

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 (Abrego *et al.* 2021; Gonzalez & Londoño 2022).
4 However, cataloging species, populations and, in particular, ecological interactions (e.g., predation, parasitism,
5 and pollination) is a substantial challenge (Pascual *et al.* 2006; Polis 1991). 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). The
16 probability that species meet each other also depends on their biological characteristics, such as the
17 synchronization of their phenology (Olesen *et al.* 2010; Singer & McBride 2012) and their discoverability (e.g.,
18 Broom & Ruxton 2005). Finally, when species do come into contact, an interaction occurs only if their traits are
19 locally compatible (Poisot *et al.* 2015), including but not limited to their body phenotypes (Bolnick *et al.* 2011;
20 Gravel *et al.* 2013; Stouffer *et al.* 2011) and behavioral choices (Choh *et al.* 2012; Pulliam 1974). Interactions
21 may also be influenced by the presence or prevalence of a third species (e.g., of a more profitable prey species,
22 Golubski & Abrams 2011; Sanders & van Veen 2012). Documenting the location and timing of interactions
23 becomes even more difficult when accounting for the spatiotemporal variability of ecological interactions
24 (Poisot *et al.* 2012, 2015). Environmental factors, such as temperature (Angilletta *et al.* 2004), drought
25 (Woodward *et al.* 2012), climate change (Araujo *et al.* 2011; Gilman *et al.* 2010; Woodward *et al.* 2010), and
26 habitat modifications (Tylianakis *et al.* 2007), contribute to this spatiotemporal variability by impacting species
27 abundance and traits. Even after satisfying all these conditions, there remains a possibility that the interaction
28 does not occur locally, either due to the intricate nature of the system or simply by chance. If it does occur, it
29 might still go unnoticed, particularly if it happens infrequently. In this context, it is unsurprising that our
30 knowledge of ecological interactions remains limited (Hortal *et al.* 2015) despite extensive biodiversity data

31 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 (Dallas *et al.* 2017; Fu *et al.* 2021;

36 Poisot *et al.* 2016). This different perspective allows us to fill in the Eltonian shortfall (Hortal *et al.* 2015) by

37 modeling the probability of occurrence of interactions, which can be an important tool for directing efforts and

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

39 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, 2016). Representing direct interactions probabilistically enables

43 us to capture the spatiotemporal variability of the aforementioned ecological processes and the uncertainties

44 associated with their occurrence. As opposed to webs of binary deterministic interactions, in which interactions

45 are regarded as either occurring or not, webs of probabilistic interactions, within a Bayesian framework, express

46 our degree of belief (or confidence) regarding the occurrence or observation of interactions. Based on the scale

47 at which they are estimated, probabilistic interactions may reflect our level of confidence in whether interactions

48 will be observed, realized locally, or biologically feasible. As an illustration, we could outline a situation in

49 which there is a 50% certainty that an interaction occurs 50% of the time, or that there is a 50% certainty that it

50 simply occurs. Our level of confidence should be more definitive (approaching either 0 or 1) as we extend our

51 sampling to a broader area and over a longer time period, thereby diminishing the uncertainty of the interactions

52 (but not necessarily the estimation of their variability). In the broadest sense, binary interactions are also a type

53 of probabilistic interaction, in which the numerical value of an interaction is restrained to 0 (non-occurring) or 1

54 (occurring). Yet, for the sake of clarity, we omit binary interactions from our discussion of probabilistic

55 interactions in this contribution. In networks of probabilistic interactions, only forbidden interactions (i.e.,

56 interactions prohibited by biological traits or species absence, Jordano *et al.* 2003; Olesen *et al.* 2010) have a

57 probability value of zero, provided that intraspecific trait variability is considered (Gonzalez-Varo & Traveset

58 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, McCann 2007; McCann 2011; Proulx *et al.* 2005; 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 (Gravel *et al.* 2013; Petchey *et al.* 2008), 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 (Godsoe *et al.* 2022; Ohlmann *et al.* 2019) 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

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

112 **Probabilistic representations of interactions**

113 Consider a scenario where a species of avian predator has just established itself in a northern habitat home to a
114 small rodent species. Suppose these species have never co-occurred before, and as a result, their interaction has
115 not been previously observed. What is the probability that the rodent is part of the diet of the avian predator, or
116 put differently, what is the probability that they interact? Answering this question requires some clarification, as
117 there are multiple ways to interpret and calculate interaction probabilities. We may calculate the probability that
118 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 in
184 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 webs
188 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 and
203 modeled. Moreover, most published networks of probabilistic interactions and methods describe probabilistic
204 interactions whose outcome is binary (whether interaction probabilities are regarded as constant or variable,
205 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
222 interactions (Weinstein & Graham 2017a, b) and mosquito biting rates (e.g., Kulkarni *et al.* 2006) at different
223 elevations. In contrast, time is defined as the specific time period within which interactions were either observed
224 or predicted. Even though space and time are continuous variables that should yield probability *densities* of
225 interactions (i.e., relative likelihoods of interactions occurring at infinitesimal locations and instants in time),
226 these definitions enable them to be conceptualized as distinct patches and time segments. Treating space and
227 time as discrete dimensions aligns with the common sampling methods of ecological networks and provides
228 actual probabilities of interactions, which can be obtained by integrating probability densities over space and
229 time. Furthermore, we can quantify both an area A and a duration t , which can be readily used in spatiotemporal
230 analyses of ecological networks. For example, when studying network-area relationships (NAR, Galiana *et al.*
231 2018), we anticipate that local probabilities of interactions scale positively with area and duration because taxa
232 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 (i.e.,
 242 $P(L_{i \rightarrow j}|X_{i,j,l} = 0) = 0$), the probability of local interaction can be obtained by multiplying the probability of
 243 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 network
 250 (Kéfi *et al.* 2012; Pilosof *et al.* 2017), as described above. Here, we use the variable E_l to describe the local
 251 ecological context in which interaction probabilities were estimated. For example, if a research team conducts a
 252 mesocosm experiment to estimate interaction probabilities between predators and prey with and without
 253 shelters (a place that offers refuge and protection for prey, shielding them from predators), E_l would represent
 254 the presence or absence of these shelters. Like co-occurrence, E_l can also be modeled probabilistically when
 255 the stochasticity or uncertainty of environmental factors is considered. In sum, E_l represents all ecological
 256 variables that were taken into consideration when measuring interaction probabilities and is, therefore, a subset
 257 of all environmental factors impacting ecological interactions. Finally, local interaction probabilities may be
 258 conditioned on higher-level properties of the network, which we denote by $f(L)$. Many topological null models
 259 (i.e., statistical models that randomize interactions by retaining certain properties of the network while
 260 excluding others) provide interaction probabilities from selected measures of network structure, such as
 261 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 probabilities
309 in the metaweb (i.e., when species' biological traits can support an interaction if they were to encounter each
310 other). Likewise, non-co-occurring taxa may have a non-zero probability of interaction in the metaweb.

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

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

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

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

322 For example, let i be a western diamondback rattlesnake (*Crotalus atrox*) and j , a wood lemming (*Myopus*
323 *schisticolor*). These two taxa never co-occur, the rattlesnake being adapted to warm regions of North America
324 (Castoe *et al.* 2007) and the lemming, to northern habitats of Eurasia (Fedorov *et al.* 2008). As we lack direct
325 observations of an interaction between these two species, we have to rely on expert knowledge or trait-matching

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

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

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

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

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

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

349 Starting from a selected set of taxa, which are usually distributed within a broad region of interest, metawebs

350 can be built using different data sources, including literature review (e.g., Maiorano *et al.* 2020), aggregated
351 local web data (e.g., Gravel *et al.* 2019; Saravia *et al.* 2022), trait-matching models Strydom *et al.* (2022), and
352 expert knowledge. Every pair of taxa that have confidently been observed to interact at least once can be given a
353 probability of 1 (i.e., $P(M_{i \rightarrow j}) = 1$) since we know that they *can* interact. This differs from local webs of
354 probabilistic interactions, where interaction events may remain stochastic (i.e., $P(L_{i \rightarrow j}) < 1$) even after
355 empirically observing interactions due to their spatiotemporal variability. Interactions that were never observed
356 typically have low probability values in local webs and vary from low to high values in metawebs, contingent
357 upon taxa traits distributions (reaching 0 for forbidden links).

358 When incorporating local network data to estimate probabilities of regional interactions, repeatedly failing to
359 observe an interaction between two co-occurring taxa (i.e., $P(O_{i \rightarrow j} = 0)$) should decrease the probability that
360 the interaction is biologically feasible. Using Bayes' theorem, the probability that the interaction is biologically
361 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:

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

362 The reduction in the probability of regional interaction after considering that it was never observed locally (i.e.,
363 $P(M_{i \rightarrow j} = 1|O_{i \rightarrow j} = 0, \dots) < P(M_{i \rightarrow j} = 1|\dots)$) occurs because $P(O_{i \rightarrow j} = 0|M_{i \rightarrow j} = 1, \dots)$ must be lower than
364 $P(O_{i \rightarrow j} = 0, \dots)$, i.e. there is a higher chance of observing an interaction when we know it is biologically
365 feasible.

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

373 **Properties of probabilistic interaction webs**

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

383 **Host-parasite network data**

384 We use the collection of tripartite host-parasite networks sampled across Europe, created by Kopelke *et al.*
385 (2017), in the following case studies. This dataset contains well-resolved binary local interactions between
386 willows (52 species), willow-galling sawflies (96 species), and their parasitoids (126 species). Given its
387 replicated webs spanning large spatiotemporal scales, this dataset is well-suited for analyzing a variety of
388 ecological hypotheses and processes. Out of a total of 374 local webs, we retained those containing at least 5
389 species, resulting in a set of 233 georeferenced local webs (networks sampled within areas of 0.1 to 0.3 km²
390 during June and/or July spanning 29 years). We built a metaweb of binary interactions by aggregating all local
391 interactions, which gave us a regional web composed of 274 species and 1080 interactions. In the first two
392 panels of Fig. 1, we show how the dissimilarity of interactions between common species (β_{OS}) and the
393 dissimilarity in species composition (β_S) between the metaweb and aggregated local webs (Poisot *et al.* 2012)
394 vary with the number of sampled local webs. This shows that networks of local interactions are highly
395 dissimilar from the metaweb, both in terms of species and interactions, especially when only a limited number
396 of sites has been sampled. Both dissimilarity indices were calculated based on the number of items shared by
397 the two webs (c_{LM}) and the number of items unique to the metaweb (u_M) and to the aggregated local web (u_L).
398 The β_S dissimilarity index uses species (nodes) as items being compared, while the β_{OS} index assesses
399 dissimilarity based on interactions between shared species (Poisot *et al.* 2012). Both indices were calculated
400 following the β_W index of Whittaker (1960):

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

401

[Figure 1 about here.]

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

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

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

421 We built local webs of probabilistic interactions using the taxa found in the empirical local networks and
 422 attributing pairwise interaction probabilities based on the metawebs of probabilistic interactions and a constant
 423 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
 424 occur locally, intermediate values around 50% suggest considerable spatiotemporal variability, while high

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

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

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

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

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

444 Spatial and temporal scaling of interactions

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

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

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

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

481 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
482 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,
483 interaction probabilities could be higher in the smaller area, contingent upon their environmental and biological
484 conditions. Likewise, interaction probabilities are expected to be lower in webs with shorter durations when
485 time intervals are nested. In Fig. 2, we show how the expected number of local host-parasite interactions scales
486 with area, represented as an expanding latitudinal window, in comparison with regional interactions. Even
487 though we employed local probabilities of interactions equal to regional interactions for the purpose of
488 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
489 more rapidly than local interactions. This is because numerous regional interactions involve species that never
490 co-occur, and as a result, these interactions are not captured in any local web.

491 [Figure 2 about here.]

492 **Box 1: A spatiotemporally explicit model of interactions**

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

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

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

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

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

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

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

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

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

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

530 the value of the λ_l and γ parameters and generate novel interaction data:

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

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

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

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

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

536 [Figure 3 about here.]

537 **Taxonomic scaling of interactions**

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

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

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

557 where $g_{1,i}$ and $g_{2,j}$ are the species of the corresponding genus and assuming independence between
 558 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
 559 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
 560 species-based network following a similar approach, by using simulated interactions between individuals
 561 derived from a neutral model (i.e., a model that assumed ecological equivalence among individuals). In
 562 contrast, a more sophisticated approach is necessary when transitioning from a broader to a finer level of
 563 organization. This is because knowledge of an interaction between two genera does not guarantee that all
 564 possible pairwise combinations of their species will also interact. One possible method is to build a finer-scale
 565 network by generating probabilities of interactions through random sampling from a beta distribution,
 566 parameterized by the broader-scale network.

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

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

583 Sampling for binary interaction webs

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

603 within a given region. Both approaches assume independence between interactions. The first approach involves
604 performing a singular Bernoulli trial for each pair of taxa based on their regional probability of interaction:

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

605 In employing this approach, we predict a single metaweb of binary interactions for each simulation. Every pair
606 of taxa predicted to interact in this metaweb will be treated as interacting in all local webs where they co-occur,
607 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.
608 The second approach is to independently sample each local web of probabilistic interactions:

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

609 This can be achieved by first generating distinct probabilistic interaction networks for each location. These local
610 webs of probabilistic interactions may vary in taxa composition and interaction probabilities. Because binary
611 interaction networks are sampled independently for each location, this second approach introduces spatial
612 variation in binary interactions.
613 In Fig. 4, we compare the average connectance of binary interaction networks resulting from these two sampling
614 techniques, where regional and local interactions are drawn from our host-parasite networks of probabilistic
615 interactions, generating a number of binary interaction web realizations for each site in the dataset. These two
616 sampling approaches yield different outcomes, particularly for lower values of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$, which represent
617 instances where regional interactions do not consistently manifest locally. Small discrepancies between these
618 techniques are also apparent when we equate the probability of local interaction to the probability of regional
619 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
620 binary interaction networks for each location is low. As anticipated, we observe that sampling binary
621 interactions from the metaweb tends to overestimate connectance on average compared to sampling them from
622 local webs. Furthermore, we observe an increase in the variability of connectance when employing a single
623 simulation, representing what we consider as a more tangible process leading to the realization of local
624 interactions in nature.

625

[Figure 4 about here.]

626 The choice of a sampling approach can influence the selection of grid cell size when delineating local
627 communities within a broader region of interest. In the first approach, pairwise interactions remain constant
628 irrespective of cell size because they are sampled only once from the metaweb. However, in the second
629 approach, local interaction probabilities are contingent on network area. For instance, consider the local webs
630 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
631 and L_2 as independent, the probability of interaction between taxa i and j in L_0 is given by:

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

632 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
633 sampling binary interactions from local webs, it is crucial to sample at the same spatial scale for which
634 probabilities were estimated. Otherwise, interaction probabilities must be adjusted to align with the intended
635 cell size, preventing systematic biases in predictions.

636 Prediction of local webs from metawebs

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

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

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

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

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

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

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

667 Conclusion

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

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

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

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

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

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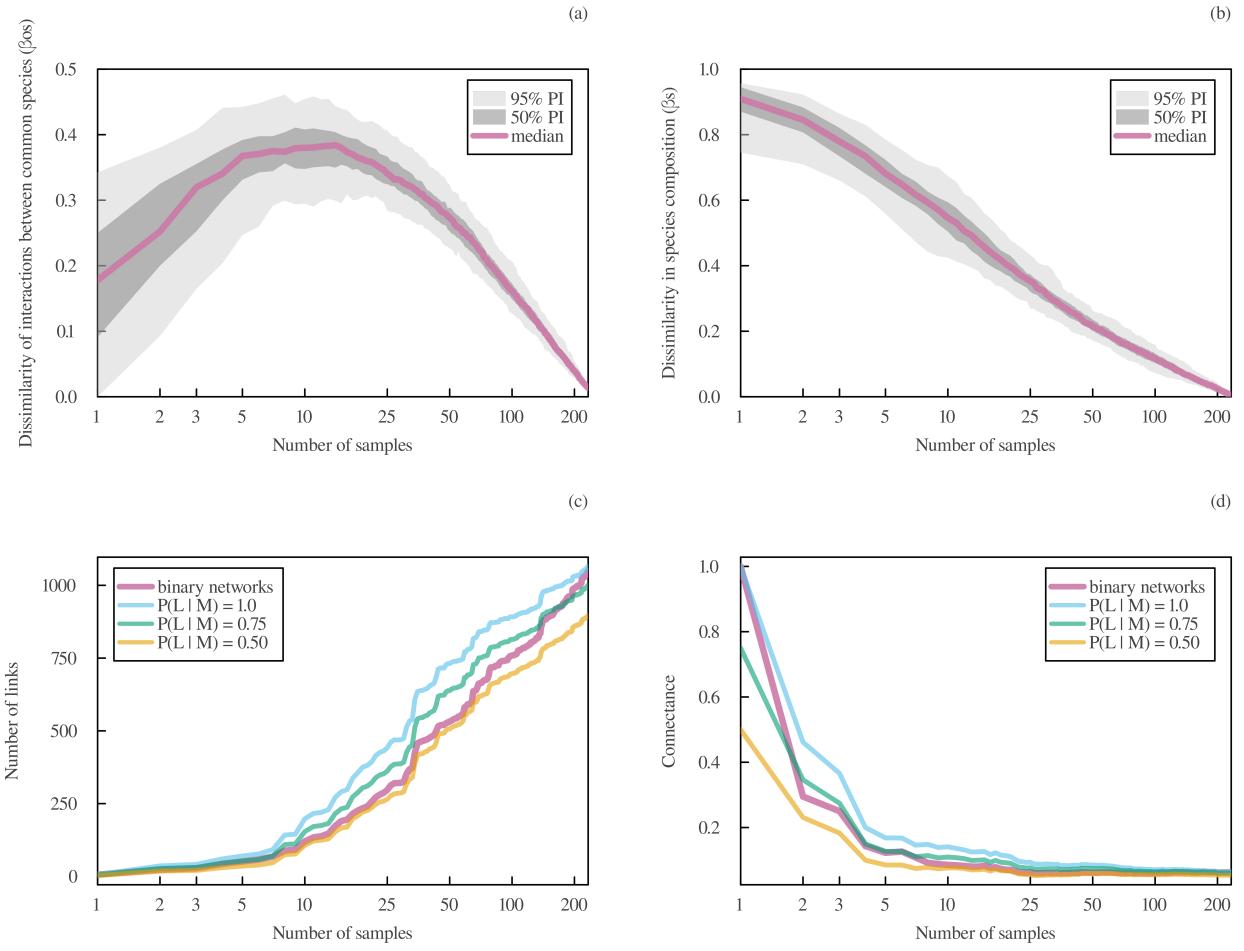


Figure 1: Network accumulation curves. (a) Dissimilarity of interactions between common species and (b) dissimilarity in species composition between aggregated local webs and the metaweb of binary host-parasite interactions. Aggregated local webs were obtained by sequentially and randomly selecting a 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 $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ (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 $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ adjusting according to Eq. 11).

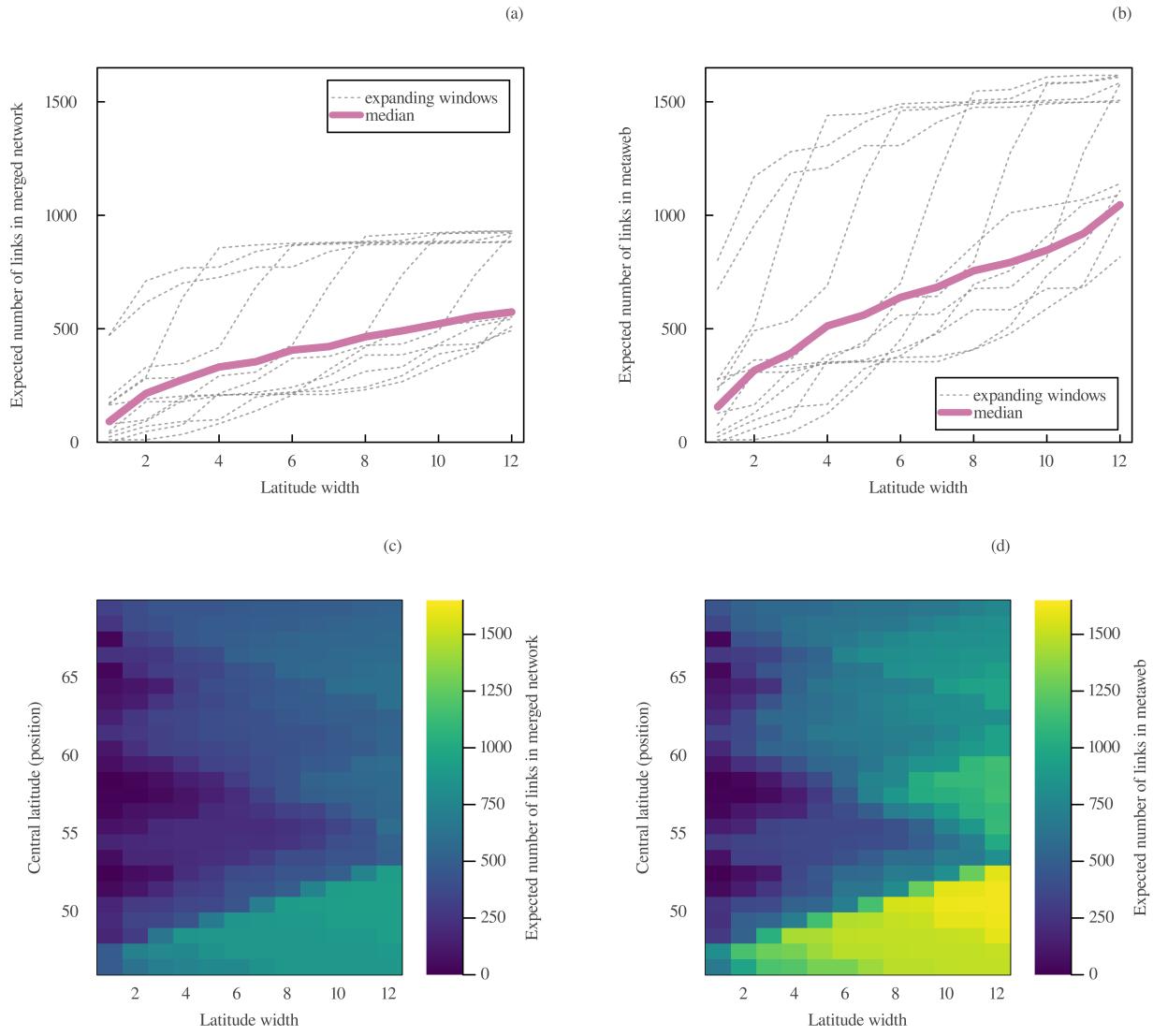


Figure 2: Spatial scaling of interactions. Expected number of host-parasite interactions in a network aggregating all (a) local and (b) regional probabilistic interactions within a latitudinal window of a given length. Every dashed curve corresponds to a different expanding window characterized by a 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.

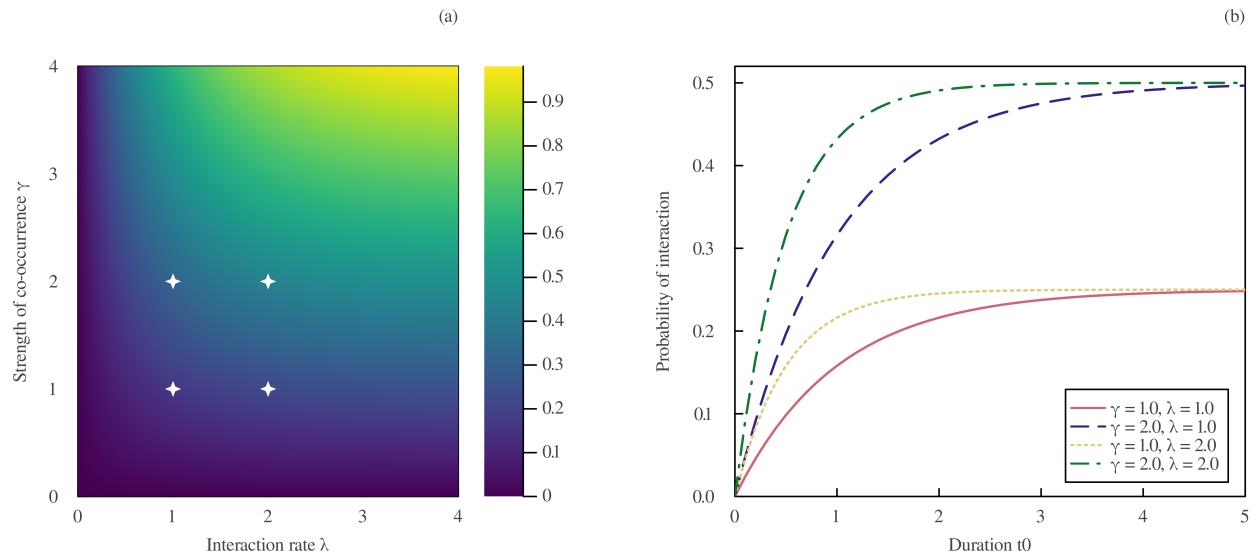


Figure 3: Parameters of the spatiotemporally explicit model of interactions. (a) Probability of local interaction given by the process model (Eq. 16) under different values of λ_l and γ , with $t_0 = 1$. The parameter values used in the right panel are denoted by the white stars. (b) Scaling of the probability of interaction with the duration parameter t_0 in Eq. 16, for different values of λ_l and γ . 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.

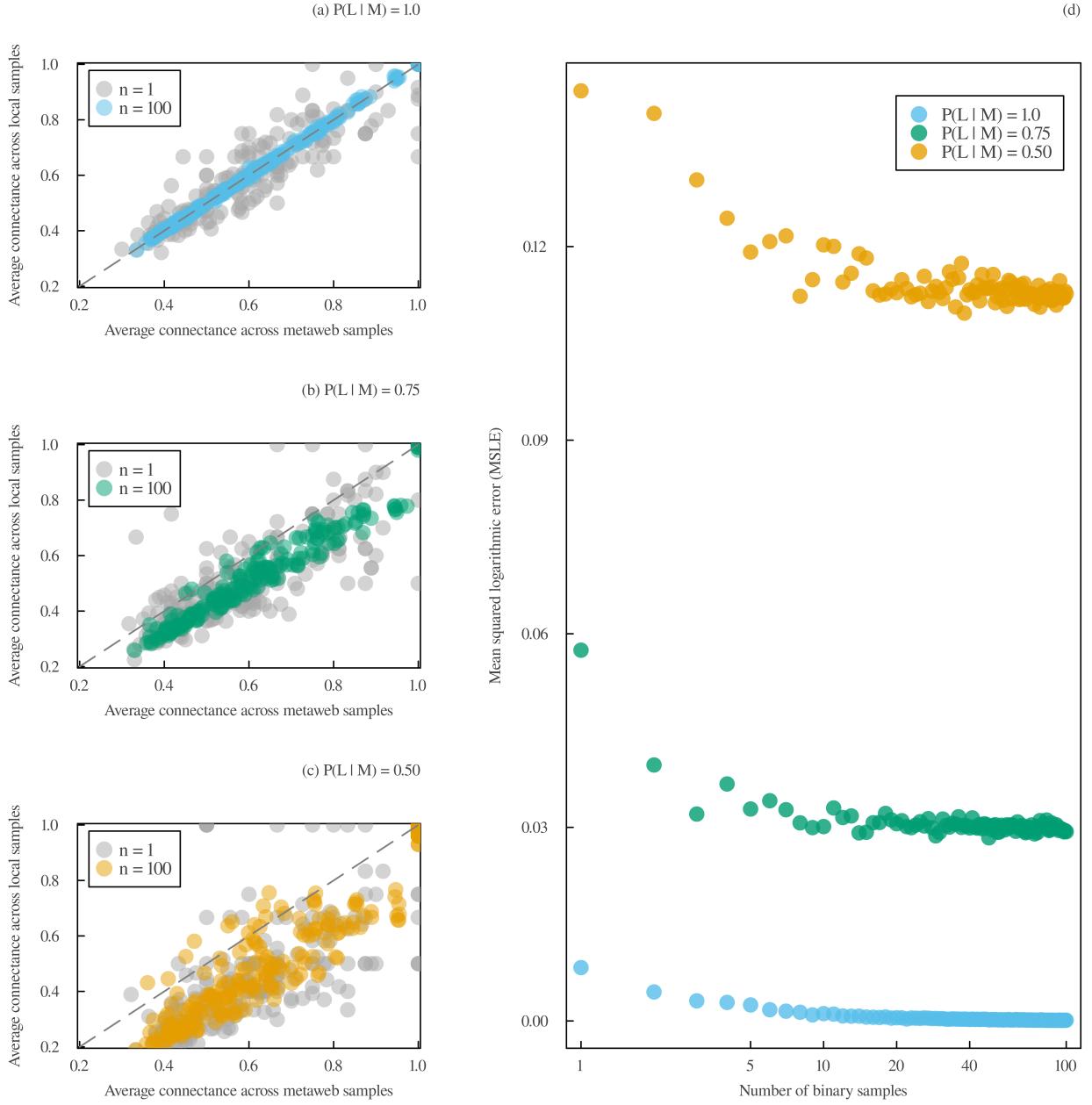


Figure 4: Connectance of sampled binary interaction webs. Comparison between the average connectance of binary interaction network samples obtained from the local and metawebs of probabilistic interactions. Each dot corresponds to a different site. The local probability of interaction between potentially 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.