (Weinstein & Graham (2017b), Weinstein & Graham (2017a)) and mosquito biting rates (e.g., Kulkarni *et al.*  
223 (2006)) at different elevations. In contrast, time is defined as the specific time period within which interactions  
224 were either observed or predicted. Even though space and time are continuous variables that should yield  
225 probability *densities* of interactions (i.e., relative likelihoods of interactions occurring at infinitesimal locations  
226 and instants in time), these definitions enable them to be conceptualized as distinct patches and time segments.

227 Treating space and time as discrete dimensions aligns with the common sampling methods of ecological  
228 networks and provides actual probabilities of interactions, which can be obtained by integrating probability  
229 densities over space and time. Furthermore, we can quantify both an area  $A$  and a duration  $t$ , which can be  
230 readily used in spatiotemporal analyses of ecological networks. For example, when studying network-area  
231 relationships (NAR, Galiana *et al.* (2018)), we anticipate that local probabilities of interactions scale positively  
232 with area and duration because taxa have more opportunities to interact as these dimensions expand.

233 The probability that two taxa  $i$  and  $j$  interact in a local web  $L_{x,y,z,t}$  (spatial and temporal subscripts hereafter  
234 omitted or replaced by the shorter subscript  $l$  for clarity) can be conditioned on many environmental and

235 biological factors. In addition to network area (or volume) and duration, they may be conditioned on taxa  
 236 co-occurrence  $X_{i,j,l}$ , which is usually a Boolean describing if the geographic distributions of both taxa overlap  
 237 within the study area. Co-occurrence may be modeled probabilistically, in which case it may conform to a  
 238 Bernoulli distribution  $X_{i,j,l} \sim \text{Bernoulli}(P(X_{i,l}, X_{j,l}))$ , where  $X_{i,l}$  and  $X_{j,l}$  are the local occurrences (presence /  
 239 absence) of both taxa. The probability of co-occurrence  $P(X_{i,l}, X_{j,l})$  can be estimated through the application of  
 240 joint species distribution models (e.g., Pollock *et al.* (2014)), potentially taking into account biotic interactions  
 241 (Staniczenko *et al.* (2017)). Given that the probability that two non-co-occurring taxa interact locally is zero  
 242 (i.e.,  $P(L_{i \rightarrow j}|X_{i,j,l} = 0) = 0$ ), the probability of local interaction can be obtained by multiplying the probability  
 243 of interaction given co-occurrence with the probability of co-occurrence:

$$P(L_{i \rightarrow j}) = P(L_{i \rightarrow j}|X_{i,j,l} = 1) \times P(X_{i,l} = 1, X_{j,l} = 1). \quad (1)$$

244 Other important factors that can impact interaction probabilities at the local scale are taxa local abundances  $N_{i,l}$   
 245 and  $N_{j,l}$ , which affect encounter probabilities (Canard *et al.* (2012)), and local traits distributions  $T_{i,l}$  and  $T_{j,l}$   
 246 (e.g., body mass, presence of given anatomical features, host resistance), which determine the ability of  
 247 individuals to interact after encountering each other (Poisot *et al.* (2015)). Moreover, local interactions may be  
 248 conditional on local environmental factors such as temperature (Angilletta *et al.* (2004)), precipitation  
 249 (Woodward *et al.* (2012)), habitat structure (Klecka & Boukal (2014)), and presence of other taxa in the  
 250 network (Pilosof *et al.* (2017), Kéfi *et al.* (2012)), as described above. Here, we use the variable  $E_l$  to describe  
 251 the local ecological context in which interaction probabilities were estimated. For example, if a research team  
 252 conducts a mesocosm experiment to estimate interaction probabilities between predators and prey with and  
 253 without shelters (a place that offers refuge and protection for prey, shielding them from predators),  $E_l$  would  
 254 represent the presence or absence of these shelters. Like co-occurrence,  $E_l$  can also be modeled probabilistically  
 255 when the stochasticity or uncertainty of environmental factors is considered. In sum,  $E_l$  represents all  
 256 ecological variables that were taken into consideration when measuring interaction probabilities and is,  
 257 therefore, a subset of all environmental factors impacting ecological interactions. Finally, local interaction  
 258 probabilities may be conditioned on higher-level properties of the network, which we denote by  $f(L)$ . Many  
 259 topological null models (i.e., statistical models that randomize interactions by retaining certain properties of the  
 260 network while excluding others) provide interaction probabilities from selected measures of network structure,  
 261 such as connectance (Fortuna & Bascompte (2006)) and the degree distribution (Bascompte *et al.* (2003)).

262 The probability that two taxa  $i$  and  $j$  interact in a local web  $L$  can thus be conditioned on their co-occurrence  
 263  $X_{i,j,l}$  (or more explicitly on their occurrences  $X_{i,l}$  and  $X_{j,l}$ ), local abundances  $N_{i,l}$  and  $N_{j,l}$ , local traits  
 264 distributions  $T_{i,l}$  and  $T_{j,l}$ , local environmental conditions  $E_l$ , network area (or volume)  $A$ , time interval  $t$ , and  
 265 network properties  $f(L)$ . Although these variables correspond to distinct ecological inquiries or mechanisms  
 266 related to ecological interactions, they may covary with each other, such as the possible dependence of  $X_{i,j,l}$  and  
 267  $E_l$  on spatial and temporal scales. When estimating interaction probabilities using e.g. a generalized linear  
 268 model with multiple explanatory variables that might not be independent, it may become important to address  
 269 collinearity. In such a case, to mitigate this issue, it may be necessary to use variable selection techniques before  
 270 fitting the model to data. The probability that a local interaction is realized is described by the following  
 271 expression when all these conditional variables are included:

$$P(L_{i \rightarrow j} | X_{i,l}, X_{j,l}, N_{i,l}, N_{j,l}, T_{i,l}, T_{j,l}, E_l, A, t, f(L)) \quad (2)$$

272 The representation of the local context in which probabilities are estimated and the variables that should be  
 273 taken into consideration depend on the study system, the objectives of the study, and the resources available to  
 274 the researchers. In other words, these variables do not systematically need to be accounted for. For example, in  
 275 Gravel *et al.* (2019), for the purpose of model comparison, some models incorporated environmental variables  
 276 as conditions of interaction probabilities, while others did not. When accounted for, these variables should be  
 277 clearly described in the documentation of the data (Brimacombe *et al.* (2023)), preferentially in mathematical  
 278 terms to avoid any confusion in their interpretation and to limit manipulation errors during their re-use. For  
 279 instance, ecologists should be explicit about their consideration of co-occurrence in their estimation of local  
 280 interaction probabilities. Indeed, it is important to specify if probability values are conditional  $P(L_{i \rightarrow j} | X_{i,j,l} = 1)$   
 281 or not  $P(L_{i \rightarrow j})$  on co-occurrence since this can significantly impact the interpretation and analysis of the data.  
 282 In [tbl. 1](#), we present examples of studies that used these different formulations of probabilistic interactions and  
 283 conditional variables. We have included the probability of empirically observing an interaction that is realized  
 284 locally  $P(O_{i \rightarrow j} | L_{i \rightarrow j})$  to underscore the distinction between local observations and actual realizations of  
 285 interactions, even though the focus of this manuscript is not on the observation of interactions.

**Table 1: Mathematical expressions of probabilistic interactions.** The probability of interaction between two taxa  $i$  and  $j$  is interpreted differently in a metaweb  $M$  of potential interactions (representing the *biological* feasibility of interactions), a metaweb  $M^*$  of potential interactions (representing the *ecological* feasibility of interactions), a local web  $L$  of realized interactions and a local web  $O$  of observed interactions. Each expression emphasizes a different conditional variable, the ellipsis serving as a placeholder for other variables not explicitly stated in the expression. The outcome of each of these probabilistic events, along with common uncertainty sources (often stemming from the model used for estimation), is presented alongside examples of studies that employed them (with specific variables indicated in parentheses, when applicable). The study marked with an asterisk has been conducted on binary interaction webs.

Expression	Type	Outcome	Uncertainty		Reference
			sources		
$P(L_{i \rightarrow j} X_{i,l}, X_{j,l}, \dots)$	local	realization of the interaction	spatiotemporal	Gravel <i>et al.</i> (2019)	
		given taxa co-occurrence	variability		
$P(L_{i \rightarrow j} N_{i,l}, N_{j,l}, \dots)$	local	realization of the interaction	neutral models	Canard <i>et al.</i> (2014)	
		given taxa abundances			
$P(L_{i \rightarrow j} T_{i,l}, T_{j,l}, \dots)$	local	realization of the interaction	trait matching	Gravel <i>et al.</i> (2016)	
		given local traits	models		
$P(L_{i \rightarrow j} E_l, \dots)$	local	realization of the interaction	environmental-	Gravel <i>et al.</i> (2019)	
		given local environmental	based models		(temperature and
		conditions			precipitation)
$P(L_{i \rightarrow j} A, \dots)$	local	realization of the interaction in	spatial models	Galiana <i>et al.</i> (2018)	
		a given area or volume			*
$P(L_{i \rightarrow j} t, \dots)$	local	realization of the interaction	temporal models	Weinstein & Graham (2017a)	
		during a given time period			
$P(L_{i \rightarrow j} f(L), \dots)$	local	realization of the interaction	topological null	Fortuna & Bascompte (2006) (connectance)	
		given network structure	models		
$P(L_{i \rightarrow j} M_{i \rightarrow j}, \dots)$	local	realization of the interaction	spatiotemporal	this study	
		given that the taxa can	variability		
$P(O_{i \rightarrow j} L_{i \rightarrow j}, \dots)$	local	observation of the interaction	sampling model	Catchen <i>et al.</i> (2023)	
		given that it is realized locally			

Expression	Type	Outcome	Uncertainty	
			sources	Reference
$P(M_{i \rightarrow j} T_i, T_j)$	regional	biological feasibility of the interaction given regional traits (non-forbiddenness)	trait matching models	Strydom <i>et al.</i> (2022)
$P(M_{i \rightarrow j}^* T_i, T_j, E)$	regional	ecological feasibility of the interaction given regional traits and environmental conditions	trait matching and environmental-based models	this study

When testing or employing multiple models to estimate local interaction probabilities, rather than selecting a single model that best fits the data, model averaging may be used to enhance our estimations. In this approach, the weighting is based on the likelihood of each model. Model weights represent the probability that each model is the most suitable for explaining the data, and may be measured using Akaike weights (Burnham & Anderson (2004), Wagenmakers & Farrell (2004)). For instance, considering two models  $mod_1$  and  $mod_2$  with respective probabilities (or weights)  $P(mod_1)$  and  $P(mod_2)$ , the average probability of interaction  $P(L_{i \rightarrow j}|...)$  can be calculated as follows:

$$P(L_{i \rightarrow j}|...) = P(L_{i \rightarrow j}|mod_1, ...) \times P(mod_1) + P(L_{i \rightarrow j}|mod_2, ...) \times P(mod_2), \quad (3)$$

where the ellipsis serves as a placeholder for the conditional variables incorporated in these models.

## 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). Potential interactions describe the biological capacity of taxa to interact, which is typically assessed at the regional scale. Metawebs of probabilistic interactions are particularly useful in situations where there is high uncertainty in the ability of taxa to interact if they were to encounter each other. This uncertainty frequently arises due to insufficient interaction data, especially for taxa that have not yet been observed to co-occur, and uncertainties in trait-matching models. As data accumulates, interactions in metawebs should tend towards binarity, approaching probability values of 0

302 (repeatedly failing to observe an interaction between two co-occurring taxa) and 1 (observing an interaction at  
303 least once). The extent of sampling effort thus influences our evaluation of probabilities of potential  
304 interactions, as sampling over a larger area or for a longer duration enables us to capture a greater number of  
305 regional interactions (McLeod *et al.* (2021)). However, in contrast with local webs of probabilistic interactions,  
306 which describe interaction stochasticity in local natural settings, regional interactions are not evaluated for any  
307 particular local context. Although *neutrally* forbidden interactions (i.e., improbable interactions between rare  
308 species, Canard *et al.* (2012)) tend to have low probability values in local webs, they may have higher  
309 probabilities in the metaweb (i.e., when species' biological traits can support an interaction if they were to  
310 encounter each other). Likewise, non-co-occurring taxa may have a non-zero probability of interaction in the  
311 metaweb.

312 Potential interactions describe what we refer to as the *biological feasibility* of interactions, which is based solely  
313 on the regional traits distributions  $T_i$  and  $T_j$  of taxa  $i$  and  $j$ , respectively. A probability of potential interaction in  
314 a metaweb  $M$  describing the biological feasibility of interactions may be expressed as:

$$P(M_{i \rightarrow j} | T_i, T_j), \quad (4)$$

315 which, in contrast with local webs, is not conditioned on any spatial, temporal, co-occurrence or environmental  
316 variables (tbl. 1). Regional traits may differ from local traits  $T_{i,l}$  and  $T_{j,l}$ , which may vary spatially and  
317 temporally due to phenotypic plasticity (Berg & Ellers (2010)). The biological feasibility of interactions  
318 expresses our degree of belief that there exists at least one combination of phenotypes that could support an  
319 interaction if they were to encounter each other, assuming they had infinite time to interact. Evaluating this  
320 probability is conducted without incorporating the environmental conditions under which they encounter each  
321 other into the model. It is the complement of the probability  $P(F_{i \rightarrow j} | T_i, T_j)$  of forbidden interactions based  
322 uniquely on biological traits (i.e., the probability that their traits do not support an interaction):

$$P(M_{i \rightarrow j} | T_i, T_j) = 1 - P(F_{i \rightarrow j} | T_i, T_j). \quad (5)$$

323 For example, let  $i$  be a western diamondback rattlesnake (*Crotalus atrox*) and  $j$ , a wood lemming (*Myopus*  
324 *schisticolor*). These two taxa never co-occur, the rattlesnake being adapted to warm regions of North America  
325 (Castoe *et al.* (2007)) and the lemming, to northern habitats of Eurasia (Fedorov *et al.* (2008)). As we lack

326 direct observations of an interaction between these two species, we have to rely on expert knowledge or  
327 trait-matching models to estimate their probability of potential interaction. To accurately estimate this  
328 probability using trait-matching models, it is crucial to ensure that the set of traits considered reflects the overall  
329 traits distributions of both taxa. We could for instance consider their average body mass and the average  
330 phylogenetic proximity of lemmings to rattlesnakes' prey. Doing so, we might find a high probability of  
331 potential interaction based on these traits.

332 The biological feasibility of interactions should not be confused with what we refer to as the *ecological*  
333 feasibility of interactions. A probability of potential interaction in a metaweb  $M^*$  describing ecological  
334 feasibility of interactions may be expressed as:

$$P(M_{i \rightarrow j}^* | T_i, T_j, E), \quad (6)$$

355 where  $E$  is the environmental conditions under which potential interactions are evaluated (tbl. 1). Unlike  $E_l$ ,  
356 these environmental conditions do not represent conditions occurring at specific locations. Ecological  
357 feasibility represents the probability that two taxa interact if they were to encounter each other under given  
358 environmental conditions, assuming they had infinite time to interact. Incorporating environmental conditions  
359 into a trait-matching model may be important when there is high covariation between the environment and  
360 biological traits. For instance, in our example involving rattlesnakes and lemmings, the probability of potential  
361 interaction between these two species may be low in most environmental conditions. Western diamondback  
362 rattlesnakes may be unactive under low temperatures (Kissner *et al.* (1997)), whereas wood lemmings may have  
363 low tolerance to high temperatures (Kausrud *et al.* (2008)). The probability that an interaction is ecologically  
364 feasible is always lower than the probability that it is biologically feasible, even across all environmental  
365 conditions:

$$\int_E P(M_{i \rightarrow j}^* | T_i, T_j, E) dE \leq P(M_{i \rightarrow j} | T_i, T_j). \quad (7)$$

346 This is because the biological feasibility of an interaction is a prerequisite for its ecological feasibility.  
347 Biological feasibility is necessary but not sufficient for an interaction to be ecologically feasible. Our discussion  
348 of metawebs will focus on the biological feasibility of interactions since most methods developed for inferring  
349 probabilities of regional interactions do not explicitly take into account environmental conditions (e.g., Strydom

350 *et al.* (2022)).

351 Starting from a selected set of taxa, which are usually distributed within a broad region of interest, metawebs  
352 can be built using different data sources, including literature review (e.g., Maiorano2020Tetraeu), aggregated  
353 local web data (e.g., Gravel *et al.* (2019), Saravia *et al.* (2022)), trait-matching models (e.g., Strydom *et al.*  
354 (2022), Shaw *et al.* (2024)), and expert knowledge. Every pair of taxa that have confidently been observed to  
355 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.  
356 This differs from local webs of probabilistic interactions, where interaction events may remain stochastic (i.e.,  
357  $P(L_{i \rightarrow j}) < 1$ ) even after empirically observing interactions due to their spatiotemporal variability. Interactions  
358 that were never observed typically have low probability values in local webs and vary from low to high values in  
359 metawebs, contingent upon taxa traits distributions (reaching 0 for forbidden links).  
360 When incorporating local network data to estimate probabilities of regional interactions, repeatedly failing to  
361 observe an interaction between two co-occurring taxa (i.e.,  $P(O_{i \rightarrow j} = 0)$ ) should decrease the probability that  
362 the interaction is biologically feasible. Using Bayes' theorem, the probability that the interaction is biologically  
363 feasible given that it was never observed locally,  $P(M_{i \rightarrow j} = 1|O_{i \rightarrow j} = 0, \dots)$ , may be calculated as follows:

$$P(M_{i \rightarrow j} = 1|O_{i \rightarrow j} = 0, \dots) = \frac{P(O_{i \rightarrow j} = 0|M_{i \rightarrow j} = 1, \dots) \times P(M_{i \rightarrow j} = 1|\dots)}{P(O_{i \rightarrow j} = 0|\dots)}. \quad (8)$$

364 The reduction in the probability of regional interaction after considering that it was never observed locally (i.e.,  
365  $P(M_{i \rightarrow j} = 1|O_{i \rightarrow j} = 0, \dots) < P(M_{i \rightarrow j} = 1|\dots)$ ) occurs because  $P(O_{i \rightarrow j} = 0|M_{i \rightarrow j} = 1, \dots)$  must be lower than  
366  $P(O_{i \rightarrow j} = 0, \dots)$  (there is a higher chance of observing an interaction when we know it is biologically feasible).  
367 Many observations of interactions are false positives because of observation errors due to taxonomic  
368 misidentifications and ecological misinterpretations (e.g., due to cryptic species and interactions, Pringle &  
369 Hutchinson (2020)). Likewise, forbidden interactions may be false negatives, e.g. if they have been evaluated  
370 based on unrepresentative or incomplete traits distributions. Employing Bayesian models could prove valuable  
371 when estimating interaction probabilities in metawebs (e.g., Bartomeus *et al.* (2016), Cirtwill *et al.* (2019)).  
372 This improvement is achieved by updating prior information regarding the feasibility of interactions (e.g.,  
373 experts' prior assessments of interaction probabilities) with empirical data on interactions and traits.

374 **Properties of probabilistic interaction webs**

375 Local and metawebs of probabilistic interactions differ in their type of interactions (i.e., realized or potential)  
376 and in the conditional variables upon which interaction values depend. These differences are significant as they  
377 influence the characteristics of probabilistic interaction networks. Neglecting to consider them may result in  
378 misleading results and interpretation errors when analyzing the properties of probabilistic interaction webs,  
379 which could be particularly problematic when addressing crucial ecological questions about networks. Here we  
380 compare the characteristics of local and metawebs through the presentation of four applications of probabilistic  
381 interactions: (1) describing their spatial and temporal scaling, (2) describing their taxonomic scaling, (3)  
382 sampling for binary interaction webs, and (4) reconstructing local webs of probabilistic interactions from  
383 metawebs. All code and data to reproduce these analyses are available at the Open Science Framework (TBD).

384 **Host-parasite network data**

385 We use the collection of tripartite host-parasite networks sampled across Europe, created by Kopelke *et al.*  
386 (2017), in the following case studies. This dataset contains well-resolved binary local interactions between  
387 willows (52 species), willow-galling sawflies (96 species), and their parasitoids (126 species). Given its  
388 replicated webs spanning large spatiotemporal scales, this dataset is well-suited for analyzing a variety of  
389 ecological hypotheses and processes. Out of a total of 374 local webs, we retained those containing at least 5  
390 species, resulting in a set of 233 georeferenced local webs (networks sampled within areas of 0.1 to 0.3 km<sup>2</sup>  
391 during June and/or July spanning 29 years). We built a metaweb of binary interactions by aggregating all local  
392 interactions, which gave us a regional web composed of 274 species and 1080 interactions. In the first two  
393 panels of fig. 1, we show how the dissimilarity of interactions between common species ( $\beta_{OS}$ ) and the  
394 dissimilarity in species composition ( $\beta_S$ ) between the metaweb and aggregated local webs (Poisot *et al.* (2012))  
395 vary with the number of sampled local webs. This shows that networks of local interactions are highly  
396 dissimilar from the metaweb, both in terms of species and interactions, especially when only a limited number  
397 of sites has been sampled. Both dissimilarity indices were calculated based on the number of items shared by  
398 the two webs ( $c_{LM}$ ) and the number of items unique to the metaweb ( $u_M$ ) and to the aggregated local web ( $u_L$ ).  
399 The  $\beta_S$  dissimilarity index uses species (nodes) as items being compared, while the  $\beta_{OS}$  index assesses  
400 dissimilarity based on interactions between shared species (Poisot *et al.* (2012)). Both indices were calculated  
401 following the  $\beta_W$  index of Whittaker (1960):

$$\beta_W = \frac{c_{LM} + u_L + u_M}{(2c_{LM} + u_L + u_M)/2} - 1. \quad (9)$$

402

[Figure 1 about here.]

403 We converted these binary interaction networks into probabilistic ones using models based on simple  
 404 assumptions. Our models are not designed to estimate the exact values of probabilistic interactions. Instead,  
 405 their purpose is to create plausible networks that serve as illustrative examples to highlight distinctions between  
 406 local and metawebs of probabilistic interactions. We created two metawebs of probabilistic interactions by  
 407 employing constant false positive and false negative rates for all regional interactions. In the first metaweb, we  
 408 set both false positive and false negative rates to zero to prevent artificially inflating the total number of links,  
 409 enabling a more accurate comparison with binary interaction webs. This gave us a probability of regional  
 410 interaction of 1 when at least one interaction has been observed locally and of 0 in the absence of any observed  
 411 interaction between a given pair of species. In the second metaweb, we introduced a 5% false positive rate to  
 412 account for spurious interactions and a 10% false negative rate to address the elevated occurrence of missing  
 413 interactions in ecological networks (Catchen *et al.* (2023)). We believe these rates represent reasonable  
 414 estimates of missing and spurious potential interactions, but confirming their accuracy is challenging due to the  
 415 unavailability of data on the actual feasibility of interaction. Observed interactions were thus given a probability  
 416 of regional interaction of 95%, whereas unobserved ones were assigned a probability of 10%.

417 To build local webs of probabilistic interactions, we first recognize that local interactions must initially be  
 418 biologically feasible before occurring at a specific time and space. A local probability of interaction  $P(L_{i \rightarrow j})$   
 419 can be expressed as the product of the probability of local interaction given that the two taxa can potentially  
 420 interact  $P(L_{i \rightarrow j}|M_{i \rightarrow j} = 1)$ , which we denote as  $P(L_{i \rightarrow j}|M_{i \rightarrow j})$  for the sake of simplicity, with their probability of  
 421 regional interaction  $P(M_{i \rightarrow j})$ :

$$P(L_{i \rightarrow j}) = P(L_{i \rightarrow j}|M_{i \rightarrow j} = 1) \times P(M_{i \rightarrow j} = 1). \quad (10)$$

422 We built local webs of probabilistic interactions using the taxa found in the empirical local networks and  
 423 attributing pairwise interaction probabilities based on the metawebs of probabilistic interactions and a constant  
 424 value of  $P(L_{i \rightarrow j}|M_{i \rightarrow j})$  across interactions. Low values of  $P(L_{i \rightarrow j}|M_{i \rightarrow j})$  indicate that feasible interactions rarely  
 425 occur locally, intermediate values around 50 suggest considerable spatiotemporal variability, while high values

426 indicate that regional interactions are nearly always realized locally. Following eq. 10, the local probability of  
427 interaction between a given pair of taxa consistently remained equal to or below their probability of regional  
428 interaction.

429 In the last two panels of fig. 1, we show how the aggregated number of links and connectance (i.e., the  
430 proportion of all of the non-forbidden links that are realized) scale with the number of sampled local webs,  
431 according to different values of  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ . When aggregating local webs of probabilistic interactions, the  
432 constancy of the probability of regional interaction across the entire study area means that any rise in the  
433 probability of local interaction is solely attributable to an increase in  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ . For example, let  $L_1$  and  $L_2$   
434 be two local networks and  $L_{1,2}$  the aggregated web. If  $P(L_{1,i \rightarrow j} | M_{i \rightarrow j})$  and  $P(L_{2,i \rightarrow j} | M_{i \rightarrow j})$  are the probabilities  
435 that two potentially interacting taxa interact respectively in  $L_1$  and  $L_2$ , the probability  $P(L_{1,2,i \rightarrow j} | M_{i \rightarrow j})$  that  
436 these taxa interact in the aggregated web  $L_{1,2}$  is obtained by:

$$P(L_{1,2,i \rightarrow j} | M_{i \rightarrow j}) = 1 - (1 - P(L_{1,i \rightarrow j} | M_{i \rightarrow j})) \times (1 - P(L_{2,i \rightarrow j} | M_{i \rightarrow j})), \quad (11)$$

437 assuming independence between the interactions of two taxa in different networks. This equation represents the  
438 probability that the interaction is realized in either (1) exclusively the local web  $L_1$ , (2) exclusively the local web  
439  $L_2$  or (3) both local webs, given that the two taxa have the biological capacity to interact.

440 By comparing the scaling relationships observed in webs of binary and probabilistic interactions, fig. 1  
441 illustrates that high values of  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$  lead to systematic overestimations in the number of links and  
442 connectance, especially when  $P(L_{i \rightarrow j} | M_{i \rightarrow j}) = 1$  (corresponding to the scenario where local probabilities of  
443 interactions are equivalent to the probabilities of regional interactions). However, these biases tend to diminish  
444 as the number of sampled webs increases.

## 445 Spatial and temporal scaling of interactions

446 The investigation of network-area relationships and interaction accumulation curves is an important area of  
447 research in network ecology. First, network-area relationships elucidate the scaling of network properties (such  
448 as modularity and trophic chain lengths) with spatial scale (e.g., Wood *et al.* (2015), Galiana *et al.* (2018)). The  
449 variations in network structure across spatial scales may stem from the scaling of species richness (species-area  
450 relationships, SARs), the number of interactions (Brose *et al.* (2004)), and many other higher-level properties of  
451 the system (e.g., environmental heterogeneity, Thompson & Townsend (2005)) with the sampled area.

452 Additionally, ecological processes occurring at distinct spatial scales, such as the spatial variability in local  
453 community composition resulting from different sequences of extinction and colonization events, can also  
454 contribute to this variation (Galiana *et al.* (2018)). Next, interaction accumulation curves describe the scaling of  
455 the number of observed interactions with sampling effort (Jordano (2016)). Sampling effort, which may  
456 correspond to the duration of the sampling period used to construct the network, can impact connectance  
457 (Bersier *et al.* (1999)) and various measures of network structure (Banašek-Richter *et al.* (2004), McLeod *et al.*  
458 (2021)). Apart from sampling effort, the temporal scaling of interactions also elucidates how network structure  
459 changes with the temporal resolution of the network (Poisot *et al.* (2012)), acknowledging that distinct  
460 interactions take place over time, ranging from short-term fluctuations of interactions to long-term trends. As  
461 local webs of probabilistic interactions may explicitly account for the spatiotemporal variability of interactions,  
462 they offer a distinct approach to investigating the scaling of network structure with space and time, in contrast to  
463 webs of binary and quantitative interactions, by making the stochasticity of interactions the focal point of the  
464 modeling process.

465 Local and metawebs exhibit distinct relationships with spatial and temporal scales. On one hand, metawebs of  
466 probabilistic interactions, representing biological feasibility, feature regional interactions that do not scale with  
467 space and time. This is because regional interactions depend solely on the biological capacity of two taxa to  
468 interact, regardless of their co-occurrence and local environmental conditions. However, probabilities of  
469 potential interactions may change (tending to become more definitive) upon updating previous estimates with  
470 increased sampling effort, even though they do not vary in a specific direction with the spatial and temporal  
471 extent (boundaries) of the network. The probability of two taxa potentially interacting should theoretically be  
472 the same in all metawebs in which they are present, provided that the data and methods used for estimation are  
473 consistent. For example, if a smaller metaweb  $M_1$  is derived from a larger metaweb  $M_0$  by selecting the subset  
474 of taxa present in the region described by  $M_1$  and retaining all their interactions, their probabilities of  
475 interaction should be identical regardless of scale, i.e.  $P(M_{1,i \rightarrow j}) = P(M_{0,i \rightarrow j})$ . With a larger or equal number of  
476 taxa in  $M_0$  as compared to  $M_1$ , the total number of interactions is expected to be higher or at least equal in the  
477 larger web, even though pairwise probabilities remain identical.

478 On the other hand, local interactions scale both spatially and temporally, given that they have more  
479 opportunities to be realized and observed in larger areas and longer durations. This is attributed to factors such  
480 as a higher number of individuals, greater trait variations, and increased opportunities for encounters, as  
481 highlighted by McLeod *et al.* (2020). For example, if a local web of probabilistic interactions  $L_1$  with an area

482  $A_1$  is derived from a larger web  $L_0$  with an area  $A_0$ , and  $A_1$  is entirely nested within  $A_0$ , interaction probabilities  
483 should be lower in the smaller web, i.e.  $P(L_{1,i \rightarrow j}|A_1 < A_0) \leq P(L_{0,i \rightarrow j}|A_0)$ . However, if  $A_1$  and  $A_0$  are disjoint,  
484 interaction probabilities could be higher in the smaller area, contingent upon their environmental and biological  
485 conditions. Likewise, interaction probabilities are expected to be lower in webs with shorter durations when  
486 time intervals are nested. In fig. 2, we show how the expected number of local host-parasite interactions scales  
487 with area, represented as an expanding latitudinal window, in comparison with regional interactions. Even  
488 though we employed local probabilities of interactions equal to regional interactions for the purpose of  
489 comparison (i.e., using  $P(L_{i \rightarrow j}|M_{i \rightarrow j}) = 1$  here), we notice that the total number of regional interactions scales  
490 more rapidly than local interactions. This is because numerous regional interactions involve species that never  
491 co-occur, and as a result, these interactions are not captured in any local web.

492 [Figure 2 about here.]

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

494 Predicting local webs across time and space is a pivotal goal of network ecology, especially given the scarcity of  
495 interaction data (Strydom *et al.* (2021)). Ecologists may resort to predictive models (e.g., generative Bayesian  
496 and machine learning models) to reconstruct networks at fine spatial and temporal scales with limited  
497 interaction data. For instance, real-time biomonitoring data coupled with appropriate numerical models (Bohan  
498 *et al.* (2017)) can be employed to reconstruct local ecological webs, opening avenues for in-depth studies on  
499 local ecosystem functioning and dynamics. The probabilistic representation of interactions describes the  
500 inherent uncertainty in these models, typically expressed through probability distributions. We introduce and  
501 develop a simple generative mechanistic model for probabilistic local interactions that takes into consideration  
502 their spatiotemporal variability (i.e., a spatiotemporally explicit model of local interactions). It is essential to  
503 note that our model is not designed for regional interactions, which are scale-independent. Rather, it could  
504 prove valuable for predicting local interactions across time and space by generating new interaction data  
505 following parameter inference.

506 As indicated by eq. 1, the probability that two taxa  $i$  and  $j$  interact at a specific location and time  $l$  may be  
507 determined by the product of their probability of interaction given co-occurrence and their probability of  
508 co-occurrence. First, their co-occurrence probability can be calculated using their individual (marginal)  
509 occurrence probabilities  $P(X_{i,l})$  and  $P(X_{j,l})$ . Given that taxa occurrences are not independent of each other, the

510 joint probability of both taxa occurring together can be calculated by multiplying the probability of one taxon  
 511 being present by the conditional probability of the other occurring when the first one is present. Alternatively,  
 512 the joint occurrence probability can be obtained by multiplying the marginal probabilities by the strength of  
 513 association  $\gamma$  between the occurrences of both taxa (Cazelles *et al.* (2016)):

$$P(X_{i,l}, X_{j,l}) = P(X_{i,l}|X_{j,l})P(X_{j,l}) = P(X_{i,l})P(X_{j,l})\gamma. \quad (12)$$

514 When  $\gamma > 1$ , it signifies a positive association in the geographic distributions of both taxa, indicating that the  
 515 presence of one taxon enhances the probability of occurrence of the other. Attractions may be the result of  
 516 positive interactions (e.g., mutualism) or positive/negative interactions (e.g., antagonism between predators and  
 517 prey, Cazelles *et al.* (2016)). In empirical webs,  $\gamma > 1$  holds true for the majority of species pairs (Catchen *et*  
 518 *al.* (2023)). In contrast, repulsions ( $\gamma < 1$ ) may be caused e.g. by strong interspecific competition (Cazelles *et*  
 519 *al.* (2016)). We model the co-occurrence  $X_{i,j,l}$  of both taxa as the outcome of a Bernoulli trial

$$X_{i,j,l} \sim \text{Bernoulli}(P(X_{i,l}, X_{j,l})). \quad (13)$$

520 Next, the probability of interaction given co-occurrence can be made temporally explicit by modeling it as a  
 521 Poisson process with rate parameter  $\lambda_l$ . This parameter represents the local expected frequency of interaction  
 522 between the taxa within a defined time interval and can be estimated using prior data on interaction strengths,  
 523 when accessible. The probability that two co-occurring taxa engage in an interaction during a time period  $t_0$  is  
 524 given by:

$$P(L_{i \rightarrow j}|X_{i,j,l} = 1) = 1 - e^{-\lambda_l t_0}, \quad (14)$$

525 which tends toward 1 as  $t_0 \rightarrow \infty$  if  $\lambda > 0$ . In other words, two co-occurring taxa with a nonzero rate of  
 526 interaction will inevitably interact in a sufficiently long time period. It is important to note that the units of  $\lambda_l$   
 527 and  $t_0$  are complementary. For instance, if the duration  $t_0$  is measured in months,  $\lambda_l$  denote the expected  
 528 number of interactions per month.

529 The occurrence of an interaction between  $i$  and  $j$  can be modeled as a Bernoulli trial with a probability of  
 530  $P(L_{i \rightarrow j})$ . Consequently, a Bayesian inference model can be built based on the preceding equations to estimate

531 the value of the  $\lambda_l$  and  $\gamma$  parameters and generate novel interaction data:

$$L_{i \rightarrow j} \sim \text{Bernoulli}(P(L_{i \rightarrow j})) \quad (15)$$

$$P(L_{i \rightarrow j}) = P(X_{i,l})P(X_{j,l})\gamma(1 - e^{-\lambda_l t_0}) \quad (16)$$

$$\gamma \sim \text{Gamma}(2, 0.5) \quad (17)$$

$$\lambda_l \sim \text{Exponential}(2) \quad (18)$$

532 In fig. 3, we show the variation in the probability of interaction under different parameter values. In the right  
533 panel, we notice that, irrespective of the interaction rate  $\lambda_l$ , the probability of interaction converges toward an  
534 asymptote determined by the probability of co-occurrence  $P(X_{i,j,l})$  (eq. 12). This model can be customized in  
535 different ways, such as by linking  $\lambda_l$  with specific environmental variables or explicitly incorporating  
536 observation errors (i.e., the probabilities of false negatives and false positives).

537 [Figure 3 about here.]

### 538 **Taxonomic scaling of interactions**

539 Probabilistic interaction networks offer a versatile approach to tackle a broad array of ecological questions,  
540 depending on their level of organization. For instance, the assemblage of interactions across ecological scales  
541 can be explored through species-based networks, while clade-based networks provide insights into  
542 macroevolutionary processes (e.g., Gomez *et al.* (2010)). Given that our interpretation of the properties and  
543 dynamics of ecological webs depends on their taxonomic level (Guimarães (2020)), investigating the taxonomic  
544 scaling of interactions (i.e., how interaction probabilities change with taxonomic level) emerges as a promising  
545 research avenue. Examining the same system at various taxonomic scales can yield meaningful and  
546 complementary ecological information, and, in our perspective, employing webs of probabilistic interactions is  
547 an effective approach for such analyses.

548 There are no inherent differences in the taxonomic scaling between local and metawebs, as only the nodes are  
 549 defined taxonomically. In other words, the probability values of edges in both local (eq. 2) and metawebs (eq. 4)  
 550 are not conditional on any taxonomic level. The taxonomic scale is tied to the definition of the event itself (i.e.,  
 551 the interaction between two taxa, defined at the desired taxonomical scale), not to the variables on which  
 552 interaction probabilities are conditional. In both types of webs, transitioning to a broader level of organization  
 553 (e.g., from a species-level web  $S$  to a genus-level web  $G$ ) can be accomplished directly by using probabilities  
 554 from finer scales. For example, in a network with  $n_1$  species from genus  $g_1$  and  $n_2$  species from genus  $g_2$ , one  
 555 can compute the probability that at least one species from genus  $g_1$  interacts with at least one species from  
 556 genus  $g_2$  (i.e., that there is a non-zero number of species-level interactions or, equivalently, that the genus-level  
 557 interaction occurs) as follows:

$$P(G_{g_1 \rightarrow g_2} = 1) = 1 - \prod_{i=1}^{n_1} \prod_{j=1}^{n_2} (1 - P(S_{g_{1i} \rightarrow g_{2j}} = 1)), \quad (19)$$

558 where  $g_{1,i}$  and  $g_{2,j}$  are the species of the corresponding genus and assuming independence between  
 559 species-level interactions. If it is known that at least two of these species interact (i.e.,  $P(S_{g_{1,i} \rightarrow g_{2,j}}) = 1$  for at  
 560 least one pair of  $(g_{1,i}, g_{2,j})$ ), it implies a probability of genus interaction equal to 1. Canard *et al.* (2012) built a  
 561 species-based network following a similar approach, by using simulated interactions between individuals  
 562 derived from a neutral model (i.e., a model that assumed ecological equivalence among individuals). In  
 563 contrast, a more sophisticated approach is necessary when transitioning from a broader to a finer level of  
 564 organization. This is because knowledge of an interaction between two genera does not guarantee that all  
 565 possible pairwise combinations of their species will also interact. One possible method is to build a finer-scale  
 566 network by generating probabilities of interactions through random sampling from a beta distribution,  
 567 parameterized by the broader-scale network.

568 Ideally, our biological interpretation of probabilistic interactions should remain consistent across a network  
 569 even if it incorporates heterogeneous levels of organization, such as a network whose nodes represent both  
 570 species and trophic species (groups of species sharing similar predators and prey). This is common in  
 571 ecological webs where taxonomic resolution is typically low (Hemprich-Bennett *et al.* (2021), Vázquez§ *et al.*  
 572 (2022)). Interaction probabilities at broader taxonomic scales should be based on probabilities of interactions  
 573 between individuals, for both local and metawebs. For instance, in local individual-based food webs, the  
 574 probability that two individuals interact reflects our degree of belief that one individual will consume the other.

575 Similarly, in local species-based food webs, the probability that two species interact represents our degree of  
576 belief that at least one individual from the predator species consumes at least another individual from the prey  
577 species. Furthermore, in local clade-based food webs, the probability that two clades interact represents our  
578 degree of belief that at least two species from these clades interact with each other or, equivalently, that at least  
579 two individuals from these clades interact with each other. Fundamentally, the taxonomic scaling of interactions  
580 involves aggregating interactions between individuals into larger groups, which may exhibit varying degrees of  
581 homogeneity based on the organisms and the study system. In that regard, taxonomic scaling is analogous to the  
582 spatial and temporal scaling of interactions, as they all represent different ways to aggregate individuals into  
583 broader groups (either spatially, temporally, or taxonomically).

#### 584 **Sampling for binary interaction webs**

585 The prediction of binary interactions through Bernoulli trials is an important application of probabilistic  
586 interaction webs. This approach proves beneficial for analyzing the structural characteristics of probabilistic  
587 interaction webs, particularly in the absence of specific analytical measures. By performing independent  
588 Bernoulli trials for each interaction, a network of binary interactions may be generated. A probability  
589 distribution of network properties can be obtained by measuring network structure across multiple randomly  
590 generated networks (Poisot *et al.* (2016)). This method enables the representation of the variability of network  
591 structure, albeit with possible biases when connectance is low (Poisot & Gravel (2014), Chagnon (2015)).  
592 Employing this strategy to generate binary interaction networks under a null model facilitates null hypothesis  
593 significance testing, wherein the observed measure is compared against the simulated distribution (e.g.,  
594 Bascompte *et al.* (2003)). Additionally, the random generation of binary interaction networks, from a  
595 probabilistic interaction web that accounts for the spatiotemporal variability of interactions, may effectively  
596 capture network structure across space and time. This facilitates the investigation of ecological hypotheses  
597 about interactions at broad spatial and temporal scales. Yet, inferring network structure through sampling for  
598 binary interactions assumes independence among interactions, which might not accurately represent reality.  
599 Covariation among interactions could exist even if we do not explicitly condition interactions on others. For  
600 example, an interaction between two taxa could be more probable when another interaction occurs. The  
601 consequences of this assumption of independence on the prediction of network structure have yet to be  
602 empirically examined.  
603 There are at least two distinct approaches to sample binary interaction networks from probabilistic interaction

604 webs across space, for example, when attempting to predict a binary interaction network for each location  $l$   
605 within a given region. Both approaches assume independence between interactions. The first approach involves  
606 performing a singular Bernoulli trial for each pair of taxa based on their regional probability of interaction:

$$M_{i \rightarrow j} \sim \text{Bernoulli}(P(M_{i \rightarrow j})).$$

607 In employing this approach, we predict a single metaweb of binary interactions for each simulation. Every pair  
608 of taxa predicted to interact in this metaweb will be treated as interacting in all local webs where they co-occur,  
609 i.e.  $L_{l,i \rightarrow j} = M_{i \rightarrow j}$  when  $X_{i,j,l} = 1$ . This will result in local pairwise interactions without spatial variation.  
610 The second approach is to independently sample each local web of probabilistic interactions:

$$L_{l,i \rightarrow j} \sim \text{Bernoulli}(P(L_{l,i \rightarrow j})).$$

611 This can be achieved by first generating distinct probabilistic interaction networks for each location. These local  
612 webs of probabilistic interactions may vary in taxa composition and interaction probabilities. Because binary  
613 interaction networks are sampled independently for each location, this second approach introduces spatial  
614 variation in binary interactions.

615 In fig. 4, we compare the average connectance of binary interaction networks resulting from these two sampling  
616 techniques, where regional and local interactions are drawn from our host-parasite networks of probabilistic  
617 interactions, generating a number of binary interaction web realizations for each site in the dataset. These two  
618 sampling approaches yield different outcomes, particularly for lower values of  $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ , which represent  
619 instances where regional interactions do not consistently manifest locally. Small discrepancies between these  
620 techniques are also apparent when we equate the probability of local interaction to the probability of regional  
621 interaction (i.e., when using  $P(L_{i \rightarrow j}|M_{i \rightarrow j}) = 1.0$  in eq. 10), especially when the number of simulations of  
622 binary interaction networks for each location is low. As anticipated, we observe that sampling binary  
623 interactions from the metaweb tends to overestimate connectance on average compared to sampling them from  
624 local webs. Furthermore, we observe an increase in the variability of connectance when employing a single  
625 simulation, representing what we consider as a more tangible process leading to the realization of local  
626 interactions in nature.

627

[Figure 4 about here.]

628 The choice of a sampling approach can influence the selection of grid cell size when delineating local  
629 communities within a broader region of interest. In the first approach, pairwise interactions remain constant  
630 irrespective of cell size because they are sampled only once from the metaweb. However, in the second  
631 approach, local interaction probabilities are contingent on network area. For instance, consider the local webs  
632  $L_1$  and  $L_2$  with an area of  $\frac{1}{2}A_0$ , both nested within  $A_0$  but disjoint from each other, forming  $L_0$ . If we treat  $L_1$   
633 and  $L_2$  as independent, the probability of interaction between taxa  $i$  and  $j$  in  $L_0$  is given by:

$$P(L_{0,i \rightarrow j}) = 1 - (1 - P(L_{1,i \rightarrow j}) \times P(L_{2,i \rightarrow j})). \quad (20)$$

634 Due to its larger area, the probability that the two taxa interact in  $L_0$  is equal or greater than in  $L_1$  and  $L_2$ . When  
635 sampling binary interactions from local webs, it is crucial to sample at the same spatial scale for which  
636 probabilities were estimated. Otherwise, interaction probabilities must be adjusted to align with the intended  
637 cell size, preventing systematic biases in predictions.

### 638 Prediction of local webs from metawebs

639 Metawebs serve as a valuable source of ecological information for predicting local webs across time and space.  
640 Local webs of binary interactions can be reconstructed by selecting a subset of taxa and interactions from the  
641 metaweb (Dunne (2006)). This implies that metawebs consistently contain more interactions than their  
642 corresponding local webs, even though their connectance is usually much smaller than the ones of local webs  
643 (Gravel *et al.* (2011)). Determining the list of taxa to select can be achieved empirically or through numerical  
644 methods like range maps or species distribution models. As species composition is arguably less difficult to  
645 sample or predict than pairwise interactions, the primary challenge lies in deciding which interactions to select  
646 from the metaweb, a task that may necessitate advanced statistical models and ecological expertise. Inferring  
647 the structure of local webs from the metaweb before predicting specific local pairwise interactions could hold  
648 promise (Strydom *et al.* (2021)), considering that the structure of local webs is constrained by the metaweb  
649 (Saravia *et al.* (2022)).

650 Building local webs of probabilistic interactions from a metaweb of probabilistic interactions involves a  
651 reduction in the value of pairwise interaction probabilities. This decrease is attributed to the prerequisite that  
652 two taxa must initially possess the capacity to interact before engaging in local interactions (eq. 10). Therefore,  
653 inferring local webs from their metaweb while maintaining identical interaction probability values would

654 introduce systematic biases into the predictions. In such cases, these networks would essentially represent  
 655 smaller-scale metawebs of potential interactions, possibly leading to misinterpretations by being perceived as  
 656 local interactions. As proposed by McLeod *et al.* (2021), although metawebs do not capture the spatiotemporal  
 657 variability of interactions, they establish an upper limit for local interactions. In other words, the probability of  
 658 two taxa interacting at a specific location and time is consistently lower or equal to the probability of their  
 659 regional interaction:

$$P(L_{i \rightarrow j} | X_{i,l}, X_{j,l}, N_{i,l}, N_{j,l}, T_{i,l}, T_{j,l}, E_l, A, t, f(L)) \leq P(M_{i \rightarrow j} | T_i, T_j). \quad (21)$$

660 Moreover, the probability that two taxa possess the biological capacity to interact must exceed the probability of  
 661 them interacting at any location and time because they may never co-occur or encounter locally. Specifically,  
 662 the cumulative probability of local interactions across all spatial, temporal, and environmental conditions must  
 663 be less than the probability of regional interaction, i.e.

$$\int_{E_l} \int_A \int_t P(L_{i \rightarrow j} | E_l, A, t) dt dA dE_l \leq P(M_{i \rightarrow j} | T_i, T_j). \quad (22)$$

664 Estimating more precisely the probability  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$  that two taxa interact locally if they can potentially  
 665 interact allows for improved predictions of local webs from the metaweb of probabilistic interactions. This task  
 666 is challenging due to the variability of this probability across space and time, as well as its variability across  
 667 pairwise interactions within a network. Using simple models of  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ , as demonstrated in our case  
 668 studies, represents an initial step toward the overarching objective of reconstructing local webs from metawebs.

## 669 Conclusion

670 In this contribution, we underline the importance of network metadata for adequately interpreting and  
 671 manipulating probabilistic interaction data. The mathematical representation of probabilities and their statistical  
 672 properties depend on the type of interactions (local or regional) and the conditions under which these  
 673 interactions were evaluated. We showed that local and metawebs of probabilistic interactions differ in their  
 674 relationship to spatial and temporal scales, with regional interactions remaining consistent across scales. In  
 675 contrast with metawebs, local interactions are measured in a specific context (e.g., in a given area, time, and  
 676 biological and environmental conditions) and depend on taxa co-occurrence. These differences bring to light

677 the need to use probabilistic data with caution, for instance when generating network realizations of binary  
678 interactions across space and predicting local webs from metawebs. Clear metadata describing the type of  
679 interaction and the variables used in their estimation are required to ensure adequate data manipulation. Sound  
680 data practices and foundations for probabilistic thinking in network ecology could facilitate reliable assessments  
681 of the spatiotemporal variability and uncertainty of biotic interactions.

682 Estimating local interaction probabilities independently for each taxa pair and assembling them into a network  
683 of probabilistic interactions comes with limitations. Predicting local networks of binary interactions based on  
684 these interaction probabilities assumes independence among interactions, a condition seldom respected in  
685 practice (Golubski & Abrams (2011)). Relaxing this assumption is the next logical step in the stochastic  
686 representation of interactions. A more accurate representation of the stochasticity of ecological networks  
687 involves creating *probabilistic networks* ( $P(L|...)$  and  $P(M|...)$ ), rather than networks of *probabilistic*  
688 *interactions* ( $P(L_{i \rightarrow j}|...)$  and  $P(M_{i \rightarrow j}|...)$ ). Probabilistic networks describe the probability that a particular  
689 network of binary (or quantitative) interactions (its whole adjacency matrix) is realized. For example, Young *et*  
690 *al.* (2021) used a Bayesian approach to estimate the probability of different plant-pollinator network structures  
691 derived from imperfect observational data. A probability distribution of ecological networks may also be  
692 derived using maximum entropy principles given some structural constrained (e.g., Park & Newman (2004),  
693 Cimini *et al.* (2019)). Regardless of the method employed, generating probabilistic local webs, bypassing the  
694 need to independently estimate local interaction probabilities, could lead to more accurate predictions of local  
695 webs. Furthermore, probabilistic networks could serve as an alternative to null hypothesis significance testing  
696 when comparing the structure of a local web to some random expectations or, as done in Pellissier *et al.* (2018),  
697 to the metaweb. These random expectations are typically derived by performing a series of Bernoulli trials on  
698 probabilistic interactions, assuming independence, to generate a distribution of networks of binary interactions  
699 and then calculate their structure (Poisot *et al.* (2016)). One could for instance compare the likelihood of an  
700 observed network to the one of the most likely network structure according to the probabilistic network  
701 distribution, thereby directly obtaining a measure of discrepancy of the empirical network. Generating  
702 probabilistic ecological networks represents a tangible challenge, one that, in the coming years, promises to  
703 unlock doors to more advanced and adequate analyses of ecological networks.

704 It is essential to enhance our comprehension of both regional and local interactions, especially considering the  
705 current scarcity of interaction data. While sampling biological communities does decrease the uncertainty of  
706 interactions by accumulating evidence for their feasibility and local realization, there is a limit to how much we

707 can reduce uncertainty. In metawebs, probabilities reflect our limited knowledge of interactions (i.e., our degree  
708 of belief that interactions are feasible), which is expected to improve with a larger volume of data. Regional  
709 interactions should become more definitive (with probabilities approaching 0 or 1) as we investigate various  
710 conditions, including different combinations of species traits. In local webs, which can be seen as random  
711 instances of metawebs, randomness cannot be reduced to the same extent. Local interaction probabilities may  
712 represent both their uncertainty and spatiotemporal variability. Owing to environmental heterogeneity, there  
713 will invariably be instances in which an interaction occurs and others in which it does not, across different times  
714 and locations, irrespective of the extent to which we can improve our knowledge of its biological feasibility and  
715 the local conditions that facilitate its occurrence. When local webs describe probabilities of observing  
716 interactions rather than their actual occurrence, we must also consider observation variability (sampling error)  
717 as an additional source of stochasticity. Every ecological process is stochastic but there is also a possibility that  
718 a phenomenon goes undetected. Quantifying and partitioning this stochasticity will enable us to make more  
719 accurate predictions about ecological interactions at various spatial and temporal scales. This will prove to be of  
720 vital importance as our time to understand nature runs out, especially at the places where the impacts of climate  
721 change and habitat loss hit harder.

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## 730 References

- 731 Abrego, N., Roslin, T., Huotari, T., Ji, Y., Schmidt, N.M., Wang, J., *et al.* (2021). Accounting for species  
732 interactions is necessary for predicting how arctic arthropod communities respond to climate change.

- 733      *Ecography*, 44, 885–896.
- 734      Andrade-Pacheco, R., Rerolle, F., Lemoine, J., Hernandez, L., Meïté, A., Juziwelo, L., *et al.* (2020). [Finding hotspots: Development of an adaptive spatial sampling approach](#). *Scientific Reports*, 10, 10939.
- 735
- 736      Angilletta, M.J., Jr., Steury, T.D. & Sears, M.W. (2004). [Temperature, Growth Rate, and Body Size in Ectotherms: Fitting Pieces of a Life-History Puzzle](#)1. *Integrative and Comparative Biology*, 44, 498–509.
- 737
- 738      Araujo, M.B., Rozenfeld, A., Rahbek, C. & Marquet, P.A. (2011). [Using species co-occurrence networks to assess the impacts of climate change](#). *Ecography*, 34, 897–908.
- 739
- 740      Banašek-Richter, C., Cattin, M.-F. & Bersier, L.-F. (2004). [Sampling effects and the robustness of quantitative and qualitative food-web descriptors](#). *Journal of Theoretical Biology*, 226, 23–32.
- 741
- 742      Bartomeus, I., Gravel, D., Tylianakis, J.M., Aizen, M.A., Dickie, I.A. & Bernard-Verdier, M. (2016). [A common framework for identifying linkage rules across different types of interactions](#). *Functional Ecology*, 30, 1894–1903.
- 743
- 744
- 745      Bascompte, J., Jordano, P., Melián, C.J. & Olesen, J.M. (2003). [The nested assembly of plant–animal mutualistic networks](#). *Proceedings of the National Academy of Sciences*, 100, 9383–9387.
- 746
- 747      Berg, M.P. & Ellers, J. (2010). [Trait plasticity in species interactions: A driving force of community dynamics](#). *Evolutionary Ecology*, 24, 617–629.
- 748
- 749      Berlow, E.L., Neutel, A.-M., Cohen, J.E., De Ruiter, P.C., Ebenman, B., Emmerson, M., *et al.* (2004). [Interaction strengths in food webs: Issues and opportunities](#). *Journal of Animal Ecology*, 73, 585–598.
- 750
- 751      Bersier, L.-F., Dixon, P. & Sugihara, G. (1999). [Scale-Invariant or Scale-Dependent Behavior of the Link Density Property in Food Webs: A Matter of Sampling Effort?](#) *The American Naturalist*, 153, 676–682.
- 752
- 753      Blanchet, F.G., Cazelles, K. & Gravel, D. (2020). [Co-occurrence is not evidence of ecological interactions](#). *Ecology Letters*, 23, 1050–1063.
- 754
- 755      Bohan, D.A., Vacher, C., Tamaddoni-Nezhad, A., Raybould, A., Dumbrell, A.J. & Woodward, G. (2017). [Next-Generation Global Biomonitoring: Large-scale, Automated Reconstruction of Ecological Networks](#). *Trends in Ecology & Evolution*, 32, 477–487.
- 756
- 757
- 758      Bolnick, D.I., Amarasekare, P., Araújo, M.S., Bürger, R., Levine, J.M., Novak, M., *et al.* (2011). [Why intraspecific trait variation matters in community ecology](#). *Trends in Ecology & Evolution*, 26, 183–192.
- 759

- 760 Borrett, S.R. & Scharler, U.M. (2019). [Walk partitions of flow in Ecological Network Analysis: Review and synthesis of methods and indicators](#). *Ecological Indicators*, 106, 105451.
- 761
- 762 Boulangeat, I., Gravel, D. & Thuiller, W. (2012). [Accounting for dispersal and biotic interactions to disentangle the drivers of species distributions and their abundances](#). *Ecology Letters*, 15, 584–593.
- 763
- 764 Brimacombe, C., Bodner, K., Michalska-Smith, M., Poisot, T. & Fortin, M.-J. (2023). [Shortcomings of reusing species interaction networks created by different sets of researchers](#). *PLOS Biology*, 21, e3002068.
- 765
- 766 Broom, M. & Ruxton, G.D. (2005). [You can run—or you can hide: Optimal strategies for cryptic prey against pursuit predators](#). *Behavioral Ecology*, 16, 534–540.
- 767
- 768 Brose, U., Ostling, A., Harrison, K. & Martinez, N.D. (2004). [Unified spatial scaling of species and their trophic interactions](#). *Nature*, 428, 167–171.
- 769
- 770 Burnham, K.P. & Anderson, D.R. (2004). [Multimodel Inference: Understanding AIC and BIC in Model Selection](#). *Sociological Methods & Research*, 33, 261–304.
- 771
- 772 Canard, E.F., Mouquet, N., Mouillot, D., Stanko, M., Miklisova, D. & Gravel, D. (2014). [Empirical Evaluation of Neutral Interactions in Host-Parasite Networks](#). *The American Naturalist*, 183, 468–479.
- 773
- 774 Canard, E., Mouquet, N., Marescot, L., Gaston, K.J., Gravel, D. & Mouillot, D. (2012). [Emergence of Structural Patterns in Neutral Trophic Networks](#). *PLOS ONE*, 7, e38295.
- 775
- 776 Castoe, T.A., Spencer, C.L. & Parkinson, C.L. (2007). [Phylogeographic structure and historical demography of the western diamondback rattlesnake \(\*Crotalus Atrox\*\): A perspective on North American desert biogeography](#). *Molecular Phylogenetics and Evolution*, 42, 193–212.
- 777
- 778
- 779 Catchen, M.D., Poisot, T., Pollock, L.J. & Gonzalez, A. (2023). The missing link: Discerning true from false negatives when sampling species interaction networks.
- 780
- 781 Cazelles, K., Araujo, M.B., Mouquet, N. & Gravel, D. (2016). [A theory for species co-occurrence in interaction networks](#). *Theoretical Ecology*, 9, 39–48.
- 782
- 783 Chagnon, P.-L. (2015). [Characterizing topology of ecological networks along gradients: The limits of metrics' standardization](#). *Ecological Complexity*, 22, 36–39.
- 784
- 785 Choh, Y., Ignacio, M., Sabelis, M.W. & Janssen, A. (2012). [Predator-prey role reversals, juvenile experience and adult antipredator behaviour](#). *Scientific Reports*, 2, 728.
- 786

- 787 Cimini, G., Squartini, T., Saracco, F., Garlaschelli, D., Gabrielli, A. & Caldarelli, G. (2019). [The statistical](#)  
788 [physics of real-world networks](#). *Nature Reviews Physics*, 1, 58–71.
- 789 Cirtwill, A.R., Eklöf, A., Roslin, T., Wootton, K. & Gravel, D. (2019). [A quantitative framework for](#)  
790 [investigating the reliability of empirical network construction](#). *Methods in Ecology and Evolution*, 10,  
791 902–911.
- 792 Dallas, T., Park, A.W. & Drake, J.M. (2017). [Predicting cryptic links in host-parasite networks](#). *PLOS*  
793 [Computational Biology, 13, e1005557.](#)
- 794 Dunne, J.A. (2006). The Network Structure of Food Webs. In: *Ecological networks: Linking structure and*  
795 *dynamics* (eds. Dunne, J.A. & Pascual, M.). Oxford University Press, pp. 27–86.
- 796 Elmasri, M., Farrell, M.J., Davies, T.J. & Stephens, D.A. (2020). [A hierarchical Bayesian model for predicting](#)  
797 [ecological interactions using scaled evolutionary relationships](#). *The Annals of Applied Statistics*, 14,  
798 221–240.
- 799 Elton, C.S. (2001). *Animal Ecology*. University of Chicago Press, Chicago, IL.
- 800 Emmerson, M.C. & Raffaelli, D. (2004). [Predator–prey body size, interaction strength and the stability of a real](#)  
801 [food web](#). *Journal of Animal Ecology*, 73, 399–409.
- 802 Fedorov, V.B., Goropashnaya, A.V., Boeskorov, G.G. & Cook, J.A. (2008). [Comparative phylogeography and](#)  
803 [demographic history of the wood lemming \(\*Myopus schisticolor\*\): Implications for late Quaternary history](#)  
804 [of the taiga species in Eurasia](#). *Molecular Ecology*, 17, 598–610.
- 805 Fortuna, M.A. & Bascompte, J. (2006). [Habitat loss and the structure of plant–animal mutualistic networks](#).  
806 *Ecology Letters*, 9, 281–286.
- 807 Fu, X., Seo, E., Clarke, J. & Hutchinson, R.A. (2021). [Link Prediction Under Imperfect Detection:](#)  
808 [Collaborative Filtering for Ecological Networks](#). *IEEE Transactions on Knowledge and Data Engineering*,  
809 33, 3117–3128.
- 810 Galiana, N., Lurgi, M., Claramunt-López, B., Fortin, M.-J., Leroux, S., Cazelles, K., et al. (2018). [The spatial](#)  
811 [scaling of species interaction networks](#). *Nature Ecology & Evolution*, 2, 782–790.
- 812 Gilman, S.E., Urban, M.C., Tewksbury, J., Gilchrist, G.W. & Holt, R.D. (2010). [A framework for community](#)  
813 [interactions under climate change](#). *Trends in Ecology & Evolution*, 25, 325–331.

- 814 Godsoe, W., Murray, R. & Iritani, R. (2022). Species interactions and diversity: A unified framework using Hill  
815 numbers. *Oikos*, n/a, e09282.
- 816 Golubski, A.J. & Abrams, P.A. (2011). Modifying modifiers: What happens when interspecific interactions  
817 interact? *Journal of Animal Ecology*, 80, 1097–1108.
- 818 Gomez, J.M., Verdu, M. & Perfectti, F. (2010). Ecological interactions are evolutionarily conserved across the  
819 entire tree of life. *Nature*, 465, 918–U6.
- 820 Gonzalez, A. & Londoño, M.C. (2022). Monitor biodiversity for action. *Science*, 378, 1147–1147.
- 821 Gonzalez-Varo, J.P. & Traveset, A. (2016). The Labile Limits of Forbidden Interactions. *Trends in Ecology &*  
822 *Evolution*, 31, 700–710.
- 823 Gravel, D., Albouy, C. & Thuiller, W. (2016). The meaning of functional trait composition of food webs for  
824 ecosystem functioning. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 371,  
825 20150268.
- 826 Gravel, D., Baiser, B., Dunne, J.A., Kopelke, J.-P., Martinez, N.D., Nyman, T., et al. (2019). Bringing Elton  
827 and Grinnell together: A quantitative framework to represent the biogeography of ecological interaction  
828 networks. *EcoGraphy*, 42, 401–415.
- 829 Gravel, D., Massol, F., Canard, E., Mouillot, D. & Mouquet, N. (2011). Trophic theory of island biogeography.  
830 *Ecology Letters*, 14, 1010–1016.
- 831 Gravel, D., Poisot, T., Albouy, C., Velez, L. & Mouillot, D. (2013). Inferring food web structure from  
832 predator–prey body size relationships. *Methods in Ecology and Evolution*, 4, 1083–1090.
- 833 Guimarães, P.R. (2020). The Structure of Ecological Networks Across Levels of Organization. *Annual Review*  
834 *of Ecology, Evolution, and Systematics*, 51, 433–460.
- 835 Guimerà, R. & Sales-Pardo, M. (2009). Missing and spurious interactions and the reconstruction of complex  
836 networks. *Proceedings of the National Academy of Sciences*, 106, 22073–22078.
- 837 Hemprich-Bennett, D.R., Oliveira, H.F.M., Le Comber, S.C., Rossiter, S.J. & Clare, E.L. (2021). Assessing the  
838 impact of taxon resolution on network structure. *Ecology*, 102, e03256.
- 839 Herrera, C.M. (1989). Pollinator abundance, morphology, and flower visitation rate: Analysis of the “quantity”  
840 component in a plant-pollinator system. *Oecologia*, 80, 241–248.

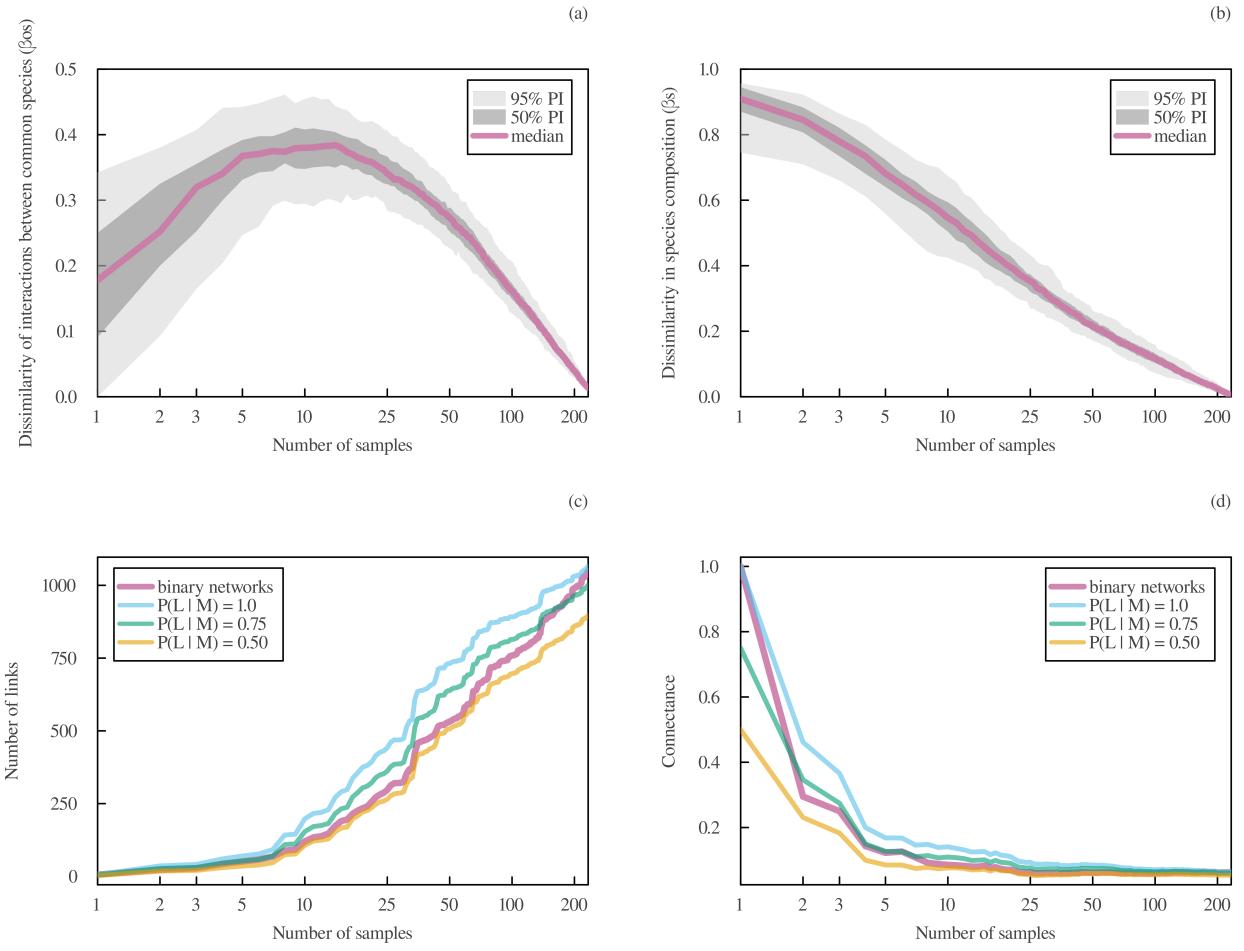
- 841 Hortal, J., de Bello, F., Diniz-Filho, J.A.F., Lewinsohn, T.M., Lobo, J.M. & Ladle, R.J. (2015). [Seven Shortfalls](#)  
842 [that Beset Large-Scale Knowledge of Biodiversity](#). *Annual Review of Ecology, Evolution, and Systematics*,  
843 46, 523–549.
- 844 Jordano, P. (1987). [Patterns of Mutualistic Interactions in Pollination and Seed Dispersal: Connectance,](#)  
845 [Dependence Asymmetries, and Coevolution](#). *The American Naturalist*, 129, 657–677.
- 846 Jordano, P. (2016). [Sampling networks of ecological interactions](#). *Functional Ecology*, 30, 1883–1893.
- 847 Jordano, P., Bascompte, J. & Olesen, J.M. (2003). [Invariant properties in coevolutionary networks of](#)  
848 [plant–animal interactions](#). *Ecology Letters*, 6, 69–81.
- 849 Kausrud, K.L., Mysterud, A., Steen, H., Vik, J.O., Østbye, E., Cazelles, B., et al. (2008). [Linking climate](#)  
850 [change to lemming cycles](#). *Nature*, 456, 93–97.
- 851 Kéfi, S., Berlow, E.L., Wieters, E.A., Joppa, L.N., Wood, S.A., Brose, U., et al. (2015). [Network structure](#)  
852 [beyond food webs: Mapping non-trophic and trophic interactions on Chilean rocky shores](#). *Ecology*, 96,  
853 291–303.
- 854 Kéfi, S., Berlow, E.L., Wieters, E.A., Navarrete, S.A., Petchey, O.L., Wood, S.A., et al. (2012). [More than a](#)  
855 [meal... integrating non-feeding interactions into food webs](#). *Ecology Letters*, 15, 291–300.
- 856 Kéfi, S., Miele, V., Wieters, E.A., Navarrete, S.A. & Berlow, E.L. (2016). [How Structured Is the Entangled](#)  
857 [Bank? The Surprisingly Simple Organization of Multiplex Ecological Networks Leads to Increased](#)  
858 [Persistence and Resilience](#). *PLOS Biology*, 14, e1002527.
- 859 Kissner, K.J., Forbes, M.R. & Secoy, D.M. (1997). [Rattling Behavior of Prairie Rattlesnakes \(\*Crotalus viridis\*](#)  
860 [viridis, Viperidae\) in Relation to Sex, Reproductive Status, Body Size, and Body Temperature](#). *Ethology*,  
861 103, 1042–1050.
- 862 Klecka, J. & Boukal, D.S. (2014). [The effect of habitat structure on prey mortality depends on predator and](#)  
863 [prey microhabitat use](#). *Oecologia*, 176, 183–191.
- 864 Kopelke, J.-P., Nyman, T., Cazelles, K., Gravel, D., Vissault, S. & Roslin, T. (2017). [Food-web structure of](#)  
865 [willow-galling sawflies and their natural enemies across Europe](#). *Ecology*, 98, 1730–1730.
- 866 Kulkarni, M.A., Kweka, E., Nyale, E., Lyatuu, E., Mosha, F.W., Chandramohan, D., et al. (2006).  
867 [Entomological Evaluation of Malaria Vectors at Different Altitudes in Hai District, Northeastern Tanzania](#).  
868 *Journal of Medical Entomology*, 43, 580–588.

- 869 McCann, K. (2007). Protecting biostructure. *Nature*, 446, 29–29.
- 870 McCann, K.S. (2011). Food webs (MPB-50). In: *Food Webs (MPB-50)*. Princeton University Press.
- 871 McLeod, A., Leroux, S.J., Gravel, D., Chu, C., Cirtwill, A.R., Fortin, M.-J., et al. (2021). [Sampling and asymptotic network properties of spatial multi-trophic networks](#). *Oikos*, n/a.
- 873 McLeod, A.M., Leroux, S.J. & Chu, C. (2020). [Effects of species traits, motif profiles, and environment on spatial variation in multi-trophic antagonistic networks](#). *Ecosphere*, 11, e03018.
- 875 Melián, C.J., Vilas, C., Baldó, F., González-Ortegón, E., Drake, P. & Williams, R.J. (2011). [Eco-evolutionary Dynamics of Individual-Based Food Webs](#). In: *Advances in Ecological Research*, The Role of Body Size in Multispecies Systems (ed. Belgrano, A.). Academic Press, pp. 225–268.
- 878 Ohlmann, M., Miele, V., Dray, S., Chalmandrier, L., O'Connor, L. & Thuiller, W. (2019). [Diversity indices for ecological networks: A unifying framework using Hill numbers](#). *Ecology Letters*, 22, 737–747.
- 880 Olesen, J.M., Bascompte, J., Dupont, Y.L., Elberling, H., Rasmussen, C. & Jordano, P. (2010). [Missing and forbidden links in mutualistic networks](#). *Proceedings of the Royal Society B: Biological Sciences*, 278, 725–732.
- 883 Park, J. & Newman, M.E.J. (2004). [Statistical mechanics of networks](#). *Physical Review E*, 70, 066117.
- 884 Pascual, M., Dunne, J.A. & Dunne, J.A. (2006). *Ecological Networks: Linking Structure to Dynamics in Food Webs*. Oxford University Press, USA.
- 886 Pellissier, L., Albouy, C., Bascompte, J., Farwig, N., Graham, C., Loreau, M., et al. (2018). [Comparing species interaction networks along environmental gradients](#). *Biological Reviews*, 93, 785–800.
- 888 Petchey, O.L., Beckerman, A.P., Riede, J.O. & Warren, P.H. (2008). [Size, foraging, and food web structure](#). *Proceedings of the National Academy of Sciences*, 105, 4191–4196.
- 890 Pilosof, S., Porter, M.A., Pascual, M. & Kéfi, S. (2017). [The multilayer nature of ecological networks](#). *Nature Ecology & Evolution*, 1, 1–9.
- 892 Plagányi, É.E. & Butterworth, D.S. (2004). [A critical look at the potential of Ecopath with ecosim to assist in practical fisheries management](#). *African Journal of Marine Science*, 26, 261–287.
- 894 Poisot, T., Canard, E., Mouillot, D., Mouquet, N. & Gravel, D. (2012). [The dissimilarity of species interaction networks](#). *Ecology Letters*, 15, 1353–1361.

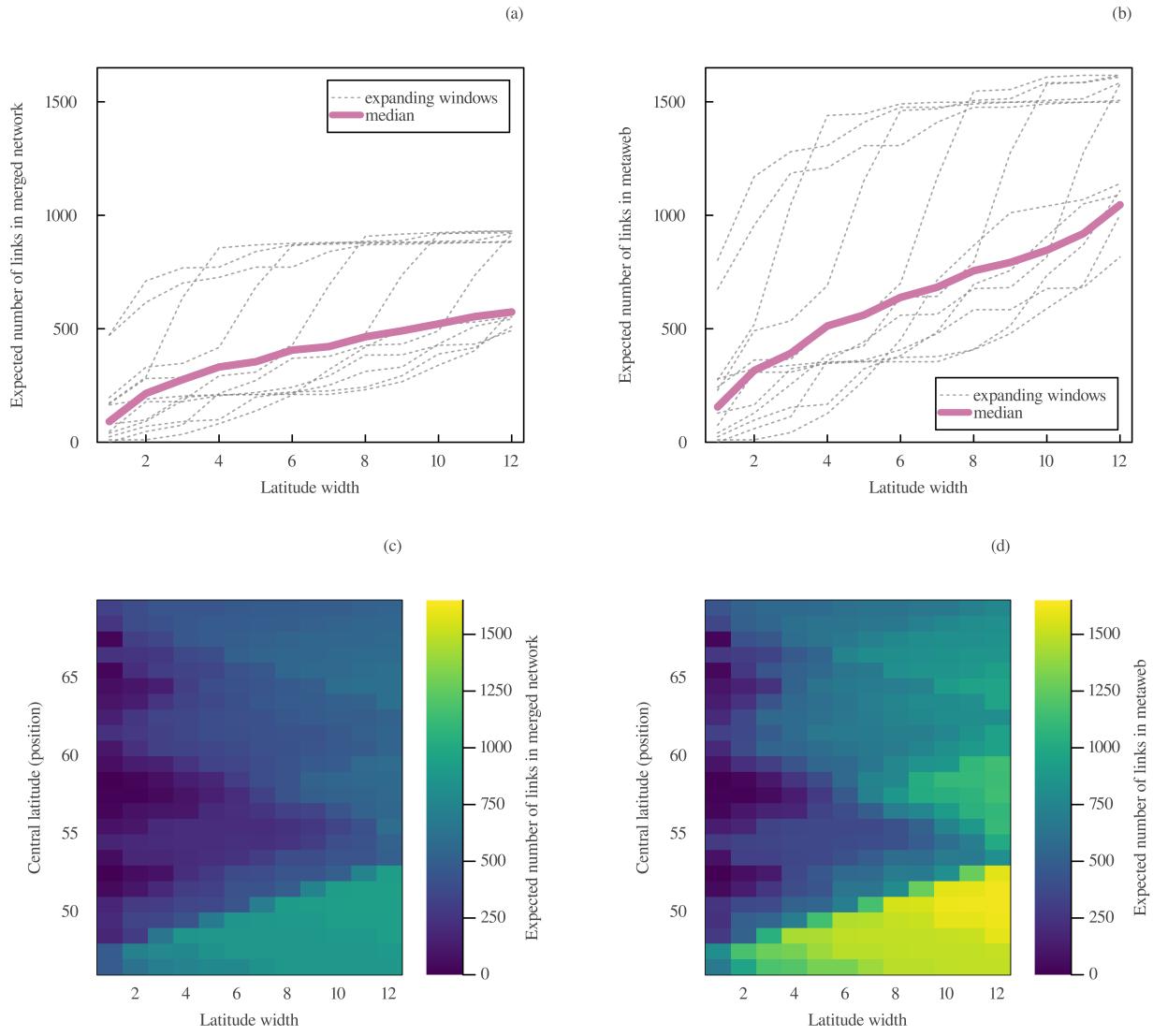
- 896 Poisot, T., Cirtwill, A.R., Cazelles, K., Gravel, D., Fortin, M.-J. & Stouffer, D.B. (2016). [The structure of probabilistic networks](#). *Methods in Ecology and Evolution*, 7, 303–312.
- 897
- 898 Poisot, T. & Gravel, D. (2014). [When is an ecological network complex? Connectance drives degree distribution and emerging network properties](#). *PeerJ*, 2, e251.
- 899
- 900 Poisot, T., Stouffer, D.B. & Gravel, D. (2015). [Beyond species: Why ecological interaction networks vary through space and time](#). *Oikos*, 124, 243–251.
- 901
- 902 Polis, G.A. (1991). [Complex Trophic Interactions in Deserts: An Empirical Critique of Food-Web Theory](#). *The American Naturalist*, 138, 123–155.
- 903
- 904 Pollock, L.J., Tingley, R., Morris, W.K., Golding, N., O’Hara, R.B., Parris, K.M., *et al.* (2014). [Understanding co-occurrence by modelling species simultaneously with a Joint Species DistributionModel \(JSMD\)](#). *Methods in Ecology and Evolution*, 5, 397–406.
- 905
- 906
- 907 Pomeranz, J.P.F., Thompson, R.M., Poisot, T. & Harding, J.S. (2019). [Inferring predator–prey interactions in food webs](#). *Methods in Ecology and Evolution*, 10, 356–367.
- 908
- 909 Pringle, R.M. & Hutchinson, M.C. (2020). [Resolving Food-Web Structure](#). *Annual Review of Ecology, Evolution, and Systematics*, 51, 55–80.
- 910
- 911 Proulx, S.R., Promislow, D.E.L. & Phillips, P.C. (2005). [Network thinking in ecology and evolution](#). *Trends in Ecology & Evolution*, SPECIAL ISSUE: BUMPER BOOK REVIEW, 20, 345–353.
- 912
- 913 Pulliam, H.R. (1974). [On the Theory of Optimal Diets](#). *The American Naturalist*, 108, 59–74.
- 914 Rooney, N. & McCann, K.S. (2012). [Integrating food web diversity, structure and stability](#). *Trends in Ecology & Evolution*, 27, 40–46.
- 915
- 916 Salim, J.A., Saraiva, A.M., Zermoglio, P.F., Agostini, K., Wolowski, M., Drucker, D.P., *et al.* (2022). [Data standardization of plant–pollinator interactions](#). *GigaScience*, 11, giac043.
- 917
- 918 Sanders, D. & van Veen, F.J.F. (2012). [Indirect commensalism promotes persistence of secondary consumer species](#). *Biology Letters*, 8, 960–963.
- 919
- 920 Saravia, L.A., Marina, T.I., Kristensen, N.P., De Troch, M. & Momo, F.R. (2022). [Ecological network assembly: How the regional metaweb influences local food webs](#). *Journal of Animal Ecology*, 91, 630–642.
- 921

- 922 Schmeller, D.S., Julliard, R., Bellingham, P.J., Böhm, M., Brummitt, N., Chiarucci, A., *et al.* (2015). Towards a  
923 global terrestrial species monitoring program. *Journal for Nature Conservation*, 25, 51–57.
- 924 Shaw, J.O., Dunhill, A.M., Beckerman, A.P., Dunne, J.A. & Hull, P.M. (2024). A framework for reconstructing  
925 ancient food webs using functional trait data.
- 926 Singer, M.C. & McBride, C.S. (2012). Geographic mosaics of species' association: A definition and an  
927 example driven by plant–insect phenological synchrony. *Ecology*, 93, 2658–2673.
- 928 Staniczenko, P.P.A., Sivasubramaniam, P., Suttle, K.B. & Pearson, R.G. (2017). Linking macroecology and  
929 community ecology: Refining predictions of species distributions using biotic interaction networks.  
930 *Ecology Letters*, 20, 693–707.
- 931 Stouffer, D.B., Rezende, E.L. & Amaral, L.A.N. (2011). The role of body mass in diet contiguity and food-web  
932 structure. *Journal of Animal Ecology*, 80, 632–639.
- 933 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M.J., *et al.* (2022). Food web  
934 reconstruction through phylogenetic transfer of low-rank network representation. *Methods in Ecology and  
935 Evolution*, 13.
- 936 Strydom, T., Catchen, M.D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., *et al.* (2021). A  
937 roadmap towards predicting species interaction networks (across space and time). *Philosophical  
938 Transactions of the Royal Society B-Biological Sciences*, 376, 20210063.
- 939 Thompson, R.M. & Townsend, C.R. (2005). Food-Web Topology Varies with Spatial Scale in a Patchy  
940 Environment. *Ecology*, 86, 1916–1925.
- 941 Tylianakis, J.M., Tscharntke, T. & Lewis, O.T. (2007). Habitat modification alters the structure of tropical  
942 host–parasitoid food webs. *Nature*, 445, 202–205.
- 943 Vázquez, D.P., Melián, C.J., Williams, N.M., Blüthgen, N., Krasnov, B.R. & Poulin, R. (2007). Species  
944 abundance and asymmetric interaction strength in ecological networks. *Oikos*, 116, 1120–1127.
- 945 Vázquez§, D.P., Peralta§, G., Cagnolo, L., Santos, M. & Igual, §.E. autores contribuyeron por. (2022).  
946 Ecological interaction networks. What we know, what we don't, and why it matters. *Ecología Austral*, 32,  
947 670–697.
- 948 Wagenmakers, E.-J. & Farrell, S. (2004). AIC model selection using Akaike weights. *Psychonomic Bulletin &  
949 Review*, 11, 192–196.

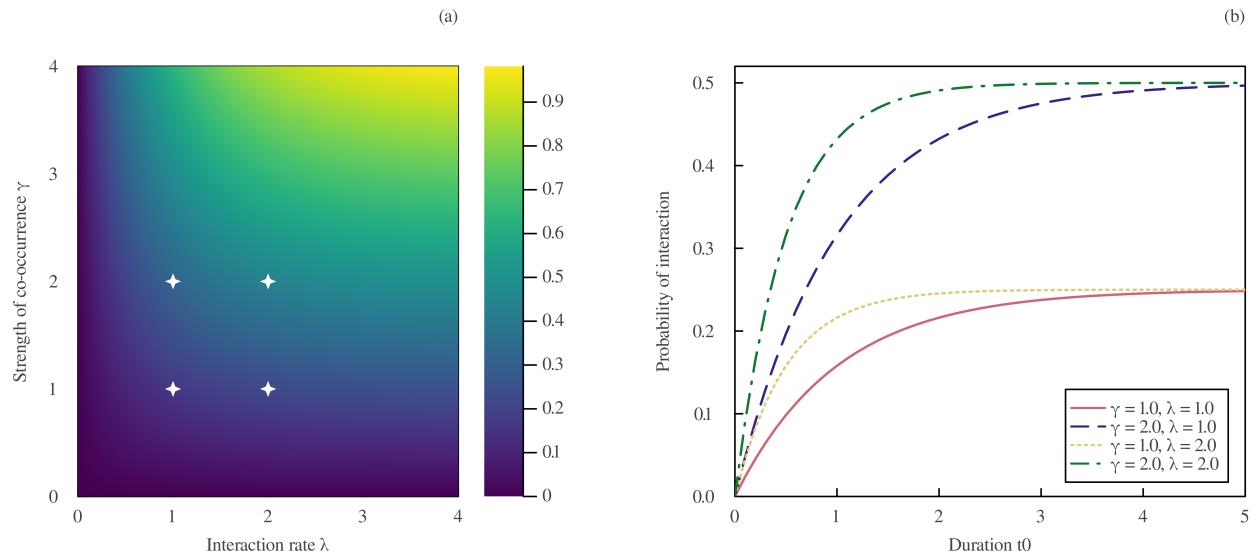
- 950 Weinstein, B.G. & Graham, C.H. (2017a). [On comparing traits and abundance for predicting species](#)  
951 [interactions with imperfect detection](#). *Food Webs*, 11, 17–25.
- 952 Weinstein, B.G. & Graham, C.H. (2017b). [Persistent bill and corolla matching despite shifting temporal](#)  
953 [resources in tropical hummingbird-plant interactions](#). *Ecology Letters*, 20, 326–335.
- 954 Whittaker, R.H. (1960). [Vegetation of the Siskiyou Mountains, Oregon and California](#). *Ecological*  
955 [Monographs](#), 30, 279–338.
- 956 Wood, S.A., Russell, R., Hanson, D., Williams, R.J. & Dunne, J.A. (2015). [Effects of spatial scale of sampling](#)  
957 [on food web structure](#). *Ecology and Evolution*, 5, 3769–3782.
- 958 Woodward, G., Benstead, J.P., Beveridge, O.S., Blanchard, J., Brey, T., Brown, L.E., *et al.* (2010). [Chapter 2 -](#)  
959 [Ecological Networks in a Changing Climate](#). In: *Advances in Ecological Research*, Ecological Networks  
960 (ed. Woodward, G.). Academic Press, pp. 71–138.
- 961 Woodward, G., Brown, L.E., Edwards, F.K., Hudson, L.N., Milner, A.M., Reuman, D.C., *et al.* (2012). [Climate](#)  
962 [change impacts in multispecies systems: Drought alters food web size structure in a field experiment](#).  
963 [Philosophical Transactions of the Royal Society B: Biological Sciences](#), 367, 2990–2997.
- 964 Young, J.-G., Valdovinos, F.S. & Newman, M.E.J. (2021). [Reconstruction of plant–pollinator networks from](#)  
965 [observational data](#). *Nature Communications*, 12, 3911.



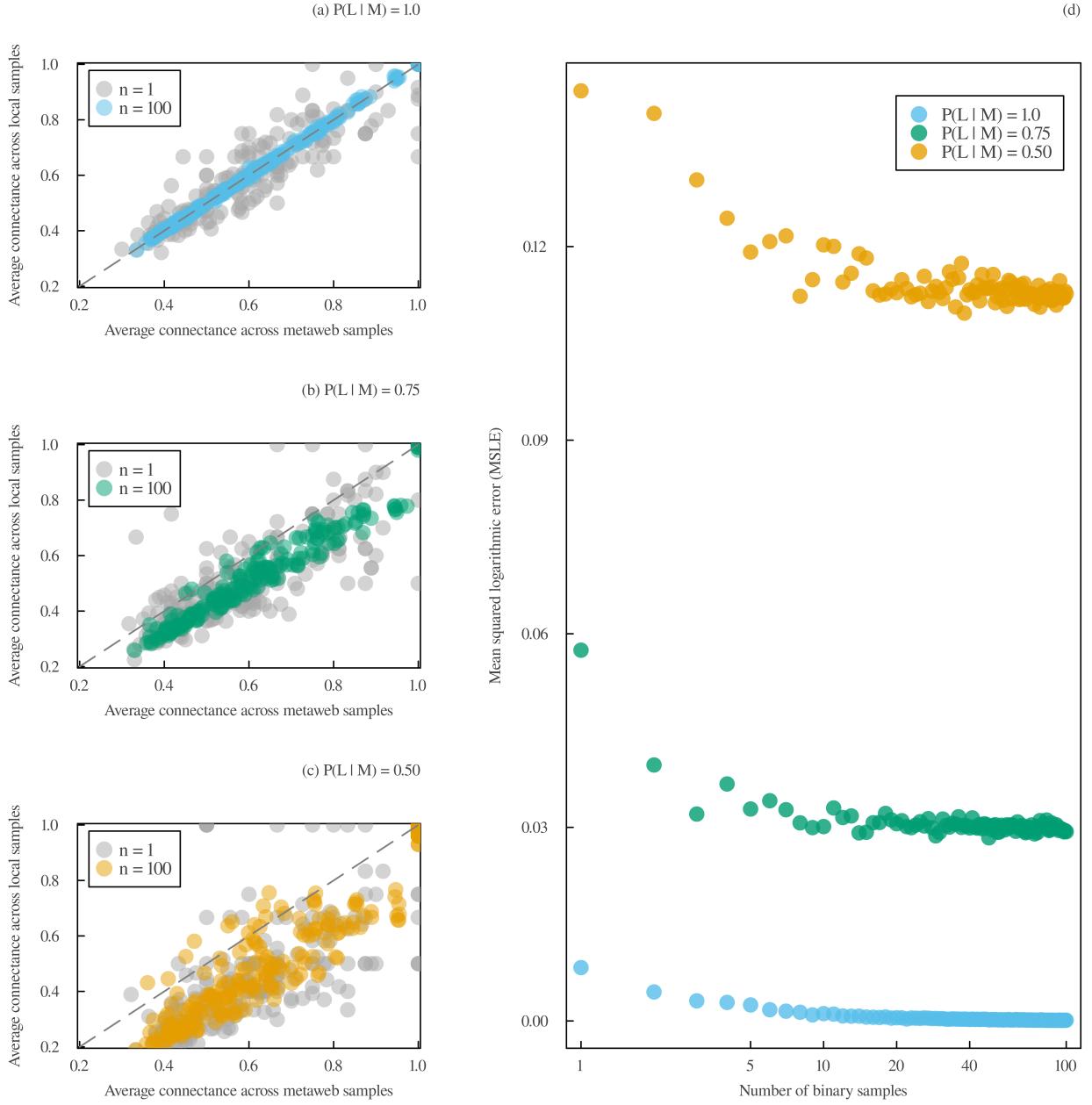
**Figure 1: Network accumulation curves.** (a) Dissimilarity of interactions between common species and (b) dissimilarity in species composition between aggregated local webs and the metaweb of binary host-parasite interactions. Aggregated local webs were obtained by sequentially and randomly selecting a number of local webs of binary interactions 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 interaction webs. For a better comparison with binary interactions, local webs of probabilistic interactions were derived from the metaweb of probabilistic interactions with a false positive and false negative rate of zero. A specific value of  $P(L_{i \rightarrow j} \mid M_{i \rightarrow j})$  (the local probability of interaction among potentially interacting species, indices omitted in the figure for simplicity) was used for all local webs within a particular curve. Aggregated local webs of probabilistic interactions were obtained by sequentially and randomly selecting a number of local webs and aggregating both their species and interactions (with the value of  $P(L_{i \rightarrow j} \mid M_{i \rightarrow j})$  adjusting according to eq. 11).



**Figure 2: Spatial scaling of interactions.** Expected number of host-parasite interactions in a network aggregating all (a) local and (b) regional probabilistic 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) regional interactions found in windows of specified length and central latitudes. Probabilities of regional interactions were obtained with a false positive rate of 5% and a false negative rate of 10%. Local probabilistic interactions were derived from probabilistic regional interactions by setting the value of  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$  (the local probability of interaction among potentially interacting species) to 1, ensuring a conservative comparison between aggregated local webs and metawebs. Aggregated local webs were obtained by aggregating both the species and interactions found within a particular latitudinal window, with the values of  $P(L_{i \rightarrow j} | M_{i \rightarrow j})$  remaining at their maximum value of 1 following eq. 11.



**Figure 3: Parameters of the spatiotemporally explicit model of interactions.** (a) Probability of local interaction given by the process model (eq. 16) under different values of  $\lambda_l$  and  $\gamma$ , with  $t_0 = 1$ . The parameter values used in the right panel are denoted by the white stars. (b) Scaling of the probability of interaction with the duration parameter  $t_0$  in eq. 16, for different values of  $\lambda_l$  and  $\gamma$ . In both panels, the marginal probabilities of occurrence  $P(X_{i,l})$  and  $P(X_{j,l})$  are set to a constant value of 0.5.



**Figure 4: Connectance of sampled binary interaction webs.** Comparison between the average connectance of binary interaction network samples obtained from the local and metawebs of probabilistic interactions. Each dot corresponds to a different site. The local probability of interaction between potentially interacting species was set to three different values: (a)  $P(L_{i \rightarrow j} \mid M_{i \rightarrow j}) = 1.0$ , (b)  $P(L_{i \rightarrow j} \mid M_{i \rightarrow j}) = 0.75$ , and (c)  $P(L_{i \rightarrow j} \mid M_{i \rightarrow j}) = 0.50$ . Grey dots represent the outcome of a single simulation, while colored dots represent the average connectance of each network across 100 simulations. (d) Reduction in the mean squared logarithmic error between the average connectance of binary interaction networks obtained from these two sampling methods as the number of simulations increases, for the same values of  $P(L_{i \rightarrow j} \mid M_{i \rightarrow j})$  used in panels a-c. Probabilities of regional interactions were obtained with a false positive rate of 5% and a false negative rate of 10%. Metaweb samples were obtained by randomly sampling binary interactions from the probabilistic interaction metaweb, and then propagating this result to all local webs that include the species potentially engaged in the interactions. Local binary interaction webs were generated by independently sampling binary interactions for each local web of probabilistic interactions.