

Deciphering probabilistic species interaction networks

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Representing species interactions probabilistically (how likely are they to occur?) as opposed to deterministically (are they occurring?) conveys uncertainties in our knowledge of interactions. The sources of uncertainty captured by interaction probabilities depend on the method used to evaluate them: uncertainty of predictive models, subjective assessment of experts, or empirical measurement of interaction spatiotemporal variability. However, guidelines for the estimation and documentation of probabilistic interaction data are still lacking. This is concerning because our understanding and analysis of interaction probabilities depend on their sometimes elusive definition and uncertainty sources. We review how probabilistic interactions are defined at different spatial scales, from local interactions to regional networks (metawebs), with a strong emphasis on host-parasite and trophic (predatory and herbivory) 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). Using host-parasite interactions in Europe, we illustrate how these two network representations differ in their statistical properties, specifically: how local networks and metawebs differ in their spatial and temporal scaling of probabilistic interactions, but not in their taxonomic scaling. We present two approaches to inferring binary interactions from probabilistic ones that account for these differences and show that systematic biases arise when directly inferring local networks from metawebs. Our results underscore the importance of more rigorous descriptions of probabilistic species interaction networks that specify their type of interaction (local or regional) and uncertainty sources.

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1 Introduction

2 Species interactions are uncertain

3 As we try to navigate global biodiversity change, filling in knowledge gaps about biodiversity becomes
4 instrumental to monitoring and mitigating those changes (Abrego *et al.* 2021; Gonzalez & Londoño 2022;
5 Hortal *et al.* 2015). However, cataloging species, populations and, in particular, ecological interactions (e.g.,
6 predation, parasitism, and pollination) is a substantial challenge (Pascual *et al.* 2006; Polis 1991). There are
7 methodological and biological constraints that hinder our ability to document species interactions, inevitably
8 leading to uncertainty in our knowledge of interactions. For example, the spatial and temporal uncoupling of
9 species (e.g., nocturnal and diurnal species coexisting in the same space with different daily activity timings,
10 Jordano 1987) and the large number of rare and cryptic interactions in a community, contribute to these
11 knowledge gaps (Jordano 2016).

12 Several conditions must be satisfied for an interaction to be observed locally. First, both species must have
13 overlapping geographic ranges, i.e. they must co-occur within the region of interest (Cazelles *et al.* 2016;
14 Morales-Castilla *et al.* 2015). Second, they must have some probability of meeting (Poisot *et al.* 2015).
15 Probabilities of interspecific encounters are typically low, especially for rare species with low abundances.
16 While species' absolute abundances may impact interaction frequencies (Vázquez *et al.* 2007), encounter
17 probabilities are determined by their relative abundances (Canard *et al.* 2012). The probability that species
18 meet also depends on their biology, such as their phenology (Olesen *et al.* 2010; Singer & McBride 2012) and
19 discoverability (Broom & Ruxton 2005). Finally, when species do come into contact, an interaction occurs only
20 if their traits are locally compatible (Poisot *et al.* 2015), including their phenotypes (Bolnick *et al.* 2011; Gravel
21 *et al.* 2013; Stouffer *et al.* 2011) and behavior (Choh *et al.* 2012; Pulliam 1974).

22 Documenting the location and timing of interactions becomes more difficult when accounting for the
23 spatiotemporal variability of ecological interactions (Poisot *et al.* 2012, 2015). Environmental factors, such as
24 temperature (Angilletta *et al.* 2004), drought (Woodward *et al.* 2012), climate change (Araujo *et al.* 2011;
25 Gilman *et al.* 2010; Woodward *et al.* 2010), and habitat modifications (Tylianakis *et al.* 2007), contribute to this
26 spatiotemporal variability by impacting species abundance and traits. Interactions may also be influenced by a
27 third species (e.g., a more profitable prey species, Golubski & Abrams 2011; Sanders & van Veen 2012). Even
28 under favorable circumstances, there remains a possibility that the interaction does not occur locally, either due
29 to the intricate nature of the system or simply by chance. If it does occur, it might go undetected, particularly if

30 it happens infrequently. In this context, it is unsurprising that our knowledge of ecological interactions remains
31 limited (Hortal *et al.* 2015) despite extensive biodiversity data collection (Schmeller *et al.* 2015).

32 Species interactions as probabilistic objects

33 Knowing the biological capacity of two species to interact directly (via e.g., trophic interactions) is necessary
34 but not sufficient for inferring their interaction at a specific time and space. The recognition of the intrinsic
35 variability of species interactions has led ecologists to expand their representation of ecological networks to
36 include a probabilistic view of interactions (Dallas *et al.* 2017; Fu *et al.* 2021; Poisot *et al.* 2016). This allows
37 filling in the Eltonian shortfall (Hortal *et al.* 2015) by modeling the probability of occurrence of interactions
38 (e.g., Gravel *et al.* 2019), which can be an important tool for directing efforts and taking action (Carlson *et al.*
39 2021), especially in places where access and resources for research are scarce. The probabilistic representation
40 of interactions has been applied to direct interactions, which are conceptually and mathematically analogous
41 regardless of their biological type (e.g., predation and pollination). This is in contrast with indirect interactions
42 (e.g., interspecific competition), which arise from distinct ecological processes and are often not directly
43 observable (Kéfi *et al.* 2015, 2016). Representing direct interactions probabilistically can capture the
44 spatiotemporal variability of the aforementioned ecological processes and the uncertainty in our knowledge of
45 interactions. By accounting for the uncertainty of interactions, networks of probabilistic interactions may
46 provide a more realistic portrait of species interactions.

47 Networks of probabilistic interactions, within a Bayesian perspective, express our degree of belief (or
48 confidence) regarding the occurrence or observation of interactions. In contrast, interactions are simply
49 regarded as either occurring or not in networks of deterministic binary interactions. Based on the scale at which
50 they are estimated, interaction probabilities may reflect our level of confidence in whether interactions will be
51 observed, realized locally, or biologically feasible. As an illustration, we could outline a situation in which there
52 is a 50% certainty that an interaction occurs 50% of the time. Our level of confidence should be more definitive
53 (approaching either 0 or 1) as we extend our sampling to a broader area and over a longer time period, thereby
54 diminishing the uncertainty of our knowledge of interactions (but not necessarily the estimation of their
55 variability). In the broadest sense, binary interactions are also a type of probabilistic interaction, in which the
56 numerical value of an interaction is restrained to 0 (non-occurring) or 1 (occurring). In networks of
57 probabilistic interactions, only forbidden interactions (i.e., interactions prohibited by biological traits or species
58 absence, Jordano *et al.* 2003; Olesen *et al.* 2010) have a probability value of zero, provided that intraspecific

59 trait variability is considered (Gonzalez-Varo & Traveset 2016).

60 The application and development of computational methods in network ecology, often based on a probabilistic
61 representation of interactions, can alleviate (and guide) the sampling efforts required to document species
62 interactions (Strydom *et al.* 2021). For example, statistical models can be used to estimate the uncertainty of
63 pairwise interactions (Cirtwill *et al.* 2019) and the probability of missing (false negatives) and spurious (false
64 positives) interactions (Guimerà & Sales-Pardo 2009). Statistical models can generate predictions of ecological
65 networks without prior knowledge of pairwise interactions. They may do so using body size (Caron *et al.* 2024;
66 Gravel *et al.* 2013; Petchey *et al.* 2008), phylogeny (Elmasri *et al.* 2020; Strydom *et al.* 2022), or a combination
67 of niche and neutral processes (Bartomeus *et al.* 2016; Pomeranz *et al.* 2019) for inference. Topological null
68 models, which generate networks of probabilistic interactions by preserving chosen characteristics of the
69 adjacency matrix of binary interactions while intentionally omitting others (Bascompte *et al.* 2003; Fortuna &
70 Bascompte 2006), are examples of common probabilistic interaction models. Null models can be used to
71 produce underlying distributions of network measures for null hypothesis significance testing. However, how
72 the uncertainty of pairwise interactions propagates to network structure (i.e., community-level properties
73 driving the functioning, dynamics, and resilience of ecosystems, McCann 2007; McCann 2011; Proulx *et al.*
74 2005; Rooney & McCann 2012) remains to be elucidated. Many measures have been developed to describe the
75 structure (Poisot *et al.* 2016) and diversity (Godsoe *et al.* 2022; Ohlmann *et al.* 2019) of probabilistic
76 interaction networks. These models and measures support the use of this approach for the study of a wide range
77 of ecological questions, from making better predictions of species distribution (Cazelles *et al.* 2016) to
78 forecasting the impact of climate change on ecological networks (Gilman *et al.* 2010).

79 We lack clear definitions of probabilistic species interactions

80 Yet, a precise definition of probabilistic interactions appears to be lacking, making the estimation and use of
81 these data more difficult. In this manuscript, we aim to take a step back by outlining different ways in which
82 probabilistic interactions are defined and used in network ecology. We distinguish two broad categories of
83 probabilistic interaction networks that necessitate distinct approaches: local networks describing probabilities
84 of realized interactions, and regional networks (metawebs) describing probabilities of potential interactions. We
85 highlight the distinctions in the ecological meaning of these two representations and examine their properties
86 and relationships (particularly with space, time, and between each other).

87 The lack of clear guidelines on the use of probabilistic interaction data is worrisome, as it affects both data
88 producers and re-users who generate and manipulate these numbers. This is concerning because sampling
89 strategies and decisions regarding network construction can affect our understanding of network properties
90 (Brimacombe *et al.* 2023). There is currently no reporting standard that could guide the documentation of all
91 types of probabilistic interactions (although Salim *et al.* 2022 discuss data standards for deterministic
92 mutualistic networks). Clear reporting standards for probabilistic interactions would support more adequate
93 manipulation and integration of interaction data from different sources and guard against possible
94 misinterpretations arising from ambiguous definitions of probabilistic interaction networks. This
95 documentation should outline the nature (i.e., local or regional) and type (e.g., predatory or pollination) of the
96 interactions, provide information regarding the taxonomic level, identities, and characteristics (e.g., life stages)
97 of the individuals involved in an interaction, present the mathematical formulation of probabilities, including
98 clearly identified conditional variables (e.g., spatial and temporal scales), and describe the methods and contexts
99 (e.g., location, time, environmental conditions) in which interactions were estimated. Inadequately documented
100 probabilistic interaction data should be used with caution when analyzing ecological networks. The broad
101 principles underlying our findings remain relevant and applicable across diverse ecological contexts involving
102 direct interactions. In the following sections, we delve into the definitions of probabilistic interactions as we
103 scale up from pairwise interactions to higher-level representations of ecological networks, i.e. local networks
104 and metawebs.

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

106 **Probabilistic interactions have different interpretations**

107 Consider a scenario where an avian predator has just established itself in a northern habitat home to a small
108 rodent. Suppose these species have never co-occurred before, and as a result, their interaction has not been
109 previously observed. What is the probability that the rodent is part of the diet of the avian predator, or put
110 differently, what is the probability that they interact? Answering this question requires some clarification, as
111 there are multiple ways to interpret and calculate interaction probabilities. We could calculate the probability
112 that the traits of these species match, i.e. that the avian predator possesses the biological attributes to capture
113 and consume the rodent. We could also calculate the probability that their traits support an interaction under the
114 typical environmental conditions of the new habitat. For example, because avian predators hunt by sight,

115 predation could be possible in the absence of snow but highly improbable when snow is present, as rodents may
116 use it as a shelter to hide from predators. Finally, we could calculate the probability that the avian predator will
117 consume the rodent at *that* particular location, for which the spatial and temporal boundaries need to be
118 specified. The estimation of interaction probabilities, whether through predictive models or prior distributions,
119 hinges on our understanding of these probabilities and the specific ecological processes we aim to capture.

120 An important aspect to consider when using interaction probabilities is knowing if they describe potential or
121 realized interactions, as these two types of interactions have distinct conceptual underpinnings and sources of
122 uncertainty. A potential (regional) interaction is defined as the biological capacity of two taxa to interact (i.e.,
123 the probability that they interact if they were to encounter each other and given sufficient time) whereas a
124 realized (local) interaction is the occurrence or observation of this interaction in a well-defined space and time
125 (i.e., the probability that they interact locally). For two co-occurring taxa and over enough time, the probability
126 of local interaction is equivalent to the probability of regional (potential) interaction.

127 We use the terms *metaweb* (Dunne 2006) to designate regional networks of potential interactions and *local*
128 *networks* (Poisot *et al.* 2012) for those of realized interactions. Metawebs are the network analogs of the species
129 pool, where local networks originate from a subset of both species (nodes) and interactions (edges) of the
130 regional metaweb (Saravia *et al.* 2022). Without clear documentation, it can be challenging to know if
131 published probabilistic interaction networks describe local or regional interactions, or if so-called probabilities
132 are in reality a form of interaction score. When probabilistic regional interactions are used and interpreted
133 incorrectly as local interactions (and conversely), this may generate misleading findings during data analysis. A
134 better understanding of probabilistic local and regional interactions would prevent interpretation errors (e.g.,
135 when studying network-area relationships with metawebs or local networks) and facilitate a more adequate use
136 of interaction data.

137 **The outcome of probabilistic interactions is usually binary**

138 Local networks and metawebs, like any type of network, are made of nodes and edges that may be represented
139 at different levels of organization. The basic units of ecological networks are individuals that interact with each
140 other (e.g., by predation in food webs, Elton 2001), forming individual-based networks (Melián *et al.* 2011).
141 The aggregation of these individuals into more or less homogeneous groups (e.g., populations, species, families,
142 feeding guilds) allows us to represent nodes at broader taxonomic scales, which affects our interpretation of the

143 properties of these systems (Guimarães 2020; Hemprich-Bennett *et al.* 2021).

144 Ecologists have traditionally represented interactions (edges) as binary objects that were considered realized
145 after observing at least one individual from group i interact with at least another individual from group j . In an
146 adjacency matrix B of binary interactions, the presence or absence of an interaction $B_{i \rightarrow j}$ between two taxa can
147 be viewed as the result of a Bernoulli trial $B_{i \rightarrow j} \sim \text{Bernoulli}(P(B_{i \rightarrow j}))$, with $P(B_{i \rightarrow j})$ being the probability of
148 interaction. This interaction probability characterizes our limited ecological knowledge and/or the intrinsic
149 spatiotemporal variability of interactions. It may be estimated through predictive models (e.g., those based on
150 biological traits and species abundances) or expert (prior) knowledge about the interaction. In networks of
151 probabilistic interactions, the edge values $P(B_{i \rightarrow j})$ are probabilistic events whose only two possible outcomes
152 are the presence ($B_{i \rightarrow j} = 1$) or absence ($B_{i \rightarrow j} = 0$) of an interaction between each pair of nodes. Depending on
153 the type of probabilistic interaction network (local or metaweb), the mathematical formulation and interpretation
154 of stochastic parameters like $P(B_{i \rightarrow j})$ can be linked to environmental and biological factors such as species
155 abundance, traits, area, and time, for example using logistic regression with continuous explanatory variables.

156 Predicting the number of local networks in which the interaction between two given taxa occurs can be achieved
157 by using a Binomial distribution, assuming a constant interaction probability and independence between
158 networks (trials). When considering uncertainties around the estimation of $P(B_{i \rightarrow j})$ or its spatiotemporal
159 variability, a Beta distribution may be used to represent the relative likelihood of different probability values.
160 For example, when calculating the probability of interaction between two taxa based on their local abundances,
161 any spatiotemporal fluctuations in their abundances would introduce variability in the interaction probability at
162 the local scale. If we take into account the stochasticity of the interaction probability, a Beta-Binomial
163 distribution can be used to predict the number of networks in which the interaction occurs. Empirically
164 observing an interaction between two taxa at a given location and time provides important information that can
165 be used to update previous estimates of $P(B_{i \rightarrow j})$, informing us on the biological capacity of both taxa to interact
166 and the environmental conditions that enabled them to interact locally.

167 **Probabilistic interactions may also describe quantitative networks**

168 Even though binary interaction networks constitute a highly valuable source of ecological information (Pascual
169 *et al.* 2006), they overlook interaction strengths. Represented in a quantitative adjacency matrix W , interaction
170 strengths better describe the energy flows, demographic impacts or frequencies of interactions between nodes

171 (Berlow *et al.* 2004; Borrett & Scharler 2019), with $W_{i \rightarrow j}$ being a natural \mathbb{N} or real \mathbb{R} number depending on the
172 measure. For example, they may represent local interaction rates between pairs of taxa (e.g., the flower-visiting
173 rates of pollinators in a mutualistic network, Herrera 1989). When interaction strengths characterize predation
174 pressure on prey, they can serve as parameters in a Lotka-Volterra model (e.g., Emmerson & Raffaelli 2004).
175 The extra amount of ecological information in quantitative networks typically comes at a cost of greater
176 sampling effort and data volume in predictive models (Strydom *et al.* 2021), which can lead to relatively high
177 levels of uncertainties when inferring quantitative networks with limited data.

178 As for binary interaction networks, the uncertainty and variability of interaction strengths can be represented
179 probabilistically. However, the need to estimate the probability distribution of interaction strengths makes the
180 inference of probabilities more challenging in quantitative networks compared to binary interaction networks.
181 Interaction strengths can follow many probability distributions depending on the method. For instance, they can
182 follow a Poisson distribution $W_{i \rightarrow j} \sim \text{Poisson}(\lambda_{i \rightarrow j})$ when predicting the number of interactions between pairs
183 of nodes, with $\lambda_{i \rightarrow j}$ being the expected rate at which individuals of taxa i and j interact (e.g., the average
184 number of prey j consumed by all predators i in a given time period). The Poisson distribution can also be
185 0-inflated after initially modeling non-interacting taxa (e.g., Boulangeat *et al.* 2012 employ a 0-inflated model
186 to analyze species abundance following the modeling of species presence and absence), which constitute the
187 majority of taxa pairs in most local networks (Jordano 2016).

188 Because of the methodological difficulties typically encountered when building deterministic quantitative
189 networks (which are only partially mitigated by models such as Ecopath, Plagányi & Butterworth 2004), binary
190 interaction networks, which are easier to sample (Jordano 2016) and predict (Strydom *et al.* 2021), have been
191 more frequently studied and modeled. Moreover, most published probabilistic interaction networks and methods
192 describe interactions whose outcome is binary (whether interaction probabilities are regarded as constant or
193 variable, e.g. represented by a Beta distribution), which underlines the need for better guidelines regarding the
194 interpretation and manipulation of these types of networks first. For these reasons, our primary focus is
195 interpreting and using interaction probabilities in Bernoulli distributions, in both local networks and metawebs.

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

197 **Species interactions occur in a local context**

198 Local networks of probabilistic interactions describe how likely taxa are to interact at a given location and time
199 period. Local interactions are contingent upon the environmental conditions of the community and the matching
200 of taxa biological traits. In local networks, edges commonly represent our degree of belief that two taxa interact
201 in nature, but can also represent the probability of empirically *observing* this interaction (Catchen *et al.* 2023).

202 **Space and time**

203 We define space as the collection of geographic coordinates (x, y, z) , with (x, y) representing longitude and
204 latitude coordinates, and z denoting either altitudes or depths. These point coordinates delineate the spatial
205 boundaries of the system, which may be portrayed as a polyhedron. Ecological interactions may exhibit
206 variations along latitudinal and altitudinal gradients, as evidenced by changes in hummingbird-plant
207 interactions (Weinstein & Graham 2017a, b) and mosquito biting rates (e.g., Kulkarni *et al.* 2006) at different
208 elevations. In contrast, time is defined as the specific time period within which interactions were either observed
209 or predicted. Even though space and time are continuous variables that should yield probability *densities* of
210 interactions (i.e., relative likelihoods of interactions occurring at infinitesimal locations and instants in time),
211 these definitions enable them to be conceptualized as distinct patches and time segments. Treating space and
212 time as discrete dimensions aligns with the common sampling methods of ecological networks and provides
213 probabilities of interactions, which can be obtained by integrating probability densities over space and time. We
214 can quantify both an area A and a duration t , which can be readily used in spatiotemporal analyses of ecological
215 networks. When studying network-area relationships (NAR, Galiana *et al.* 2018), we anticipate that local
216 probabilities of interactions scale positively with area and duration because taxa have more opportunities to
217 interact as these dimensions expand.

218 **Co-occurrence**

219 The probability that two taxa i and j interact in a local network $L_{x,y,z,t}$ (spatial and temporal subscripts hereafter
220 omitted or replaced by the shorter subscript k for clarity) can be conditioned on many environmental and
221 biological factors. In addition to network area (or volume) and duration, they may be conditioned on taxa

222 co-occurrence $X_{i,j,k}$, which is usually a Boolean describing if the geographic distributions of both taxa overlap
223 within the study area. As illustrated in Box 1, co-occurrence may be modeled probabilistically, in which case it
224 may conform to a Bernoulli distribution $X_{i,j,k} \sim \text{Bernoulli}(P(X_{i,k}, X_{j,k}))$, where $X_{i,k}$ and $X_{j,k}$ are the local
225 occurrences of both taxa. The probability of co-occurrence $P(X_{i,k}, X_{j,k})$ can be estimated through the
226 application of joint species distribution models (e.g., Pollock *et al.* 2014), potentially taking into account biotic
227 interactions (Staniczenko *et al.* 2017). Given that the probability that two non-co-occurring taxa interact locally
228 is zero (i.e., $P(L_{i \rightarrow j}|X_{i,j,k} = 0) = 0$), the probability of local interaction can be obtained by multiplying the
229 probability of interaction given co-occurrence with the probability of co-occurrence:

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

230 Biological and environmental factors

231 Local interactions may be conditioned on local environmental factors such as temperature (Angilletta *et al.*
232 2004), precipitation (Woodward *et al.* 2012), habitat structure (Klecka & Boukal 2014), and presence of other
233 taxa in the network (Kéfi *et al.* 2012; Pilosof *et al.* 2017). We use the variable E_k to describe the local
234 environmental context in which interaction probabilities were estimated. For example, in a mesocosm
235 experiment estimating interaction probabilities between predators and prey with and without shelters, E_k would
236 represent the presence or absence of these shelters. Like co-occurrence, E_k can also be modeled
237 probabilistically when the stochasticity or uncertainty of environmental factors is considered. E_k represents all
238 environmental variables that were taken into consideration when measuring interaction probabilities; it is a
239 subset of all environmental factors acting on ecological interactions.

240 Other important factors that can impact interaction probabilities at the local scale are taxa local abundances $N_{i,k}$,
241 and $N_{j,k}$, which affect encounter probabilities (Canard *et al.* 2012), and local traits distributions $T_{i,k}$ and $T_{j,k}$
242 (e.g., body mass, longevity, and habitat breadth, Caron *et al.* 2024), which determine the ability of individuals
243 to interact after encountering each other (Poisot *et al.* 2015). Local interaction probabilities may also be
244 conditioned on higher-level properties of the network, which we denote by $f(L)$. Many topological null models
245 (i.e., statistical models that randomize interactions by retaining certain properties of the network while
246 excluding others) provide interaction probabilities from selected measures of network structure, such as
247 connectance (Fortuna & Bascompte 2006) and the degree distribution (Bascompte *et al.* 2003).

248 **Local interactions must be biological feasible**

249 Local interactions must be biologically feasible before occurring at a specific time and space. A local
250 probability of interaction $P(L_{i \rightarrow j})$ can be expressed as the product of the probability of local interaction given
251 that the two taxa can potentially interact $P(L_{i \rightarrow j}|M_{i \rightarrow j} = 1)$, which we sometimes denote as $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ for the
252 sake of simplicity, with their probability of regional interaction $P(M_{i \rightarrow j})$:

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

253 Low values of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ indicate that feasible interactions rarely occur locally, intermediate values around
254 50% suggest considerable spatiotemporal variability, while high values indicate that regional interactions are
255 nearly always realized locally. The local probability of interaction between a given pair of taxa is always equal
256 to or below their probability of regional interaction.

257 **The variables used must be explicitly stated**

258 The probability that two taxa i and j interact in a local network L can thus be conditioned on their co-occurrence
259 $X_{i,j,k}$ (or more explicitly on their occurrences $X_{i,k}$ and $X_{j,k}$), local abundances $N_{i,k}$ and $N_{j,k}$, local traits
260 distributions $T_{i,k}$ and $T_{j,k}$, local environmental conditions E_k , network area (or volume) A , time interval t ,
261 network properties $f(L)$, and biological feasibility $M_{i \rightarrow j}$.

262 Although these variables correspond to distinct ecological inquiries or mechanisms related to ecological
263 interactions, they may covary with each other, such as the possible dependence of $X_{i,j,k}$ and E_k on spatial and
264 temporal scales. When estimating interaction probabilities using e.g. a generalized linear model with multiple
265 explanatory variables that might not be independent, it may become important to address collinearity. In such a
266 case, to mitigate this issue, it may be necessary to use variable selection techniques before fitting the model to
267 data. The probability that a local interaction is realized is described by the following expression when all these
268 conditional variables are included:

$$P(L_{i \rightarrow j}|X_{i,k}, X_{j,k}, N_{i,k}, N_{j,k}, T_{i,k}, T_{j,k}, E_k, A, t, f(L), M_{i \rightarrow j}) \quad (3)$$

269 The representation of the local context in which probabilities are estimated and the variables that should be

270 taken into consideration depend on the study system, the objectives of the study, and the resources available to
271 the researchers. In other words, these variables do not systematically need to be accounted for. For example,
272 Gravel *et al.* (2019) analyzed local European trophic networks of willow-galling sawflies and their natural
273 enemies, all referenced in space and time, to infer probabilities of local interactions between co-occurring
274 species. This was achieved by including temperature and precipitation as conditional variables in their models.
275 In Box 2, we reuse these data to show the extent of variation among these local host-parasite networks. We do
276 so by measuring their dissimilarity with the regional network (metaweb aggregating all local interactions), both
277 in terms of species composition and interactions. We build local probabilistic networks following eq. 2,
278 showing that insufficient local variation (high probability of local interaction among potentially interacting
279 species) results in an overestimation in both the number of interactions and connectance (i.e., the proportion of
280 all of the non-forbidden links that are realized).

281 When accounted for, conditional variables should be clearly described in the documentation of the data
282 (Brimacombe *et al.* 2023), preferentially in mathematical terms to avoid any confusion in their interpretation
283 and to limit manipulation errors during their re-use. For instance, ecologists should be explicit about their
284 consideration of co-occurrence in their estimation of local interaction probabilities. Indeed, it is important to
285 specify if probability values are conditional ($P(L_{i \rightarrow j}|X_{i,j,k} = 1)$) or not ($P(L_{i \rightarrow j})$) on co-occurrence, as this can
286 change the interpretation of the data. In Tbl. 1, we present examples of studies that used different expressions of
287 probabilistic interactions. We have included the probability of empirically observing an interaction that is
288 realized locally $P(O_{i \rightarrow j}|L_{i \rightarrow j})$ to underscore the distinction between local observations and actual realizations of
289 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 local network L of realized interactions and a metaweb M of potential interactions (representing the *biological* feasibility of 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 networks. Note that we also included the expression for a local network O of observed interactions and a metaweb M^* of potential interactions (representing the *ecological* feasibility of interactions) as they were mentioned in the main text, even though they are not the focus of this manuscript.

| Expression | Type | Outcome | Variability sources | Reference |
|---|-------|-----------------------------------|---------------------|---|
| $P(L_{i \rightarrow j} X_{i,k}, X_{j,k}, \dots)$ | local | realization of the interaction | spatiotemporal | Gravel <i>et al.</i> (2019) |
| | | given taxa co-occurrence | variability | |
| $P(L_{i \rightarrow j} N_{i,k}, N_{j,k}, \dots)$ | local | realization of the interaction | neutral models | Canard <i>et al.</i> (2014) |
| | | given taxa abundances | | |
| $P(L_{i \rightarrow j} T_{i,k}, T_{j,k}, \dots)$ | local | realization of the interaction | trait matching | Caron <i>et al.</i> (2024) |
| | | given local traits | models | |
| $P(L_{i \rightarrow j} E_k, \dots)$ | local | realization of the interaction | environmental- | Gravel <i>et al.</i> (2019) |
| | | given local environmental | based models | |
| | | conditions | | |
| $P(L_{i \rightarrow j} A, \dots)$ | 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 | |
| | | biologically interact | | |
| $P(O_{i \rightarrow j} L_{i \rightarrow j}, \dots)$ | local | observation of the interaction | sampling model | Catchen <i>et al.</i> (2023) |
| | | given that it is realized locally | | |

| Expression | Type | Outcome | Variability 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 |

290 **Interaction probabilities may be estimated with multiple models**

291 When using multiple models to estimate local interaction probabilities, rather than selecting a single model that
 292 best fits the data, model averaging may enhance our estimations. In this approach, the weighting is based on the
 293 likelihood of each model. Model weights represent the probability that each model is the most suitable for
 294 explaining the data, and may be measured using Akaike weights (Burnham & Anderson 2004; Wagenmakers &
 295 Farrell 2004). For instance, considering two models mod_1 and mod_2 with respective probabilities (or weights)
 296 $P(mod_1)$ and $P(mod_2)$, the average probability of interaction $P(L_{i \rightarrow j} | \dots)$ can be calculated as follows:

$$P(L_{i \rightarrow j} | \dots) = P(L_{i \rightarrow j} | mod_1, \dots) \times P(mod_1) + P(L_{i \rightarrow j} | mod_2, \dots) \times P(mod_2), \quad (4)$$

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

Box 1: A spatiotemporally explicit model of interactions

Ecologists may resort to predictive models (e.g., generative Bayesian models) to reconstruct local networks across time and space (Strydom *et al.* 2021). Uncertainty in model parameters, model structure, and input data leads to probabilistic interactions. We introduce and develop a simple generative mechanistic model for probabilistic local interactions that takes into consideration their spatiotemporal variability (i.e., a spatiotemporally explicit model of local interactions). This model is not designed for regional interactions, which do not vary spatially and temporally. Rather, it may prove valuable for predicting local interactions across time and space by generating new interaction data following parameter inference.

As indicated by Eq. 1, the probability that two taxa i and j interact at a specific location and time k may be determined by the product of their probability of interaction given co-occurrence and their probability of co-occurrence. First, their co-occurrence probability can be calculated using their individual (marginal) occurrence probabilities $P(X_{i,k})$ and $P(X_{j,k})$. Given that taxa occurrences are not independent of each other, the joint probability of both taxa occurring together can be calculated by multiplying the probability of one taxon being present by the conditional probability of the other occurring when the first one is present. Alternatively, the joint occurrence probability can be obtained by multiplying the marginal probabilities by the strength of association γ between the occurrences of both taxa (Cazelles *et al.* 2016):

$$P(X_{i,k}, X_{j,k}) = P(X_{i,k}|X_{j,k})P(X_{j,k}) = P(X_{i,k})P(X_{j,k})\gamma. \quad (5)$$

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

$$X_{i,j,k} \sim \text{Bernoulli}(P(X_{i,k}, X_{j,k})). \quad (6)$$

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

$$P(L_{i \rightarrow j}|X_{i,k}, X_{j,k}) = 1 - e^{-\lambda_k t_0}, \quad (7)$$

which tends toward 1 as $t_0 \rightarrow \infty$ if $\lambda > 0$. In other words, two co-occurring taxa with a nonzero rate of interaction will inevitably interact in a sufficiently long time period. It is important to note that the units

of λ_k and t_0 are complementary. For instance, if the duration t_0 is measured in months, λ_k would denote the expected number of interactions per month.

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

$$L_{i \rightarrow j} \sim \text{Bernoulli}(P(L_{i \rightarrow j})) \quad (8)$$

$$P(L_{i \rightarrow j}) = P(X_{i,k})P(X_{j,k})\gamma(1 - e^{-\lambda_k t_0}) \quad (9)$$

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

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

In Fig. 1, we show the variation in the probability of interaction under different parameter values. In the right panel, we notice that, irrespective of the interaction rate λ_k , the probability of interaction converges toward an asymptote determined by the probability of co-occurrence $P(X_{i,k}, X_{j,k})$ (Eq. 5). This model can be customized in different ways, such as by linking λ_k with specific environmental variables or explicitly incorporating observation errors (i.e., the probabilities of false negatives and false positives).

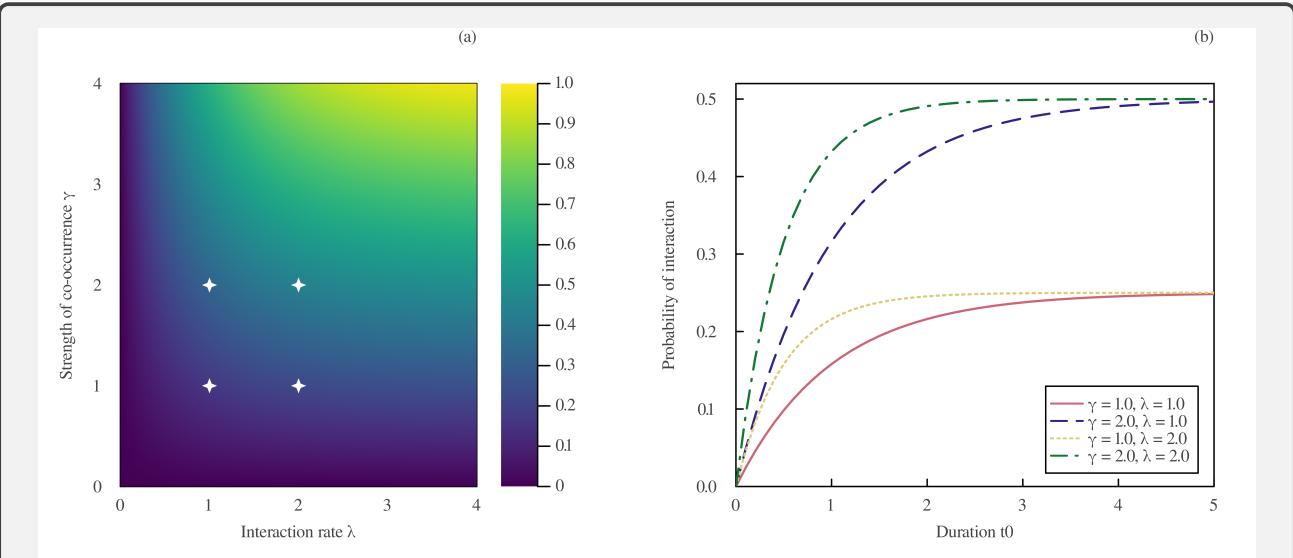


Figure 1: Parameters of the spatiotemporally explicit model of interactions. (a) Probability of local interaction given by the process model (Eq. 9) under different values of λ_k (interaction rate) and γ (strength of co-occurrence), with $t_0 = 1$ (duration). Parameters t_0 and λ_k have complementary units (e.g., t_0 in months and λ_k in number of interactions per month). 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. 9, for different values of λ_k and γ . In both panels, the marginal probabilities of occurrence $P(X_{i,k})$ and $P(X_{j,k})$ are set to a constant value of 0.5.

301

Box 2: Dissimilarity of local host-parasite networks

We use the collection of tripartite host-parasite networks of Kopelke *et al.* (2017), consisting of willows, willow-galling sawflies, and their natural enemies, sampled across Europe (233 local networks used). Given its replicated networks spanning large spatiotemporal scales, this dataset is well-suited for analyzing network variability, both in terms of species composition and interactions. Further details regarding data manipulation and network construction can be found in the supplementary material. All code and data to reproduce these analyses are available at the Open Science Framework (TBD).

In Fig. 2a-b, we show how the dissimilarity between the metaweb of binary interactions and aggregated local networks varies with the number of sampled local networks. To do so, we randomly selected one local network of binary interactions and sequentially sampled additional networks while aggregating both their species and interactions. We compared the metaweb and the aggregated local networks using the dissimilarity in species composition (β_S , Fig. 2a) and the dissimilarity of interactions between common species (β_{OS} , Fig. 2b) indices (Poisot *et al.* 2012). We repeated this sampling process one hundred times and highlighted the median dissimilarity values across simulations, as well as the 50% and 95%

302

percentile intervals. Both dissimilarity indices were calculated based on the number of items shared by the two networks (c_{LM}) and the number of items unique to the metaweb (u_M) and the aggregated local network (u_L). The β_S dissimilarity index uses species (nodes) as items being compared, while the β_{OS} index assesses dissimilarity based on interactions between shared species. Both indices were calculated following the β_W index of Whittaker (1960):

$$\beta_W = \frac{c_{LM} + u_L + u_M}{(2c_{LM} + u_L + u_M)/2} - 1. \quad (12)$$

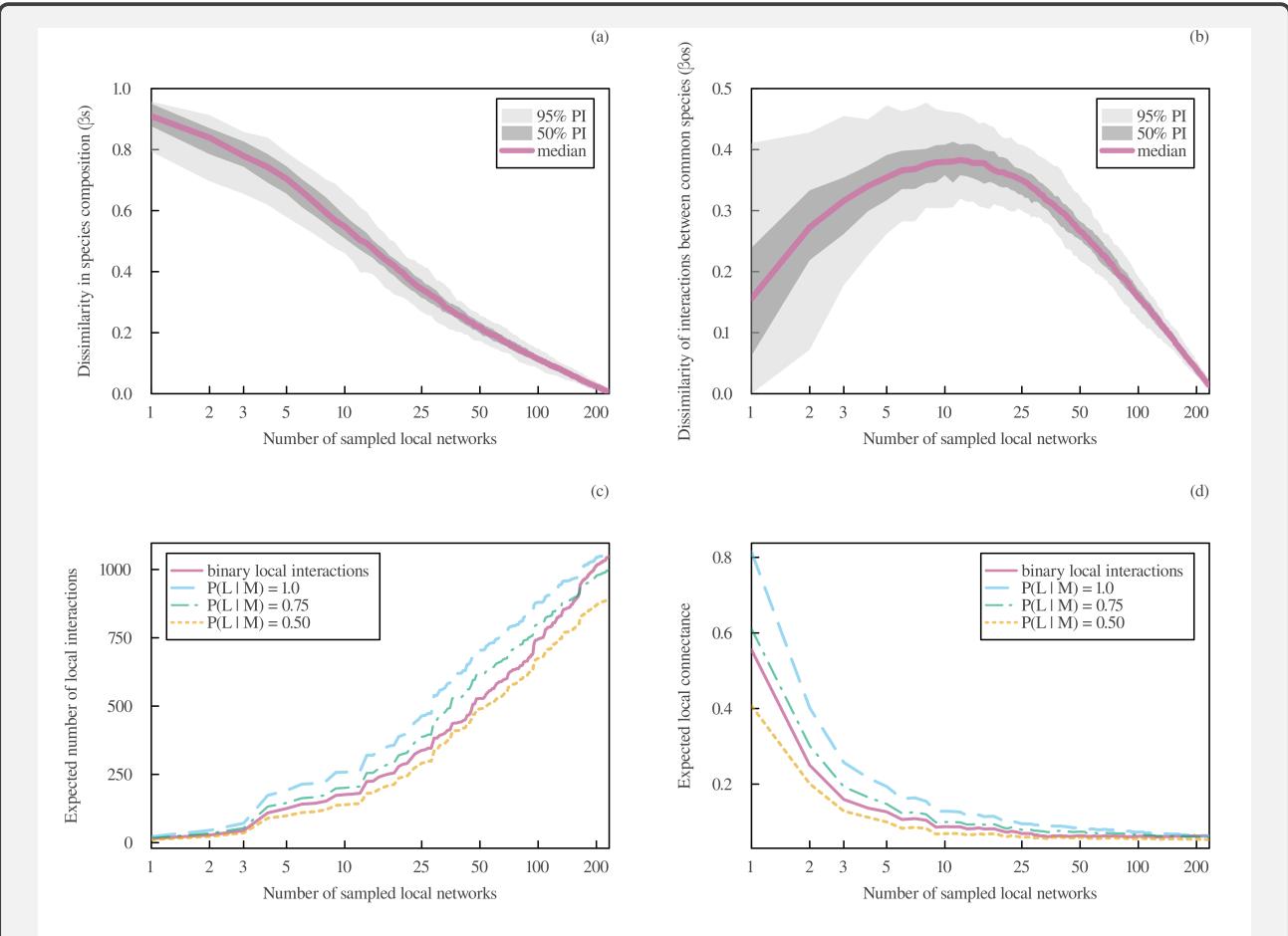


Figure 2: Network accumulation curves. (a) Dissimilarity in species composition and (b) dissimilarity of interactions between common species between aggregated local networks and the metaweb of binary host-parasite interactions. Aggregated local networks were obtained by sequentially and randomly selecting a number of local networks 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 interactions and (d) scaling of connectance with the number of sampled (aggregated) binary and probabilistic local interaction networks. For a better comparison with binary interactions, local networks of probabilistic interactions were derived from a metaweb of probabilistic interactions with a false positive and false negative rate of zero. A specific value of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ (the local probability of interaction among potentially interacting species, indices omitted in the figure for simplicity) was used for all local networks within a particular curve. Aggregated local networks of probabilistic interactions were obtained by sequentially and randomly selecting a number of local networks and aggregating both their species and interactions (with the value of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ adjusting according to Eq. 13).

Expectingly, local networks are highly dissimilar from the metaweb in terms of species composition, especially when only a limited number of sites has been sampled. This is because species in the metaweb form the regional species pool, and few species occur locally. Moreover, we observe a peak in the dissimilarity of interactions between common species at intermediate sampling levels. This suggests that

species are collected faster than their interactions. With a limited number of sampled local networks, few regional interactions are observed locally. Adding more sites brings new species, but not always their interactions. Interactions are more comprehensively captured when the number of sampled sites is high. Quadratic relationships of network properties with sampling effort were also observed by McLeod *et al.* (2021).

Next, we investigate how the number of local interactions and connectance scale with the number of sampled (aggregated) local networks of probabilistic or binary interactions (Fig. 2c-d). We built probabilistic local networks following Eq. 2, and set $P(M_{i \rightarrow j})$ to 1 when the interaction was observed at least once, and to 0 otherwise (i.e., no false positive or false negative in the metaweb). We used a constant value of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ for all interactions.

When aggregating local networks of probabilistic interactions, the constancy of the probability of regional interaction across the entire study area means that any rise in the 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 be two local networks and $L_{1,2}$ the aggregated network. 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 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 these taxa interact in the aggregated network $L_{1,2}$ is obtained by:

$$P(L_{1,2,i \rightarrow j} | M_{i \rightarrow j}) = 1 - [1 - P(L_{1,i \rightarrow j} | M_{i \rightarrow j})] \times [1 - P(L_{2,i \rightarrow j} | M_{i \rightarrow j})], \quad (13)$$

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

By comparing the scaling relationships observed in local networks of binary (empirical) and probabilistic (modeled) interactions, Fig. 2c-d shows that high values of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ lead to systematic overestimations in the number of interactions and connectance, especially when $P(L_{i \rightarrow j} | M_{i \rightarrow j}) = 1$ (corresponding to the scenario where local probabilities of interactions are equivalent to the probabilities of regional interactions). This suggests that high values of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ do not adequately capture the variability of local interactions. However, these biases tend to diminish as the number of sampled networks increases, indicating that most interactions are eventually captured when $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ is high. In contrast,

low values of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ lead to missing interactions, resulting in an underestimation of the number of interactions and connectance. These results underscore the importance of using the appropriate level of variability when estimating local interaction probabilities.

306

307 Metawebs: regional catalogs of interactions

308 Metawebs (Dunne 2006) are networks of potential interactions over broad spatial, temporal, and taxonomic
309 scales (e.g., food webs at the continental scale). Potential interactions describe the biological capacity of taxa to
310 interact, which is typically assessed at the regional scale. Metawebs of probabilistic interactions are particularly
311 useful in situations where there is uncertainty in the ability of taxa to interact. This uncertainty frequently arises
312 due to insufficient interaction data, especially for taxa that have not yet been observed to co-occur, and
313 uncertainties in trait-matching models. As data accumulates, interactions in metawebs should tend towards
314 binarity, approaching probability values of 0 (repeatedly failing to observe an interaction between two
315 co-occurring taxa) and 1 (observing an interaction at least once). The extent of sampling effort thus influences
316 our evaluation of probabilities of potential interactions, as sampling over a larger area or for a longer duration
317 enables us to capture a greater number of regional interactions (McLeod *et al.* 2021). However, in contrast with
318 local networks of probabilistic interactions, which describe local interaction stochasticity, regional interactions
319 are not evaluated for any particular local context. In Box 3, we discuss the differences in spatial and temporal
320 scaling of regional interactions compared to local interactions. We do so by using the host-parasite networks of
321 Kopelke *et al.* (2017) as an illustration of spatial scaling. Although *neutrally* forbidden interactions (i.e.,
322 between rare species, Canard *et al.* 2012) tend to have low probability values in local networks, they may have
323 higher probabilities in the metaweb (i.e., when species' biological traits can support an interaction if they were
324 to encounter each other). Likewise, non-co-occurring taxa may have a non-zero probability of interaction in the
325 metaweb.

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

$$P(M_{i \rightarrow j} | T_i, T_j), \quad (14)$$

which, in contrast with local networks, is not conditioned on any spatial, temporal, co-occurrence or environmental variables (Tbl. 1). Regional traits may differ from local traits $T_{i,k}$ and $T_{j,k}$, which may vary spatially and temporally due to phenotypic plasticity (Berg & Ellers 2010). The taxonomic level at which interactions are evaluated influences the distribution of regional and local traits. However, as explained in Box 4, there is no fundamental difference in the taxonomic scaling of regional and local interactions (i.e., how interaction probabilities change with taxonomic level), unlike their spatial and temporal scaling.

The biological feasibility of interactions expresses our degree of belief that there exists at least one combination of phenotypes that could support an interaction if they were to encounter each other, assuming they had infinite time to interact. Evaluating this probability is conducted without incorporating the environmental conditions under which they encounter each other into the model, as the complement of the probability $P(F_{i \rightarrow j}|T_i, T_j)$ of forbidden interactions based uniquely on biological traits (i.e., the probability that their traits do not support an interaction):

$$P(M_{i \rightarrow j}|T_i, T_j) = 1 - P(F_{i \rightarrow j}|T_i, T_j). \quad (15)$$

For example, let i be a western diamondback rattlesnake (*Crotalus atrox*) and j , a wood lemming (*Myopus schisticolor*). These two taxa never co-occur, the rattlesnake being adapted to warm regions of North America (Castoe *et al.* 2007) and the lemming, to northern habitats of Eurasia (Fedorov *et al.* 2008). As we lack direct observations of an interaction between these two species, we have to rely on expert knowledge or trait-matching models to estimate their probability of potential interaction. To accurately estimate this probability using trait-matching models, it is crucial to ensure that the set of traits considered reflects the overall traits distributions of both taxa. We could for instance consider their average body mass and the average phylogenetic proximity of lemmings to rattlesnakes' prey. Doing so, we might find a high probability of potential interaction based on these traits.

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

$$P(M_{i \rightarrow j}^*|T_i, T_j, E), \quad (16)$$

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

$$\int_E P(M_{i \rightarrow j}^* | T_i, T_j, E) dE \leq P(M_{i \rightarrow j} | T_i, T_j). \quad (17)$$

363 This is because the biological feasibility of an interaction is a prerequisite for its ecological feasibility.
 364 Biological feasibility is necessary but not sufficient for an interaction to be ecologically feasible. Our discussion
 365 of metawebs will focus on the biological feasibility of interactions since most methods developed for inferring
 366 probabilities of regional interactions do not explicitly take into account environmental conditions (e.g., Strydom
 367 *et al.* 2022).

368 Starting from a selected set of taxa, which are usually distributed within a broad region of interest, metawebs
 369 can be built using different data sources, including literature review (e.g., Maiorano *et al.* 2020), aggregated
 370 interaction data (e.g., Gravel *et al.* 2019; Saravia *et al.* 2022), trait-matching models (e.g., Shaw *et al.* 2024;
 371 Strydom *et al.* 2022), and expert knowledge. Every pair of taxa that have confidently been observed to interact
 372 at least once can be given a probability of 1 (i.e., $P(M_{i \rightarrow j}) = 1$) since we know that they *can* interact. This
 373 differs from local networks of probabilistic interactions, where interaction events may remain stochastic (i.e.,
 374 $P(L_{i \rightarrow j}) < 1$) even after empirically observing interactions due to their spatiotemporal variability. Interactions
 375 that were never observed typically have low probability values in local networks and vary from low to high
 376 values in metawebs, contingent upon taxa traits distributions (reaching 0 for forbidden links).

377 When incorporating local network data to estimate probabilities of regional interactions, repeatedly failing to
 378 observe an interaction between two co-occurring taxa (i.e., $P(O_{i \rightarrow j} = 0)$) should decrease the probability that
 379 the interaction is biologically feasible. Using Bayes' theorem, the probability that the interaction is biologically

380 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:

$$P(M_{i \rightarrow j} = 1 | O_{i \rightarrow j} = 0, \dots) = \frac{P(O_{i \rightarrow j} = 0 | M_{i \rightarrow j} = 1, \dots) \times P(M_{i \rightarrow j} = 1 | \dots)}{P(O_{i \rightarrow j} = 0 | \dots)}. \quad (18)$$

381 The reduction in the probability of regional interaction after considering that it was never observed locally (i.e.,
382 $P(M_{i \rightarrow j} = 1 | O_{i \rightarrow j} = 0, \dots) < P(M_{i \rightarrow j} = 1 | \dots)$) occurs because $P(O_{i \rightarrow j} = 0 | M_{i \rightarrow j} = 1, \dots)$ must be lower than
383 $P(O_{i \rightarrow j} = 0, \dots)$, i.e. there is a higher chance of observing an interaction when we know it is biologically
384 feasible.

385 Many observations of interactions are false positives because of observation errors due to taxonomic
386 misidentifications and ecological misinterpretations (e.g., due to cryptic species and interactions, Pringle &
387 Hutchinson 2020). Likewise, forbidden interactions may be false negatives, e.g. if they have been evaluated
388 based on unrepresentative or incomplete traits distributions. Employing Bayesian models proves valuable when
389 estimating interaction probabilities in metawebs (e.g., Bartomeus *et al.* 2016; Cirtwill *et al.* 2019). This
390 improvement is achieved by updating prior information regarding the feasibility of interactions (e.g., experts'
391 prior assessments of interaction probabilities) with empirical data on interactions and traits.

Box 3: Spatial and temporal scaling of interactions

Network-Area Relationships document the scaling of network properties (such as modularity and connectance) with spatial scale (e.g., Galiana *et al.* 2018; Wood *et al.* 2015). The variation in network structure across spatial scales may stem from the scaling of species richness (species-area relationships, SARs), the number of interactions (Brose *et al.* 2004), and many other higher-level properties of the system (e.g., environmental heterogeneity, Thompson & Townsend 2005) with the sampled area. Likewise, interaction accumulation curves describe the scaling of the number of observed interactions with sampling effort (Jordano 2016). Sampling effort, which may correspond to the duration of the sampling period used to construct the network, can impact connectance (Bersier *et al.* 1999) and various measures of network structure (Banašek-Richter *et al.* 2004; McLeod *et al.* 2021). Apart from sampling effort, the temporal scaling of interactions also describes how network structure changes with the temporal resolution of the network, acknowledging that distinct interactions take place over time, ranging from short-term fluctuations of interactions to long-term trends. As local networks of probabilistic interactions may explicitly account for the spatiotemporal variability of interactions, they offer a distinct approach to

investigating the scaling of network structure with space and time.

Local networks and metawebs exhibit distinct relationships with spatial and temporal scales. On one hand, metawebs of probabilistic interactions feature regional interactions that do not scale with space and time. This is because regional interactions depend solely on the biological capacity of two taxa to interact, regardless of their co-occurrence and local environmental conditions. However, probabilities of potential interactions may change, tending to become more definitive with increased sampling effort (even though they do not vary with the spatial and temporal extent (boundaries) of the network). The probability of two taxa potentially interacting should be the same in all metawebs in which they are present, provided that the data and methods used for estimation are consistent. For example, if a smaller metaweb M_1 is derived from a larger metaweb M_0 by selecting the subset of taxa present in the region described by M_1 and retaining all their interactions, their probabilities of 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 taxa in M_0 as compared to M_1 , the total number of interactions is expected to be higher in the larger network, even though pairwise probabilities remain identical.

On the other hand, local interactions scale both spatially and temporally, given that they have more opportunities to be realized and observed in larger areas and longer durations. This is attributed to factors such as a higher number of individuals, greater trait variations, and increased opportunities for encounters, as highlighted by McLeod *et al.* (2020). For example, if a local network of probabilistic interactions L_1 with an area A_1 is derived from a larger network L_0 with an area A_0 , and A_1 is entirely nested within A_0 , interaction probabilities should be lower in the smaller network, 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, interaction probabilities could be higher in the smaller area, contingent upon their environmental and biological conditions. Likewise, interaction probabilities should be lower in networks with shorter durations when time intervals are nested. In Fig. 3, we show how the expected number of local host-parasite interactions scales with area, represented as an expanding latitudinal window, in comparison with regional interactions (data from Kopelke *et al.* 2017). Even though we employed local probabilities of interactions equal to regional interactions for the purpose of 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 more rapidly than local interactions. This is because numerous regional interactions involve species that never co-occur, and as a result, these interactions are not captured in local networks.

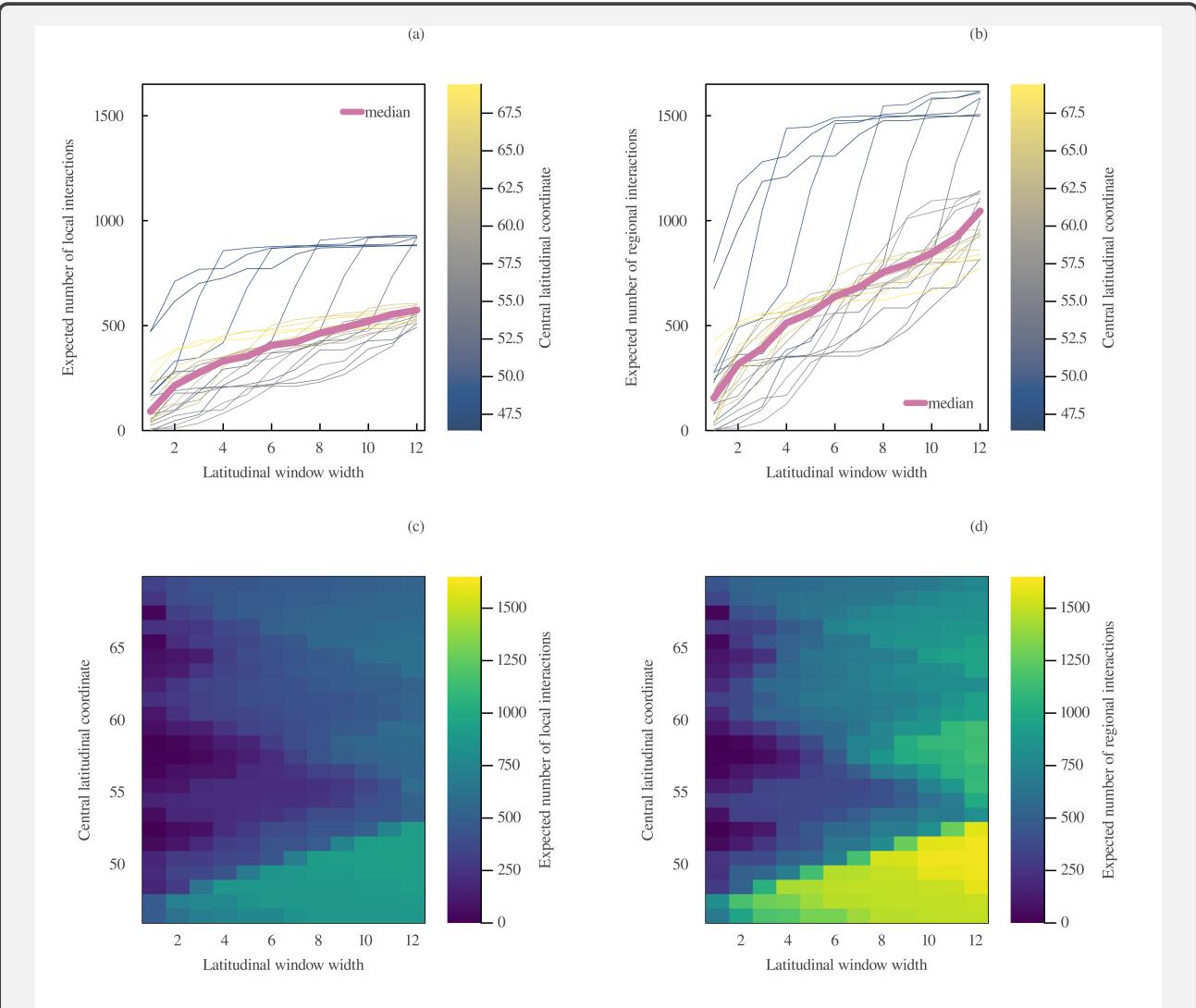


Figure 3: Spatial scaling of interactions. Expected number of host-parasite interactions in a network aggregating all (a) local and (b) regional probabilistic interactions within a latitudinal window of a given width. Every dashed curve corresponds to a different window centered at a given latitude (color bar), with the pink solid line representing the median number of interactions across windows. Heatmaps of the expected number of (c) local and (d) regional interactions found in windows of specified width 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 networks and metawebs. Aggregated local networks were obtained by aggregating both the species and interactions found within a particular latitudinal window, with the values of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ remaining at their maximum value of 1 following Eq. 13. Further details on the data and network construction are presented in the supplementary material.

Box 4: Taxonomic scaling of interactions

Probabilistic interaction networks offer a versatile approach to tackle a broad array of ecological questions, depending on their level of organization. For instance, the assemblage of interactions across ecological scales can be explored through species-based networks, while clade-based networks provide insights into macroevolutionary processes (Gomez *et al.* 2010). Given that our interpretation of the properties and dynamics of ecological networks depends on their taxonomic level (Guimarães 2020), investigating the taxonomic scaling of interactions (i.e., how interaction probabilities change with taxonomic level) emerges as a promising research avenue.

There are no inherent differences between the taxonomic scaling of local networks and metawebs. Interaction probabilities in both local networks (Eq. 3) and metawebs (Eq. 14) are not directly conditioned on taxonomic level. The taxonomic scale is tied to the definition of the event itself (i.e., the interaction between two taxa, defined at the desired taxonomical scale), not to the variables on which interaction probabilities are conditioned. However, some conditional variables (e.g. trait distribution) may vary with taxonomic scale. In such cases, interaction probabilities would vary taxonomically following the scaling of these variables.

In both types of networks, transitioning to a broader level of organization (e.g., from a species-level network S to a genus-level network G) can be accomplished directly by using probabilities 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 can compute the probability that at least one species from genus g_1 interacts with at least one species from genus g_2 (i.e., that there is a non-zero number of species-level interactions or, equivalently, that the genus-level interaction occurs) as follows:

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

where $g_{1,i}$ and $g_{2,j}$ are the species of the corresponding genus and assuming independence between 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 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 species-based network following a similar approach, by using simulated interactions between individuals derived from a neutral model (i.e., a model that assumed ecological equivalence among individuals).

In contrast, a more sophisticated approach is necessary when transitioning from a broader to a finer level of organization. This is because the knowledge of an interaction between two genera does not guarantee that all possible pairwise combinations of their species will also interact. One possible method is to build a finer-scale network by generating probabilities of interactions through random sampling from a beta distribution, parameterized by the broader-scale network.

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

396

Box 5: Sampling for binary interaction networks

The prediction of binary interactions through Bernoulli trials is an important application of probabilistic interaction networks. This approach proves beneficial for analyzing the structural characteristics of probabilistic interaction networks, particularly in the absence of specific analytical formulas for measures of network structure (Poisot *et al.* 2016). By performing independent Bernoulli trials for each interaction, a network of binary interactions may be generated. A probability distribution of network properties can be obtained by measuring network structure across multiple randomly generated networks (Poisot *et al.*

397

2016). This method enables the representation of the variability or uncertainty of network structure, albeit with possible biases when connectance is low (Chagnon 2015; Poisot & Gravel 2014). Employing this strategy to generate binary interaction networks under a null model facilitates null hypothesis significance testing, wherein the observed measure is compared against the simulated distribution (e.g., Bascompte *et al.* 2003). Yet, inferring network structure through sampling for binary interactions assumes independence among interactions, which might not accurately represent reality. Covariation among interactions could exist even if we do not explicitly condition interactions on others. For example, an interaction between two taxa could be more probable when another interaction occurs. The consequences of this assumption of independence on the prediction of network structure have yet to be empirically examined.

There are at least two approaches to sampling binary interaction networks across space from probabilistic interaction networks (i.e., when predicting a binary interaction network for each location k within a given region). Both approaches assume independence between interactions. The first approach involves performing a singular Bernoulli trial for each pair of taxa based on their regional probability of interaction:

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

In employing this approach, we predict a single metaweb of binary interactions for each simulation. Every pair of taxa predicted to interact in this metaweb will be treated as interacting in all localized networks where they co-occur, i.e. $L_{k,i \rightarrow j} = M_{i \rightarrow j}$ when $X_{i,j,k} = 1$. This will result in local pairwise interactions without spatial variation.

The second approach is to independently sample each local network of probabilistic interactions:

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

This can be achieved by first generating distinct probabilistic interaction networks for each location. These local networks of probabilistic interactions may vary in taxa composition and interaction probabilities. Because binary interaction networks are sampled independently for each location, this second approach introduces spatial variation in binary interactions. This approach may more effectively capture network structure across space and time, facilitating the investigation of ecological hypotheses about interactions at broad spatial and temporal scales.

In Fig. 4, we compare the average connectance of binary interaction networks resulting from these

two sampling techniques. We drew regional and local interactions from our host-parasite networks of probabilistic interactions (Kopelke *et al.* 2017), generating a number of binary interaction network realizations for each site in the dataset. These two sampling approaches yield different outcomes, particularly for intermediate values of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$, which represent instances where regional interactions do not consistently manifest locally (i.e., with the largest local variability). Small differences between these techniques are also apparent when we equate the probability of local interaction to the probability of regional interaction (i.e., when using $P(L_{i \rightarrow j}|M_{i \rightarrow j}) = 1.0$, Fig. 4a,d), especially when the number of samples of binary interaction networks for each location is low. As anticipated, we observe that sampling binary interactions from the metaweb tends to overestimate connectance on average compared to sampling them from local networks (Fig. 4a-c). Furthermore, we observe an increase in the variability of connectance when employing a single simulation (Fig. 4, cross markers), which is a more tangible representation of the process leading to the realization of local interactions in nature.

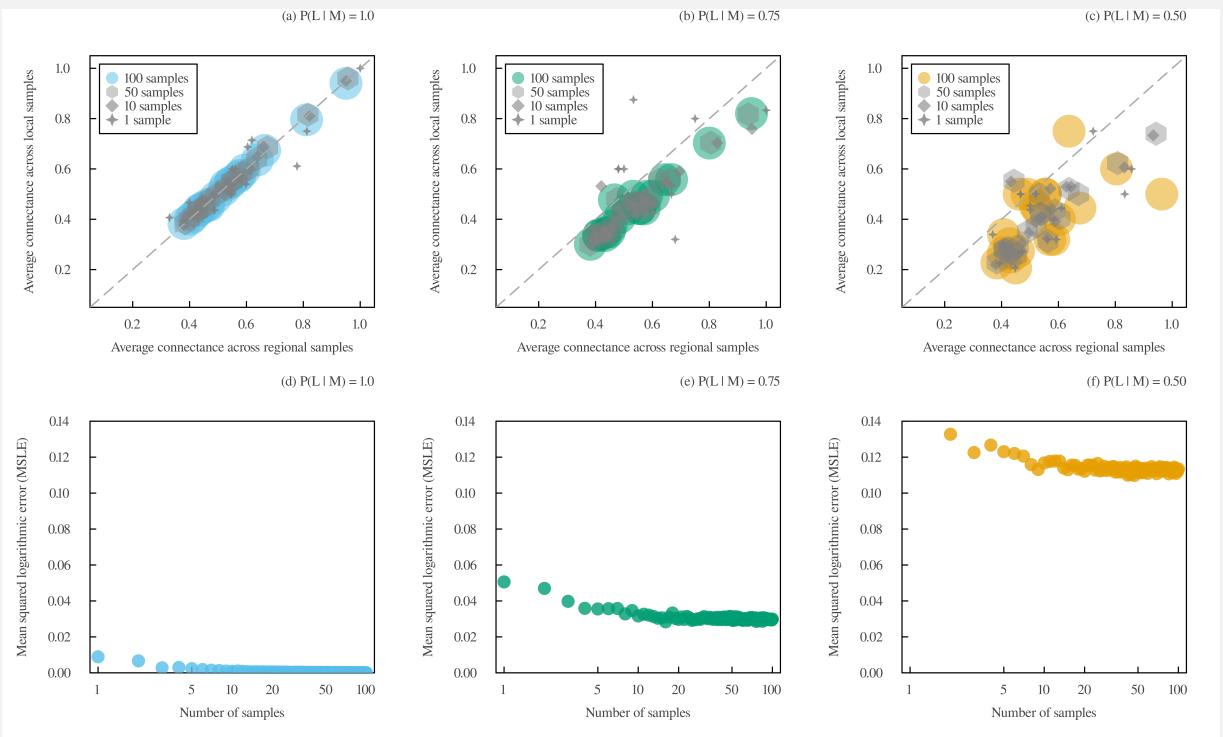


Figure 4: Connectance of sampled binary interaction networks. (a-c) Average connectance of binary interaction networks obtained from the two sampling approaches for 20 randomly selected host-parasite networks. Cross markers represent the connectance of a single sample for each network, diamond markers the average connectance across 10 samples, hexagon markers the average connectance across 50 samples, and the colored circles the average connectance across 100 samples (marker size proportional to the number of samples). (d-f) Reduction in the mean squared logarithmic error between the average connectance of binary interaction networks (all 233 host-parasite networks) obtained from these two sampling methods as the number of samples increases. The local probability of interaction between potentially interacting species was set to three different values: (a,d) $P(L_{i \rightarrow j}|M_{i \rightarrow j}) = 1.0$, (b,e) $P(L_{i \rightarrow j}|M_{i \rightarrow j}) = 0.75$, and (c,f) $P(L_{i \rightarrow j}|M_{i \rightarrow j}) = 0.50$. Probabilities of regional interactions were obtained with a false positive rate of 5% and a false negative rate of 10%. Further details on the data and network construction are presented in the supplementary material. Regional samples were obtained by randomly sampling binary interactions from the probabilistic interaction metaweb, and then propagating this result to all local networks that include the species potentially engaged in the interactions. Local binary interaction networks were generated by independently sampling binary interactions for each local network of probabilistic interactions.

The choice of sampling approach can influence the selection of grid cell size when delineating local communities within a broader region of interest. In the first approach, pairwise interactions remain constant irrespective of cell size because they are sampled only once from the metaweb. However, in the second approach, local interaction probabilities are contingent on network area. For instance, consider the local networks 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 and L_2 as independent, the probability of interaction between taxa i and j in L_0

is given by:

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

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 sampling binary interactions from local networks, it is crucial to sample at the same spatial scale for which probabilities were estimated. Otherwise, interaction probabilities must be adjusted to align with the intended cell size, preventing systematic biases in predictions.

401

402 Conclusion

403 In this contribution, we underline the importance of network documentation for adequately interpreting and
404 manipulating probabilistic interaction data. The mathematical representation of probabilities and their statistical
405 properties depend on the type of interactions (local or regional) and the conditions under which these
406 interactions were evaluated. We showed that local networks and metawebs of probabilistic interactions differ in
407 their relationship to spatial and temporal scales (Box 3), with regional interactions remaining consistent across
408 scales. In contrast with metawebs, local interactions are measured in a specific context (e.g., in a given area,
409 time, and biological and environmental conditions) and depend on taxa co-occurrence. These differences bring
410 to light the need to use probabilistic data with caution, for instance when generating network realizations of
411 binary interactions across space (Box 5). Clear documentation describing the type of interaction and the
412 variables used in their estimation are required to ensure adequate data manipulation. Sound data practices and
413 foundations for probabilistic thinking in network ecology facilitate reliable assessments of the spatiotemporal
414 variability and uncertainty of biotic interactions. Here we identify key research priorities for improving our
415 understanding of local and regional interactions and their stochasticity.

416 Predicting local networks from metawebs

417 Metawebs are a valuable source of ecological information for predicting local networks across time and space.
418 Local networks of binary interactions can be reconstructed by selecting a subset of taxa and interactions from
419 the metaweb (Dunne 2006). Metawebs thus contain more interactions than local networks, even though their
420 connectance is usually much smaller than the one of local networks (Gravel *et al.* 2011). Determining the list of

421 taxa to select can be achieved empirically (e.g., observed occurrence data for a site) or numerically (e.g., species
422 distribution models). As species composition is arguably easier to sample or predict than pairwise interactions,
423 the primary challenge lies in deciding which interactions to select from the metaweb. Inferring the structure of
424 local networks from the metaweb before predicting local pairwise interactions could hold promise (Strydom *et
425 al.* 2021), considering that the structure of local networks is constrained by the metaweb (Saravia *et al.* 2022).

426 Inferring local networks of probabilistic interactions from a metaweb comes with its own set of challenges. For
427 example, Dansereau *et al.* (2023) inferred spatially-explicit food webs from a metaweb of probabilistic trophic
428 interactions between Canadian mammals. Their predicted localized food webs are downscaled versions of the
429 metaweb (i.e., localized metawebs with the same interaction probabilities as those in the regional metaweb). To
430 infer local networks as defined in this manuscript (i.e., describing local realizations of interactions), local
431 interaction probabilities must be smaller than regional interaction probabilities. This decrease is due to the
432 prerequisite that two taxa must initially possess the capacity to interact before engaging in local interactions
433 (Eq. 2). Inferring local networks from a metaweb by maintaining identical interaction probability values
434 introduces systematic biases into the predictions, as discussed in Box 2 (unless networks are seen as downscaled
435 metawebs).

436 As suggested by McLeod *et al.* (2021), although metawebs do not capture the spatiotemporal variability of
437 interactions, they establish an upper limit for local interactions (similarly for metawebs of probabilistic
438 interactions, Strydom *et al.* 2023). In other words, the probability that two taxa interact at a specific location
439 and time is consistently lower or equal to the probability of their regional interaction, regardless of the
440 conditional variables considered:

$$P(L_{i \rightarrow j} | \dots) \leq P(M_{i \rightarrow j} | T_i, T_j). \quad (21)$$

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

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

445 Estimating more precisely the probability $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ that two taxa interact locally if they can potentially
446 interact allows for improved predictions of local networks from the metaweb of probabilistic interactions. This
447 task is challenging due to the variability of this probability across space and time, as well as its variability
448 across pairwise interactions within a network. Using simple models of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$, as shown in Box 2,
449 represents an initial step toward the overarching objective of reconstructing local networks from metawebs.

450 Quantifying and reducing interaction uncertainty

451 While sampling biological communities decreases the uncertainty of interactions by accumulating evidence for
452 their feasibility and local realization, there is a limit to how much we can reduce uncertainty. In metawebs,
453 probabilities reflect our limited knowledge of interactions (i.e., our degree of belief that interactions are
454 feasible), which is expected to improve with a larger volume of data. Regional interactions should become more
455 definitive (with probabilities approaching 0 or 1) as we investigate various conditions, including different
456 combinations of species traits.

457 In comparison, although local networks can be seen as random instances of metawebs, their stochasticity cannot
458 be reduced to the same extent. Local interaction probabilities may represent both their uncertainty and
459 spatiotemporal variability. Owing to environmental heterogeneity, there will invariably be instances in which an
460 interaction occurs and others in which it does not, across different times and locations, irrespective of the extent
461 to which we can improve our knowledge of its biological feasibility and the local conditions that facilitate its
462 occurrence. When local networks describe probabilities of observing interactions rather than their actual
463 occurrence, we must also consider observation variability (sampling error) as an additional source of
464 stochasticity. Every ecological process is stochastic but there is also a possibility that a phenomenon goes
465 undetected. Quantifying and partitioning this stochasticity will enable us to make more accurate predictions
466 about ecological interactions at various spatial and temporal scales. This will prove to be of vital importance as
467 our time to understand nature runs out, especially at locations where the impacts of climate change and habitat
468 loss hit harder.

469 Relaxing the independence assumption

470 Estimating local interaction probabilities independently for each taxa pair and assembling them into a network
471 of probabilistic interactions comes with limitations. Predicting local networks of binary interactions based on

472 these interaction probabilities assumes independence among interactions, a condition seldom respected in
473 practice (Golubski & Abrams 2011). Relaxing this assumption is the next logical step in the stochastic
474 representation of interactions.

475 A more accurate representation of the stochasticity of ecological networks involves creating *probabilistic*
476 *networks* ($P(L|...)$ and $P(M|...)$), rather than networks of *probabilistic interactions* ($P(L_{i \rightarrow j}|...)$ and $P(M_{i \rightarrow j}|...)$).
477 Probabilistic networks describe the probability that a particular network of binary (or quantitative) interactions
478 (its whole adjacency matrix) is realized. For example, Young *et al.* (2021) used a Bayesian approach to estimate
479 the probability of different plant-pollinator network structures derived from imperfect observational data. A
480 probability distribution of ecological networks may also be derived using the principle of maximum entropy
481 given structural constrained (e.g., Cimini *et al.* 2019; Park & Newman 2004).

482 Regardless of the method employed, generating probabilistic local networks could lead to more accurate
483 predictions of local networks of binary interactions by bypassing the independence assumption. Probabilistic
484 networks could serve as an alternative to null hypothesis significance testing when comparing the structure of a
485 local network to some random expectations or, as done in Pellissier *et al.* (2018), to the metaweb. These random
486 expectations are typically derived by performing a series of Bernoulli trials on probabilistic interactions,
487 assuming independence, to generate a distribution of networks of binary interactions to calculate their structure
488 (Poisot *et al.* 2016). One could for instance compare the likelihood of an observed network to the one of the
489 most likely network structure (according to the probabilistic network distribution), thereby directly obtaining a
490 measure of discrepancy of the empirical network. Generating probabilistic ecological networks represents a
491 tangible challenge, one that, in the coming years, promises to unlock doors to more advanced and adequate
492 analyses of ecological networks.

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