

The ecological interpretation of probabilistic networks

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

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

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1 Introduction

2 As we try to navigate global biodiversity change, filling in knowledge gaps about biodiversity becomes
3 instrumental to monitoring and mitigating those changes (Gonzalez & Londoño (2022), Abrego *et al.* (2021)).
4 However, cataloging species, populations and, in particular, ecological interactions is a substantial challenge.
5 There are methodological and biological constraints that hinder our ability to observe all interactions, such as
6 the spatial and temporal uncoupling of species (Jordano (1987)) and the large number of possible interactions in
7 a community, of which the vast majority are rare (Jordano (2016)). More generally, a handful of conditions
8 must be satisfied for an interaction to be observed locally. First, both species must have overlapping geographic
9 ranges, i.e. they must co-occur within the region of interest (Blanchet *et al.* (2020)). Second, they must have
10 some probability of meeting. Probabilities of interspecific encounters are typically low, especially for rare
11 species with low relative abundances (Canard *et al.* (2012)). Finally, their traits must be locally compatible
12 (Poisot *et al.* (2015)), including but not limited to phenology (Olesen *et al.* (2010), Singer & McBride (2012)),
13 behavioral choices (Pulliam (1974), Choh *et al.* (2012)), and phenotypes (Bolnick *et al.* (2011), Stouffer *et al.*
14 (2011), Gravel *et al.* (2013)). Interactions may also be influenced by the presence or prevalence of a third
15 species (e.g., of a more profitable prey species) (Golubski & Abrams (2011), Sanders & van Veen (2012)).
16 Documenting the location and timing of interactions becomes even more difficult when accounting for the
17 spatiotemporal variability of ecological networks (Poisot *et al.* (2012), Poisot *et al.* (2015)). Environmental
18 factors, such as temperature (Angilletta *et al.* (2004)), drought (Woodward *et al.* (2012)), climate change
19 (Gilman *et al.* (2010), Woodward *et al.* (2010), Araujo *et al.* (2011)), and habitat modifications (Tylianakis *et*
20 *al.* (2007)), contribute to this spatiotemporal variability of interactions by impacting species abundance and
21 traits. In this context, it is unsurprising that our knowledge of ecological interactions remains limited (Hortal *et*
22 *al.* (2015)) despite extensive biodiversity data collection (Schmeller *et al.* (2015)).
23 Knowing the biological capacity of two species to interact is necessary but not sufficient for inferring their
24 interaction at a specific time and space. The recognition of the intrinsic variability of species interactions has
25 led ecologists to expand their representation of ecological networks to include a probabilistic view of
26 interactions (Poisot *et al.* (2016), Dallas *et al.* (2017), Fu *et al.* (2021)). This different perspective allows us to
27 fill in the Eltonian shortfall by modeling the probability of detecting interactions, which can be an important
28 tool for directing efforts and take action, especially in places where access and resources for research are scarce.
29 As opposed to binary deterministic networks, in which interactions are regarded as either occurring or not,

30 probabilistic networks represent our degree of belief about the realization or feasibility of pairwise interactions
31 at the local or regional scale, respectively. In other words, representing interactions probabilistically takes into
32 account inherent uncertainties and variability associated with ecological data. In the broadest sense, binary
33 networks are also a type of probabilistic network, in which the numerical value of an interaction is restrained to
34 0 (non-occurring) or 1 (occurring). In probabilistic networks, only forbidden interactions (i.e., interactions
35 prohibited by biological traits, Jordano *et al.* (2003), Olesen *et al.* (2010)) have a probability value of zero,
36 provided that intraspecific trait variability is considered (Gonzalez-Varo & Traveset (2016)). However, *neutrally*
37 forbidden interactions (i.e., improbable interactions between rare species, Canard *et al.* (2012)) could have low
38 probability values in local networks but high probability in a regional network (metaweb) describing the
39 biological capacity of species to interact.

40 By accounting for the uncertainty of interactions, probabilistic networks provide a more realistic portrait of
41 species interactions and network structure (i.e. community-level properties), which is a major driver of the
42 functioning, dynamics, and resilience of ecosystems worldwide (Proulx *et al.* (2005), McCann (2007), McCann
43 (2011), Rooney & McCann (2012)). Moreover, the application and development of computational methods in
44 network ecology, often based on a probabilistic representation of interactions, can alleviate (and guide) the
45 sampling efforts required to document species interactions (Strydom *et al.* (2021)). For example, statistical
46 models can be used to estimate the uncertainty of pairwise interactions (Cirtwill *et al.* (2019)) and the
47 probability of missing (false negatives) and spurious (false positives) interactions (Guimerà & Sales-Pardo
48 (2009)). Considering the high rate of false negatives in species interaction data due to the difficulty of
49 witnessing rare interactions (Catchen *et al.* (2023)), these models could inform the identification of priority
50 sampling locations of ecological networks where data collection would yield the most valuable information,
51 thereby reducing errors. Optimization models for sampling locations have mostly found applications in
52 biological systems that are not networks, such as identifying priority sampling sites for disease hotspots
53 (Andrade-Pacheco *et al.* (2020)), but there is substantial promise in applying them to probabilistic ecological
54 interactions. Statistical models can also be used to generate network predictions without prior knowledge of
55 pairwise interactions, for instance using body size (Petchey *et al.* (2008), Gravel *et al.* (2013)), phylogeny
56 (Elmasri *et al.* (2020), Strydom *et al.* (2022)), or a combination of niche and neutral processes (Bartomeus *et*
57 *al.* (2016), Pomeranz *et al.* (2019)) for inference. Topological null models (e.g., Bascompte *et al.* (2003),
58 Fortuna & Bascompte (2006)), which can be used to generate underlying distributions of network measures for
59 null hypothesis significance testing, are other examples of common probabilistic network models. Many

measures have been developed to describe the structure (Poisot *et al.* (2016)) and diversity (Ohlmann *et al.* (2019), Godsoe *et al.* (2022)) of probabilistic networks. These models and measures support the use of this approach for the study of a wide range of ecological questions, from making better predictions of species distribution (Cazelles *et al.* (2016)) to forecasting the impact of climate change on ecological networks (Gilman *et al.* (2010)).

The lack of clear guidelines on the use of probabilistic interaction data is worrisome (Brimacombe *et al.* (2023)), both for data producers and re-users who generate and manipulate these numbers. Besides methodological difficulties that may arise when assessing probabilistic interactions, a precise definition of probabilistic interactions appears to be lacking, making the estimation and use of these data more difficult. We aim to take a step back by outlining different ways in which probabilistic interactions are defined and used in network ecology. We distinguish two broad categories of probabilistic networks that necessitate distinct approaches when applied to key ecological questions: local networks of realized interactions, and regional networks (metawebs) of potential interactions. We highlight the distinctions in the ecological meaning of these two representations and show that they yield different statistical outcomes regarding e.g. the spatial and temporal scaling of interactions and the prediction of binary networks across space. Moreover, there is currently no metadata standard that could guide the documentation of all types of probabilistic interactions (although see e.g., Salim *et al.* (2022) who discuss data standards for deterministic mutualistic networks). Well-defined metadata for probabilistic networks would support more adequate manipulation and integration of interaction data from different sources and guard against the potential misinterpretations arising from ambiguous definitions of probabilistic networks. These metadata should outline the nature (i.e., potential or local) and type (e.g., predatory or pollination) of the interactions, provide information regarding the taxonomic level, identities, and characteristics (e.g., life stages) of the individuals involved in an interaction, present the mathematical formulation of probabilities, including clearly identified conditional variables, and describe the methods and contexts (e.g., location, time, environmental conditions) in which interactions were estimated. Inadequately documented probabilistic interaction data should be used with caution when analyzing ecological networks.

Although our contribution focuses on food webs, our observations and advice can be applied to other types of ecological networks, from plant-pollinator to host-virus networks. Indeed, excluding networks of indirect interactions such as competition and facilitation networks (Kéfi *et al.* (2015), Kéfi *et al.* (2016)), most ecological networks describe probabilities of direct interactions, which are conceptually and mathematically analogous regardless of their biological type (e.g., trophic and mutualistic interactions).

90 Probabilistic representations of interactions

91 One of the first aspects to take into consideration when estimating or interpreting probabilities of interactions is
92 knowing if they describe potential or realized interactions. A potential interaction is defined as the biological
93 capacity of two taxa to interact (i.e., the probability that they *can* theoretically interact) whereas a realized
94 interaction is the materialization or observation of this interaction in a well-defined space and time (i.e., the
95 probability that they interact locally). Here, we use the terms *metaweb* (Dunne (2006)) to designate networks of
96 potential interactions and *local networks* (Poisot *et al.* (2012)) for those of realized interactions. Metawebs are
97 the network analogues of the species pool, where local networks originate from a subset of both species (nodes)
98 and interactions (edges) of the regional metaweb (Saravia *et al.* (2022)). Without clear documentation, it can be
99 challenging to know if published probabilistic networks describe potential or realized interactions, or if
100 so-called probabilities are in reality *interaction scores* (i.e., non-probabilistic quantitative interactions). When
101 probabilistic potential interactions are used and interpreted as local interactions (and conversely), this may
102 generate misleading findings during data analysis. We believe that a better understanding of the differences,
103 similarities, and relationships between these two probabilistic representations of ecological networks would
104 alleviate interpretation errors and facilitate a more adequate utilization of interaction data.

105 Pairwise interactions: the building blocks of ecological networks

106 Local ecological networks and metawebs, like any type of network, are made of nodes and edges that can be
107 represented at different levels of organization and precision. The basic unit of food webs and other ecological
108 networks are individuals that interact with each other (e.g., by predation, Elton (2001)), forming
109 individual-based networks (Melián *et al.* (2011)). The aggregation of these individuals into more or less
110 homogeneous groups (e.g., populations, species, trophic species, families) allows us to represent nodes at
111 broader taxonomic scales, which affects our interpretation of the properties of these systems (Guimarães
112 (2020)). Moreover, edges linking these nodes can describe a variety of interaction measures. Ecologists have
113 traditionally represented interactions as binary objects that were considered realized after observing at least one
114 individual from group i interact with at least another individual from group j . Boolean interactions can be
115 viewed as the result of a Bernoulli process $A_{i,j} \sim \text{Bernoulli}(P(i \rightarrow j))$, with $P(i \rightarrow j)$ being the probability of
116 interaction between i and j that characterizes our limited knowledge of the system and its intrinsic
117 spatiotemporal variability. Depending on the type of networks (local or metaweb), the mathematical

118 formulation and interpretation of stochastic parameters like $P(i \rightarrow j)$ can be linked to environmental and
119 biological factors such as species relative abundance, traits, area, and time (tbl. 1), for example using logistic
120 regression with a logit link function with continuous explanatory variables. In these probabilistic network
121 representations in which $P(i \rightarrow j)$ are edge values, the only two possible outcomes are the presence ($A_{i,j} = 1$) or
122 absence ($A_{i,j} = 0$) of an interaction between each pair of nodes. When considering uncertainties around the
123 estimation of $P(i \rightarrow j)$, a Beta distribution $\text{Beta}(\alpha, \beta)$ can also be used to encompass all possible probability
124 values. Observing an interaction between two taxa at a given location and time provides important information
125 that can be used to update previous estimates of $P(i \rightarrow j)$, informing us on the biological capacity of both taxa
126 to interact and the environmental conditions that enabled them to interact locally.

127 Even though binary networks constitute a highly valuable source of ecological information (Pascual *et al.*
128 (2006)), they overlook important factors regarding interaction strengths. These are represented using
129 quantitative interactions, which better describe the energy flows, demographic impacts or frequencies of
130 interactions between nodes (Berlow *et al.* (2004), Borrett & Scharler (2019)), with $A_{i,j}$ being a natural number
131 \mathbb{N} or a real number \mathbb{R} depending on the measure. For example, they may represent local interaction rates
132 between pairs of taxa (e.g., the flower visiting rates of pollinators in a mutualistic network, Herrera (1989)).
133 Because quantitative interactions can also describe predation pressure on prey taxa in food webs, they can be
134 good estimators of the parameters describing species interactions in a Lotka-Volterra model (e.g., Emmerson &
135 Raffaelli (2004)). The extra amount of ecological information in quantitative networks typically comes at a cost
136 of greater sampling effort and data volume in predictive models (Strydom *et al.* (2021)), which can lead to
137 relatively high levels of uncertainties when inferring quantitative networks with limited data.

138 Just like binary networks, the uncertainty and spatiotemporal variability of quantitative interactions can be
139 represented probabilistically. However, the need to estimate the probability distribution of all possible values of
140 interaction strengths can make the inference of probabilities more challenging in quantitative networks
141 compared to binary networks, which require only one probability estimate for each interaction. Quantitative
142 interactions can follow various probability distributions depending on the measure used, the event's outcome
143 being the value of interaction strength. For instance, quantitative interactions can follow a Poisson distribution
144 $A_{i,j} \sim \text{Poisson}(\lambda_{i \rightarrow j})$ when predicting frequencies of interactions between pairs of nodes, with $\lambda_{i \rightarrow j}$ being the
145 expected rate at which individuals of taxa i and j interact (e.g., the average number of prey j consumed by all
146 predators i in a given time period). The Poisson distribution can also be 0-inflated after initially modeling
147 non-interacting taxa (e.g., Boulangeat *et al.* (2012) employ a 0-inflated model to analyze species abundance

148 following the modeling of species presence and absence), which constitute the majority of taxa pairs in most
149 local networks due to their typically high sparseness (Jordano (2016)). Because of the methodological
150 difficulties typically encountered when building deterministic quantitative networks, binary networks, which are
151 easier to sample (Jordano (2016)) and predict (Strydom *et al.* (2021)), are documented and modeled more
152 frequently in the literature. Moreover, most published probabilistic networks and methods describe Bernoulli
153 interactions (whether interaction probabilities are regarded as constant or variable, e.g. represented by Beta
154 distributions), which underlines the need for better guidelines regarding the interpretation and manipulation of
155 these types of networks. For these reasons, our primary focus in this contribution will be on addressing the
156 challenges in interpreting and using Bernoulli interactions, in both probabilistic local networks and metawebs.

157 Local networks: communities interacting in space and time

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

167 We define space as the set of geographic coordinates (x, y, z) of the spatial boundaries delineating the system,
168 whether sampled or targeted. Ecological interactions may exhibit variations spatially and along altitudinal
169 gradients, as evidenced by changes in hummingbird-plant interactions (Weinstein & Graham (2017b) and
170 Weinstein & Graham (2017a)) and mosquitoes biting rates (e.g., Kulkarni *et al.* (2006)) at different elevations.

171 In contrast, time is defined as the specific time period within which interactions were either observed or
172 predicted. With these definitions in mind, space and time can be conceptualized as distinct patches or time
173 segments. Treating them as discrete dimensions aligns with the common sampling methods of ecological
174 networks and provides actual probabilities of interactions across space and time. This differs from the approach
175 of treating them as continuous variables, where edge values represent probability densities (i.e., relative
176 likelihoods of interactions occurring at infinitesimal locations and instants in time) rather than discrete

177 probability values (which can be obtained by integrating probability densities). By employing discrete locations
178 and time periods, we can quantify both an area A and a duration t , which can be readily used in spatiotemporal
179 analyses of ecological networks. For example, when studying network-area relationships (NAR, Galiana *et al.*
180 (2018)), we anticipate that local probabilities of interactions scale positively with area and duration because
181 taxa have more opportunities to interact as these dimensions expand.

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

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

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

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

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

204 The representation of the local context in which probabilities are estimated and the variables that should be
 205 taken into consideration depend on the study system, the objectives of the study, and the resources available to
 206 the researchers. In other words, these variables do not systematically need to be accounted for. For example, in
 207 Gravel *et al.* (2019), for the purpose of model comparison, some models incorporated environmental variables
 208 as conditional factors to estimate interaction probabilities, while others did not. When accounted for, these
 209 variables should be clearly described in the documentation of the data (Brimacombe *et al.* (2023)),
 210 preferentially in mathematical terms to avoid any confusion in their interpretation and to limit manipulation
 211 errors during their re-use. For instance, ecologists should be explicit about their consideration of co-occurrence
 212 in their estimation of local interaction probabilities. Indeed, it is important to specify if probability values are
 213 conditional $P_N(i \rightarrow j|C = 1)$ or not $P_N(i \rightarrow j)$ on co-occurrence since this can significantly impact the
 214 interpretation and analysis of the data. In [tbl. 1](#), we present examples of studies that used these diverse
 215 formulations of probabilistic interactions and conditional variables.

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

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

| Notation | Type | Description | Reference |
|-------------------------------|-------|---|---|
| $P_N(i \rightarrow j \Omega)$ | local | realization of the interaction given environmental conditions | Gravel <i>et al.</i> (2019) (temperature and precipitation) |

216 Metawebs: regional catalogs of interactions

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

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

232 which, in contrast with eq. 2, is not conditional on any spatial, temporal, or environmental variables (tbl. 1).
 233 Starting from a selected set of taxa, which are usually distributed within a broad region of interest, probabilistic
 234 metawebs can be built using different data sources, including literature review, fieldwork, and predictive models
 235 (e.g., the metaweb of trophic interactions between Canadian mammals inferred by Strydom *et al.* (2022)).
 236 Every pair of taxa that have confidently been observed to interact at least once can be given a probability of 1
 237 (i.e., $P_M(i \rightarrow j) = 1$) since we know that they *can* interact. This is not the case in local probabilistic networks,

238 in which interaction events usually remain stochastic (i.e., $P_N(i \rightarrow j) < 1$) after empirically observing
239 interactions because of their intrinsic spatiotemporal variability. Similarly, although rare interactions typically
240 have low probabilities in local networks, they can have high probabilities in metawebs when the traits of both
241 taxa are congruent. On the other hand, interactions that were never observed can have low probability values in
242 both metawebs and local networks, going as low as 0 for forbidden links. However, because of observation
243 errors due to taxonomic misidentifications and ecological misinterpretations (e.g., due to cryptic species and
244 interactions, Pringle & Hutchinson (2020)), many observations of interactions are in reality false positives.
245 Likewise, forbidden interactions can be false negatives in metawebs, e.g. if they have been assessed for specific
246 phenotypes, locations or time. Employing Bayesian models, whether they are mechanistic or
247 phenomenological, has the potential to enhance the accuracy of our estimation of interaction probabilities
248 within both local and potential networks (e.g., Bartomeus *et al.* (2016), Cirtwill *et al.* (2019)). This
249 improvement is achieved in potential networks by leveraging prior information regarding the feasibility of
250 interactions along with the empirical data on observed interactions.

251 **Properties of probabilistic networks**

252 Probabilistic local networks and metawebs differ in their type of interactions (i.e., local or potential) and in the
253 conditional variables upon which interaction values depend. These differences are significant as they influence
254 the characteristics of probabilistic networks. Neglecting to consider them may result in misleading results and
255 interpretation errors when analyzing the properties of probabilistic networks, which could be particularly
256 problematic when addressing crucial ecological questions about networks. Here we compare the characteristics
257 of local networks and metawebs through the presentation of four common applications of probabilistic
258 interactions. All code and data to reproduce these analyses are available at the Open Science Framework (TBD).

259 **Host-parasite network data**

260 We use the collection of tripartite host-parasite networks sampled across Europe, created by Kopelke *et al.*
261 (2017), in most of our case studies. This dataset contains well-resolved binary local interactions between
262 willows (52 species), willow-galling sawflies (96 species), and their parasitoids (126 species). Given its
263 replicated networks spanning large spatiotemporal scales, this dataset is well-suited for analyzing a variety of
264 ecological hypotheses and processes. Out of a total of 374 local networks, we retained those containing at least

265 5 species, resulting in a set of 233 georeferenced local networks. We built a binary metaweb by aggregating all
266 local interactions, which gave us a regional metaweb composed of 274 species and 1080 interactions. In the first
267 two panels of fig. 1, we show how the dissimilarity of interactions between common species (β_{OS}) and the
268 dissimilarity in species composition (β_S) between the metaweb and aggregated local networks (Poisot *et al.*
269 (2012)) vary with the number of sampled local networks. This shows that networks of local interactions are
270 highly dissimilar from the metaweb, both in terms of species and interactions, especially when only a limited
271 number of sites has been sampled.

272 [Figure 1 about here.]

273 We converted these binary networks into probabilistic ones using models based on simple assumptions. Our
274 models do not aim to precisely estimate the actual values of probabilistic interactions but rather to offer
275 simplified networks as illustrative examples to underscore the differences between probabilistic local networks
276 and metawebs. We created two probabilistic metawebs by employing constant false positive and false negative
277 rates for all potential interactions. In the first metaweb, we set both false positive and false negative rates to zero
278 to prevent artificially inflating the total number of links, enabling a more accurate comparison with binary
279 networks. This gave us a probability of potential interaction of 1 when at least one interaction has been observed
280 and of 0 in the absence of any observed interaction between a given pair of species. In the second metaweb, we
281 introduced a 5% false positive rate to account for spurious interactions and a 10% false negative rate to capture
282 the elevated occurrence of false negatives in ecological networks (Catchen *et al.* (2023)). Observed potential
283 interactions were thus given a probability of 95%, whereas unobserved ones were assigned a probability of 10%.
284 To build probabilistic local networks, we first recognize that local interactions must initially be biologically
285 feasible before occurring at a specific time and space. A local probability of interaction $P_N(i \rightarrow j)$ can be
286 expressed as the product of the probability of local interaction given that the two taxa can potentially interact
287 $P_N(i \rightarrow j|M_{i \rightarrow j} = 1)$, which we denote as p for the sake of simplicity, with their probability of potential
288 interaction $P_M(i \rightarrow j)$:

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

289 We built the probabilistic local networks from the binary ones by using the probabilistic metawebs and a
290 constant value of p across interactions. Lower values of p indicate that feasible interactions rarely occur locally,

291 intermediate values around 50% suggest considerable spatiotemporal variability, while higher values indicate
292 that potential interactions are nearly always realized. Following eq. 4, the local probabilities of interaction
293 between a given pair of taxa consistently remained equal to or below their probability of potential interaction.

294 In the last two panels of fig. 1, we show how the aggregated number of links and connectance (i.e., the
295 proportion of all of the S^2 possible links that are realized, where S represents species richness) scale with the
296 number of sampled local probabilistic networks, according to different values of p . When aggregating local
297 probabilistic networks, the constancy of the probability of potential interaction across the entire study area
298 means that any rise in the probability of local interaction is solely attributable to an increase in p . The
299 probability $p_{1,2}$ of local interaction among potentially interacting species in an aggregated network $N_{1,2}$ is
300 obtained by:

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

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

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

307 Taxonomic scaling of interactions

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

316 There are no inherent differences in the taxonomic scaling between local networks and metawebs, as only the
317 nodes are defined taxonomically. In other words, the probability values of edges in both local networks (eq. 2)
318 and metawebs (eq. 3) are not conditional on any taxonomic scale. The phylogenetic scale is tied to the definition
319 of the event itself (i.e., the interaction between two taxa), not to the conditional variables. In both types of
320 networks, transitioning to a broader level of organization can be accomplished directly by using probabilities
321 from finer scales. For example, in a network with n_A species from genus A and n_B species from genus B, one
322 can compute the probability that at least one species from genus A interacts with at least one species from genus
323 B as follows:

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

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

333 Ideally, our biological interpretation of probabilistic interactions should remain consistent across a network
334 even if it incorporates heterogenous levels of organization (e.g., a network whose nodes are composed of both
335 species and trophic species). This is common in ecological networks where taxonomic resolution is typically
336 low (Hemprich-Bennett *et al.* (2021), Vázquez *et al.* (2022)). Interaction probabilities at broader taxonomic
337 scales should be based on probabilities of interactions between individuals, for both local networks and
338 metawebs. For instance, in local individual-based food webs, the probability that two individuals interact
339 reflects our degree of belief that one individual will consume the other. Similarly, in local species-based food
340 webs, the probability that two species interact represents our degree of belief that at least one individual from
341 the predator species consumes at least another individual from the prey species. Furthermore, in local
342 clade-based food webs, the probability that two clades interact represents our degree of belief that at least two

343 species from these clades interact with each other or, equivalently, that at least two individuals from these clades
344 interact with each other. Fundamentally, the taxonomic scaling of interactions involves aggregating interactions
345 between individuals into larger groups, which may exhibit varying degrees of homogeneity based on the
346 organisms and the study system. In that regard, taxonomic scaling is analogous to the spatial and temporal
347 scaling of interactions, as they all represent different ways to aggregate individuals into broader groups (either
348 spatially, temporally, or taxonomically).

349 **Spatial and temporal scaling of interactions**

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

364 Metawebs and local networks exhibit distinct relationships with spatial and temporal scales. On one hand,
365 probabilistic metawebs, being independent of any local context, feature potential interactions that do not scale
366 with space and time. This is because potential interactions depend solely on the biological capacity of two taxa
367 to interact, regardless of their co-occurrence and specific environmental conditions. This implies that the
368 probability of two taxa potentially interacting should theoretically be the same in all metawebs in which they are
369 present, provided that the data and methods used for estimation are consistent. As a result, if a smaller metaweb
370 M_1 is derived from subsampling a regional metaweb M_0 to represent potential interactions among a subset of
371 taxa in a smaller region, their probabilities of interaction should be identical regardless of scale,

372 i.e. $P_{M_1}(i \rightarrow j) = P_{M_0}(i \rightarrow j)$. However, because the number of taxa may be higher in the larger metaweb, it is
373 expected that the overall number of interactions would be higher in the larger network, despite pairwise
374 probabilities being identical.

375 On the other hand, local interactions scale both spatially and temporally, given that they have more opportunities
376 to be realized and observed in larger areas and longer durations. This is attributed to factors such as a higher
377 number of individuals, greater trait variations, and increased opportunities for encounters, as highlighted by
378 McLeod *et al.* (2020). For example, if a local probabilistic network N_1 with an area A_1 is derived from a larger
379 network N_0 with an area A_0 , and A_1 is entirely nested within A_0 , interaction probabilities should be lower in the
380 smaller network, i.e. $P_{N_1}(i \rightarrow j | A_1 < A_0) \leq P_{N_0}(i \rightarrow j | A_0)$. However, if A_1 and A_0 are disjoint, interaction
381 probabilities could potentially be higher in the smaller area, contingent upon their environmental and biological
382 conditions. Likewise, interaction probabilities are expected to be lower in networks with shorter durations when
383 time intervals are nested. In fig. 2, we show how the expected number of local host-parasite interactions scales
384 with area, represented as an expanding latitudinal window, in comparison with potential interactions. Even
385 though we employed local probabilities of interactions equal to potential interactions for the purpose of
386 comparison (i.e., using $p = 1$ here), we notice that the total number of potential interactions scales more rapidly
387 than local interactions. This is due to the fact that numerous potential interactions involve species that never
388 co-occur, and as a result, these interactions are not captured in local networks.

389 [Figure 2 about here.]

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

391 Predicting local networks across time and space is a pivotal goal of network ecology (Strydom *et al.* (2021)). In
392 a context of scarcity of interaction data (Jordano (2016)), ecologists must resort to predictive models for
393 reconstructing networks at fine spatial and temporal scales. For instance, real-time biomonitoring data coupled
394 with appropriate numerical models (Bohan *et al.* (2017)) can be employed to reconstruct local ecological
395 networks, opening avenues for in-depth studies on local ecosystem functioning and dynamics. Apart from their
396 predictive applications, statistical models can also be crafted for descriptive purposes, elucidating key
397 parameters of interest such as probabilities of interactions. In such instances, the parameter values themselves
398 offer valuable ecological insights. Various types of models (e.g., Bayesian and machine learning models) have
399 been used for both predictive and descriptive purposes in the realm of ecological interactions (Strydom *et al.*

400 (2021)). The probabilistic representation of interactions acknowledges the inherent uncertainty in these models,
 401 typically expressed through probability distributions. We introduce and develop a simple generative mechanistic
 402 model for probabilistic local interactions that takes into consideration their spatiotemporal variability (i.e. a
 403 spatiotemporally explicit model of local interactions). It is essential to note that our model is not designed for
 404 potential interactions, which are scale-independent. Rather, it could prove valuable for predicting local
 405 interactions across time and space by generating new interaction data following parameter inference.

406 As indicated by eq. 1, the probability that two taxa i and j interact at a specific location (x, y, z) is determined by
 407 the product of their probability of interaction given co-occurrence and their probability of co-occurrence. First,
 408 their co-occurrence probability can be calculated using their individual occurrence probabilities $P_i(x, y, z)$ and
 409 $P_j(x, y, z)$, along with the strength of association γ between their occurrences and co-occurrence (Cazelles *et al.*
 410 (2016)):

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

411 When $\gamma > 1$, it signifies a positive association in the geographic distributions of both taxa, indicating that the
 412 presence of one taxon enhances the probability of occurrence of the other. In empirical networks, $\gamma > 1$ holds
 413 true for the majority of species pairs (Catchen *et al.* (2023)). The co-occurrence of both taxa is modeled as the
 414 outcome of a Bernoulli trial

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

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

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

420 which tends toward 1 as $t_0 \rightarrow \infty$. It is important to note that the units of λ and t_0 are complementary. For

421 instance, if the duration t_0 is measured in months, λ denote the expected number of interactions per month.
 422 The occurrence of an interaction between i and j can be modeled as a Bernoulli trial with a probability of
 423 $P_N(i \rightarrow j)$. Consequently, a Bayesian inference model can be built based on the preceding equations to estimate
 424 the value of the λ and γ parameters and generate novel interaction data:

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

425

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

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

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

426 In fig. 3, we show the variation in the probability of interaction under different parameter values. In the right
 427 panel, we notice that, irrespective of the interaction rate λ , the probability of interaction converges toward an
 428 asymptote determined by the co-occurrence $P_{i,j}(x, y, z)$ (eq. 7). This model can be customized in different ways,
 429 such as by linking λ with specific environmental variables or explicitly incorporating observation errors (i.e.,
 430 the probabilities of false negatives and false positives).

431

[Figure 3 about here.]

432 Sampling binary networks

433 The prediction of binary interactions through random draws is an important application of probabilistic
 434 networks. This approach proves beneficial for analyzing the structural characteristics of probabilistic networks,
 435 particularly in the absence of specific analytical measures. By simulating independent Bernoulli trials for each
 436 interaction, a binary network can be generated. A probability distribution of network properties can be obtained
 437 by measuring network structure across multiple randomly generated networks (Poisot *et al.* (2016)). This
 438 method enables the representation of the variability of network structure, albeit with potential biases when
 439 connectance is low (Poisot & Gravel (2014), Chagnon (2015)). Employing this strategy to generate binary

440 networks under a null model facilitates null hypothesis significance testing, wherein the observed measure is
441 compared against the simulated distribution (e.g., Bascompte *et al.* (2003)). Additionally, randomly generating
442 binary networks across spatial and temporal dimensions aids in representing the spatiotemporal variability of
443 network structure, allowing the testing of ecological hypotheses regarding interactions on large spatial and
444 temporal scales.

445 There are at least two distinct approaches to sample binary networks from probabilistic webs across space, for
446 example, when attempting to predict a binary network for each of a number of locations within a given region.
447 The first approach involves performing a singular Bernoulli trial for each pair of taxa within the region of
448 interest based on their regional probability of potential interaction. In employing this approach, every pair of
449 taxa predicted to interact in the binary metaweb realization will be treated as interacting in all local networks
450 where they co-occur. This will result in local pairwise interactions without spatial variation. The second
451 approach is to independently sample each of the local probabilistic networks, which can be achieved by first
452 generating distinct probabilistic networks for each location. These local probabilistic networks may vary in taxa
453 composition and interaction probabilities. Subsequently, binary networks can be independently sampled for
454 each location, introducing spatial variation in binary interactions.

455 In fig. 4, we compare the average connectance of binary networks resulting from these two sampling techniques,
456 where potential and local interactions are drawn from our host-parasite probabilistic networks, generating a
457 number of binary network realizations for each site in the dataset. These two sampling approaches yield
458 different outcomes, particularly for lower values of p , which denote instances when potential interactions do not
459 consistently manifest locally. Small discrepancies are also apparent between these techniques when we equate
460 the probability of local interaction to the probability of potential interaction (i.e., when using $p = 1.0$ in eq. 4),
461 especially when the number of binary network samples for each location is low. As anticipated, we observe that
462 sampling binary interactions from the metaweb tends to overestimate connectance on average compared to
463 sampling them from local networks. Furthermore, we observe an increase in the variability of connectance
464 when employing a single sample, representing what we consider as a more tangible process leading to the
465 realization of local and potential interactions in nature.

466 [Figure 4 about here.]

467 The choice of a sampling approach can influence the selection of grid cell size when delineating local
468 communities within a broader region of interest. In the first approach, pairwise interactions remain constant

469 irrespective of cell size since they are sampled only once from the regional network. However, in the second
470 approach, local interaction probabilities are contingent on the network area. For instance, consider networks N_1
471 and N_2 with an area of $\frac{1}{2}A_0$, both nested within A_0 but disjoint from each other, forming N_0 . If we treat N_1 and
472 N_2 as independent, the probability of interaction between taxa i and j in N_0 is given by:

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

473 Due to its larger area, the probability that the two taxa interact in N_0 is equal or greater than in N_1 and N_2 .
474 When sampling binary interactions from local networks, it is crucial to sample at the same spatial scale for
475 which probabilities were estimated. Otherwise, interaction probabilities must be adjusted to align with the
476 intended cell size, preventing potential systematic biases in predictions.

477 Prediction of local networks from metawebs

478 Metawebs serve as a valuable source of ecological information for predicting local networks across time and
479 space. Binary local networks can be reconstructed by selecting a subset of taxa and interactions from the
480 metaweb (Dunne (2006)). This implies that metawebs consistently contain more interactions than their
481 corresponding local networks. Determining the list of taxa to select can be achieved empirically or through
482 methods like range maps or species distribution models. As the species composition of a community is arguably
483 less difficult to sample or predict than its interactions, the primary challenge lies in deciding which interactions
484 to select from the metaweb, a task that may necessitate advanced statistical models and ecological expertise.
485 Inferring the structure of local networks from the metaweb before predicting specific local pairwise interactions
486 could hold promise (Strydom *et al.* (2021)), considering that the structure of local networks is constrained by
487 the metaweb (Saravia *et al.* (2022)).

488 Building probabilistic local networks from a probabilistic metaweb involves a reduction in the value of pairwise
489 interaction probabilities. This decrease is attributed to the prerequisite that two taxa must initially possess the
490 capacity to interact before engaging in local interactions (eq. 4). Therefore, inferring local networks from their
491 metaweb while maintaining identical interaction probability values would introduce systematic biases into the
492 predictions. In such cases, these networks would essentially represent smaller-scale metawebs of potential
493 interactions, potentially leading to misinterpretations by being perceived as local interactions. As proposed by
494 McLeod *et al.* (2021b), although metawebs lack the ability to capture the spatiotemporal variability of

495 interactions, they establish an upper limit for local interactions. In other words, the probability of two taxa
496 interacting at a specific location and time is consistently lower or equal to the probability of their potential
497 interaction:

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

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

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

502 Estimating more precisely the probability p that two taxa interact locally if they can potentially interact allows
503 for improved predictions of local networks from a probabilistic metaweb. This task is challenging due to the
504 variability of this probability across space and time, as well as its potential variations among pairwise
505 interactions within a network. Using simple models of p , as demonstrated in our case studies, represents an
506 initial step toward the overarching objective of reconstructing local networks from metawebs.

507 Conclusion

508 In this contribution, we underline the importance of network metadata for adequately interpreting and
509 manipulating probabilistic interaction data. The mathematical representation of probabilities and their statistical
510 properties depend on the type of interactions (local or potential) and the conditions in which they were
511 estimated. We showed that probabilistic local networks and metawebs differ in their relationship to spatial and
512 temporal scales, with potential interactions remaining consistent across scales. In contrast with metawebs, local
513 interactions are measured in a specific context (e.g., in a given area, time, and biological and environmental
514 conditions) and depend on taxa co-occurrence. These important conceptual differences bring to light the need
515 to use probabilistic data with caution, for instance when generating binary network realizations across space and
516 predicting local networks from metawebs. Clear metadata describing the type of interaction and the variables
517 used in their estimation are required to ensure adequate data manipulation. Better data practices and

518 foundations for probabilistic thinking in network ecology could enable more reliable assessments of the
519 spatiotemporal variability and uncertainty of biotic interactions.

520 It is essential to enhance our comprehension of both potential and local interactions, especially considering the
521 current scarcity of interaction data. However, while sampling biological communities does decrease the
522 uncertainty of interactions by accumulating evidence for their feasibility and local realization, there is a limit to
523 how much we can diminish their inherent randomness. In metawebs, probabilities reflect our limited knowledge
524 of interactions (i.e., our degree of belief that interactions are feasible), which is expected to improve with a
525 larger volume of data. We should anticipate that potential interactions will become more definitive (with
526 probabilities approaching 0 or 1) as we investigate various conditions, including different combinations of
527 species traits. Conversely, in the case of local networks, which can be seen as random instances of metawebs,
528 randomness cannot be as reduced. In local interactions, probabilities can be divided into a component
529 representing uncertainty and another representing spatiotemporal variability. Owing to environmental
530 heterogeneity, there will invariably be instances in which an interaction occurs and others in which it does not,
531 across different times and locations, irrespective of the extent to which we can improve our knowledge of its
532 biological feasibility and the local conditions that facilitate its occurrence. When local networks depict
533 probabilities of observing interactions rather than just their actual occurrence, we must also consider the
534 observation variability as an additional source of randomness. Every ecological process is stochastic but there is
535 also a possibility that a phenomenon goes undetected. Quantifying and partitioning this stochasticity will
536 enable us to make more accurate predictions about ecological interactions at various spatial and temporal
537 scales. This will prove to be of vital importance as our time to understand nature runs out, especially at the
538 places where the climate change impacts hit harder.

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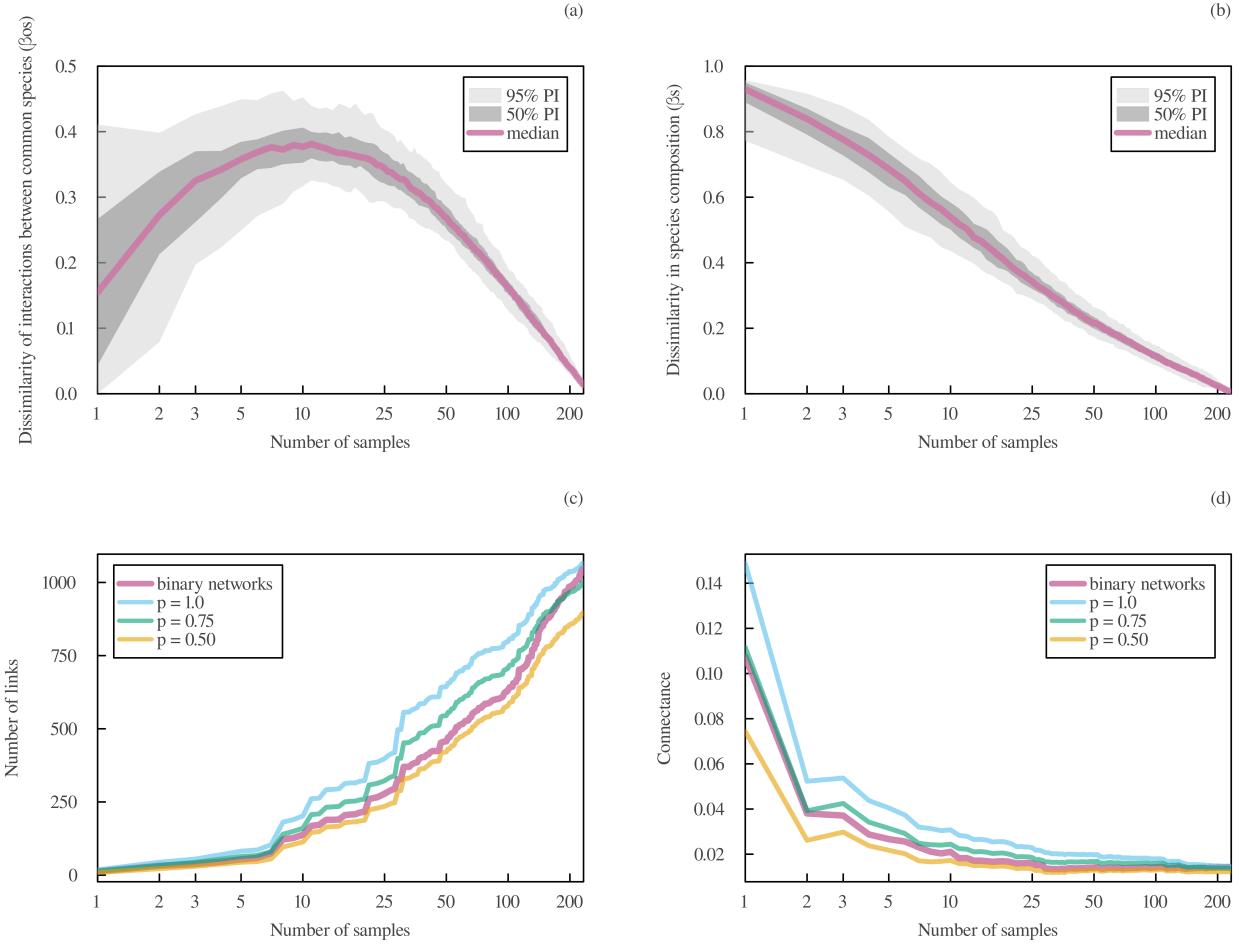


Figure 1: Network accumulation curves. (a) Dissimilarity of interactions between common species and (b) dissimilarity in species composition between aggregated local networks and the binary metaweb of host-parasite interactions. Aggregated local networks were obtained by sequentially and randomly selecting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

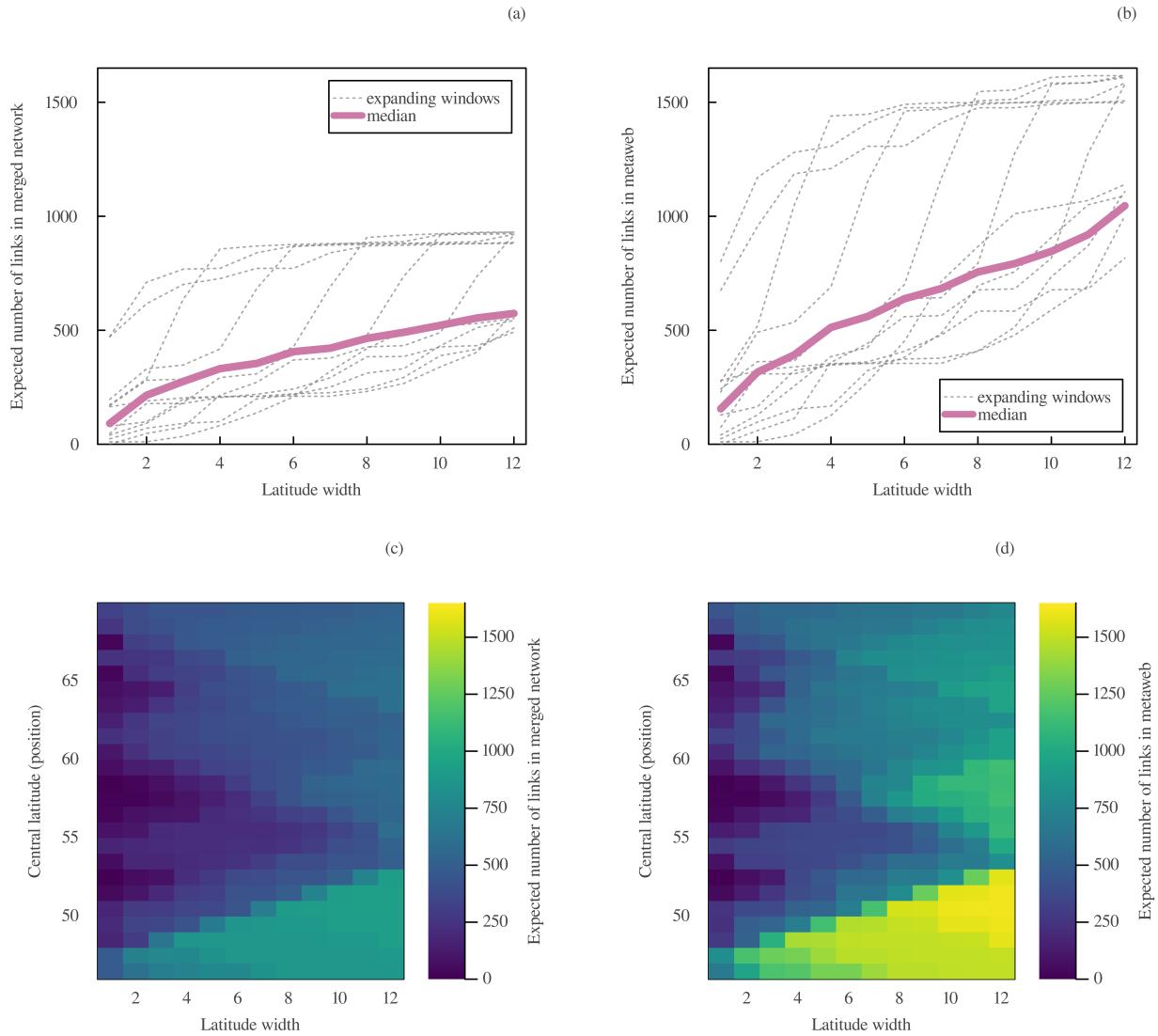


Figure 2: Spatial scaling of interactions. Expected number of host-parasite interactions in a network aggregating all probabilistic (a) local and (b) potential interactions within a latitudinal window of a given length. Every dashed curve corresponds to a different expanding window characterized by a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

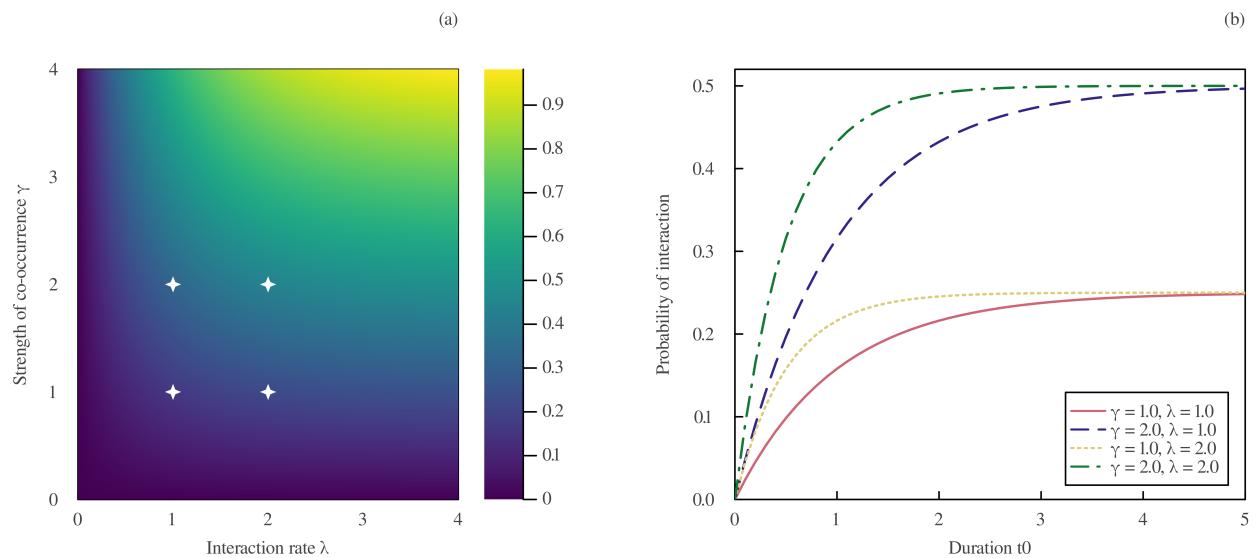


Figure 3: **Parameters of the spatiotemporally explicit model of interactions.** (a) Probability of local interaction given by the process model (eq. 11) under different values of λ and γ , with $t_0 = 1$. The parameter values used in the right panel are denoted by the white stars. (b) Scaling of the probability of interaction with the duration parameter t_0 in eq. 11, for different values of λ and γ . In both panels, the individual probabilities of occurrence $P_i(x, y, z)$ and $P_j(x, y, z)$ are set to a constant value of 0.5.

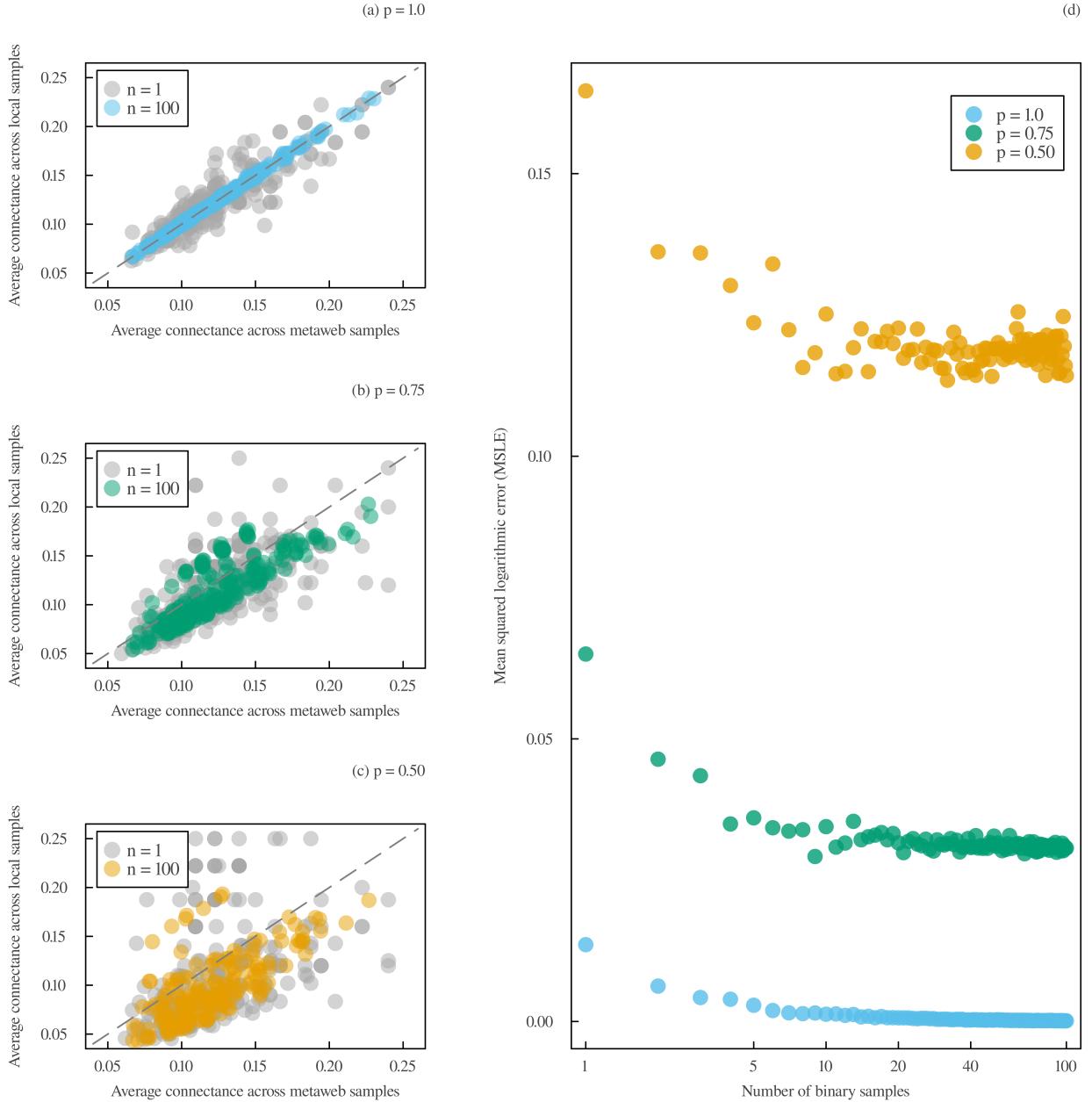


Figure 4: Connectance of sampled binary networks. Comparison between the average connectance of binary network samples obtained from the probabilistic local networks and metaweb. Each dot corresponds to a different site. The local probability of interaction between potentially interacting species was set to three different values: (a) $p = 1.0$, (b) $p = 0.75$, and (c) $p = 0.50$. Grey dots represent the outcome of a single trial, while colored dots represent the average connectance of each network across 100 trials. (d) Reduction in the mean squared logarithmic error between the average connectance of binary networks obtained from these two sampling methods as the number of trials increases, for the same values of p used in panels a-c. Probabilities of potential 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 metaweb, and then propagating this result to all local networks that include the species potentially engaged in the interactions. Local binary networks were generated by independently sampling binary interactions for each local probabilistic network.