

# The missing link: discerning true from false negatives when sampling species interaction networks

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## Abstract

Ecosystems are composed of networks of interacting species. These interactions allow communities of species to persist through time through both neutral and adaptive processes. Despite their importance, a robust understanding of (and ability to predict and forecast) interactions among species remains elusive. This knowledge-gap is largely driven by a shortfall of data—although species occurrence data has rapidly increased in the last decade, species interaction data has not kept pace, largely due to the effort required to sample interactions. This means there are many interactions between species that occur in nature, but we do not know these interactions occur because we have never observed them. These so-called *false-negatives* bias data and hinder inference about the structure and dynamics of interaction networks. Here, we show the realized number of false-negatives in data can be quite high, even in thoroughly sampled systems, due to variation in abundances in a community. We provide a naive model of occurrence detection to estimate the false-negative rate in a given dataset. We also show how to directly incorporate uncertainty due to observation error into model-based predictions of interactions between species. One hypothesis is interactions between “rare” species are themselves rare because these species are less likely to encounter one-another than species of higher relative abundance, and this can (in part) explain the common pattern of nestedness in bipartite interaction networks. We demonstrate that across several datasets of spatial/temporally replicated networks, there are positive associations between species co-occurrence and interactions, and we show how this is evidence of “neutrally forbidden links” between rare species. Finally, we assess how false negatives influence various models of network prediction, and recommend directly accounting for observation error in predictive models. We conclude by discussing how the understanding of false-negatives can inform how we design monitoring schemes for species interaction surveys.

## 1. Introduction

When you measure, include the measurer.  
—MC Hammer

Species interactions drive many processes in evolution and ecology. A better understanding of species interactions is an imperative to understand the evolution of life on Earth, to mitigate the impacts of anthropogenic change on biodiversity (Makiola et al. 2020), and for predicting zoonotic spillover of disease to prevent future pandemics (Becker et al. 2022). At the moment we lack sufficient data to meet these challenges (Poisot et al. 2021), largely because species interactions are hard to sample (Jordano 2016a; Jordano 2016b). Over the past few decades biodiversity data has become increasingly available through remotely collected data and adoption of open data practices (Kenall et al. 2014; Stephenson 2020). Still, interaction data remains relatively scarce because sampling typically requires direct human observation. This induces a constraint on the amount, spatial scale, and temporal frequency of resulting data that it is feasible to collect by humans. Many

crowdsourced methods for biodiversity data aggregation (e.g. GBIF, eBird) rely on automated identification of species, which does not easily generalize to interaction sampling. There is interest in using remote methods for interaction sampling, which primarily detect co-occurrence and derive properties like species avoidance from this data (Niedballa et al. 2019). However, co-occurrence itself is not necessarily indicative of an interaction (Blanchet et al. 2020). This is an example of semantic confusion around the word *interaction*—for example one might consider competition a type of species interaction, even though it is marked by a lack of co-occurrence between species, unlike other types of interactions, like predation or parasitism, which require both species to be together at the same place and time. Here we consider interaction in the latter sense, where two species can only interact if (and only if) they are in the sample place at the same time. In addition, here we only consider direct (not higher-order) interactions.

We cannot feasibly observe all (or even most) of the interactions that occur in an ecosystem. This means we can be confident two species actually interact if we have a record of it (assuming they are correctly identified), but not at all confident that a pair of species *do not* interact if we have *no record* of those species observed together. In other words, it is difficult to distinguish *true-negatives* (two species never interact) from *false-negatives* (two species interact sometimes, but we do not have a record of this interaction). For a concrete example of a false-negative in a food web, see Figure 1. Because even the most highly sampled systems will still contain false-negatives, there is increasing interest in combining species-level data (e.g. traits, abundance, range, phylogenetic relatedness, etc.) to build models to predict interactions between species we haven't observed together before (Strydom et al. 2021). However, false-negatives could impact the efficacy of our predictive models and have practical consequences for answering questions about interactions (de Aguiar et al. 2019). This constraint is amplified as the interaction data we have is geographically biased toward the usual suspects (Poisot et al. 2021). We therefore need a statistical approach to assess these biases in the observation process and their consequences for our understanding of interaction networks.

The importance of *sampling effort* and its impact on resulting ecological data has produced a rich body of literature. The recorded number of species in a dataset or sample depends on the total number of observations (Walther et al. 1995; Willott 2001), as do estimates of population abundance (Griffiths 1998). This relationship between sampling effort, spatial coverage, and species detectability has motivated more quantitatively robust approaches to account for error in sampling data in many contexts: to determine if a given species is extinct (Boakes et al. 2015), to determine sampling design (Moore and McCarthy 2016), and to measure species richness across large scales (Carlson et al. 2020). In the context of interactions, an initial concern was the compounding effects of limited sampling effort combined with the amalgamation of data (across both study sites, time of year, and taxonomic scales) would lead any empirical set of observations to inadequately reflect the reality of how species interact (Paine 1988) or the structure of the network as a whole (Martinez et al. 1999; McLeod et al. 2021). Martinez et al. (1999) showed that in a plant-endophyte trophic network, network connectance is robust to sampling effort, but this was done in the context of a system for which observation of 62,000 total interactions derived from 164,000 plant-stems was feasible. In some systems (e.g. megafauna food-webs) this many observations is either impractical or infeasible due to the absolute abundance of the species in question.

The intrinsic properties of ecological communities create several challenges for sampling: first, species are not observed with equal probability—we are much more likely to observe a species of high abundance than one of very low abundance (Poisot et al. 2015). Canard et al. (2012) presents a null model of food-web structure where species encounter one-another in proportion to each species' relative-abundance. This assumes that there are no associations in species co-occurrence due to an interaction (perhaps because this interaction is “important” for both species; Cazelles et al.

(2016)). Second, observed co-occurrence is often equated with meaningful interaction strength, but this is not necessarily the case (Blanchet et al. 2020) —a true non-interaction would require that neither of two species, regardless of whether they co-occur, ever exhibit any meaningful effect on the fitness of the other. So, although co-occurrence is not directly indicative of the type of interactions we discuss here, it is a precondition for these types of interactions.

Here, we illustrate how our confidence that a pair of species never interacts highly depends on sampling effort. We demonstrate how the realized false-negative-rate of interactions is related to the relative abundance of the species pool, and introduce a method to produce an estimate of the false-negative-rate given total sampling effort (the total count of all interactions seen among all species-pairs) and a method for including uncertainty into model predictions of interaction probabilities to account for observation error. We then confront these models with data, by showing that positive associations in co-occurrence data are rampant in network datasets, which suggests interactions between rare species are “neutrally forbidden links” (Canard et al. 2012). We conclude by recommending that the simulation of sampling effort and species occurrence can and should be used to help design surveys of species interaction diversity (Moore and McCarthy 2016), and by advocating use of models like those presented here as a tool for both guiding design of surveys of species interactions and for including detection error into predictive models.

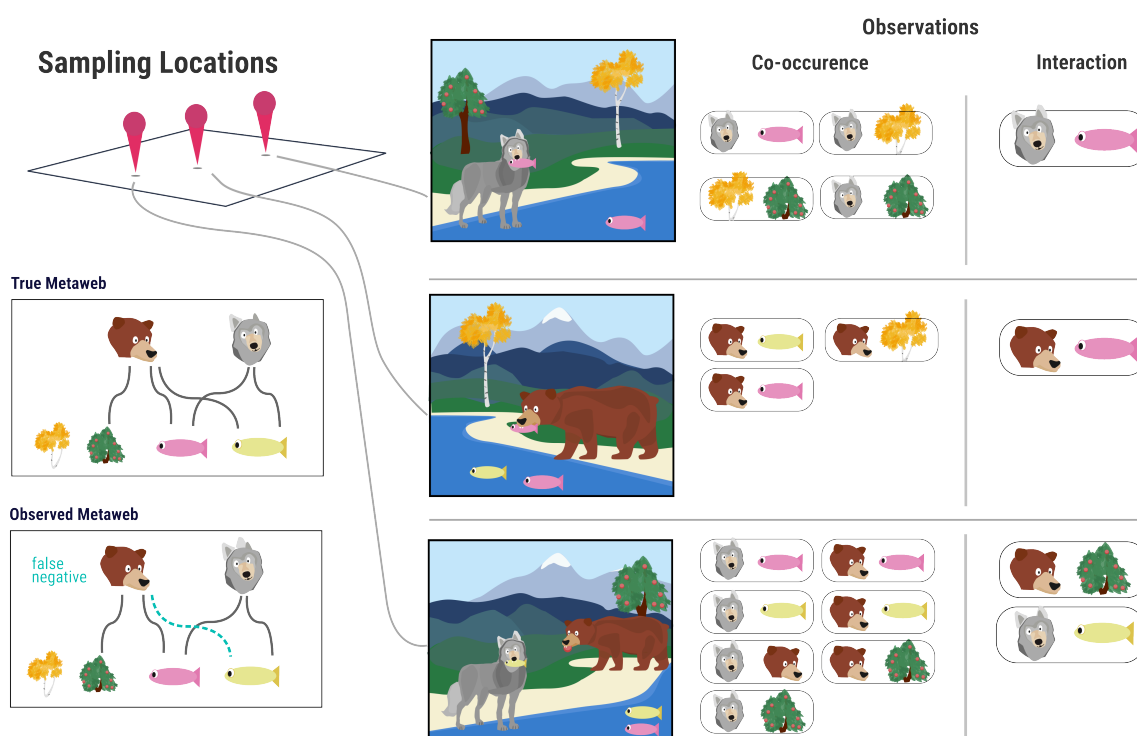


Figure 1: This conceptual example considers a sample of the trophic community of bears, wolves, salmon (pink fish), pike (yellow fish), berry trees, and aspen trees. The true metaweb (all realized interactions across the entire spatial extent) is shown on the left. In the center is what a hypothetical ecologist samples at each site. Notice that although bears are observed co-occurring with both salmon and pike, there was never a direct observation of bears eating pike, even though they actually do interact. Therefore, this interaction between bears and pike is a *false-negative*.

## 2. Accounting for false-negatives in species interactions

In this section, we demonstrate how differences in species' relative-abundance can lead to many false-negatives in interaction data. We also introduce a method for producing an estimate of the false-negative-rate in datasets via simulation. Because the true false-negative-rate is latent, we can never actually be sure how many false-negatives are in our data. However, here we outline an approach to deal with this fact—first by using simulation to estimate the false-negative-rate for a dataset of a fixed size using neutral models of observation. We then illustrate how to incorporate uncertainty directly into predictions of species interactions to account for observation error based on null estimates of both the false-positive rate (as an *a priori* estimate of species misidentification probability) and false-negative rate (as generated via the method we introduce).

### 2.1. How many observations of a non-interaction do we need to be confident it's a true negative?

We start with a naive model of interaction detection: we assume that every interacting pair of species is incorrectly observed as not-interacting with an independent and fixed probability, which we denote  $p_{fn}$  and subsequently refer to as the False-Negative-Rate (FNR). If we observe the same species not-interacting  $N$  times, then the probability of a true-negative (denoted  $p_{tn}$ ) is given by  $p_{tn} = 1 - (p_{fn})^N$ . This relation (the cumulative-distribution-function of geometric distribution, a special case of the negative-binomial distribution) is shown in Figure 2(a) for varying values of  $p_{fn}$  and illustrates the confidence with which we can say an interaction never occurs —  $p_{tn}$  — is highly dependent on the number of times  $N$  we have observed a given pair of species co-occurring. In addition, note that there is no non-zero  $p_{fn}$  for which we can ever *prove* that an interaction does not exist — no matter how many observations of co-occurrence without interaction we have,  $p_{tn} < 1$ .

From Figure 2(a) it is clear that the more often we see two species co-occurring, but *not interacting*, the more likely the interaction is a true-negative. This has several practical consequences: first it means negatives taken outside the overlap of the range of each species aren't informative because co-occurrence was not possible, and therefore neither was an interaction. In the next section we demonstrate that the distribution of abundance in ecosystems can lead to very high realized values of FNR ( $p_{fn}$ ) simply as an artifact of sampling effort. Second, we can use this relation to compute the expected number of total observations needed to obtain a “goal” number of observations of a particular pair of species (Figure 2). As an example, if we hypothesize that species  $A$  and  $B$  do not interact, and we want to see species  $A$  and  $B$  both co-occurring and *not interacting* 10 times to be confident this is a true negative, then we need an expected 1000 observations of co-occurrence among all species if the relative abundances of  $A$  and  $B$  are both 0.1.

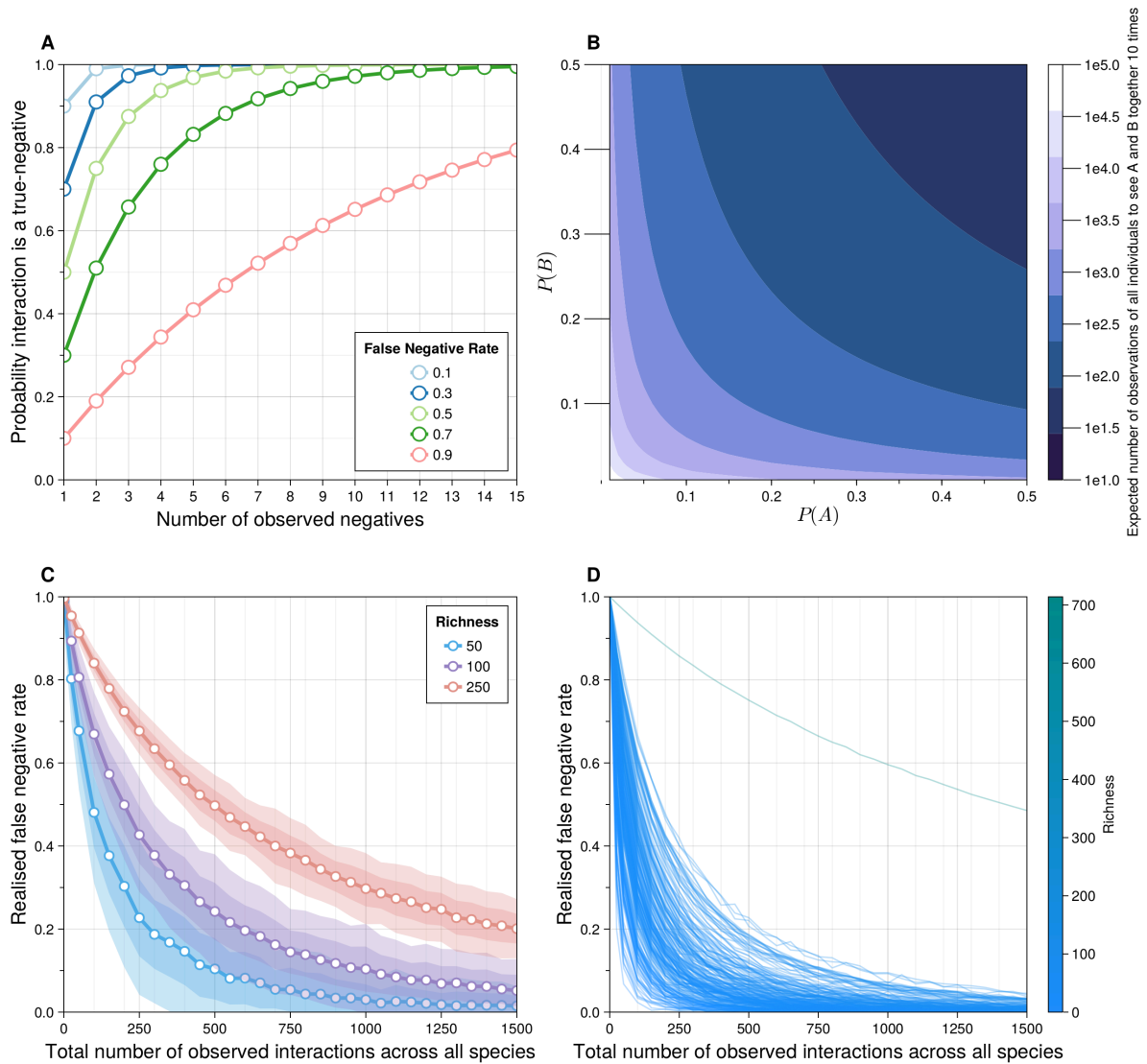


Figure 2: **(a)** The probability that an observed interaction is a true negative (y-axis) given how many times it has been sampled as a non-interaction (x-axis). Each color reflects a different value of  $p_{fn}$ , the false-negative-rate (FNR)—this is effectively the cumulative distribution function (cdf) of the geometric distribution. **(b)** The expected number of total observations needed (colors) to observe 10 co-occurrences between a species with relative abundance  $P(A)$  (x-axis) and a second species with relative abundance  $P(B)$ . **(c)** false-negative-rate (y-axis) as a function of total sampling effort (x-axis) and network size, computed using the method described above. For 500 independent draws from the niche model (Williams and Martinez 2000) at varying levels of species richness (colors) with connectance drawn according to the flexible-links model (MacDonald et al. 2020) as described in the main text. For each draw from the niche model, 200 sets of 1500 observations are simulated, for which the mean false-negative-rate at each observation-step is computed. Means denoted with points, with 1 in the first shade and 2 in the second. **(d)**: Same as (c), except using empirical food webs from Mangal (Poisot et al. 2016). The outlier on (d) is a 714 species food-web.

## 2.2. False-negatives as a product of relative abundance

We now show that the realized FNR changes drastically with sampling effort due to the intrinsic variation of the abundance of individuals of each species within a community. We do this by simulating the process of observation of species interactions, applied both to 243 empirical food webs from the Mangal database (Poisot et al. 2016; Banville et al. 2021) and random food-webs

generated using the niche model, a simple generative model of food-web structure that accounts for allometric scaling (Williams and Martinez 2000). Our neutral model of observation assumes each observed species is drawn in proportion to each species' abundance at that place and time. The abundance distribution of a community can be reasonably-well described by a log-normal distribution (Preston 1948; Volkov et al. 2003). In addition to the log-normal distribution, we also tested the case where the abundance distribution is derived from power-law scaling  $Z^{\log(T_i)-1}$  where  $T_i$  is the trophic level of species  $i$  and  $Z$  is a scaling coefficient (Savage et al. 2004), which yields the same qualitative behavior. The practical consequence of abundance distributions spanning many orders of magnitude is that observing two rare species interacting requires two low probability events: observing two rare species *at the same time*.

To simulate the process of observation, for an ecological network  $M$  with  $S$  species, we sample relative abundances for each species from a standard-log-normal distribution, and then renormalize to form a distribution. For each true interaction in the adjacency matrix (i.e.  $M_{ij} = 1$ ) we estimate the probability of observing both species  $i$  and  $j$  at a given place and time by simulating  $n$  observations of all individuals of any species, where the species of the individual observed at the  $\{1, 2, \dots, n\}$ -th observation is drawn from the generated categorical distribution of relative abundances. For each pair of species  $(i, j)$ , if both  $i$  and  $j$  are observed within the  $n$ -observations, the interaction is tallied as a true positive if  $M_{ij} = 1$ . If only one of  $i$  or  $j$  are observed—but not both—in these  $n$  observations, and  $M_{ij} = 1$ , this is counted as a false-negative. This process is illustrated conceptually in Figure 3(a).

In Figure 2(c) we see this model of observation applied to niche model networks across varying levels of species richness, and in Figure 2(d) the observation model applied to Mangal food webs. For all niche model simulations in this manuscript, for a given number of species  $S$  the number of interactions is drawn from the flexible-links model fit to Mangal data (MacDonald et al. 2020), meaning the number of interactions  $L$  for a random niche model food-web is sampled as

$$L \sim \text{BetaBinomial}(S^2 - S + 1, \mu\varphi, 1 - \mu\varphi)$$

where the maximum *a posteriori* (MAP) estimate of  $(\mu, \varphi)$  applied to Mangal data from MacDonald et al. (2020) is  $(\mu = 0.086, \varphi = 24.3)$ . All simulations were done with 500 independent replicates of unique niche model networks per unique number of total interactions observed  $n$ . All analyses presented here are done in Julia v1.8 (Bezanson et al. 2015) using both EcologicalNetworks.jl v0.5 and Mangal.jl v0.4 (Banville et al. 2021) and are hosted on Github. Note that the empirical food web data, for the reasons described above, very likely already contains many false-negatives — we'll revisit this issue in the final section.

From Figure 2(c) it is evident that the number of species considered in a study is inseparable from the false-negative-rate in that study, and this effect should be taken into account when designing samples of ecological networks in the future. We see a similar qualitative pattern in empirical networks Figure 2(d) where the FNR drops off quickly as a function of observation effort, mediated by total richness. The practical consequence of the bottom row of Figure 2 when conducting an analysis is whether there are enough total number of observed interactions (the x-axis) for the threshold FNR we deem acceptable (the y-axis) is feasible. This raises two points: first, empirical data on interactions are subject to the practical limitations of funding and human-work hours, and therefore existing data tend to fall on the order of hundreds or thousands observations of individuals per site. Clear aggregation of data on sampling effort has proven difficult to find and a meta-analysis of network data and sampling effort seems both pertinent and necessary, in addition to the effects of aggregation of interactions across taxonomic scales (Gauzens et al. 2013; Giacomuzzo and Jordán 2021). This inherent limitation on in-situ sampling means we should optimize where we sample



across space so that for a given number of samples, we obtain the maximum information possible. Second, what is meant by “acceptable” FNR? This raises the question: does a shifting FNR lead to rapid transitions in our ability inference and predictions about the structure and dynamics of networks, or does it produce a roughly linear decay in model efficacy? We explore this in the final section.

We conclude this section by advocating for the use of neutral models similar to above to generate expectations about the number of false-negatives in a dataset of a given size. This could prove fruitful both for designing surveys of interactions but also because we may want to incorporate models of imperfect detection error into predictive interactions models, as Joseph (2020) does for species occupancy modeling. Additionally, we emphasize that one must consider the context for sampling—is the goal to detect a particular species (as in Figure 2(c), or to get a representative sample of interactions across the species pool? These arguments are well-considered when sampling individual species (Willott 2001), but have not yet been adopted for designing samples of communities.

### 2.3. Including observation error in interaction predictions

Here we show how to incorporate uncertainty into model predictions of interaction probability to account for imperfect observation (both false-negatives and false-positives). Models for interaction prediction typically yield a probability of interaction between each pair of species,  $p_{ij}$ . When these are considered with uncertainty, it is usually bootstrap-uncertainty, i.e. the variance in the interaction probability prediction across several cross-validation folds, where the data is split into training and test sets several times. In contrast, the method we introduce adjusts the value of a model’s predictions to produce a distribution of interaction probabilities corrected by a given false-negative-rate  $p_{fn}$  and false-positive-rate  $p_{fp}$  (outlined in figure Figure 3). First we describe how to sample from this distribution of adjusted interaction probabilities via simulation, and show that this distribution can be well-approximated analytically.

To get an estimate of each interaction probability that accounts for observation error, we resample the output prediction from an arbitrary model for each interaction  $p_{ij}$  by simulating a set of several *particles*. Each particle is a realization of an interaction being *realized* assuming  $p_{ij}$  is a correct estimate of the probability of an interaction being *feasible*. Each particle starts by being drawn as either true or false according to  $p_{ij}$ , and then adjusting the *observed* state of the particle by the rate of observation error  $p_{fp}$  and  $p_{fn}$  to yield a single boolean outcome for each particle (*Resampling* within Figure 3(b)). Across of many particles, the resulting frequency of *true* outcomes is a single resample of the probability  $p_{ij}^*$  that the interaction is *feasible*, not just that it was *observed*. Across several samples each of several particles, this forms a distribution of probabilities which are adjusted by the true and false-negative-rates.

There is also an analytic way to approximate this distribution using the Normal approximation to Binomial distribution. As a reminder, as the total number of samples  $N$  from a binomial distribution for  $n$  trials with success probability  $p$  approaches infinity, the sum of total successes across all samples approaches a normal distribution with mean  $np$  and variance  $np(1 - p)$ . Here we denote a Normal distribution with mean  $\mu$  and standard-deviation  $\sigma$  as  $\mathcal{N}(\mu, \sigma)$ . We can use this to correct the estimate  $p_{ij}$  based on the false-negative-rate  $p_{fn}$  and false-positive rate  $p_{fp}$  to obtain the limiting distribution as the number of resamples approaches infinity for the resampled  $p_{ij}^*$  for a given number of particles  $n_p$ . We do this by first adjusting for the rates of observation error to get the mean resampled probability,  $\mathbb{E}[p_{ij}^*]$ , as

$$\mathbb{E}[p_{ij}^*] = p_{ij}(1 - p_{fp}) + (1 - p_{ij})p_{fn}$$

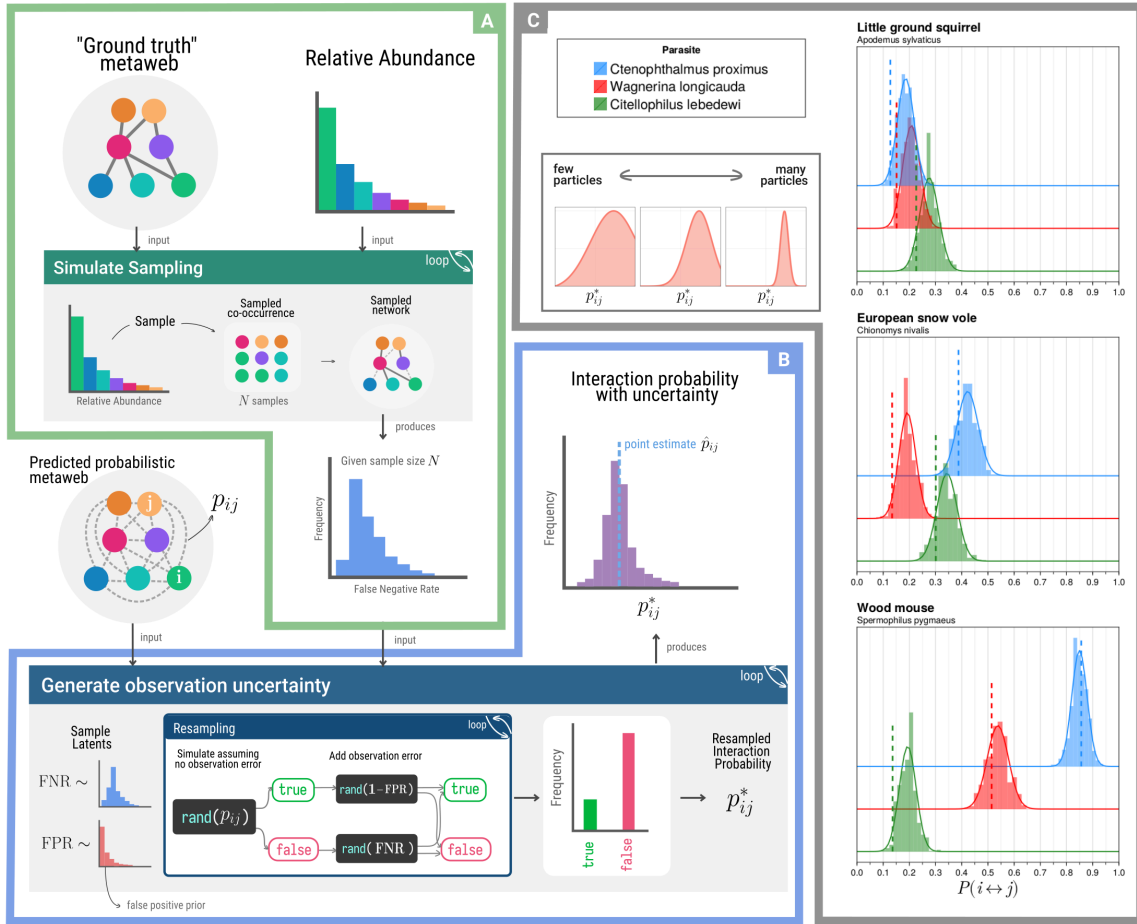


Figure 3: **(a)** The process for estimating the false-negative-rate (FNR) for an interaction dataset consisting of  $N$  total observed interactions. **(b)** The method for resampling interaction probability based on estimates of false-negative and false-positive rates. **(c)** The method for interaction probability resampling applied to three mammals and three parasites from the [Hadfield et al. \(2014\)](#) dataset. The original probability  $p_{ij}$  is indicated with a vertical dashed line. The histogram is simulated from the resampling process, and the line indicates the gaussian approximation to this distribution. Both resampling simulations and the gaussian approximation is applied with  $n_p = 150$

This yields the Normal approximation

$$\sum_{i=1}^{n_p} p_{ij}^* \sim \mathcal{N}\left(n_p \cdot \mathbb{E}[p_{ij}^*], \sqrt{n_p \mathbb{E}[p_{ij}^*] (1 - \mathbb{E}[p_{ij}^*])}\right)$$

which then can be converted back to a distribution of frequency of successes to yield the final approximation

$$p_{ij}^* \sim \mathcal{N}\left(\mathbb{E}[p_{ij}^*], \sqrt{\frac{\mathbb{E}[p_{ij}^*] (1 - \mathbb{E}[p_{ij}^*])}{n_p}}\right)$$

We can then further truncate this distribution to remain on the interval  $(0, 1)$ , as the output is a probability, although in practice often the probability mass outside  $(0, 1)$  is extremely low except for  $p_{ij}$  values very close to 0 or 1. As an example case study, we use a boosted-regression-tree to predict



interactions in a host-parasite network (Hadfield et al. 2014) (with features derived in the same manner as Strydom et al. (2021)) to produce a set of interaction predictions. We then applied this method to a set of a few resampled interaction probabilities between mammals and parasite species shown in Figure 3(c).

Why is this useful? For one, this analytic method avoids the extra computation required by simulating samples from this distribution directly. Further, it enables a natural analogue between  $n_p$  (the number of particles) and the number of observations of co-occurrence for a given pair of species—the fewer the particles, the higher the variance of the resulting approximation.

The normal approximation is undefined for 0 particles (i.e. 0 observations co-occurrence), although as  $n_p$  approaches 0 in the limit, the approximated normal (once truncated) approaches the uniform distribution on the interval  $(0, 1)$ , the maximum entropy distribution where we have no information about the possibility of an interaction.

This also has implications for what we mean by *uncertainty* in interaction predictions. A model's prediction can be uncertain in two different ways: (1) the model's predictions may have high variance across bootstrap iterations, or (2) the model's predictions may be centered around a probability of interaction of 0.5, where we are the most unsure about whether this interaction exists. Improving the incorporation of different forms of uncertainty in probabilistic interaction predictions seems a necessary next step toward understanding what pairs of species we know the least about, in order to prioritize sampling to provide the most new information possible.

### 3. Positive associations in co-occurrence decrease the false-negative-rate

The model above doesn't consider the possibility that there are positive or negative associations which shift the probability of species co-occurrence away from what is expected based on their relative abundances due to their interaction (Cazelles et al. 2016). If we denote the probability that we observe the co-occurrence of two species  $A$  and  $B$  as  $P(AB)$  and if there is no association between the marginal probabilities of observing  $A$  and observing  $B$  denoted  $P(A)$  and  $P(B)$  respectively, then the probability of observing their co-occurrence is the product of the marginal probabilities for each species,  $P(AB) = P(A)P(B)$ . In the other case where there is some positive strength of association between observing both  $A$  and  $B$  because this interaction is "important" for each species, then the probability of observation both  $A$  and  $B$ ,  $P(AB)$ , is greater than  $P(A)P(B)$  as  $P(A)$  and  $P(B)$  are not independent and instead are positively correlated, i.e.  $P(AB) > P(A)P(B)$ . In this case, the probability of observing a single false-negative in our naive model from Figure 2(a) is  $p_{fn} = 1 - P(AB)$ , which due to the above inequality implies  $p_{fn} < 1 - P(A)P(B)$ . This indicates an decreasing probability of a false negative as the strength of association gets stronger, e.g. if  $P(AB) \gg P(A)P(B)$ . Still, this does not consider variation in species abundance in space and time (Poisot et al. 2015). If positive or negative associations between species structure variation in the distribution of  $P(AB)$  across space/time, then the spatial biases induced by data collection would further impact the realized false-negative-rate, as the false negative rate would not be constant for each pair of species across sites.

To test for these positive associations in data we scoured Mangal for datasets with many spatial or temporal replicates of the same system, which led to the resulting seven datasets set in figure Figure 4. For each dataset, we compute the marginal probability  $P(A)$  of occurrence of each species  $A$  across all networks in the dataset. For each species pair observed interacting,  $A$  and  $B$ , we then compute and compare the probability of co-occurrence if each species occurs independently,  $P(A)P(B)$ , to the empirical probability of co-occurrence,  $P(AB)$ . Following our analysis above, if

$P(AB)$  is greater than  $P(A)P(B)$ , then we expect our neutral estimates of the FNR above to overestimate the realized FNR. In Figure 4, we see the difference between  $P(AB)$  and  $P(A)P(B)$  for the seven suitable datasets with enough spatiotemporal replicates and a shared taxonomic backbone (meaning all individual networks use common species identifiers) found on Mangal to perform this analysis.

In each of these datasets, the joint probability of co-occurrence  $P(AB)$  is decisively greater than our expectation if species co-occur in proportion to their relative abundance  $P(A)P(B)$ . This is one potential cause of the widely observed property of nestedness seen in bipartite networks (Bascompte and Jordano 2007) – that interactions between rare species are *neutrally forbidden links* (Canard et al. 2012).

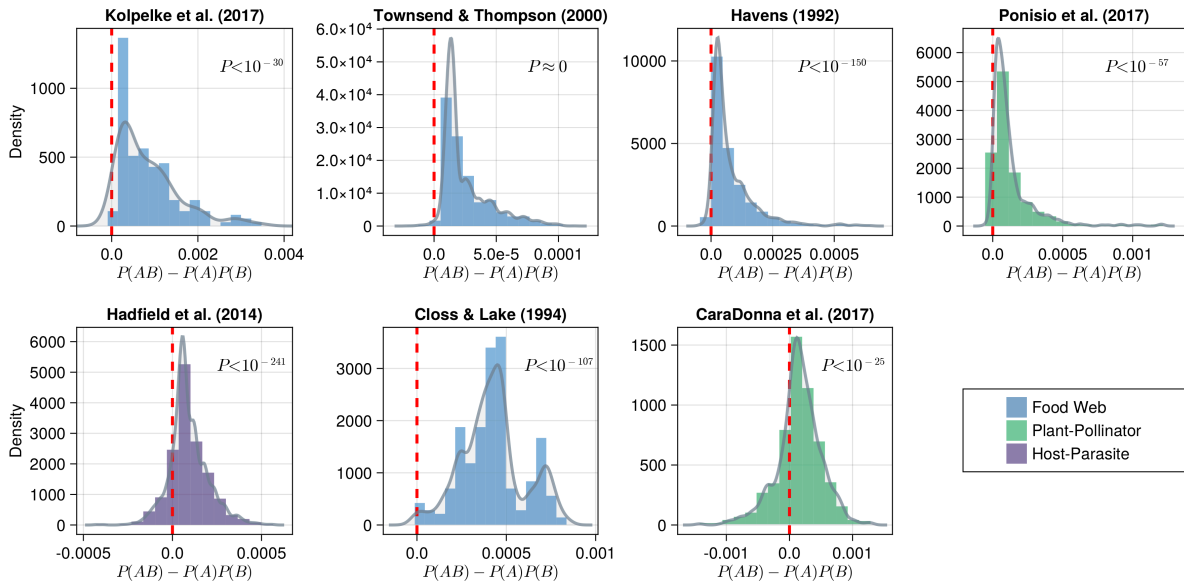


Figure 4: The difference between joint-probability of co-occurrence  $P(AB)$  and expected probability of co-occurrence under independence ( $P(A)P(B)$ ) for interacting species for each dataset. The red-dashed line indicates 0 (no association). Each histogram represents a density, meaning the area of the entire curve sums to 1. The continuous density estimate (computed using local smoothing) is shown in grey. The p-value on each plot is the result of a one-sided t-test comparing the mean of each distribution to 0.

#### 4. The impact of false-negatives on network properties and prediction

Here, we assess the effect of false-negatives on our ability to make predictions about interactions, as well as their effect on network structure. The prevalence of false-negatives in data is the catalyst for interaction prediction in the first place, and as a result methods have been proposed to counteract this bias (Stock et al. 2017; Poisot et al. 2022). However, it is feasible that the FNR in a given dataset is so high that it could induce too much noise for an interaction prediction model to detect the signal of possible interaction between species.

To test this we use the dataset from Hadfield et al. (2014) that describes host-parasite interaction networks sampled across 51 sites, and the same method as Strydom et al. (2021) to extract latent features for each species in this dataset based on applying PCA to the co-occurrence matrix. We then predict a metaweb (equivalent to predicting true or false for an interaction between each species pair, effectively a binary classification problem) from these species-level features using four

candidate models for binary classification—three often used machine-learning (ML) methods (Boosted Regression Tree (BRT), Random Forest (RF), Decision Tree (DT)), and one simpler model from classic statistics (Logistic Regression (LR)). Each of the ML models are bootstrap aggregated (or bagged) with 100 replicates each. We partition the data into 80-20 training-test splits, and then seed the training data with false negatives at varying rates, but crucially do *nothing* to the test data. We fit all of these models using MLJ.jl, a high-level Julia framework for a wide-variety of ML models (Blaom et al. 2020). We evaluate the efficacy of these models using two common measures of binary classifier performance: the area under the receiver-operator curve (ROC-AUC) and the area under the precision-recall curve (PR-AUC), for more details see Poisot (2022). Here, PR-AUC is slightly more relevant as it is a better indicator of prediction of false-negatives. The results of these simulations are shown in Figure 5(a & b).

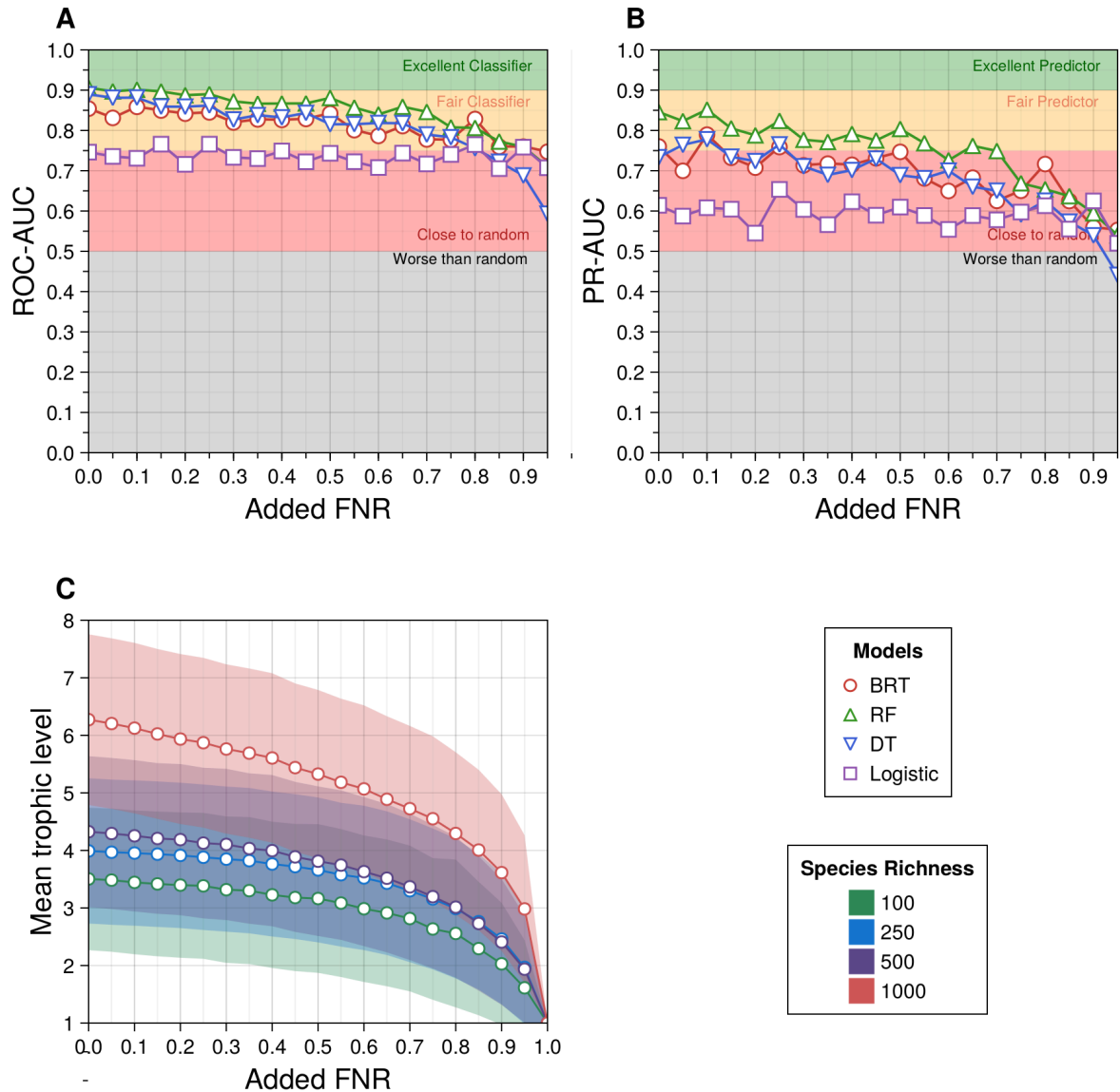


Figure 5: **(a)** The area-under the receiver-operator curve (ROC-AUC) and **(b)** The area-under the precision-recall curve (PR-AUC; right) for each different predictive model (colors/shapes) across a spectrum of the proportion of added false-negatives (x-axis). **(c)** The mean trophic-level of all species in a network generated with the niche model across different species richnesses (colors). For each value of the FNR, the mean trophic level was computed across 50 replicates. The shaded region for each line is one standard-deviation across those replicates.

One interesting result seen in Figure 5(a & b) is that the ROC-AUC value does not approach random in the same way the PR-AUC curve does as we increase the added FNR. The reason for this is that ROC-AUC is fundamentally not as useful a metric in assessing predictive capacity as PR-AUC. As we keep adding more false-negatives, the network eventually becomes a zeros matrix, and these models can still learn to predict *non-interaction* for all possible species pairs, which scores far better ROC-AUC values than random guessing (ROC-AUC = 0.5). This highlights a more broad issue of label class imbalance, meaning there are far more non-interactions than interactions in data. A full treatment of the importance of class-balance is outside the scope of this paper, but is explored in-depth in Poisot (2022). Further we see, if anything, gradual decline in the performance of the model until we reach very high FNR levels (i.e.  $p_{fn} > 0.7$ ). This is consistent with other recent work (Gupta

et al. 2023), although it must be considered that the empirical data on which these models are trained already are almost certain to already contain false-negatives.

Although these ML models are surprisingly performant at link prediction given their simplicity, there have been several major developments in applying deep-learning methods to many tasks in network inference and prediction—namely graph-representation learning (Zhang et al. 2019; Khoshraftar and An 2022) At this time, these advances can not yet be applied to ecological networks because they typically require far more network data than we currently have perform better than simpler models. We already have lots of features that could be used as inputs into these models (i.e. species level data about occurrence, genomes, abundance, etc.), but our network datasets barely get into the hundreds of local networks sampled across space and time. As the number of locally sampled networks grows, these models will become more useful, but this scaling up of network data can only be done with systematic monitoring of interactions.

We also consider how the FNR affects network properties. In Figure 5(c) we see the mean trophic level across networks simulated using the niche model (as above), across a spectrum of FNR values. In addition to the clear dependence on richness, we see that mean trophic level, despite varying widely between niche model simulations, tends to be relatively robust to false-negatives and does not deviate widely from the true value until very large FNRs. This is not entirely unsurprising. Removing links randomly from a food-web is effectively the inverse problem of the emergence of a giant component (more than half of the nodes are in a connected network) in random graphs (Li et al. 2021) for a thorough review). The primary difference being that we are removing edges, not adding them, and thus we are witnessing the dissolution of a giant component, rather than the emergence of one. Further applications of percolation theory to the topology of sampled ecological networks could improve our understanding of how false-negatives impact the inferences about the structure and dynamics on these networks.

## 5. Discussion

Species interactions enable the persistence and functioning of ecosystems, but our understanding of interactions is limited due to the intrinsic difficulty of sampling them. Here we have provided a naive model for the expected number of false-negatives in an interaction dataset. We demonstrated that we expect many false-negatives in species interaction datasets purely due to the intrinsic variation of abundances within a community. We also, for the first time to our knowledge, measured the strength of association between co-occurrence and interactions (Cazelles et al. 2016) across many empirical systems, and found that these positive associations are both very common. We have also demonstrated how the false-negative-rate decreases as the covariance between co-occurrence and interaction increases, and that this provides evidence in support of “neutrally-forbidden links” (Canard et al. 2012) in networks. We have also shown that false-negatives could further impact our ability to both predict interactions and infer properties of the networks, which highlights the need for further research into methods for correcting this bias in existing data.

A better understanding of how false-negatives impact species interaction data is a practical necessity—both for inference of network structure and dynamics, but also for prediction of interactions by using species level information. False-negatives could pose a problem for many forms of inference in network ecology. For example, inferring the dynamic stability of a network could be prone to error if the observed network is not sampled “enough”. What exactly “enough” means is then specific to the application, and should be assessed via methods like those here when designing samples. Further, predictions about network rewiring (Thompson and Gonzalez 2017) due to range shifts in response to climate change could be error-prone without accounting for interactions that have not been observed but that still may become climatically infeasible. As is evident from Figure 2(a), we can

never guarantee there are no false-negatives in data. In recent years, there has been interest toward explicitly accounting for false-negatives in models (Stock et al. 2017; Young et al. 2021), and a predictive approach to networks—rather than expecting our samples to fully capture all interactions (Strydom et al. 2021). As a result, better models for predicting interactions are needed for interaction networks. This includes explicitly accounting for observation error (Johnson and Larremore 2021) — certain classes of models have been used to reflect hidden states which account for detection error in occupancy modeling (Joseph 2020), and could be integrated in the predictive models of interactions in the future.

Future work on improving this family of models could include directly accounting for the rate of interactions between species by modeling each interaction as its own stochastic process. Further, this approach could be used to directly account for spatial and temporal variance in species occurrence, which is a property of interactions that we have not focused on in our naive model of network sampling. This could enable further extension on the particle filter method developed earlier to associate uncertainty with interaction predictions, as these methods were initially developed for observations where there is structure in the sequence of observations. A natural extension would be accounting this method to account for phenology differences between species.

This work has several practical consequences for the design of surveys for species' interactions. Simulating the process of observation could be a powerful tool for estimating the sampling effort required by a study that takes relative abundance into account, and provides a baseline for expected FNR. It is necessary to take the size of the species pool into account when deciding how many total samples is sufficient for an “acceptable” FNR (Figure 2(c & d)). Further the spatial and temporal turnover of interactions means any approach to sampling prioritization must be spatiotemporal. We demonstrated earlier that observed negatives outside of the range of both species aren't informative, and therefore using species distribution models could aid in this spatial prioritization of sampling sites.

We also should address the impact of false-negatives on the inference of process and causality in community ecology. We demonstrated that in model food webs, false-negatives do not impact the measure of total trophic levels until very high FNR (Figure 5(c)), although we cannot generalize this further to other properties. This has immediate practical concern for how we design what taxa to sample—does it matter if the sampled network is fully connected? It has been shown that the stability of subnetworks can be used to infer the stability of the metaweb beyond a threshold of samples (Song et al. 2022). But does this extend to other network properties? And how can we be sure we are at the threshold at which we can be confident our sample characterizes the whole system? We suggest that modeling observation error as we have done here can address these questions and aid in the design of samples of species interactions. To try to survey to avoid all false-negatives is a fool's errand. Species ranges overlap to form mosaics, which themselves are often changing in time. Communities and networks don't end in space, and the interactions that connect species on the *periphery* of a given network to species outside the spatial extent of a given sample will inevitably appear as false-negatives in practical samples. The goal should instead be to sample a system enough to have a statistically robust estimate of the current state and empirical change over time of an ecological community at a given spatial extent and temporal resolution, and to determine what the sampling effort required should be prior to sampling.

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