

Deciphering probabilistic species interaction networks

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

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1

Introduction

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

Several conditions must be satisfied for an interaction to be observed locally. First, both species must have overlapping geographic ranges, i.e. they must co-occur within the region of interest (Cazelles *et al.* 2016; Morales-Castilla *et al.* 2015). Second, they must have some probability of meeting (Poisot *et al.* 2015). Probabilities of interspecific encounters are typically low, especially for rare species with low abundances. While species' absolute abundances may impact interaction frequencies (Vázquez *et al.* 2007), encounter

probabilities are determined by their relative abundances (Canard *et al.* 2012). The probability that species meet also depends on their biology, such as their phenology (Olesen *et al.* 2010; Singer & McBride 2012) and discoverability (Broom & Ruxton 2005). Finally, when species do come into contact, an interaction occurs only if their traits are locally compatible (Poisot *et al.* 2015), including their phenotypes (Bolnick *et al.* 2011; Gravel *et al.* 2013; Stouffer *et al.* 2011) and behavior (Choh *et al.* 2012; Pulliam 1974).

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

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

Networks of probabilistic interactions, within a Bayesian perspective, express our degree of belief (or confidence) regarding the occurrence or observation of interactions. In contrast, interactions are simply regarded as either occurring or not in networks of deterministic binary interactions. Based on the scale at which they are estimated, interaction probabilities may reflect our level of confidence in whether interactions will be observed, realized locally, or biologically feasible. As an illustration, we could outline a situation in which there is a 50% certainty that an interaction occurs 50% of the time. Our level of confidence should be more definitive (approaching either 0 or 1) as we extend our sampling to a broader area and over a longer time period, thereby diminishing the uncertainty of our knowledge of interactions (but not necessarily the estimation of their variability). In the broadest sense, binary interactions are also a type of probabilistic interaction, in which the numerical value of an interaction is restrained to 0 (non-occurring) or 1 (occurring). In networks of probabilistic interactions, only forbidden interactions (i.e., interactions prohibited by biological traits or species absence, Jordano *et al.* 2003; Olesen *et al.* 2010) have a probability value of zero, provided that intraspecific trait variability is considered (Gonzalez-Varo & Traveset 2016).

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). Statistical models can generate predictions of ecological networks without prior knowledge of pairwise interactions. They may do so using body size (Caron *et al.* 2024; 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), are examples of common probabilistic interaction models. Null models can be used to produce underlying distributions of network measures for null hypothesis significance testing. 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. 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 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).

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

The lack of clear guidelines on the use of probabilistic interaction data is worrisome, as it affects both 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). There is currently no reporting standard that could guide the documentation of all types of probabilistic interactions (although Salim *et al.* 2022 discuss data standards for deterministic mutualistic networks). Clear reporting standards for probabilistic interactions would support more adequate manipulation and integration of interaction data from different sources and guard against possible misinterpretations arising from ambiguous definitions of probabilistic interaction networks. This documentation should outline the nature (i.e., local or regional) and type (e.g., predatory or pollination) of the interactions, provide information regarding the taxonomic level, identities, and characteristics (e.g., life stages) of the individuals involved in an interaction, present the mathematical formulation of probabilities, including clearly identified conditional variables (e.g., spatial and temporal scales), and describe the methods and contexts (e.g., location, time, environmental conditions) in which interactions were estimated. Inadequately documented probabilistic interaction data should be used with caution when analyzing ecological networks. The broad principles underlying our findings remain relevant and applicable across diverse ecological contexts involving direct interactions. In the following sections, we delve into the definitions of probabilistic interactions as we scale up from pairwise interactions to higher-level representations of ecological networks, i.e. local networks and metawebs.

2

Pairwise interactions: the building blocks of ecological networks

2.1. Probabilistic interactions have different interpretations Consider a scenario where an avian predator has just established itself in a northern habitat home to a small rodent. Suppose these species have never co-occurred before, and as a result, their interaction has not been previously observed. What is the probability that the rodent is part of the diet of the avian predator, or put differently, what is the probability that they interact? Answering this question requires some clarification, as there are multiple ways to interpret and calculate interaction probabilities. We could calculate the probability that the traits of these species match, i.e. that the avian predator possesses the biological attributes to capture and consume the rodent. We could also calculate the probability that their traits support an interaction under the typical environmental conditions of the new habitat. For example, because avian predators hunt by sight, predation could be possible in the absence of snow but highly improbable when snow is present, as rodents may use it as a shelter to hide from predators. Finally, we could calculate the probability that the avian predator will consume the rodent at *that* particular location, for which the spatial and temporal boundaries need to be specified. The estimation of interaction probabilities, whether through predictive models or prior distributions, hinges on our understanding of these probabilities and the specific ecological processes we aim to capture.

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

time (i.e., the probability that they interact locally). For two co-occurring taxa and over enough time, the probability of local interaction is equivalent to the probability of regional (potential) interaction.

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

2.2. The outcome of probabilistic interactions is usually binary Local networks and metawebs, like any type of network, are made of nodes and edges that may be represented at different levels of organization. The basic units of ecological networks are individuals that interact with each other (e.g., by predation in food webs, Elton 2001), forming individual-based networks (Melián *et al.* 2011). The aggregation of these individuals into more or less homogeneous groups (e.g., populations, species, families, feeding guilds) allows us to represent nodes at broader taxonomic scales, which affects our interpretation of the properties of these systems (Guimarães 2020; Hemprich-Bennett *et al.* 2021).

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

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

2.3. Probabilistic interactions may also describe quantitative networks Even though binary interaction networks constitute a highly valuable source of ecological information (Pascual *et al.* 2006), they overlook interaction strengths. Represented in a quantitative adjacency matrix W , interaction strengths better describe the energy flows, demographic impacts or frequencies of interactions between nodes (Berlow *et al.* 2004; Borrett & Scharler 2019), with $W_{i \rightarrow j}$ being a natural \mathbb{N} or real \mathbb{R} number depending on the measure. For example, they may represent local interaction rates between pairs of taxa (e.g., the flower-visiting rates of pollinators in a mutualistic network, Herrera 1989). When interaction strengths characterize predation pressure on prey, they can serve as parameters in a Lotka-Volterra model (e.g., Emmerson & Raffaelli 2004). The extra amount of ecological information in quantitative networks typically comes at a cost of greater sampling effort and data volume in predictive models (Strydom *et al.* 2021), which can lead to relatively high levels of uncertainties when inferring quantitative networks with limited data.

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

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

3

Local networks: communities interacting in space and time

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

3.1.1 Space and time We define space as the collection of geographic coordinates (x, y, z) , with (x, y) representing longitude and latitude coordinates, and z denoting either altitudes or depths. These point coordinates delineate the spatial boundaries of the system, which may be portrayed as a polyhedron. Ecological interactions may exhibit variations along latitudinal and altitudinal gradients, as evidenced by changes in hummingbird-plant interactions (Weinstein & Graham 2017a, b) and mosquito biting rates (e.g., Kulkarni *et al.* 2006) at different elevations. In contrast, time is defined as the specific time period within which interactions were either observed or predicted. Even though space and time are continuous variables that should yield probability *densities* of interactions (i.e., relative likelihoods of interactions occurring at infinitesimal locations and instants in time), these definitions enable them to be conceptualized as distinct patches and time segments. Treating space and time as discrete dimensions aligns with the common sampling methods of ecological networks and provides probabilities of interactions, which can be obtained by integrating probability densities over space and time. We can quantify both an area A and a duration t , which can readily be used in spatiotemporal analyses of ecological networks (Box 1).

3.1.2 Co-occurrence The probability that two taxa i and j interact in a local network $L_{x,y,z,t}$ (spatial and temporal subscripts hereafter omitted or replaced by the shorter subscript k for clarity) can be conditioned on many environmental and biological factors. In addition to network area (or volume) and duration, they may be conditioned on taxa co-occurrence $X_{i,j,k}$, which is usually a Boolean describing if the geographic distributions of both taxa overlap within the study area. As illustrated in Box 1, co-occurrence may be modeled probabilistically, in which case it may conform to a Bernoulli distribution $X_{i,j,k} \sim \text{Bernoulli}(P(X_{i,k}, X_{j,k}))$, where $X_{i,k}$ and $X_{j,k}$ are the local occurrences of both taxa. The probability of co-occurrence $P(X_{i,k}, X_{j,k})$ can be estimated through the application of joint species distribution models (e.g., Pollock *et al.* 2014), potentially taking into account biotic interactions (Staniczenko *et al.* 2017). Given that the probability that two non-co-occurring taxa interact locally is zero (i.e., $P(L_{i \rightarrow j}|X_{i,j,k} = 0) = 0$), the probability of local interaction can be obtained by multiplying the probability of interaction given co-occurrence with the probability of co-occurrence:

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

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

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

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

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

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

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

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

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

The representation of the local context in which probabilities are estimated and the variables that should be taken into consideration depend on the study system, the objectives of the study, and the resources available to the researchers. In other words, these variables do not systematically need to be accounted for. For example, Gravel *et al.* (2019) analyzed local European host-parasite networks of willow-galling sawflies and their natural enemies, all referenced in space and time, to infer probabilities of local interactions between co-occurring species. This was achieved by including temperature and precipitation as conditional variables in

their models. In Box 2, we reuse these data to show the extent of variation among these local networks. We do so by measuring their dissimilarity with the regional network (metaweb aggregating all local interactions), both in terms of species composition and interactions. We build local probabilistic networks following eq. 2, showing that insufficient local variation (high probability of local interaction among potentially interacting species) results in an overestimation in both the number of interactions and connectance (i.e., the proportion of all of the non-forbidden links that are realized).

When accounted for, conditional variables should be clearly described in the documentation of the data (Brimacombe *et al.* 2023), preferentially in mathematical terms to avoid any confusion in their interpretation and to limit manipulation errors during their re-use. For instance, ecologists should be explicit about their consideration of co-occurrence in their estimation of local interaction probabilities. Indeed, it is important to specify if probability values are conditional ($P(L_{i \rightarrow j}|X_{i,j,k} = 1)$) or not ($P(L_{i \rightarrow j})$) on co-occurrence, as this can change the interpretation of the data. In Tbl. 1, we present examples of studies that used different expressions of probabilistic interactions. We have included the probability of empirically observing an interaction that is realized locally $P(O_{i \rightarrow j}|L_{i \rightarrow j})$ to underscore the distinction between local observations and actual realizations of interactions.

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

| Expression | Type | Outcome | Common models | Reference |
|---|----------|--|---|--|
| $P(L_{i \rightarrow j} X_{i,k}, X_{j,k}, \dots)$ | local | realization of the interaction given taxa co-occurrence | species distribution models | Gravel <i>et al.</i> (2019), Dansereau <i>et al.</i> (2023) |
| $P(L_{i \rightarrow j} N_{i,k}, N_{j,k}, \dots)$ | local | realization of the interaction given taxa abundances | neutral models | Canard <i>et al.</i> (2014) |
| $P(L_{i \rightarrow j} T_{i,k}, T_{j,k}, \dots)$ | local | realization of the interaction given local traits | trait matching models | Caron <i>et al.</i> (2024) |
| $P(L_{i \rightarrow j} E_k, \dots)$ | local | realization of the interaction given local environmental conditions | environmental-based models | Gravel <i>et al.</i> (2019) (temperature and precipitation) |
| $P(L_{i \rightarrow j} A, \dots)$ | local | realization of the interaction in a given area or volume | spatial models | Galiana <i>et al.</i> (2018)* |
| $P(L_{i \rightarrow j} t, \dots)$ | local | realization of the interaction during a given time period | temporal models | Weinstein & Graham (2017a) |
| $P(L_{i \rightarrow j} f(L), \dots)$ | local | realization of the interaction given network structure | topological models | Fortuna & Bascompte (2006) (connectance), Stock <i>et al.</i> (2017) |
| $P(L_{i \rightarrow j} M_{i \rightarrow j}, \dots)$ | local | realization of the interaction given that the taxa can biologically interact | spatiotemporal models | Dansereau <i>et al.</i> (2023) |
| $P(O_{i \rightarrow j} L_{i \rightarrow j}, \dots)$ | local | observation of the interaction given that it is realized locally | sampling models | Catchen <i>et al.</i> (2023) |
| $P(M_{i \rightarrow j} T_i, T_j)$ | 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 |

3.4. Interaction probabilities may be estimated with multiple models When using multiple models to estimate local interaction probabilities, rather than selecting a single model that best fits the data, model averaging may 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 $P(L_{i \rightarrow j} | \dots)$ can be calculated as follows:

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

where the ellipsis serves as a placeholder for the conditional variables incorporated in these models. Model structure constitutes another source of uncertainty that needs to be documented and quantified when estimating interaction probabilities.

Box 1: A spatiotemporally explicit model of interactions Ecologists may resort to predictive models (e.g., generative Bayesian models) to reconstruct local networks across time and space (Strydom *et al.* 2021). Uncertainty in model parameters, model structure, and input data leads to probabilistic interactions. We introduce and develop a simple generative mechanistic model for probabilistic local interactions that takes into consideration their spatiotemporal variability (i.e., a spatiotemporally explicit model of local interactions). This model is not designed for regional interactions, which do not vary spatially and temporally. Rather, it may prove valuable for predicting local interactions across time and space by generating new interaction data following parameter inference.

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

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

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

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

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

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

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

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

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

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

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

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

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

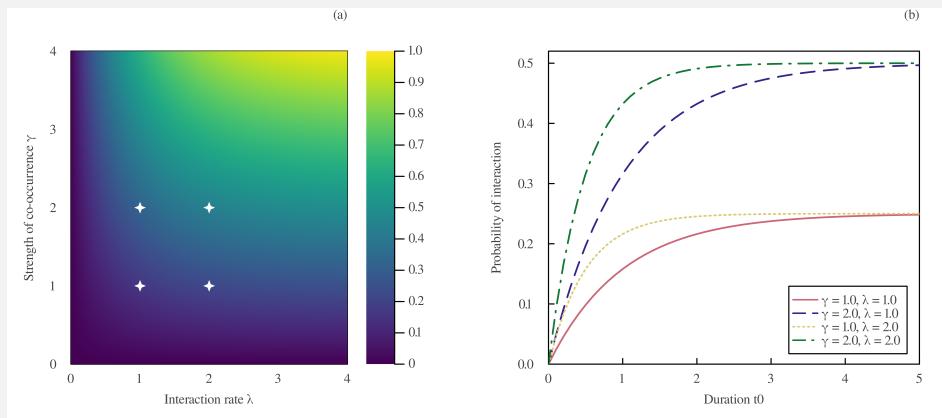


Figure 1 Parameters of the spatiotemporally explicit model of interactions. (a) Probability of local interaction given by the process model (Eq. 9) under different values of λ_k (interaction rate) and γ (strength of co-occurrence), with $t_0 = 1$ (duration). Parameters t_0 and λ_k have complementary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

Box 2: Dissimilarity of local host-parasite networks We use the collection of tripartite host-parasite networks of Kopelke *et al.* (2017), consisting of willows, willow-galling sawflies, and their natural enemies, sampled across Europe (233 local networks used). Given its replicated networks spanning large spatiotemporal scales, this dataset is well-suited for analyzing network variability, both in terms of species composition and interactions. Further details regarding data manipulation and network construction can be found in the supplementary material. All code and data to reproduce these analyses are available at the Open Science Framework (TBD).

In Fig. 2a-b, we show how the dissimilarity between the metaweb of binary interactions and aggregated local networks varies with the number of sampled local networks. To do so, we randomly selected one local network of binary interactions and sequentially sampled additional networks while aggregating both their species and interactions. We compared the metaweb and the aggregated local networks using the dissimilarity in species composition (β_S , Fig. 2a) and the dissimilarity of interactions between common species (β_{OS} , Fig. 2b) indices (Poisot *et al.* 2012). We repeated this sampling process one hundred times and highlighted the median dissimilarity values across simulations, as well as the 50% and 95% percentile intervals. Both dissimilarity indices were calculated based on the number of items shared by the two networks (c_{LM}) and the number of items unique to the metaweb (u_M) and the aggregated local network (u_L). The β_S dissimilarity index uses species (nodes) as items being compared, while the β_{OS} index assesses dissimilarity based on interactions between shared species. Both indices were calculated following the β_W index of Whittaker (1960):

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

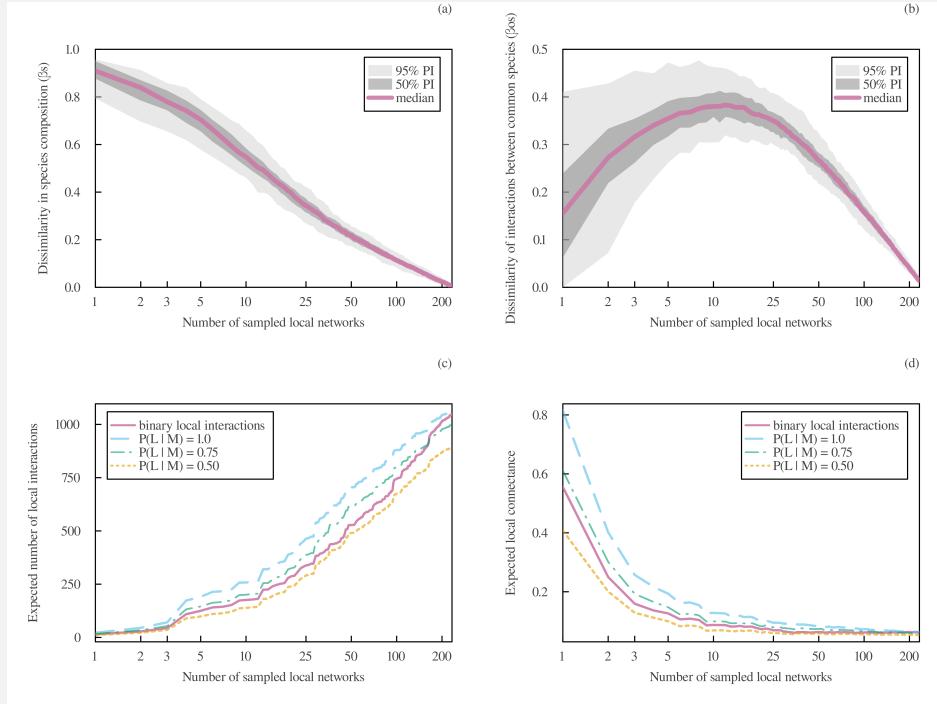


Figure 2 Network accumulation curves. (a) Dissimilarity in species composition and (b) dissimilarity of interactions between common species between aggregated local networks and the metaweb of binary host-parasite interactions. Aggregated local networks were obtained by sequentially and randomly selecting a number of local networks of binary interactions and aggregating both their species and interactions. In both panels, the colored line represents the median dissimilarity across simulations and the grey areas cover the 50% and 95% percentile intervals. (c) Scaling of the number of interactions and (d) scaling of connectance with the number of sampled (aggregated) binary and probabilistic local interaction networks. For a better comparison with binary interactions, local networks of probabilistic interactions were derived from a metaweb of probabilistic interactions with a false positive and false negative rate of zero. A specific value of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ (the local probability of interaction among potentially interacting species, indices omitted in the figure for simplicity) was used for all local networks within a particular curve. Aggregated local networks of probabilistic interactions were obtained by sequentially and randomly selecting a number of local networks and aggregating both their species and interactions (with the value of $P(L_{i \rightarrow j}|M_{i \rightarrow j})$ adjusting according to Eq. 13).

Expectingly, local networks are highly dissimilar from the metaweb in terms of species composition, especially when only a limited number of sites has been sampled. This is because species in the metaweb form the regional species pool, and few species occur locally. Moreover, we observe a peak in the dissimilarity of interactions between common species at intermediate sampling levels. This suggests that species are collected faster than their interactions. With a limited number of sampled local networks, few regional interactions are observed locally. Adding more sites brings new species, but not always their interactions. Interactions are more comprehensively captured when the number of sampled sites is high. Quadratic relationships of network properties with sampling effort were also observed by McLeod *et al.* (2021).

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

When aggregating local networks of probabilistic interactions, the constancy of the probability of regional interaction across the entire study area means that any rise in the probability of local interaction is solely attributable to an increase in $P(L_{i \rightarrow j}|M_{i \rightarrow j})$. For example, let L_1 and L_2 be two

local networks and $L_{1,2}$ the aggregated network. If $P(L_{1,i \rightarrow j}|M_{i \rightarrow j})$ and $P(L_{2,i \rightarrow j}|M_{i \rightarrow j})$ are the probabilities that two potentially interacting taxa interact respectively in L_1 and L_2 , the probability $P(L_{1,2,i \rightarrow j}|M_{i \rightarrow j})$ that these taxa interact in the aggregated network $L_{1,2}$ is obtained by:

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

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

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

4

Metawebs: regional catalogs of interactions

4.1. Unobserved interactions should be probabilistic Metawebs (Dunne 2006) are networks of potential interactions over broad spatial, temporal, and taxonomic scales (e.g., 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 uncertainty in the ability of taxa to interact. 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 (repeatedly failing to observe an interaction between two co-occurring taxa) and 1 (observing an interaction at least once). Although *neutrally* forbidden interactions (i.e., between rare species, Canard *et al.* 2012) tend to have low probability values in local networks, they may have higher probabilities in the metaweb (i.e., when species' biological traits can support an interaction if they were to encounter each other). Likewise, non-co-occurring taxa may have a non-zero probability of interaction in the metaweb.

The extent of sampling effort influences our evaluation of probabilities of potential interactions, as sampling over a larger area or for a longer duration enables us to capture a greater number of regional interactions (McLeod *et al.* 2021). However, in contrast with local networks of probabilistic interactions, which describe local interaction stochasticity, regional interactions are not evaluated for any particular local context. In Box 3, we discuss the differences in spatial and temporal scaling of regional interactions compared to local interactions. We do so by using the host-parasite networks of Kopelke *et al.* (2017) as an illustration of spatial scaling.

4.2. Potential interactions are sometimes linked to environmental conditions

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

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

which, in contrast with local networks, is not conditioned on any spatial, temporal, co-occurrence or environmental variables (Tbl. 1). Regional traits may differ from local traits $T_{i,k}$ and $T_{j,k}$, which may vary spatially

and temporally due to phenotypic plasticity (Berg & Ellers 2010). The taxonomic level at which interactions are evaluated influences the distribution of regional and local traits. However, as explained in Box 4, there is no fundamental difference in the taxonomic scaling of regional and local interactions (i.e., how interaction probabilities change with taxonomic level), unlike their spatial and temporal scaling.

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

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

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

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

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

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

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

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

4.3. Metawebs are built with interaction data and trait-matching models Starting from a selected set of taxa, which are usually distributed within a broad region of interest, metawebs can be built using different data sources, including literature review (e.g., Maiorano *et al.* 2020), aggregated interaction data (e.g., Gravel *et al.* 2019; Saravia *et al.* 2022), trait-matching models (e.g., Shaw *et al.* 2024; Strydom *et al.* 2022), and expert knowledge. Every pair of taxa that have confidently been observed to interact at least once can be given a probability of 1 (i.e., $P(M_{i \rightarrow j}) = 1$) since we know that they *can* interact. This differs from local networks of probabilistic interactions, where interaction events may remain stochastic (i.e., $P(L_{i \rightarrow j}) < 1$) even after empirically observing interactions due to their spatiotemporal variability. Interactions that were

never observed typically have low probability values in local networks and vary from low to high values in metawebs, contingent upon taxa traits distributions (reaching 0 for forbidden links).

When incorporating local network data to estimate probabilities of regional interactions, repeatedly failing to observe an interaction between two co-occurring taxa (i.e., $P(O_{i \rightarrow j} = 0)$) should decrease the probability that the interaction is biologically feasible. Using Bayes' theorem, the probability that the interaction is biologically feasible given that it was never observed locally, $P(M_{i \rightarrow j} = 1|O_{i \rightarrow j} = 0, \dots)$, may be calculated as follows:

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

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

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

Box 3: Spatial and temporal scaling of interactions Network-Area Relationships document the scaling of network properties (such as modularity and connectance) with spatial scale (e.g., Galiana *et al.* 2018; Wood *et al.* 2015). The variation in network structure across spatial scales may stem from the scaling of species richness (species-area relationships, SARs), the number of interactions (Brose *et al.* 2004), and many other higher-level properties of the system (e.g., environmental heterogeneity, Thompson & Townsend 2005) with the sampled area. Likewise, interaction accumulation curves describe the scaling of the number of observed interactions with sampling effort (Jordano 2016). Sampling effort, which may correspond to the duration of the sampling period used to construct the network, can impact connectance (Bersier *et al.* 1999) and various measures of network structure (Banašek-Richter *et al.* 2004; McLeod *et al.* 2021). Apart from sampling effort, the temporal scaling of interactions also describes how network structure changes with the temporal resolution of the network, acknowledging that distinct interactions take place over time, ranging from short-term fluctuations of interactions to long-term trends. As local networks of probabilistic interactions may explicitly account for the spatiotemporal variability of interactions, they offer a distinct approach to investigating the scaling of network structure with space and time.

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

On the other hand, local interactions scale both spatially and temporally, given that they have more opportunities to be realized and observed in larger areas and longer durations. This is attributed to factors such as a higher number of individuals, greater trait variations, and increased opportunities for encounters, as highlighted by McLeod *et al.* (2020). For example, if a local network of probabilistic interactions L_1 with an area A_1 is derived from a larger network L_0 with an area A_0 , and A_1 is entirely nested within A_0 , interaction probabilities should be lower in the smaller network, i.e. $P(L_{1,i \rightarrow j}|A_1 < A_0) \leq P(L_{0,i \rightarrow j}|A_0)$. However, if A_1 and A_0 are disjoint, interaction probabilities could be higher in the smaller area, contingent upon their environmental and biological conditions.

Likewise, interaction probabilities should be lower in networks with shorter durations when time intervals are nested. In Fig. 3, we show how the expected number of local host-parasite interactions scales with area, represented as an expanding latitudinal window, in comparison with regional interactions (data from Kopelke *et al.* 2017). Even though we employed local probabilities of interactions equal to regional interactions for the purpose of comparison (i.e., using $P(L_{i \rightarrow j} | M_{i \rightarrow j}) = 1$ here), we notice that the total number of regional interactions scales more rapidly than local interactions. This is because numerous regional interactions involve species that never co-occur, and as a result, these interactions are not captured in local networks.

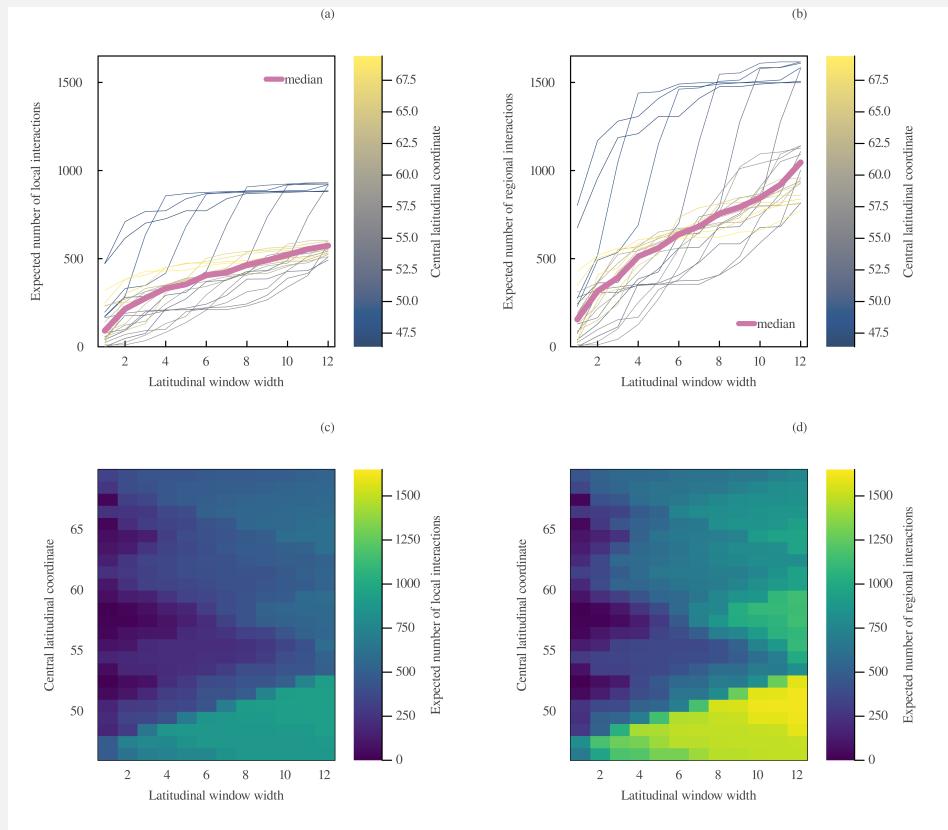


Figure 3 Spatial scaling of interactions. Expected number of host-parasite interactions in a network aggregating all (a) local and (b) regional probabilistic interactions within a latitudinal window of a given width. Every dashed curve corresponds to a different window centered at a given latitude (color bar), with the pink solid line representing the median number of interactions across windows. Heatmaps of the expected number of (c) local and (d) regional interactions found in windows of specified width and central latitudes. Probabilities of regional interactions were obtained with a false positive rate of 5% and a false negative rate of 10%. Local probabilistic interactions were derived from probabilistic regional interactions by setting the value of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ (the local probability of interaction among potentially interacting species) to 1, ensuring a conservative comparison between aggregated local networks and metawebs. Aggregated local networks were obtained by aggregating both the species and interactions found within a particular latitudinal window, with the values of $P(L_{i \rightarrow j} | M_{i \rightarrow j})$ remaining at their maximum value of 1 following Eq. 13. Further details on the data and network construction are presented in the supplementary material.

Box 4: Taxonomic scaling of interactions Probabilistic interaction networks offer a versatile approach to tackle a broad array of ecological questions, depending on their level of organization. For instance, the assemblage of interactions across ecological scales can be explored through species-based networks, while clade-based networks provide insights into macroevolutionary processes (Gomez *et al.* 2010). Given that our interpretation of the properties and dynamics of ecological networks depends on their taxonomic level (Guimarães 2020), investigating the taxonomic scaling of interactions (i.e., how interaction probabilities change with taxonomic level) emerges as a

promising research avenue.

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

In both types of networks, transitioning to a broader level of organization (e.g., from a species-level network S to a genus-level network G) can be accomplished directly by using probabilities from finer scales. For example, in a network with n_1 species from genus g_1 and n_2 species from genus g_2 , one can compute the probability that at least one species from genus g_1 interacts with at least one species from genus g_2 (i.e., that there is a non-zero number of species-level interactions or, equivalently, that the genus-level interaction occurs) as follows:

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

where $g_{1,i}$ and $g_{2,j}$ are the species of the corresponding genus and assuming independence between species-level interactions. If it is known that at least two of these species interact (i.e., $P(S_{g_1,i \rightarrow g_2,j}) = 1$ for at least one pair of $(g_{1,i}, g_{2,j})$), it implies a probability of genus interaction equal to 1. Canard *et al.* (2012) built a species-based network following a similar approach, by using simulated interactions between individuals derived from a neutral model (i.e., a model that assumed ecological equivalence among individuals).

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

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

Box 5: Sampling for binary interaction networks The prediction of binary interactions through Bernoulli trials is an important application of probabilistic interaction networks. This approach proves beneficial for analyzing the structural characteristics of probabilistic interaction networks, particularly in the absence of specific analytical formulas for measures of network structure (Poisot *et al.* 2016). By performing independent Bernoulli trials for each interaction, a network of binary interactions may be generated. A probability distribution of network properties can be obtained by measuring network structure across multiple randomly generated networks (Poisot *et al.* 2016). This method enables the representation of the variability or uncertainty of network structure, albeit with possible biases when connectance is low (Chagnon 2015; Poisot & Gravel 2014). Employing this strategy to generate binary interaction networks under a null model facilitates null hypothesis significance testing, wherein the observed measure is compared against the simulated distribution (e.g.,

Bascompte *et al.* 2003). Yet, inferring network structure through sampling for binary interactions assumes independence among interactions, which might not accurately represent reality. Covariation among interactions could exist even if we do not explicitly condition interactions on others. For example, an interaction between two taxa could be more probable when another interaction occurs. The consequences of this assumption of independence on the prediction of network structure have yet to be empirically examined.

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

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

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

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

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

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

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

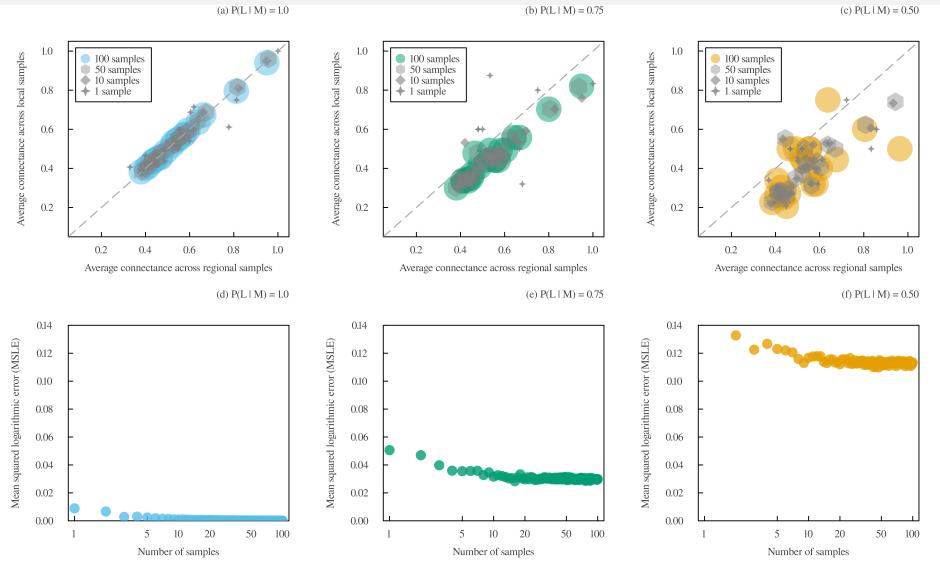


Figure 4 Connectance of sampled binary interaction networks. (a-c) Average connectance of binary interaction networks obtained from the two sampling approaches for 20 randomly selected host-parasite networks. Cross markers represent the connectance of a single sample for each network, diamond markers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

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

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

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

Conclusion

In this contribution, we underline the importance of network documentation for adequately interpreting and manipulating probabilistic interaction data. The mathematical representation of probabilities and their statistical properties depend on the type of interactions (local or regional) and the conditions under which these interactions were evaluated. We showed that local networks and metawebs of probabilistic interactions differ

in their relationship to spatial and temporal scales (Box 3), with regional interactions remaining consistent across scales. In contrast with metawebs, local interactions are measured in a specific context (e.g., in a given area, time, and biological and environmental conditions) and depend on taxa co-occurrence. These differences bring to light the need to use probabilistic data with caution, for instance when generating network realizations of binary interactions across space (Box 5). Clear documentation describing the type of interaction and the variables used in their estimation are required to ensure adequate data manipulation. Sound data practices and foundations for probabilistic thinking in network ecology facilitate reliable assessments of the spatiotemporal variability and uncertainty of biotic interactions. Here we identify key research priorities for improving our understanding of local and regional interactions and their stochasticity.

5.1. Predicting local networks from metawebs Metawebs are a valuable source of ecological information for predicting local networks across time and space. Local networks of binary interactions can be reconstructed by selecting a subset of taxa and interactions from the metaweb (Dunne 2006). Metawebs thus contain more interactions than local networks, even though their connectance is usually much smaller than the one of local networks (Gravel *et al.* 2011). Determining the list of taxa to select can be achieved empirically (e.g., observed occurrence data for a site) or numerically (e.g., species distribution models). As species composition is arguably easier to sample or predict than pairwise interactions, the primary challenge lies in deciding which interactions to select from the metaweb. Inferring the structure of local networks from the metaweb before predicting local pairwise interactions could hold promise (Strydom *et al.* 2021), considering that the structure of local networks is constrained by the metaweb (Saravia *et al.* 2022).

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

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

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

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

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

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

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

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

5.3. Relaxing the independence assumption Estimating local interaction probabilities independently for each taxa pair and assembling them into a network of probabilistic interactions comes with limitations. Predicting local networks of binary interactions based on these interaction probabilities assumes independence among interactions, a condition seldom respected in practice (Golubski & Abrams 2011). Relaxing this assumption is the next logical step in the stochastic representation of interactions.

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

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

6

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