

The biological interpretation of probabilistic food webs

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Community ecologists are increasingly thinking probabilistically when it comes to food webs and other ecological networks. Assuredly, the benefits of representing ecological interactions as probabilistic events (e.g., how likely are species to interact?) instead of binary objects (e.g., do species interact?) are numerous, from a better assessment of the spatiotemporal variation of trophic interactions to an increase capacity to reconstruct networks from sparse data. However, probabilities need to be used with caution when working with species interactions. Indeed, depending on the system at hand and the method used to build probabilistic networks, probabilities can have different interpretations that imply different ways to manipulate them. At the core of these differences lie the distinction between assessing the likelihood that two groups of individuals *can* interact and the likelihood that they *will* interact. This impacts the spatial, temporal, and taxonomic scaling of interaction probabilities, thus enlightening the need to properly define them in their ecological context. Published data on probabilistic species interactions are poorly documented in the literature, which impedes our ability to use them appropriately. With these challenges in mind, we propose a general approach to thinking about probabilities in regards to ecological interactions, with a strong focus on food webs, and call for better definitions and conceptualizations of probabilistic ecological networks, both at the local and regional scales.

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spatial scale
species interactions
temporal scale

1

Introduction

Cataloging species interactions across space is a gargantuan task. At the core of this challenge lies the spatiotemporal variability of ecological networks (Poisot *et al.* 2012, 2015), which makes documenting the location and timing of interactions difficult. Indeed, it is not sufficient to know that two species have the biological capacity to interact to infer the realization of their interaction at a specific time and space (Dunne 2006). Taking food webs as an example, a predator species and its potential prey must first co-occur in order for a trophic interaction to take place (Blanchet *et al.* 2020). They must then encounter, which is conditional on their relative abundances in the ecosystem and the matching of their phenology (Poisot *et al.* 2015). Finally, the interaction occurs only if the predators have a desire to consume their prey and are able to capture and ingest them (Pulliam 1974). Environmental (e.g. temperature and presence of shelters) and biological (e.g. physiological state of both species and availability of other prey species) factors contribute to this variability by impacting species co-occurrence (Araujo *et al.* 2011) and the realization of their interactions (Poisot *et al.* 2015). In this context, the development of computational methods in ecology can help alleviate the colossal sampling efforts required to document species interactions across time and space (Strydom *et al.* 2021). Having a better portrait of species interactions and the emerging structure of their food webs is important since it lays the groundwork for understanding the functioning, dynamics, and resilience of ecosystems worldwide (e.g., Proulx *et al.* 2005; Pascual *et al.* 2006; Delmas *et al.* 2019).

The recognition of the intrinsic variability of species interactions and the emergence of numerical methods have led ecologists to rethink their representation of ecological networks, slowly moving from a binary to a probabilistic view of species interactions (Poisot *et al.* 2016). This has several benefits. For example, probabilities represent the limit of our knowledge about species interactions and can inform us about the expected number of interactions and emerging network properties despite this limited knowledge (Poisot *et al.* 2016). They are also very helpful in predicting the spatial distribution of species within networks (Cazelles *et al.* 2016) and the temporal variability of interactions (Poisot *et al.* 2015), generating new ecological data (e.g., Strydom *et al.* 2022), and identifying priority sampling locations of species interactions (see Andrade-Pacheco *et al.* 2020 for an ecological example of a sampling optimization problem). Moreover, the high rate of false negatives in ecological network data, resulting from the difficulty of witnessing interactions between rare species, makes it hard to interpret non-observations of species interactions ecologically (Catchen *et al.* 2023). Using probabilities instead of yes-no interactions accounts for these observation errors; in that case, only forbidden interactions (Jordano *et al.* 2003; Olesen *et al.* 2010) would have a probability value of zero (but see Gonzalez-Varo & Traveset 2016). 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 interactions, which shows the potential of this framework in the study of a variety of ecological phenomena.

However, representing species interactions probabilistically can also be challenging. Beyond methodological difficulties in estimating these numbers, there are important conceptual challenges in defining what we mean by “probability of interactions.” To the best of our knowledge, because the building blocks of this mathematical representation of food webs are still being laid, there is no clear definition found in the literature. This is worrisome, since working with probabilistic species interactions without clear guidelines could be misleading as much for field ecologists as for computational ecologists who use and generate these data. In this contribution, we outline different ways to define and interpret interactions probabilities in network ecology and propose an approach to thinking about them. These definitions mostly depend on the study system (e.g. local network or metaweb) and on the method used to generate them. We show that different definitions can have different ecological implications, especially regarding spatial, temporal, and taxonomic scaling. Although we will focus on food webs, our observations and advice can be applied to all types of ecological networks, from plant-pollinator to host-parasite networks. Specifically, we argue that probabilities should be better documented, defined mathematically, and used with caution when describing species interactions.

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Definitions and interpretations

2.1. Food-web representations The basic unit of food webs and other ecological networks are individuals that interact with each others (e.g., by predation; Elton 2001), forming individual-based networks. The aggregation of these individuals into more or less homogeneous groups (e.g., populations, species, trophic species, families) allows us to represent networks at broader scales, which impacts the properties and behaviour of these systems (Guimarães 2020). A network’s nodes can thus designate distinct levels of organization, whereas the edges linking these nodes can describe a variety of interaction measures. When using a Boolean (yes-no) representation of biotic interactions, the observation that one individual from group (or node) i interacts with another individual from group j is enough to set the interaction $A_{i,j}$ to 1. This simplified representation of food webs is a highly valuable source of ecological information (Pascual *et al.* 2006) even though it overlooks important factors regarding interaction strengths. These, in turn, can be represented using weighted interactions, which better describe the energy flows, demographic impacts or frequencies of interactions between nodes (Berlow *et al.* 2004; Borrett & Scharler 2019), with $A_{i,j} \in \mathbb{N}$ or \mathbb{R} depending on the measure. For example, they can be used to estimate the average number of prey individuals consumed by the predators in a given time period. This extra amount of ecological information typically comes at a cost of greater sampling effort or data requirement in predictive models (Strydom *et al.* 2021), which can lead to high uncertainties when building these types of networks. Therefore, important methodological and conceptual decisions must be made when sampling and building food webs.

The uncertainty and spatiotemporal variability of both types of trophic interactions (Boolean and weighted) can be represented probabilistically. On one hand, Boolean interactions follow a Bernoulli distribution $A_{i,j} \sim \text{Bernoulli}(p)$, with p being the probability of interactions. The only two possible outcomes are the presence ($A_{i,j} = 1$) or absence ($A_{i,j} = 0$) of an interaction between the two nodes. Weighted interactions, on the other hand, can follow various probability distributions depending on the measure

used. In this case, the event's outcome is the value of interaction strength. For instance, weights can follow a Poisson distribution $A_{i,j} \sim \text{Poisson}(\lambda)$ when predicting frequencies of interactions between pairs of nodes, with λ being the expected rate of interaction. The definition and interpretation of parameters like p and λ are inextricably linked to environmental and biological factors such as species relative abundance, traits, area, and time, depending on the type of interaction. Because Boolean species interactions are much more documented in the literature, our primary focus in this contribution will be on addressing the challenges in defining and interpreting p for pairwise species interactions.

The first aspect to take into consideration when estimating or interpreting probabilities of interactions is knowing if they describe the likelihood of potential or realized interactions. A potential interaction is defined as the biological capacity of two species to interact (i.e., the probability that they *can* interact) whereas a realized interaction refers to the materialization or observation of this interaction in a delineated space and time period (i.e., the probability that they interact). Here, we will use the terms *metaweb* to designate networks of potential interactions and *local networks* for those of realized interactions. Frequent confusion arises among ecologists over the use of these two terms, especially in a probabilistic context. Indeed, in many studies of probabilistic ecological networks, it remains unclear when authors describe potential or realized interactions, or when so-called probabilities are actually *interaction scores*. Likewise, probabilistic potential interactions are often used as realized interactions (and conversely), even when the type of interaction is clearly indicated. We believe that a better understanding of these differences and concepts would alleviate interpretation errors and help ecologists use these numbers more appropriately.

2.2. Probabilistic metawebs Metawebs are networks of potential interactions, representing the probability that two taxa can interact regardless of biological plasticity, environmental variability or co-occurrence. They are the network analogue to the species pool, where local networks originate from a subset of both species (nodes) and interactions (edges). For this reason, they have been initially designed for broad spatial, temporal, and taxonomic scales (e.g. species food webs at the continental scale). However, in the next section, we argue that this concept can also be used at smaller scales, with similar ecological meaning.

We can express the probability that two taxa i and j can interact in a metaweb M as

$$P_M(i \rightarrow j), \quad (1)$$

which is context independent. In other words, the probability that two species can interact is not contingent on location, time, and environmental factors. Nevertheless, one aspect of a metaweb that could be conditional on these factors is the list of species (or taxa) it is built from when assembled for a specific region.

Starting from a selected set of species, metawebs can be built using different data sources, including literature review, field work, and predictive models (e.g., the metaweb of Canadian mammals inferred by Strydom *et al.* 2022). Every pair of species that has been observed to interact at least once can be given a probability of interaction of 1; we know that they *can* interact. This means that rare interactions can technically be given high probabilities in the metaweb. Unobserved interactions, on the other hand, are given lower probabilities, going as low as 0 for forbidden links. Two important nuances must however be made here. Because of observation errors due to taxonomic misidentifications and ecological misinterpretations, many observations of interactions are actually false positives. Similarly, forbidden interactions can be false negatives if e.g. they have been assessed for specific phenotypes, locations or time. Implementing a Bayesian framework, which updates prior probabilities of interactions with empirical data, could lessen these errors.

2.3. Probabilistic local networks As opposed to metawebs, probabilistic local food webs represent the likelihood that two species will interact at a specific location and within a given time period; in other words, they are context dependant. To be specific, space is defined here as the geographic coordinates x, y of the spatial boundaries delineating the system, whereas time is the time interval t during which interactions were sampled or for which they were predicted. We put these variables in bold to emphasize that they are not single values, but rather continued dimensions that could be outlined differently depending on the study system. Regardless of how they were defined, they always delineate a specific area A and duration D . These could refer to the sampled area and duration or to the targeted location and time period.

Many factors could be taken into consideration when estimating the probability that a predator species i interacts with a given prey species j locally. One of the most important is species co-occurrence, which describes if both species can be found at location and time x, y, t . Surely, the probability that the interaction is realized must be 0 when species do not co-occur. Similarly, species relative abundance is another important predictor of the probability of interaction, because it impacts the probability that species will randomly encounter (Canard *et al.* 2012; Canard *et al.* 2014; Poisot *et al.* 2015). Interaction probabilities can also be conditional on other biological and environmental variables, such as temperature, precipitation, presence of shelters, phenotypic plasticity, phenology, and presence of other interacting species in the network. These conditions can affect species traits, which greatly impact the likelihood of interactions (Poisot *et al.* 2015). When probabilities of interactions are estimated using specific values of these variables, ecologists should make them explicit in their metadata, preferably using mathematical equations to avoid any ambiguity. In the next section, we will see examples of why this matters when it comes to spatial, temporal, and taxonomic scaling of biotic interactions. Here, we will use the variable Ω as a substitute for the biological and ecological context in which interaction probabilities were estimated. This gives us the following equation for the probability that species (or taxa) i and j interact in a local network N :

$$P_N(i \rightarrow j | x, y, t, \Omega). \quad (2)$$

2.4. From potential to realized interactions Even though the spatiotemporal variation of interactions is not considered in metawebs, they can still be useful to reconstruct local networks of realized interactions. Indeed, local networks are formed from subsets of their metaweb (called subnetworks), which are obtained by selecting a subset of both species and interactions (Dunne 2006). Because a community's composition is arguably easier to sample (or predict) than its interactions, the biggest challenge is to sample links from the metaweb. This becomes a conceptual issue when we consider how potential and realized interactions differ. Despite these concerns, metawebs remain an important source of ecological information that can be leveraged for realistically predicting spatially explicit networks. First, metawebs set the upper limit of species interactions (McLeod *et al.* 2021), i.e. the probability that two species interact at a specific location is always lower or equal to the probability of their potential interaction:

$$P_N(i \rightarrow j | x, y, t, \Omega) \leq P_M(i \rightarrow j). \quad (3)$$

Therefore, building local networks from their metaweb keeping the same values of interaction probability would generate systematic biases in the prediction. Second, the structure of local networks is constrained by the one of their metaweb (Saravia *et al.* 2022). This suggests that a metaweb not only constraints the pairwise interactions of its corresponding local networks, but also their emerging properties. Inferring the structure of local networks from the metaweb could thus help estimate more realistically the likelihood that potential interactions are realized and observed locally (Strydom *et al.* 2021).

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Scaling

- We should expect a certain number of interactions to be realized depending on the probability value. This number depends on the number of trials, which also depends on the ecological context (e.g., environmental conditions, scale) in which probabilities were estimated. This is in contrast with probabilities in metawebs.

3.1. Spatial and temporal scales How do interaction probabilities scale spatially and temporally?

- Why do probabilistic local food webs scale with area and time but not probabilistic metawebs?
- In metawebs, interaction probabilities do not scale with space and time because they depend solely on the biological capacity of two species to interact.
- In local food webs, interaction probabilities scale with space and time because there are more opportunities of interactions (e.g., more environmental conditions) in a larger area and longer time period.

- What are some network area relationships in probabilistic local food webs?
- We know that local networks can inform regional networks. However, can regional networks inform local networks?

Figure: Empirical example of the association between the number of interactions in realized local food webs and the number of interactions in the corresponding species subnetworks of regional networks. We should expect the interaction to be linear below the 1:1 line.

Papers: there might be something in these McLeod *et al.* (2020); McLeod *et al.* (2021); Wood *et al.* (2015)

3.2. Taxonomic scale How do interaction probabilities scale taxonomically?

- There are different biological interpretations of probabilities in food webs at the individual level and at higher taxonomic levels.
- How does the scaling up of the nodes from an individual to population to any higher taxonomic group change our interpretation of interaction probabilities? How does the aggregation change our interpretation?
- How is it similar and different to spatial and temporal scaling? Basically, all kinds of scaling are just different ways to aggregate individuals or nodes.

Figure: Conceptual figure of how a scale up of the nodes from an individual to a population to any higher taxonomic group change our interpretation of the probability of interaction.

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Concluding remarks

Here we present some advice moving forward.

- What can we learn from other systems/fields (e.g., social networks, probabilistic graph theory)?
- What even are probabilities? What is the probability that we will ever know the answer to that?
- Be careful of how we define probabilities. Be sure to be explicit about these things. Be sure to specify the type of interaction, the spatial, temporal, and taxonomic scale when presenting new data on interaction probabilities. We need better metadata documentation.
- Be careful to use and manipulate interaction probabilities properly depending on how they were defined and obtained. Different interpretations imply different scaling, and thus different ways to manipulate these numbers.
- Maybe mention thinking about a workflow to predict probabilistic local food webs from probabilistic metawebs.

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