

# 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 intrinsic difficulty and effort required to sample interactions. This means there are many interactions between species that occur in nature, but we do not think this interaction occurs because we have no record of it. These so-called “false-negatives” bias data and hinder inference about the structure and dynamics of interaction networks. Here, we demonstrate the realized rate of false-negatives in data can be quite high, even in thoroughly sampled systems, due to the intrinsic variation in abundances across species in a community. We illustrate how a null model of occurrence detection can be used 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 interaction probabilities between species. One hypothesis is that interactions between “rare” species are themselves rare because these species are less likely to encounter one-another than species of higher relative abundance, and that this can (in part) explain the common pattern of nestedness in bipartite interaction networks. However, we demonstrate that across several datasets of spatial or temporally replicated networks, there are positive associations between species co-occurrence and interactions, which suggests these interactions among “rare” species actually exist but simply are not observed. 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 interactions.

# 1 Introduction

2 Species interactions drive many processes in evolution and ecology. A better understanding of species  
3 interactions is an imperative to understand the evolution of life on Earth, to mitigate the impacts of  
4 anthropogenic change on biodiversity (Makiola *et al.* 2020), and for predicting zoonotic spillover of  
5 disease to prevent future pandemics (Becker *et al.* 2021). At the moment we lack sufficient data to meet  
6 these challenges (Poisot *et al.* 2021), largely because species interactions are hard to sample (Jordano  
7 2016). Over the past few decades biodiversity data has become increasingly available through remotely  
8 collected data and adoption of open data practices (Kenall *et al.* 2014; Stephenson 2020). Still, interaction  
9 data remains relatively scarce because sampling typically requires human observation. This induces a  
10 constraint on the amount, spatial scale, and temporal frequency of resulting data that it is feasible to  
11 collect by humans. Many crowdsourced methods for biodiversity data aggregation (e.g. GBIF, eBird) still  
12 rely on automated identification of species, which does not easily generalize to interaction sampling.  
13 There is interest in using remote methods for interaction sampling, which primarily detect co-occurrence  
14 and derive properties like species avoidance from this data (Niedballa *et al.* 2019). However, co-occurrence  
15 itself is not necessarily indicative of an interaction (Blanchet *et al.* 2020). This is an example of semantic  
16 confusion around the word “interaction”—for example one might consider competition a type of species  
17 interaction, even though it is marked by a lack of co-occurrence between species, unlike other types of  
18 interactions, like predation or parasitism, which require both species to be together at the same place and  
19 time. Here we consider interaction in the latter sense, where two species have fitness consequences on  
20 one-another if (and only if) they are in the sample place at the same time. In addition, here we only  
21 consider direct (not higher-order) interactions.

22 We cannot feasibly observe all (or even most) of the interactions that occur in an ecosystem. This means  
23 we can be confident two species actually interact if we have a record of it (assuming they are correctly  
24 identified), but not at all confident that a pair of species *do not* interact if we have *no record* of those  
25 species observed together. In other words, it is difficult to distinguish *true-negatives* (two species never  
26 interact) from *false-negatives* (two species interact sometimes, but we do not have a record of this  
27 interaction). For a concrete example of a false-negative in a food web, see fig. 1. Because even the most  
28 highly sampled systems will still contain false-negatives, there is increasing interest in combining  
29 species-level data (e.g. traits, abundance, range, phylogenetic relatedness, etc.) to build models to predict

30 interactions between species we haven't observed together before (Strydom *et al.* 2021). However, the  
31 noise of false-negatives could impact the efficacy of our predictive models and have practical  
32 consequences for answering questions about interactions (de Aguiar *et al.* 2019). This data constraint is  
33 amplified as the interaction data we have is geographically biased toward the usual suspects (Poisot *et al.*  
34 2021). We therefore need a statistical approach to assessing these biases in the observation process and  
35 their consequences for our understanding of interaction networks.

36 The importance of *sampling effort* and its impact on resulting ecological data has produced a rich body of  
37 literature. The recorded number of species in a dataset or sample depends on the total number of  
38 observations (Walther *et al.* 1995; Willott 2001), as do estimates of population abundance (Griffiths 1998).  
39 This relationship between sampling effort and spatial coverage and species detectability has motivated  
40 more quantitatively robust approaches to account for error in sampling data in many contexts: to  
41 determine if a given species is extinct (Boakes *et al.* 2015), to determine sampling design (Moore &  
42 McCarthy 2016), and to measure species richness across large scales (Carlson *et al.* 2020). In the context of  
43 interactions, an initial concern was the compounding effects of limited sampling effort combined with the  
44 amalgamation of data (across both study sites, time of year, and taxonomic scales) could lead any  
45 empirical set of observations to inadequately reflect the reality of how species interact (Paine 1988) or the  
46 structure of the network as a whole (Martinez *et al.* 1999; McLeod *et al.* 2021). Martinez *et al.* (1999)  
47 showed that in a plant-endophyte trophic network, network connectance is robust to sampling effort, but  
48 this was done in the context of a system for which observation of 62,000 total interactions derived from  
49 164,000 plant-stems was feasible. In some systems (e.g. megafauna food-webs) this many observations is  
50 either impractical or infeasible due to the absolute abundance of the species in question.

51 The intrinsic properties of ecological communities create several challenges for sampling: first, species are  
52 not observed with equal probability—we are much more likely to observe a species of high abundance  
53 than one of very low abundance (Poisot *et al.* 2015). Canard *et al.* (2012) presents a null model of food-web  
54 structure where species encounter one-another in proportion to each species' relative-abundance. This  
55 assumes that there are no associations in species co-occurrence due to an interaction (perhaps because  
56 this interaction is “important” for both species; Cazelles *et al.* (2016)), but in this paper we later show  
57 increasing strength of associations leads to increasing probability of false-negatives in interaction data,  
58 and that these positive associations are common in existing network data. Second, observed co-occurrence  
59 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 an interaction, it is a precondition for an interaction.

Here, we illustrate how our confidence that a pair of species never interacts highly depends on sampling effort. We suggest that surveys of species interactions can benefit from simulation modeling of the sampling process. 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 a null 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 show that positive associations in co-occurrence data can increase the realized number of false-negatives, and demonstrate these positive associations are rampant in network datasets, and 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 & McCarthy 2016), and by advocating use of null models like those presented here as a tool for both guiding design of surveys of species interactions and for modeling detection error in predictive models.

[Figure 1 about here.]

## Accounting for false-negatives in species interactions

In this section, we demonstrate how difference in relative-abundance can lead to many false-negatives in interaction data. We also introduce a method for producing a null estimate of the false-negative-rate in datasets via simulation, and a method for incorporating uncertainty directly into predictions of species interactions to account for observation error.

### 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

<sup>86</sup>  $N$  times, then the probability of a true-negative (denoted  $p_{tn}$ ) is given by  $p_{tn} = 1 - (p_{fn})^N$ . This relation  
<sup>87</sup> (the probability-mass-function of geometric distribution, a special case of the negative-binomial  
<sup>88</sup> distribution) is shown in fig. 2(A) for varying values of  $p_{fn}$  and illustrates a fundamental link between our  
<sup>89</sup> ability to reliably say an interaction doesn't exist— $p_{tn}$ —and the number of times  $N$  we have observed a  
<sup>90</sup> given species. In addition, note that there is no non-zero  $p_{fn}$  for which we can ever *prove* that an  
<sup>91</sup> interaction does not exist—no matter how many observations of non-interactions  $N$  we have,  $p_{tn} < 1$ .  
<sup>92</sup> From fig. 2(A) it is clear that the more often we see two species co-occurring, but *not interacting*, the more  
<sup>93</sup> likely the interaction is a true-negative. This has several practical consequences: first it means negatives  
<sup>94</sup> taken outside the overlap of the range of each species aren't informative because co-occurrence was not  
<sup>95</sup> possible, and therefore neither was an interaction. Second, we can use this relation to compute the  
<sup>96</sup> expected number of total observations needed to obtain a “goal” number of observations of a particular  
<sup>97</sup> pair of species (fig. 2(B)). As an example, if we hypothesize that  $A$  and  $B$  do not interact, and we want to see  
<sup>98</sup> species  $A$  and  $B$  both co-occurring and *not interacting* 10 times to be confident this is a true negative, then  
<sup>99</sup> we need an expected 1000 observations of all species if the relative abundances of  $A$  and  $B$  are both 0.1.  
<sup>100</sup> Because the true FNR is latent, we can never actually be sure what the actual number of false-negatives in  
<sup>101</sup> our data—however, we can use simulation to estimate the FNR for datasets of a given size using neutral  
<sup>102</sup> models of observation. If some of the “worst-case” FNRs presented in fig. 2(A) seem unrealistically high,  
<sup>103</sup> considering that species are observed in proportion to their relative abundance. In the next section we  
<sup>104</sup> demonstrate that the distribution of abundance in ecosystems can lead to very high realized values of FNR  
<sup>105</sup> ( $p_{fn}$ ) simply as an artifact of sampling effort.

<sup>106</sup> [Figure 2 about here.]

## <sup>107</sup> **False-negatives as a product of relative abundance**

<sup>108</sup> We now show that the realized FNR changes drastically with sampling effort due to the intrinsic variation  
<sup>109</sup> of the abundance of individuals of each species within a community. We do this by simulating the process  
<sup>110</sup> of observation of species interactions, applied both to 243 empirical food webs from the Mangal database  
<sup>111</sup> (Banville *et al.* 2021) and random food-webs generated using the niche model, a simple generative model  
<sup>112</sup> of food-web structure that accounts for allometric scaling (Williams & Martinez 2000). Our neutral model  
<sup>113</sup> 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 (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 of abundance 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 abundances for each species from a standard-log-normal distribution. For each true interaction in the adjacency matrix  $M$  (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 a species, where the species of the individual observed at the  $\{1, 2, \dots, n\}$ -th observation is drawn from the generated log-normal distribution of 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, but  $M_{ij} = 1$ , this is counted as a false-negative, and a true-negative otherwise. 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, but  $M_{ij} = 1$ , this is counted as a false-negative, and a true-negative otherwise ( $M_{ij} = 0$ ). This process is illustrated conceptually in fig. 3(A).

In fig. 2(C) we see this model of observation applied to niche model networks across varying levels of species richness, and in fig. 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), effectively drawing the number of interactions  $L$  for a random niche model food-web as

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

where the maximum *a posteriori* (MAP) estimate of  $(\mu, \phi)$  applied to Mangal data from (MacDonald *et al.* 2020) is  $(\mu = 0.086, \phi = 24.3)$ . All simulations were done with 500 independent replicates of unique niche model networks per unique number of observations  $n$ . 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

141 are hosted on [Github](#)). Note that the empirical data, for the reasons described above, very likely already  
142 contains many false-negatives, we'll revisit this issue in the final section.

143 From fig. 2(C) it is evident that the number of species considered in a study is inseparable from the  
144 false-negative-rate in that study, and this effect should be taken into account when designing samples of  
145 ecological networks in the future. We see a similar qualitative pattern in fig. 2(D) where the FNR drops off  
146 quickly as a function of observation effort, mediated by total richness. The practical consequence of the  
147 bottom row of fig. 2 is whether the total number of observations of all species (the x-axis) for the threshold  
148 FNR we deem acceptable (the y-axis) is feasible. This raises two points: first, empirical data on  
149 interactions are subject to the practical limitations of funding and human-work hours, and therefore  
150 existing data tend to fall on the order of hundreds or thousands observations of individuals per site. Clear  
151 aggregation of data on sampling effort has proven difficult to find and a meta-analysis of network data and  
152 sampling effort seems both pertinent and necessary, in addition to the effects of aggregation of interactions  
153 across taxonomic scales (Gauzens *et al.* 2013; Giacomuzzo & Jordán 2021). This inherent limitation on  
154 in-situ sampling means we should optimize where we sample across space so that for a given number of  
155 samples, we obtain the maximum information possible. Second, what is meant by “acceptable” FNR? This  
156 raises the question: does a shifting FNR lead to rapid transitions in our ability inference and predictions  
157 about the structure and dynamics of networks, or does it produce a roughly linear decay in model efficacy?  
158 We explore this in the next section.

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



## 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 model-uncertainty, e.g. the variance in the interaction probability prediction across several cross-validation folds, where the data is split into training and test sets several times. The method we introduce adjusts the value of a model's predictions to produce a distribution of interaction probabilities, which are adjusted by a given false-negative-rate  $p_{fn}$  and false-positive-rate  $p_{fp}$  (outlined in figure fig. 3). We describe first how to sample from this distribution of adjusted interaction probabilities via simulation, and show that this distribution can be well-approximated analytically.

[Figure 3 about here.]

We then consider the output prediction from an arbitrary prediction model, which is the probability  $p_{ij}$  that two species  $i$  and  $j$  interact. To get an estimate of  $p_{ij}$  that accounts for observation error, we resample the probability of each interaction  $p_{ij}$  by simulating a set of several 'particles,' where each particle is a realization of an interaction occurring (either true or false with probabilities  $p_{ij}$  and  $1 - p_{ij}$  respectively) and then being correctly observed with probabilities given by  $p_{fp}$  and  $p_{fn}$  to yield a single boolean outcome for each particle. ("Resampling" within fig. 3 (B)). Over many samples of particles, the resulting frequency of 'true' outcomes is a single resample of the interaction probability  $p_{ij}^*$ . 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. As a reminder, as the total number of samples  $n$  from a binomial distribution with success probability  $p$  from approaches infinity, the sum of total successes across all samples approaches a normal distribution with mean  $np$  and variance  $np(1 - p)$ . We can use this to correct the estimate  $p_{ij}$  based on the expected 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

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

194 which yields the normal approximation

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

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

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

197 We can then further truncate to remain on the interval (0, 1) (as the output is a probability, although in  
198 practice often the probability mass outside (0, 1) is extremely low. As an example case study, we use a  
199 boosted-regression-tree to predict interactions in a host-parasite network (Hadfield *et al.* 2014) (with  
200 features derived in the same manner as Strydom *et al.* (2021) derives features on this data) to produce a set  
201 of interaction predictions. We then applied this method to a set of a few resampled interaction  
202 probabilities between mammals and parasite species shown in figure fig. 3(C).

203 Why is this useful? For one, this analytic method avoids the extra computation required by simulating  
204 samples from this distribution directly. Further, it enables continuous examination of the number of  
205 particles  $n_p$  as a uncertainty width. The natural analogue for the number of particles sampled is the  
206 number of observations of co-occurrence for a given pair of species—the fewer the particles, the higher  
207 the variance of the resulting approximation. The normal approximation is undefined for 0 particles (i.e. 0  
208 observations co-occurrence), although as  $n_p$  approaches 0 the approxated normal (once truncated)  
209 approaches a uniform distribution on the interval (0, 1), the maximum entropy distribution where we  
210 have no information about the possibility of an interaction.

211 This also has implications for what we mean by ‘uncertainty’ in interaction predictions. A model’s  
212 prediction can be ‘uncertain’ in two different ways: (1) the model’s predictions may have high variance, or  
213 (2) the model’s predictions may be centered around a probability of interaction of 0.5, where we are the  
214 most unsure about whether this interaction exists. Improving the incorporation of different forms of

215 uncertainty in probabilistic interaction predictions seems a necessary next step toward understanding  
216 what pairs of species we know the least about, in order to prioritize sampling to provide the most new  
217 information possible.

## 218 **Positive associations in co-occurrence increase the false-negative-rate**

219 The model above doesn't consider the possibility that there are positive or negative associations which shift  
220 the probability of species cooccurrence away from what is expected based on their relative abundances due  
221 to their interaction (Cazelles *et al.* 2016). However, here we demonstrate that the probability of having a  
222 false-negative can be higher if there is some positive association in the occurrence of species  $A$  and  $B$ . If  
223 we denote the probability that we observe the co-occurrence of two species  $A$  and  $B$  as  $P(AB)$  and if there  
224 is no association between the marginal probabilities of observing  $A$  and observing  $B$ , denoted  $P(A)$  and  
225  $P(B)$  respectively, then the probability of observing their co-occurrence is the product of the marginal  
226 probabilities for each species,  $P(AB) = P(A)P(B)$ . In the other case where there is some positive strength  
227 of association between observing both  $A$  and  $B$  because this interaction is "important" for each species,  
228 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  
229 not independent and instead are positively correlated, i.e.  $P(AB) > P(A)P(B)$ . In this case, the probability  
230 of observing a single false-negative in our naive model from fig. 2(A) is  $p_{fn} = 1 - P(AB)$ , which due to the  
231 above inequality implies  $p_{fn} > 1 - P(A)P(B)$ . This indicates an increasingly greater probability of a false  
232 negative as the strength of association gets stronger,  $P(AB) \rightarrow P(AB) \gg P(A)P(B)$ . However, this still does  
233 not consider variation in species abundance in space and time (Poisot *et al.* 2015). If positive or negative  
234 associations between species structure variation in the distribution of  $P(AB)$  across space/time, then the  
235 spatial/temporal biases induced by data collection would further impact the realized false-negative-rate, as  
236 the probability of false negative would not be constant for each pair of species across sites.

237 To test for these positive associations in data we scoured Mangal for datasets with many spatial or temporal  
238 replicates of the same system, which led to the resulting seven datasets set in figure fig. 4. For each  
239 dataset, we compute the marginal probability  $P(A)$  of occurrence of each species  $A$  across all networks in  
240 the dataset. For each pair of interacting species  $A$  and  $B$ , we then compute and compare the probability of  
241 co-occurrence if each species occurs independently,  $P(A)P(B)$ , to the empirical joint probability of  
242 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 underestimate the realized FNR. In fig. 4, we see the difference between  $P(AB)$  and  $P(A)P(B)$  for the seven suitable datasets with enough spatio-temporal replicates and a shared taxonomic backbone (meaning all individual networks use common species identifiers) found on Mangal to perform this analysis. Further details about each dataset are reported in tbl. 1.

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 suggests that there may not be as many “neutrally forbidden links” (Canard *et al.* 2012) as we might think, and that the reason we do not have records of interactions between rare species is probably due to observation error. This has serious ramifications for the widely observed property of nestedness seen in bipartite networks (Bascompte & Jordano 2007)—perhaps the reason we have lots of observations between generalists is because they are more abundant, and this is particularly relevant as we have strong evidence that generalism drives abundance (Song *et al.* 2022a), not vice-versa.

[Figure 4 about here.]

Table 1: The datasets used in the above analysis (Fig 2). The table reports the type of each dataset, the total number of networks in each dataset ( $N$ ), the total species richness in each dataset ( $S$ ), the connectance of each metaweb (all interactions across the entire spatial-temporal extent) ( $C$ ), the mean species richness across each local network  $\bar{S}$ , the mean connectance of each local network  $\bar{C}$ , the mean  $\beta$ -diversity among overlapping species across all pairs of network species ( $\bar{\beta}_{OS}$ ), and the mean  $\beta$ -diversity among all species in the metaweb ( $\bar{\beta}_{WN}$ ). Both metrics are computed using KGL  $\beta$ -diversity (Koleff *et al.* 2003)

Network	Type	$N$	$S$	$C$	$\bar{S}$	$\bar{C}$	$\bar{\beta}_{OS}$	$\bar{\beta}_{WN}$
Kopelke <i>et al.</i> (2017)	Food Web	100	98	0.037	7.87	0.142	1.383	1.972
Thompson & Townsend (2000)	Food Web	18	566	0.014	80.67	0.049	1.617	1.594
Havens (1992)	Food Web	50	188	0.065	33.58	0.099	1.468	1.881
Ponisio <i>et al.</i> (2017)	Pollinator	100	226	0.079	23.0	0.056	1.436	1.870
Hadfield <i>et al.</i> (2014)	Host-Parasite	51	327	0.085	32.71	0.337	1.477	1.952
Closs & Lake (1994)	Food Web	12	61	0.14	29.09	0.080	1.736	1.864
CaraDonna <i>et al.</i> (2017)	Pollinator	86	122	0.18	21.42	0.312	1.527	1.907

## 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 naive 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 split, 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 fig. 5(A&B).

[Figure 5 about here.]

One interesting result seen in fig. 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 “no-interaction” for all possible species pairs, which does far better than random guessing (ROC-AUC =

0.5) in terms of the false positive rate (one of the components of ROC-AUC). 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).

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 (GRL, Khoshraftar & An (2022)) and graph convolutional networks (Zhang *et al.* 2019). At this time, these advances can not yet be applied to ecological networks because they require far more data than we currently have. 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 (tbl. 1). Once we start to get into the thousands, these models will become more useful, but this can only be done with systematic monitoring of interactions. This again highlights the need to optimize our sampling effort to maximize the amount of information contained in our data given the expense of sampling interactions.

We also consider how the FNR affects network properties. In fig. 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, i.e.  $p_{fn} > 0.7$ . 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 (see 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 (Li *et al.* 2021) 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.

## 310 Discussion

311 Species interactions enable the persistence and functioning of ecosystems, but our understanding of  
312 interactions is limited due to the intrinsic difficulty of sampling them. Here we have provided a null  
313 model for the expected number of false-negatives in an interaction dataset. We demonstrated that we  
314 expect many false-negatives in species interaction datasets purely due to the intrinsic variation of  
315 abundances within a community. We also, for the first time to our knowledge, measured the strength of  
316 association between co-occurrence and interactions (Cazelles *et al.* 2016) across many empirical systems,  
317 and found that these positive associations are both very common, and showed algebraically that they  
318 increase the realized FNR. We have also shown that false-negatives could further impact our ability to  
319 both predict interactions and infer properties of the networks, which highlights the need for further  
320 research into methods for correcting this bias in existing data.

321 A better understanding of how false-negatives impact species interaction data is a practical  
322 necessity—both for inference of network structure and dynamics, but also for prediction of interactions by  
323 using species level information. False-negatives could pose a problem for many forms of inference in  
324 network ecology. For example, inferring the dynamic stability of a network could be prone to error if the  
325 observed network is not sampled “enough.” What exactly “enough” means is then specific to the  
326 application, and should be assessed via methods like those here when designing samples. Further,  
327 predictions about network rewiring (Thompson & Gonzalez 2017) due to range shifts in response to  
328 climate change could be error-prone without accounting for interactions that have not been observed but  
329 that still may become climatically infeasible. As is evident from fig. 2(A), we can never guarantee there are  
330 no false-negatives in data. In recent years, there has been interest toward explicitly accounting for  
331 false-negatives in models (Stock *et al.* 2017; Young *et al.* 2021), and a predictive approach to  
332 networks—rather than expecting our samples to fully capture all interactions (Strydom *et al.* 2021). As a  
333 result, better models for predicting interactions are needed for interaction networks. This includes  
334 explicitly accounting for observation error (Johnson & Larremore 2021)—certain classes of models have  
335 been used to reflect hidden states which account for detection error in occupancy modeling (Joseph 2020),  
336 and could be integrated in the predictive models of interactions in the future.

337 This work has several practical consequences for the design of surveys for species’ interactions.

338 Simulating the process of observation could be a powerful tool for estimating the sampling effort required

339 by a study that takes relative abundance into account, and provides a null baseline for expected FNR. It is  
340 necessary to take the size of the species pool into account when deciding how many total samples is  
341 sufficient for an “acceptable” FNR (fig. 2(C & D)). Further the spatial and temporal turnover of  
342 interactions means any approach to sampling prioritization must be spatiotemporal. We demonstrated  
343 earlier that observed negatives outside of the range of both species aren’t informative, and therefore using  
344 species distribution models could aid in this spatial prioritization of sampling sites.

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

361 Our work highlights the need for a quantitatively robust approach to sampling design, both for  
362 interactions (Jordano 2016) and all other aspects of biodiversity (Carlson *et al.* 2020). As anthropogenic  
363 forces create rapid shifts in our planet’s climate and biosphere, this is an imperative to maximize the  
364 amount of ecological information we get in our finite samples, and make our inferences and decisions  
365 based on this data as robust as possible. Where we choose to sample, and how often we choose to sample  
366 there, has strong impacts on the inferences we make from data. Incorporating a better understanding of  
367 sampling effort and bias to the design of biodiversity monitoring systems, and the inference and predictive  
368 models we apply to this data, is imperative in understanding how biodiversity is changing, and making



369 forecasts that can guide conservation action.

## 370 **Acknowledgements**

371 AG & MDC acknowledge the support of the Liber Ero Chair for Biodiversity conservation and NSERC.

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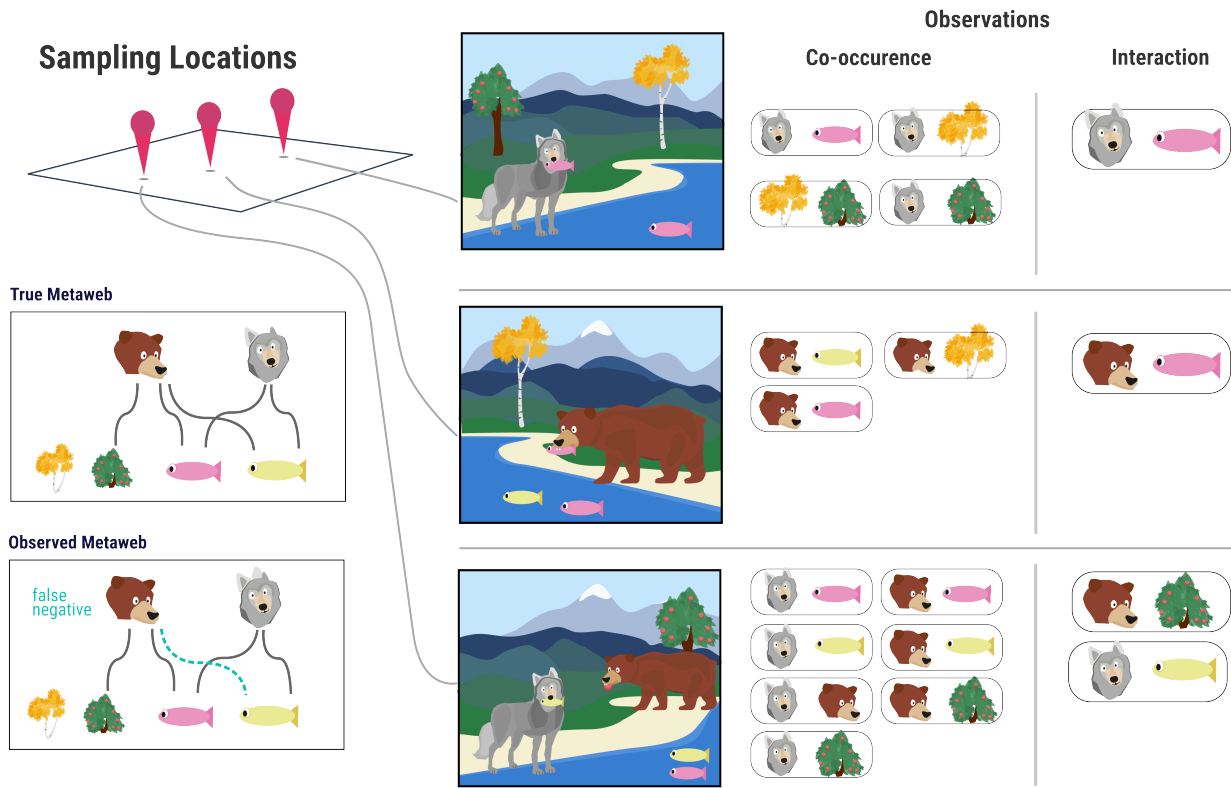


Figure 1: This conceptual example considers a sample of the trophic community of bears, wolves, salmon (pink fish), pike (yellow fish), berry trees, and aspen trees. The true metaweb (all realized interactions across the entire spatial extent) is shown on the left. In the center is what a hypothetical 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. Therefore, this interaction between bears and pike is a false-negative.

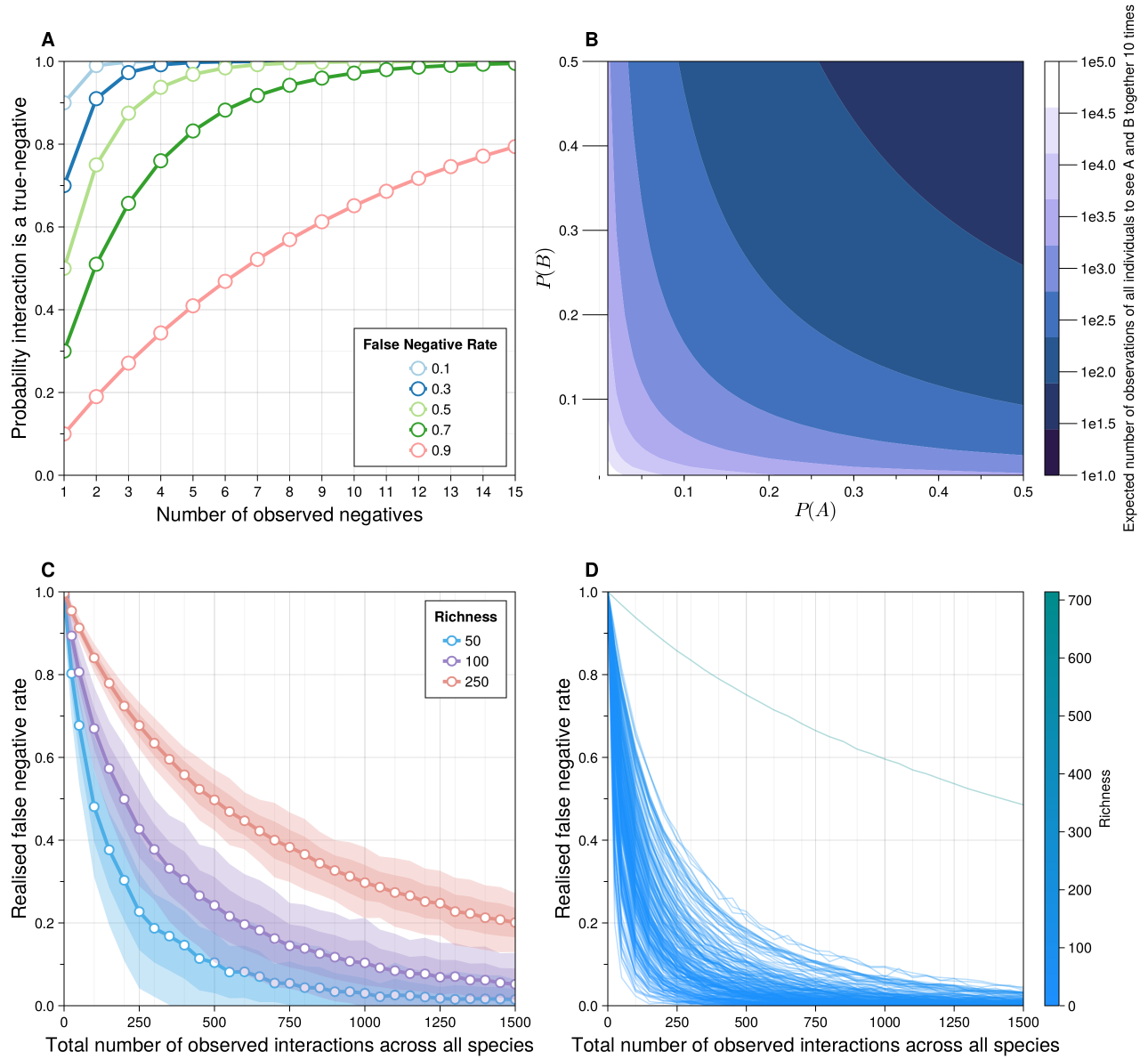


Figure 2: **(A)** The probability that an observed interaction is a true negative (y-axis) given how many times it has been sampled as a non-interaction (x-axis). Each color reflects a different value of  $p_{fn}$ , the false-negative-rate (FNR)—this is effectively the cdf of the geometric distribution. **(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  $P(Y)$ . **(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 & 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 database, where richness. The outlier on **(D)** is a 714 species food-web.

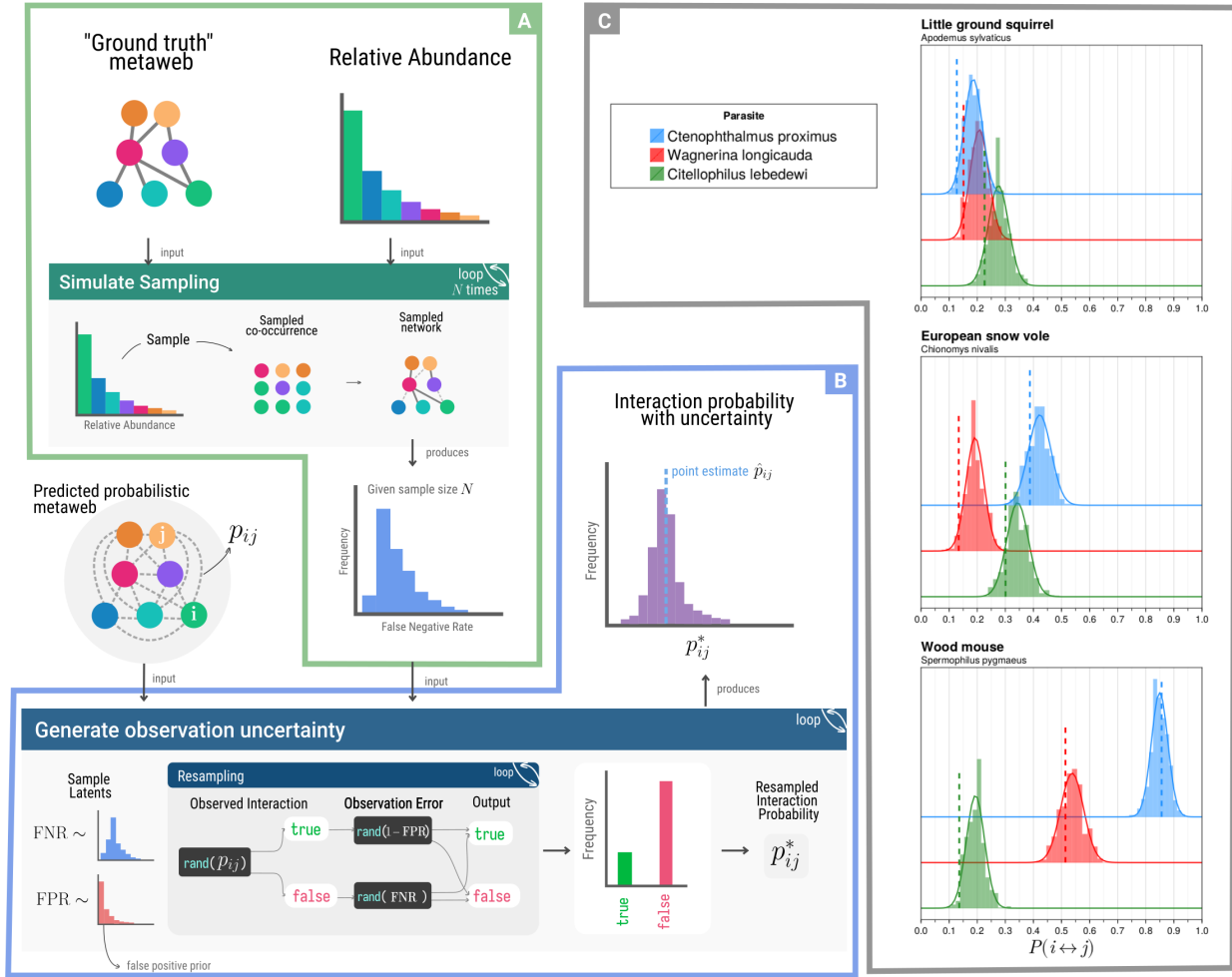


Figure 3: (A) The process for estimating the false-negative-rate (FNR) for an interaction dataset consisting of  $N$  total observed interactions. (B) The method for resampling interaction probability based on estimates of false-negative and false-positive rates. (C) The method for interaction probability resampling applied to three mammals and three parasites from the Hadfield *et al.* (2014) dataset.



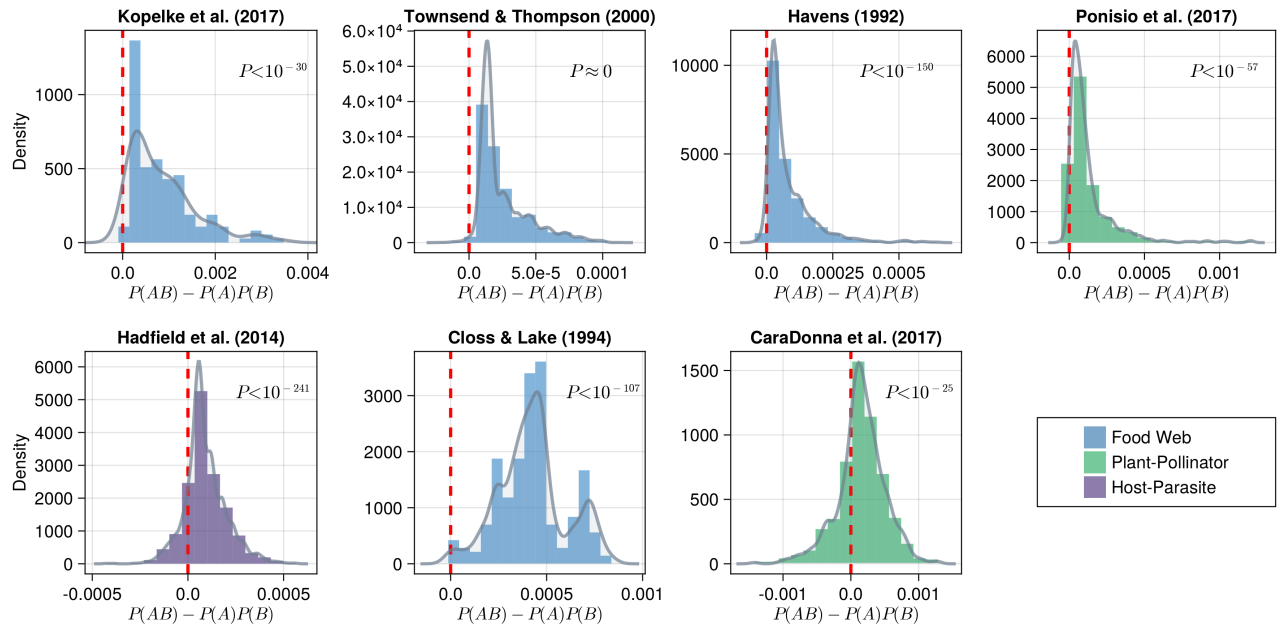


Figure 4: The difference between joint-probability of co-occurrence ( $P(AB)$ ) and expected probability of co-occurrence under independence ( $P(A)P(B)$ ) for interacting species for each dataset. The red-dashed line indicates 0 (no association). Each histogram represents a density, meaning the area 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.

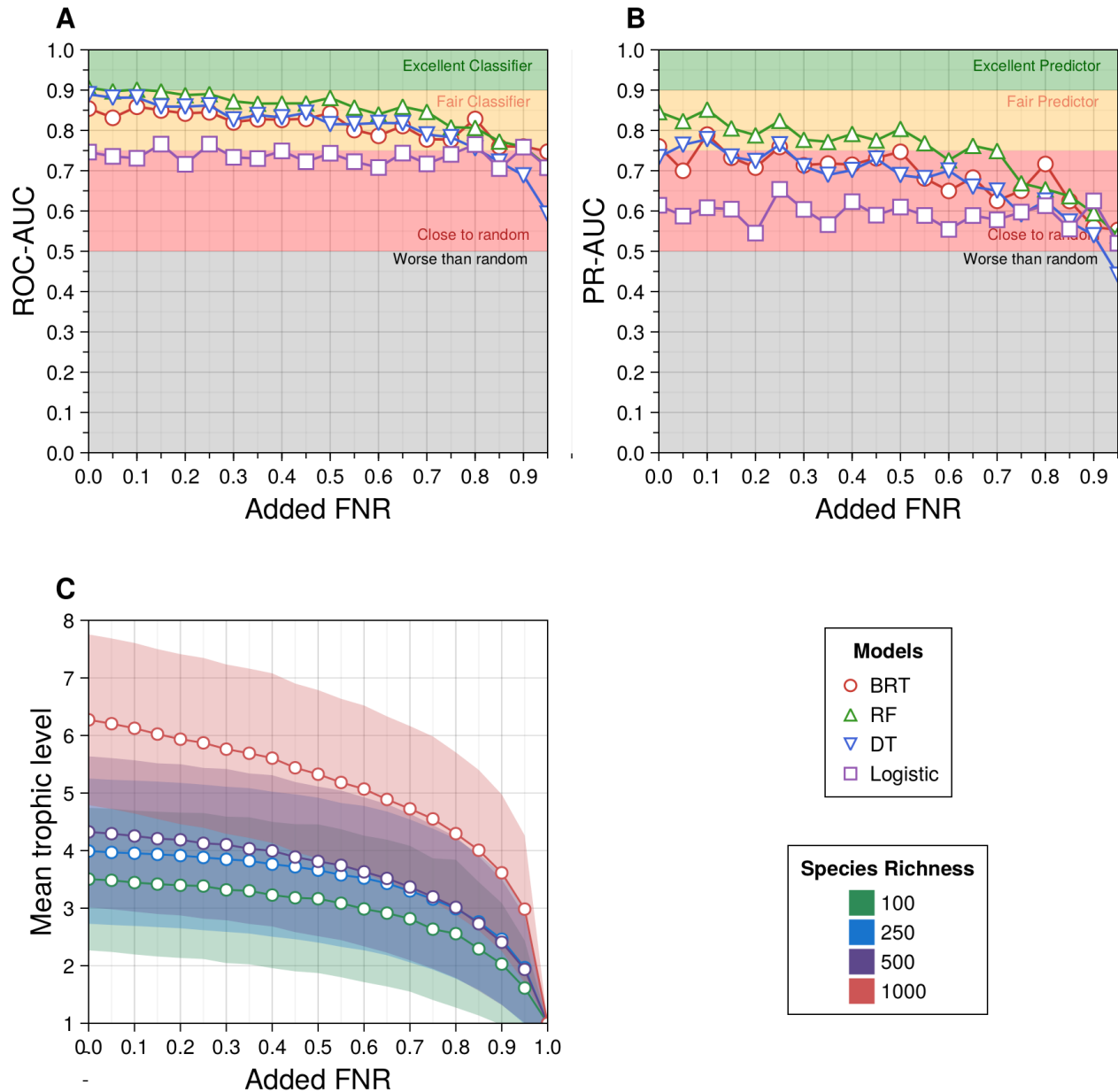


Figure 5: **(A)** The area-under the receiver-operator curve (ROC-AUC) and **(B)** The area-under the precision-recall curve (PR-AUC; right) for each different predictive model (colors/shapes) across a spectrum of the proportion of added false-negatives (x-axis). **(C)** The mean trophic-level of all 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.