

THE STRUCTURE OF PROBABILISTIC NETWORKS

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ABSTRACT

1. There is a growing realization among community ecologists that interactions between species vary in space and time. Yet, our current numerical framework to analyze the structure of interactions, largely based on graph-theoretical approaches, is unsuited to this type of data. Since the variation of species interactions holds much information, there is a need to develop new metrics to exploit it.
2. We present analytical expressions of key network metrics, using a probabilistic framework. Our approach is based on modeling each interaction as a Bernoulli event, and using basic calculus to express the expected value, and when mathematically tractable, its variance. We provide a free and open-source implementation of these measures.
3. We show that our approach allows to overcome limitations of both neglecting the variation of interactions (over-estimation of rare events) and using simulations (extremely high computational demand). We present a few case studies that highlight how these measures can be used.
4. We conclude this contribution by discussing how the sampling and data representation of ecological network can be adapted to better allow the application of a fully probabilistic numerical framework.

Keywords: ecological networks, connectance, degree distribution, nestedness, modularity

Ecological networks are an efficient way to represent biotic interactions between individuals, populations, or species. Historically, their study focused on describing their structure, with a particular attention on food webs (Dunne 2006) and plant-pollinator interactions (Jordano 1987; Bascompte *et al.* 2003). The key result of this line of research was linking this structure to community or ecosystem-level properties such as stability (McCann 2014), coexistence (Bastolla *et al.* 2009; Haerter *et al.* 2014), or ecosystem functioning (Duffy 2002; Thébault & Loreau 2003; Poisot ~~2012~~*et al.* 2013b). To a large extent, the description of ecological networks resulted in the emergence of questions about how functions ~~emerged from~~ and properties of communities emerged from their structure, and this stimulated the development of a rich methodological literature, defining a wide array of structural properties.

Given a network (*i.e.* a structure where nodes, most often species, are linked by edges, representing ecological interactions) as input, measures of network structure return a *property* based on one or several *units* from this network. Some of the properties are *direct* properties (they only require knowledge of the unit on which they are applied), whereas others are *emergent* (they require knowledge of, and describe, higher-order structures). For example, connectance, the realized proportion of potential interactions, is a direct property of a network. The degree of a node (how many interactions it is involved in) is a direct property of the node. The nestedness of a network (that is, the extent to which specialists and generalists overlap), on the other hand, is an emergent property that is not directly predictable from the degree of all nodes. Though the difference may appear to be semantics, establishing a difference between direct and emergent properties is important when interpreting their values; direct properties are conceptually equivalent to means, in that they tend to be the first moment of network units, whereas emergent properties are conceptually equivalent to variances or other higher-order moments.

In the recent years, the interpretation of the properties of network structure (as indicators of the action of ecological or evolutionary processes) has been somewhat complicated by the observation that network structure varies through space and time. This happens because, contrary to a long-standing assumption of network studies, species from the same pool do not interact in a consistent

1 way (Poisot *et al.* 2012). Empirical and theoretical studies suggest that the network is not the right
 2 unit to understand this variation; rather, network variation is an emergent property of the response
 3 of ecological interactions to environmental factors and chance events (~~???~~[see Poiset *et al.* 2015 for](#)
 4 [a review](#)). Interactions can vary because of local mismatching in phenology (Olesen *et al.* 2011;
 5 [Vizentin-Bugoni *et al.* 2014; Maruyama *et al.* 2014](#)), populations fluctuations preventing the inter-
 6 action (Canard *et al.* 2014), or a combination of both (Chamberlain *et al.* 2014; Olito & Fox 2014).
 7 For example, Olito & Fox (2014) show that accounting for neutral (population-size driven) and trait-
 8 based effects allows the prediction of the cumulative change in network structure, but not of the
 9 change at the level of individual interactions. In addition, Carstensen *et al.* (2014) show that within
 10 a meta-community, not all interactions are equally variable: some are highly consistent, whereas
 11 others are extremely rare. These empirical results all point to the fact that species interactions can-
 12 not always be adequately ~~modeled~~[represented](#) as yes-no events; since it is well established that they
 13 do vary, it is necessary to represent them as probabilities. To the question of *Do these two species*
 14 *interact?*, we should substitute the question of *How likely is it that they will interact?*. [This also](#)
 15 [requires the considerable methodological adjustment of re-writing measures of network structure to](#)
 16 [account for the fact that interactions are not consistent; in this paper, we re-develop a unified toolkit](#)
 17 [of measures to characterize the structure of probabilistic interaction networks.](#)

18 The current way of dealing with probabilistic interactions are either to ignore variability entirely or
 19 to generate random networks. Probabilistic metrics are a mathematically rigorous alternative to both.
 20 When ignoring the probabilistic nature of interactions (henceforth *binary* networks), every non-zero
 21 element of the network is assumed to be 1. This leads to over-representation of some rare events, and
 22 increases the number of interactions; [as a result, this changes the estimated value of different network](#)
 23 [properties, in a way that is not understood at all. Issues are most likely to arise for connectances](#)
 24 [where the topological \(Chagnon 2015\) or permutational \(Poisot & Gravel 2014\) space of random](#)
 25 [network is small, leading to over-replication or uncharacterized biases.](#) An alternative is to consider
 26 only the interactions above a given threshold, which leads to an under-representation of rare events
 27 and decreases the effective number of interactions [\(in addition to the problem that there is no robust](#)
 28 [criterion to decide on a treshold\). More importantly, this introduces the risk of removing species that](#)

1 establish a lot of interactions that each have a low probability. Taken together, these considerations
2 highlight the need to amend our current methodology for the description of ecological networks, in
3 order to give more importance to the variation of individual interactions — current measures neglect
4 the variability of interactions, and are therefore discarding valuable ecological information. Because
5 the methodological corpus available to describe ecological networks had first been crafted at a time
6 when it was assumed that interactions were invariants, it is unsuited to address the questions that
7 probabilistic networks allow us to ask.

8 In this paper, we show that several direct and emergent core properties of ecological networks
9 (both bipartite and unipartite) can be re-formulated in a probabilistic context (Yeakel *et al.* 2012;
10 ~~???~~Poisot *et al.* 2015); we conclude by showing how this methodology can be applied to ex-
11 ploit the information contained in the variability of networks, and to reduce the computational
12 burden of current methods in network analysis. ~~We also provide a free and open-source (MIT~~
13 ~~license) implementation of this suite of measures in a library for the julia language, available~~
14 ~~at <http://github.com/PoisotLab/ProbabilisticNetwork.jl>.~~

15 SUITE OF PROBABILISTIC NETWORK METRICS

16 Throughout this paper, we use the following notation. \mathbf{A} is a matrix wherein A_{ij} is $P(ij)$, *i.e.* the
17 probability that species i establishes an interaction with species j . If \mathbf{A} represents a unipartite net-
18 work (*e.g.* a food web), it is a square matrix and contains the probabilities of each species interacting
19 with all others, including itself. If \mathbf{A} represents a bipartite network (*e.g.* a pollination network), it
20 will not necessarily be square. We call S the number of species, and R and C respectively the number
21 of rows and columns. $S = R = C$ in unipartite networks, and $S = R + C$ in bipartite networks.

1 Note that all of the measures defined below can be applied on a bipartite network that has been made
 2 unipartite; ~~the~~. The only bipartite-only measure is nestedness. The unipartite transformation of a
 3 bipartite matrix \mathbf{A} is the block matrix

$$(1) \quad \mathbf{B} = \begin{pmatrix} 0_{(R,R)} & \mathbf{A} \\ 0_{(C,R)} & 0_{(C,C)} \end{pmatrix},$$

4 where $0_{(C,R)}$ is a matrix of C rows and R columns (noted $C \times R$) filled with 0s, etc. Note that for
 5 centrality to be relevant in bipartite networks, this matrix should be made symmetric: $\mathbf{B}_{ij} = \mathbf{B}_{ji}$.

6 We will also assume that all interactions are independent (so that $P(ij|kl) = P(ij)P(kl)$ for any
 7 species), and can be represented as a series of Bernoulli trials (so that $0 \leq P(ij) \leq 1$). A Bernoulli
 8 trial is simply the realization of a probability event, giving 1 with probability $P(ij)$, and 0 else. The
 9 latter condition allows us to derive estimates for the *variance* ($\text{var}(X) = p(1 - p)$), and expected
 10 values ($E(X) = p$). We can therefore estimate the variance of most properties, using the fact that the
 11 variance of additive independent events is the sum of their individual variances, and that the variance
 12 of multiplicative independent events is

$$(2) \quad \text{var}(X_1 X_2 \dots X_n) = \prod_i (\text{var}(X_i) + [E(X_i)]^2) - \prod_i [E(X_i)]^2$$

13 As a final note, all of the measures described below can be applied on the binary (0/1) versions of the
 14 networks ~~and will give the exact value of the non-probabilistic measure~~ in which case they effectively
 15 are the non-probabilistic version of the measure as usually calculated. This property is particularly
 16 desirable as it allows our framework to be used on any network, whether they are represented in a
 17 probabilistic or binary way. Nonetheless, this approach is different from using *weighted* networks, in
 18 that it answers a completely different question. Probabilistic networks describe the probability that
 19 any interaction will happen, whereas weighted networks describe the effect of the interaction when
 20 it happens. Although there are several measures for *quantitative* networks (Bersier *et al.* 2002),
 21 in which interactions happen but with different outcomes, these are not relevant for probabilistic

1 networks, which require to account for the fact that interactions are probabilistic event, *i.e.* they
2 display a variance that will cascade up to the network level. Actually, the weight of each interaction
3 is best viewed as a second modeling step, focusing only on the non-zero cases (*i.e.* the interactions
4 that are realized); this is similar to the method now frequently used in species distribution models,
5 where the species presence is modeled first, and its abundance second, using a (possibly) different
6 set of predictors (Boulangéat *et al.* 2012).

7 **Direct properties.**

8 *Connectance and number of interactions.* Connectance (or network density) is the proportion of
9 possible interactions that are realized, defined as $Co = L/(R \times C)$, where L is the total number
10 of interactions. As all interactions in a probabilistic network are assumed to be independent, the
11 expected value of L , is

$$(3) \quad \hat{L} = \sum A_{ij},$$

12 and $\hat{Co} = \hat{L}/(R \times C)$. Likewise, the variance of the number of interactions is $\text{var}(\hat{L}) = \sum (A_{ij}(1 -$
13 $A_{ij}))$.

14 *Node degree.* The degree distribution of a network is the distribution of the number of interactions
15 established (number of successors) and received (number of predecessors) by each node. The ex-
16 pected degree of species i is

$$(4) \quad \hat{k}_i = \sum_j (A_{ij} + A_{ji})$$

17 The variance of the degree of each species is $\text{var}(\hat{k}_i) = \sum_j (A_{ij}(1 - A_{ij}) + A_{ji}(1 - A_{ji}))$. Note also
18 that as expected, $\sum \hat{k}_i = 2\hat{L}$.

1 *Generality and vulnerability.* By simplification of the above, generality \hat{g}_i and vulnerability \hat{v}_i are
 2 given by, respectively, $\sum_j A_{ij}$ and $\sum_j A_{ji}$, with their variances $\sum_j A_{ij}(1 - A_{ij})$ and $\sum_j A_{ji}(1 - A_{ji})$.

3 ~~emergent~~Emergent properties.

4 *Path length.* Networks can be used to describe indirect interactions between species through the use
 5 of paths. The existence of a path of length 2 between species i and j means that they are connected
 6 through at least one additional species k . In a probabilistic network, unless some elements are 0, all
 7 pairs of species i and j are connected through a path of length 1, with probability A_{ij} . The expected
 8 number of paths of length k between species i and j is given by

$$(5) \quad n_{ij}^{(k)} = \left(\mathbf{A}^k \right)_{ij},$$

9 where \mathbf{A}^k is the matrix multiplied by itself k times.

10 It is possible to calculate the probability of having at least one path of length k between the two
 11 species: this can be done by calculating the probability of having no path of length k , then taking
 12 the running product of the resulting array of probabilities. For the example of length 2, species i and
 13 j are connected through g with probability $A_{ig}A_{gj}$, and so this path does not exist with probability
 14 $1 - A_{ig}A_{gj}$. For any pair i, j , let \mathbf{m} be the vector such as $m_g = A_{ig}A_{gj}$ for all $g \notin (i, j)$ (Mirchandani
 15 1976). The probability of not having any path of length 2 is $\prod (1 - \mathbf{m})$. Therefore, the probability of
 16 having a path of length 2 between i and j is

$$(6) \quad \hat{p}_{ij}^{(2)} = 1 - \prod_7 (1 - \mathbf{m}).$$

1 In most situations, one would be interested in knowing the probability of having a path of length 2
 2 *without* having a path of length 1; this is simply expressed as $(1 - A_{ij})\hat{p}_{ij}^{(2)}$. One can, by the same
 3 logic, generate the expression for having at least one path of length 3:

$$(7) \quad \hat{p}_{ij}^{(3)} = (1 - A_{ij})(1 - \hat{p}_{ij}^{(2)}) \left(1 - \prod_{x,y} (1 - \mathbf{m})\right) \prod_{x,y} ((1 - A_{ix})(1 - A_{xy})(1 - A_{yj})),$$

4 where \mathbf{m} is the vector of all $A_{ix}A_{xy}A_{yj}$ for $x \notin (i, j), y \neq x$. This gives the probability of having at least
 5 one path from i to j , passing through any pair of nodes x and y , without having any shorter path.
 6 In theory, this approach can be generalized up to an arbitrary path length, but it becomes rapidly
 7 untractable.

8 *Unipartite projection of bipartite networks.* The unipartite projection of a bipartite network is ob-
 9 tained by linking any two nodes of one mode that are connected through at least one node of the
 10 other mode; for example, to plants are connected if they share at least one pollinator. It is readily
 11 obtained using the formula in the *Path length* section. This yields either the probability of an edge
 12 in the unipartite projection (of the upper or lower nodes), or if using the matrix multiplication, the
 13 expected number of such nodes.

14 *Nestedness.* Nestedness is an important measure of (bipartite) network structure that tells the extent
 15 to which the interactions of specialists and generalists overlap. We use the formula for nestedness
 16 proposed by Bastolla et al. (2009). ~~They define nestedness;~~ this measure is a correction of NODF
 17 (Almeida-Neto et al. 2008) for ties in species degree. Nestedness for each margin of the matrix ~~is~~
 18 defined as $\eta^{(R)}$ and $\eta^{(C)}$ for, respectively, rows and columns. As per Almeida-Neto et al. (2008),
 19 we define a global statistic for nestedness as $\eta = (\eta^{(R)} + \eta^{(C)})/2$.

20 Nestedness, in a probabilistic network, is defined as

$$(8) \quad \eta^{(R)} = \sum_{i < j} \frac{\sum_k A_{ik}A_{jk}}{\min(g_i, g_j)},$$

1 where g_i is the expected generality of species i . The reciprocal holds for $\eta^{(C)}$ when using v_i (the
2 vulnerability) instead of g_i .

3 The values returned are within $[0; 1]$, with $\eta = 1$ indicating complete nestedness.

4 *Modularity*. Modularity represents the extent to which networks are compartmentalized, *i.e.* the
5 tendency for subsets of species to be strongly connected together, while they are weakly connected
6 to the rest of the network (Stouffer & Bascompte 2011). Modularity is measured as the proportion
7 of interactions between nodes of an arbitrary number of modules, as opposed to the random expect-
8 ation. Assuming a vector \mathbf{s} which, for each node in the network, holds the value of the module it
9 belongs to (an integer in $[1, c]$), Newman (2004) proposed a general measure of modularity, which is

$$\mathcal{Q} = \sum_{m=1}^c (e_{mm} - a_m^2)$$

10 , where c is the number of modules,

$$e_{mm} = \sum_{ij} \frac{A_{ij}}{2c} \delta(\mathbf{s}_i, \mathbf{s}_j)$$

11 , and

$$a_m = \sum_n e_{mn}$$

12 ,

13 with δ being Kronecker's function, returning 1 if its arguments are equal, and 0 otherwise. This
14 formula can be *directly* applied to probabilistic networks. Modularity takes values in $[0; 1]$, where 1
15 indicates perfect modularity.

16 *Centrality*. Although node degree is a rough first order estimate of centrality, other measures are
17 often needed. We derive the expected value of centrality according to Katz (1953). This **measures**
18 measure generalizes to directed acyclic graphs (whereas other do not). For example, although eigen-
19 vector centrality is often used in ecology, it cannot be measured on probabilistic graphs. Eigenvector

centrality requires the matrix's largest eigenvalues to be real, which is not the case for all probabilistic matrices. The measure proposed by Katz is a useful replacement, because it accounts for the paths of all length between two species instead of focusing on the shortest path.

As described above, the expected number of paths of length k between i and j is $(\mathbf{A}^k)_{ij}$. Based on this, the expected centrality of species i is

$$(9) \quad C_i = \sum_{j=1}^n \sum_{k=1}^{\infty} \alpha^k (\mathbf{A}^k)_{ji}.$$

The parameter $\alpha \in [0; 1]$ regulates how important long paths are. When $\alpha = 0$, only first-order paths are accounted for (and the centrality is equal to ~~generality~~). ~~DG: to the degree or generality?~~ the degree). When $\alpha = 1$, paths of all length are equally important. As C_i is sensitive to the size of the matrix, we suggest normalizing by $\mathbf{C} = \sum C$, so that

$$(10) \quad C_i = \frac{C_i}{\mathbf{C}}.$$

This results in the *expected relative centrality* of each node in the probabilistic network, which sums to unity.

Species with no outgoing links. Estimating the number of species with no outgoing links (successors) can be useful when predicting whether, *e.g.*, predators will go extinct. Alternatively, when prior information about traits are available, this can allow predicting the invasion success of a species in a novel community. A species has no successors if it manages *not* to establish any outgoing interaction, which for species i happens with probability

$$(11) \quad \prod_j (1 - A_{ij}).$$

1 The number of expected such species is therefore the sum of the above across all species:

$$(12) \quad \hat{P}P = \sum_i \left(\prod_j (1 - A_{ij}) \right).$$

2 and its variance is

$$(13) \quad \text{var}(\hat{P}P) = \sum_i \left(\prod_j (1 - A_{ij}^2) - \left(\prod_j (1 - A_{ij}) \right)^2 \right)$$

3 Note that in a non-probabilistic context, species with no outgoing links would be considered primary
 4 producers. This is not the case here: if interactions are probabilistic events, then *e.g.* a top predator
 5 may have no preys, which do not mean it will not become a primary producer. For this reason, the
 6 trophic position of the species may better be measured on the binary version of the matrix.

7 *Species with no incoming links.* Using the same approach as for the number of species with no
 8 outgoing links, the expected number of species with no incoming links is therefore

$$(14) \quad \hat{T}P = \sum_i \left(\prod_{j \neq i} (1 - A_{ji}) \right)$$

9 Note that we exclude self-interactions, as top-predators can, and often do, engage in cannibalism.

10 *Number of species with no interactions.* Predicting the number of species with no interactions (or
 11 whether any species will have at least one interaction) is useful when predicting whether species will
 12 be able to integrate into an existing network, for example. Note that from a methodological point of
 13 view, this can be a helpful *a priori* measure to determine whether null models of networks will have
 14 a lot of species with no interactions, and so will require intensive sampling.

1 A species has no interactions with probability

$$(15) \quad \prod_{j \neq i} (1 - A_{ij})(1 - A_{ji})$$

2 As for the above, the expected number of species with no interactions (*free species*) is the sum of
 3 this quantity across all i :

$$(16) \quad \hat{FS} = \sum_i \prod_{j \neq i} (1 - A_{ij})(1 - A_{ji})$$

4 The variance of the number of species with no interactions is

$$(17) \quad \text{var}(\hat{FS}) = \sum_i (A_{ij}(1 - A_{ij})A_{ji}(1 - A_{ji}) + A_{ij}(1 - A_{ij})A_{ji}^2 + A_{ji}(1 - A_{ji})A_{ij}^2)$$

5 *Self-loops.* Self-loops (the existence of an interaction of a species onto itself) is only meaningful
 6 in unipartite networks. The expected proportion of species with self-loops is very simply defined
 7 as $\text{Tr}(\mathbf{A})$, that is, the sum of all diagonal elements. The variance is $\text{Tr}(\mathbf{A} \diamond (1 - \mathbf{A}))$, where \diamond is the
 8 element-wise product operation ([Hadamard product](#)).

9 *Motifs.* Motifs are sets of pre-determined interactions between a fixed number of species (Milo *et*
 10 *al.* 2002; Stouffer *et al.* 2007), such as for example one predator sharing two preys. As there are an
 11 arbitrarily large number of motifs, we will illustrate the approach with only two examples.

12 The probability that three species form an apparent competition motif (one predator, two prey) where
 13 i is the predator, j and k are the prey, is

$$(18) \quad P(i, j, k \in \text{app. comp}) = A_{ij}(1 - A_{ji})A_{ik}(1 - A_{ki})(1 - A_{jk})(1 - A_{kj})$$

1 Similarly, the probability that these three species form an omnivory motif, in which i and j consume
 2 k and i consumes j , is

$$(19) \quad P(i, j, k \in \text{omniv.}) = A_{ij}(1 - A_{ji})A_{ik}(1 - A_{ki})A_{jk}(1 - A_{kj})$$

3 The probability of the number of *any* motif m with three species in a network is given by

$$(20) \quad \hat{N}_m = \sum_i \sum_{j \neq i} \sum_{k \neq j} P(i, j, k \in m)$$

4 It is indeed possible to have an expression of the variance of this value, or of the variance of any
 5 three species forming a given motif, but their expressions become rapidly untractable and are better
 6 computed than written.

7 **Network comparison.** The dissimilarity of a pair of (ecological) networks can be measured using
 8 the framework set forth by Koleff et al. (2003). Measures of β -diversity compute the dissimilarity
 9 between two networks based on the cardinality of three sets, a , c , and b , which are respectively the
 10 shared items, items unique to superset (network) 1, and items unique to superset 2 (the identity of
 11 which network is 1 or 2 matters for asymmetric measures). Supersets can be the species within each
 12 network, or the interactions between species. Following Poisot et al. (2012), the dissimilarity of
 13 two networks can be measured as either β_{WN} (all interactions), or β_{OS} (interactions involving only
 14 common species), with $\beta_{OS} \leq \beta_{WN}$.

15 Within our framework, these measures can be applied to probabilistic networks. The expected values
 16 of \bar{a} , \bar{c} , and \bar{b} are, respectively, $\sum \mathbf{A}_1 \diamond \mathbf{A}_2$, $\sum \mathbf{A}_1 \diamond (1 - \mathbf{A}_2)$, and $\sum (1 - \mathbf{A}_1) \diamond \mathbf{A}_2$. Whether β_{OS} or β_{WN}
 17 is measured requires to alter the matrices \mathbf{A}_1 and \mathbf{A}_2 . To measure β_{OS} , one must remove all unique
 18 species; to measure β_{WN} , one must expand the two matrices so that they have the same species at
 19 the same place, and give a weight of 0 to the added interactions.

In this section, we contrast the use of probabilistic measures to the current approaches of either using binary networks, or working with null models through simulations. When generating random networks, what we call *Bernoulli trials* from here on, a binary network is generated by doing a Bernoulli trial with probability A_{ij} , for each element of the matrix. This generates networks that have only 0/1 interactions, and are realizations of the probabilistic network. This is problematic because higher order structures involving rare events will be under-represented in the sample, and because most naive approaches (i.e. not controlling for species degree) are likely to generate ~~free-species species with no interactions~~, especially in sparsely connected networks frequently encountered in ecology (Milo *et al.* 2003; Poisot & Gravel 2014) – on the other hand, non-naive approaches (e.g. based on swaps or quasi-swaps as explained in Jordano & Bascompte 2013) break the assumption of independence between interactions.

Comparison of probabilistic networks. In this sub-section, we apply the above measures to a bacteria–phage interaction network. Poullain *et al.* (2008) have measured the probability that 24 phages can infect 24 strains of bacteria of the *Pseudomonas fluorescens* species (group SBW25). ~~Each probability has been observed~~ The (probabilistic) adjacency matrix was constructed by estimating the probability of each phage–bacteria interaction though independent infection assays, and can take values of 0, 0.5 (interaction is variable), and 1.0. We have generated a “Binary” network by setting all interactions with a probability higher than 0 to unity, to simulate the results that would have been obtained in the absence of estimates of interaction probability.

Measuring the structure of the Binary, Bernoulli trials, and Probabilistic network gives the following result (average, and variance when there is an analytical expression):

Measure	Binary	Bernoulli trials	Probabilistic
links	336	221.58 ± 57.57	221.52 ± 57.25
η	0.73	0.528	0.512
$\eta^{(R)}$	0.72	0.525	0.507

Measure	Binary	Bernoulli trials	Probabilistic
$\eta^{(C)}$	0.75	0.531	0.518

As these results show, ~~transforming the probabilistic matrix into a binary one~~ treating all interactions as having the same probability, i.e. removing the information about variability, (i) overestimates nestedness by ≈ 0.2 , and (ii) overestimates the number of links by 115. For the number of links, both the probabilistic measures and the average and variance of 10^4 Bernoulli trials were in strong agreement (they differ only by the second decimal place).

Using Bernoulli trials had the effect of slightly over-estimating nestedness. The overestimation is statistically significant from a purely frequentist point of view, but significance testing is rather meaningless when the number of replicates is this large and can be increased arbitrarily; what is important is that the relative value of the error is small enough that Bernoulli trials are able to adequately reproduce the probabilistic structure of the network. It is not unexpected that Bernoulli trials are this close to the analytical expression of the measures; due to the experimental design of the Poullain et al. (2008) study, probabilities of interactions are bound to be high, and so variance is minimal (most elements of \mathbf{A} have a value of either 0 or 1, and so their individual variance is 0 – though their confidence interval varies as a function of the number of observations from which the probability is derived). Still, despite overall low variance, the binary approach severely misrepresents the structure of the network.

Null-model based hypothesis testing. In this section, we analyse 59 pollination networks from the literature using two usual null models of network structure, and two models with intermediate constraints. These data cover a wide range of situations, from small to large, and from densely to sparsely connected networks. They provide a good demonstration of the performance of probabilistic metrics. Data come from the *InteractionWeb Database*, and were queried on Nov. 2014.

1 We use the following null models. First (Type I, Fortuna & Bascompte (2006)), any interaction
 2 between plant and animals happens with the fixed probability $P = Co$. This model controls for con-
 3 nectance, but removes the effect of degree distribution. Second, (Type II, Bascompte et al. (2003)),
 4 the probability of an interaction between animal i and plant j is $(k_i/R + k_j/C)/2$, the average of the
 5 richness-standardized degree of both species. In addition, we use the models called Type III in and
 6 out (Poisot *et al.* ~~2013~~[2013a](#)), that use the row-wise and column-wise probability of an interaction
 7 respectively, as a way to understand the impact of the degree distribution of upper and lower level
 8 species.

9 Note that these null models will take a binary network, and through some rules turn it into a prob-
 10 abilistic one. Typically, this probabilistic network is used as a template to generate Bernoulli trials
 11 and measure some of their properties, the distribution of which is compared to the empirical net-
 12 work. This approach is computationally inefficient (Poisot & Gravel 2014), especially using naive
 13 models (Milo *et al.* 2003), and as we show in the previous section, can yield biased estimates of the
 14 true average of nestedness (and presumably other properties).

15 We measured the nestedness of the 59 (binary) networks, then generated the random networks under
 16 the four null models, and calculated the expected nestedness using the probabilistic measure. For
 17 each null model i , the difference $\Delta_N^{(i)}$ in nestedness N is expressed as $\Delta_N^{(i)} = N - \mathcal{N}^{(i)}(N)$, where
 18 $\mathcal{N}^{(i)}(N)$ is the nestedness of null model i . Our results are presented in [Figure 1](#).

19 There are two striking results. First, empirical data are consistently *more* nested than the null expec-
 20 tation, as evidenced by the fact that all Δ_N values are strictly positive. Second, this underestimation
 21 is *linear* between null models I and II (in that it does not depends on how nested the empirical net-
 22 work is), although null model II is always closer to the nestedness of the empirical network (which
 23 makes sense, since null model II incorporates the higher order constraint of respecting the degree
 24 distribution of both levels). That the nestedness of the null model probability matrix is so strongly
 25 determined by the nestedness of the empirical networks calls for a closer evaluation of how the
 26 results of null models are interpreted (especially since Bernoulli simulations revealed a very low
 27 variance in the simulated nestedness).

1 There is a strong, and previously unaccounted for, circularity in this approach: empirical networks
2 are compared to a null model which, as we show, has a systematic bias *and* a low variance (in
3 simulations), meaning that differences in nestedness that are small (thus potentially ecologically
4 irrelevant) have a good chance of being reported as significant. Interestingly, models III in and III
5 out made overall *fewer* mistakes at estimating nestedness – resp. 0.129 and 0.123, compared to resp.
6 0.219 and 0.156 for model I and II. Although the error is overall sensitive to model type (Kruskal-
7 Wallis $\chi^2 = 35.80$, d.f. = 3, $p \leq 10^{-4}$), the three pairs of models that were significantly different
8 after controlling for multiple comparisons are I and II, I and III in, and I and III out (model II is not
9 different from either models III in or out).

10 In short, this analysis reveals that (i) the null expectation of a network property under randomization
11 scenarios can be obtained through the analysis of the probabilistic matrix, instead of the analysis of
12 simulated Bernoulli networks; (ii) Different models have different systematic biases, with models of
13 the type III performing overall better for nestedness than any other models. This can be explained
14 by the fact that nestedness of a network, as expressed by Bastolla et al. (2009), is the average of a
15 row-wise and column-wise nestedness. These depend on the species degree, and as such should be

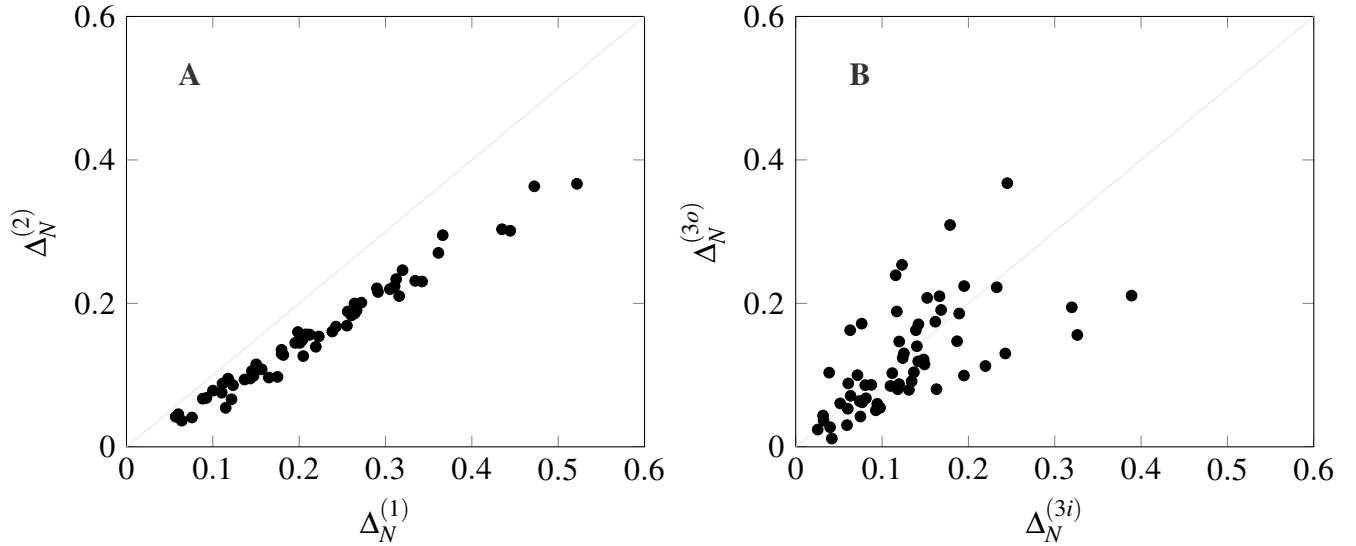


FIGURE 1. Results of the null model analysis of 59 plant-pollination networks. **A.** There is a consistent tendency for (i) both models I and II to estimate less nestedness than in the empirical network, although null model II yields more accurate estimates. **B.** Models III in and III out also estimate less nestedness than the empirical network, but neither has a systematic bias.

1 well predicted by models III. The novelty of this approach is that, instead of having to evaluate the
2 measure for thousands of replicates, an *unbiased* estimate of its mean can be obtained in a fraction of
3 the time using the measures described here. This is particularly important since, as demonstrated by
4 Chagnon (2015), the generation of null randomization is subject to biases in the range of connectance
5 where most ecological networks are. Our approach is essentially a bias-free, time-effective way of
6 estimating the expected value of a network property.

7 ~~IMPLICATIONS FOR DATA COLLECTION~~DISCUSSION

8 Understanding the structure of ecological networks, and whether it relates to ecosystem properties,
9 is emergent as a key challenge for community ecology. A proper estimation of this structure requires
10 tools that address all forms of complexity, the most oft-neglected yet pervasive of which is the fact
11 that interactions are variable. By developing these metrics, we allow future analyses of network
12 structure to account for this phenomenon. There are two main considerations highlighted by this
13 methodological development. First, in what way are probabilistic data independent; second, what
14 are the implications for data collection.

15 **Non-independance of interactions.** We developed and presented a set of measures to quantify the
16 expected network structure, using the probability that each interaction is observed or happens, in a
17 way that do not require time-consuming simulations. Our framework is set up in such a way that
18 the probabilities of interactions are considered to be independent. This is an over-simplification
19 of the ecological reality, where different interactions are known to have effects on one another
20 (Golubski & Abrams 2011; Sanders & Veen 2012; Ims *et al.* 2013). Yet we feel that, as a
21 first approximation, this assumption is reasonable. There is a strong methodological argument for
22 which the non-independance of interactions cannot currently be robustly accounted for: analytical
23 expectations for non-independant Bernoulli events require to know the full dependence structure.
24 Not only does it severely limits the ability to provide measures of network structure, it requires a far
25 more extensive sampling that what is needed to obtain an estimate of the probability of interactions
26 one by one.

Estimates of interaction probabilities.

Estimating interaction probabilities based on species abundances (Olito & Fox 2014; Canard *et al.* 2014) do not ~~,for example,~~ yield independent probabilities: changing the abundance of one species changes all probabilities in the network. They are not Bernoulli events either, as the sum of all probabilities derived this way sums to unity. On the other hand, “cafeteria experiments” (in which individuals from two species are directly exposed to one another to observe whether or not an interaction occurs) give truly independent probabilities of interactions; even a simple criteria, such as the frequency of interactions when the two species are put together, is a way of estimating probability. Using the approach ~~outline by (???)~~outlined by Poisot et al. (2015), both sources of information (species abundance, trait distribution, and the outcome of experiments) can be combined to estimate the probability that interactions will happen in empirical communities. This effort requires improved communications between scientists collecting data and scientists developing methodology to analyze them.

Another way to obtain approximation of the probability of interactions is to use spatially replicated sampling. Some studies (Tylianakis *et al.* 2007; Olito & Fox 2014; Carstensen *et al.* 2014; Trøjsgaard *et al.* 2015) surveyed the existence of interactions at different locations, and a simple approach of dividing the number of observations of an interaction by the number of co-occurrence of the species involved will provide a (somewhat crude) estimate of the probability of this interaction. This approach requires extensive sampling, especially since interactions are harder to observe than species (Poisot *et al.* 2012; Gilarranz *et al.* 2014), yet it enables the re-analysis of existing datasets in a probabilistic context.

~~Understanding the structure of ecological networks, and whether it relates to ecosystem properties, is emergent as a key challenge for community ecology. A proper estimation of this structure requires tools that address all forms of complexity, the most oft-neglected yet pervasive of which is the fact that interactions are variable. By developing these metrics, we allow future analyses of network structure to account for this phenomenon~~

Implications for data collection.

An important development is that, when estimating probabilities from observational data, it becomes possible to have an estimate of how robust the sampling is. How completely a networks is sampled is a key, yet an often overlooked one, driver of some measures of

structure (Nielsen & Bascompte 2007; Chacoff *et al.* 2011). The probabilistic approach allows to estimate the *confidence interval* of the interaction probability, knowing the number of samples used for the estimation. Assuming normally distributed observational error (this can be generalized for other structure of error), the confidence interval around a probability p estimated from n samples is

$$\varepsilon = z \sqrt{\frac{1}{n} p(1-p)}$$

For a 95% confidence interval, $z \approx 1.96$. If an interaction is estimated to happen at $p = 0.3$, its 95% confidence interval is $[0; 0.74]$ when estimated from four samples, $[0.01; 0.58]$ when estimated from ten, and $[0.21; 0.38]$ when estimated from a hundred. This points out to a fundamental issue with the sampling of networks: a correct estimate of the probability of interaction from observational data is tremendously difficult to achieve, and the development of predictive models should be a research priority since it partly alleviates this difficulty.

IMPLEMENTATION

We provide these measures in a free and open-source (MIT license) library for the `julia` language, available at <http://github.com/PoisotLab/ProbabilisticNetwork.jl>. The code can be cited using the following DOI: **TODO**. A user guide, and API reference, can be found at <http://probabilisticnetwork.org>. The code library undergoes automated testing and coverage analysis, the results of which can be accessed from the *GitHub* page given above.

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REFERENCES

Almeida-Neto, M., Guimarães, P., Guimarães, P.R., Loyola, R.D. & Ulrich, W. (2008). A consistent metric for nestedness analysis in ecological systems: reconciling concept and measurement. *Oikos*, **117**, 1227–1239. Retrieved October 10, 2014,

- 1 Bascompte, J., Jordano, P., Melián, C.J. & Olesen, J.M. (2003). The nested assembly of plant-animal
2 mutualistic networks. *Proc. Natl. Acad. Sci. U. S. A.*, **100**, 9383–9387.
- 3 Bastolla, U., Fortuna, M.A., Pascual-García, A., Ferrera, A., Luque, B. & Bascompte, J. (2009). The
4 architecture of mutualistic networks minimizes competition and increases biodiversity. *Nature*, **458**,
5 1018–1020. Retrieved October 10, 2014,
- 6 [Bersier, L.F., Banavsek-Richter, C. & Cattin, M.F. \(2002\). Quantitative descriptors of food-web
7 matrices. *Ecology*, **83**, 2394–2407.](#)
- 8 [Boulangéat, I., Gravel, D. & Thuiller, W. \(2012\). Accounting for dispersal and biotic interactions to
9 disentangle the drivers of species distributions and their abundances. *Ecol. Lett.*, **15**, 584–593.](#)
- 10 Canard, E.F., Mouquet, N., Mouillot, D., Stanko, M., Miklisova, D. & Gravel, D. (2014). Empirical
11 evaluation of neutral interactions in host-parasite networks. *The American Naturalist*, **183**, 468–479.
- 12 Carstensen, D.W., Sabatino, M., Trøjelsgaard, K. & Morellato, L.P.C. (2014). Beta Diversity of
13 Plant-Pollinator Networks and the Spatial Turnover of Pairwise Interactions. *PLoS ONE*, **9**, e112903.
14 Retrieved November 19, 2014,
- 15 [Chacoff, N.P., Vázquez, D.P., Lomáscolo, S.B., Stevani, E.L., Dorado, J. & Padrón, B. \(2011\).
16 Evaluating sampling completeness in a desert plant-pollinator network. *J. Anim. Ecol.*, no-no.](#)
- 17 [Chagnon, P.-L. \(2015\). Characterizing topology of ecological networks along gradients: The limits
18 of metrics' standardization. *Ecological Complexity*, **22**, 36–39. Retrieved March 9, 2015.](#)
- 19 Chamberlain, S.A., Cartar, R.V., Worley, A.C., Semmler, S.J., Gielens, G., Elwell, S., Evans, M.E.,
20 Vamosi, J.C. & Elle, E. (2014). Traits and phylogenetic history contribute to network structure
21 across Canadian plant-pollinator communities. *Oecologia*, 1–12. Retrieved September 11, 2014,
22 from <http://link.springer.com/article/10.1007/s00442-014-3035-2>
- 23 Duffy, J.E. (2002). Biodiversity and ecosystem function: the consumer connection. *Oikos*, **99**,
24 201–219.
- 25 Dunne, J.A. (2006). The Network Structure of Food Webs. *Ecological networks: Linking structure
26 and dynamics* (eds J.A. Dunne & M. Pascual), pp. 27–86. Oxford University Press.

- 1 Fortuna, M.A. & Bascompte, J. (2006). Habitat loss and the structure of plant-animal mutualistic
2 networks. *Ecol. Lett.*, **9**, 281–286. Retrieved January 21, 2015,
- 3 Gilarranz, L.J., Sabatino, M., Aizen, M.A. & Bascompte, J. (2014). Hot spots of mutualistic net-
4 works. *J Anim Ecol*, n/a–n/a. Retrieved November 17, 2014,
- 5 [Golubski, A.J. & Abrams, P.A. \(2011\). Modifying modifiers: what happens when interspecific](#)
6 [interactions interact? *J. Anim. Ecol.*, **80**, 1097–1108.](#)
- 7 Haerter, J.O., Mitarai, N. & Sneppen, K. (2014). Phage and bacteria support mutual diversity in a
8 narrowing staircase of coexistence. *ISME Journal*.
- 9 [Ims, R.A., Henden, J.-A., Thingnes, A.V. & Killengreen, S.T. \(2013\). Indirect food web interactions](#)
10 [mediated by predator-rodent dynamics: relative roles of lemmings and voles. *Biology Letters*, **9**,](#)
11 [20130802. Retrieved November 6, 2013.](#)
- 12 Jordano, P. (1987). Patterns of mutualistic interactions in pollination and seed dispersal: con-
13 nectance, dependence asymmetries, and coevolution. *Am. Nat.*, **129**, 657–677.
- 14 [Jordano, P. & Bascompte, J. \(2013\). *Mutualistic Networks*. Princeton Univ Press. Retrieved from](#)
15 <http://press.princeton.edu/titles/10161.html>
- 16 Katz, L. (1953). A new status index derived from sociometric analysis. *Psychometrika*, **18**, 39–43.
17 Retrieved October 9, 2014,
- 18 Koleff, P., Gaston, K.J. & Lennon, J.J. (2003). Measuring beta diversity for presence-absence data.
19 *J. Anim. Ecol.*, **72**, 367–382.
- 20 [Maruyama, P.K., Vizentin-Bugoni, J., Oliveira, G.M., Oliveira, P.E. & Dalsgaard, B. \(2014\). Morphological](#)
21 [and Spatio-Temporal Mismatches Shape a Neotropical Savanna Plant-Hummingbird Network. *Biotropica*,](#)
22 [46, 740–747. Retrieved October 30, 2014.](#)
- 23 McCann, K.S. (2014). Diversity and Destructive Oscillations: Camerano, Elton, and May. *Bulletin*
24 *of the Ecological Society of America*, **95**, 337–340. Retrieved October 7, 2014,

1 Milo, R., Kashtan, N., Itzkovitz, S., Newman, M.E.J. & Alon, U. (2003). On the uniform generation
2 of random graphs with prescribed degree sequences. *ArXivcond-Mat0312028*. Retrieved October 9,
3 2014, from <http://arxiv.org/abs/cond-mat/0312028>

4 Milo, R., Shen-Orr, S., Itzkovitz, S., Kashtan, N., Chklovskii, D. & Alon, U. (2002). Network
5 motifs: simple building blocks of complex networks. *Science*, **298**, 824–7.

6 Mirchandani, P.B. (1976). Shortest distance and reliability of probabilistic networks. *Comput. Oper.*
7 *Res.*, **3**, 347–355. Retrieved October 12, 2014, from [http://www.sciencedirect.com/science/](http://www.sciencedirect.com/science/article/pii/0305054876900174)
8 [article/pii/0305054876900174](http://www.sciencedirect.com/science/article/pii/0305054876900174)

9 Newman, M.E.J. (2004). Fast algorithm for detecting community structure in networks. *Phys. Rev.*
10 *E*, **69**, 066133. Retrieved February 24, 2015,

11 [Nielsen, A. & Bascompte, J. \(2007\). Ecological networks, nestedness and sampling effort. *Ecology*,](#)
12 [95, 1134–1141.](#)

13 Olesen, J.M., Bascompte, J., Dupont, Y.L., Elberling, H., Rasmussen, C. & Jordano, P. (2011).
14 Missing and forbidden links in mutualistic networks. *Proc. R. Soc. B*, **278**, 725–732. Retrieved
15 October 7, 2014,

16 Olito, C. & Fox, J.W. (2014). Species traits and abundances predict metrics of plantpollinator net-
17 work structure, but not pairwise interactions. *Oikos*, n/a–n/a. Retrieved January 19, 2015,

18 ~~Poisot, T. (2012). L’ABC de la spécialisation: apparition, biodiversité, conservation. *Prisme À*~~
19 ~~*Idées*, **4**, 49–52.~~

20 ~~Poisot, T.~~ & Gravel, D. (2014). When is an ecological network complex? Connectance drives degree
21 distribution and emerging network properties. *PeerJ*, **2**, e251. Retrieved September 13, 2014,

22 Poisot, T., Canard, E., Mouillot, D., Mouquet, N. & Gravel, D. (2012). The dissimilarity of species
23 interaction networks. *Ecol Lett*, **15**, 1353–1361. Retrieved November 3, 2014,

24 Poisot, T., Lounnas, M. & Hochberg, M.E. (~~2013~~[2013a](#)). The structure of natural microbial enemy-
25 victim networks. *Ecol. Process.*, **2**, 13. Retrieved March 27, 2015,

- 1 [Poisot, T., Mouquet, N. & Gravel, D. \(2013b\). Trophic complementarity drives the biodiversityecosystem](#)
2 [functioning relationship in food webs. *Ecol. Lett.*, n/a–n/a. Retrieved May 22, 2013,](#)
- 3 [Poisot, T., Stouffer, D.B. & Gravel, D. \(2015\). Beyond species: why ecological interaction networks](#)
4 [vary through space and time. *Oikos*, **124**, 243–251. Retrieved November 5, 2014,](#)
- 5 Poullain, V., Gandon, S., Brockhurst, M.A., Buckling, A. & Hochberg, M.E. (2008). The Evolution
6 of Specificity in Evolving and Coevolving Antagonistic Interactions Between a Bacteria and Its
7 Phage. *Evolution*, **62**, 1–11. Retrieved October 10, 2014,
- 8 [Sanders, D. & Veen, F.J.F. van. \(2012\). Indirect commensalism promotes persistence of secondary](#)
9 [consumer species. *Biology Letters*, 960–963.](#)
- 10 Stouffer, D.B. & Bascompte, J. (2011). Compartmentalization increases food-web persistence. *Proc.*
11 *Natl. Acad. Sci. U.S.A.*, **108**, 3648–3652.
- 12 Stouffer, D.B., Camacho, J., Jiang, W. & Amaral, L.A.N. (2007). Evidence for the existence of a
13 robust pattern of prey selection in food webs. *Proc. R. Soc. B Biol. Sci.*, **274**, 1931–40.
- 14 Thébault, E. & Loreau, M. (2003). Food-web constraints on biodiversityecosystem functioning
15 relationships. *Proc. Natl. Acad. Sci. U. S. A.*, **100**, 14949–14954.
- 16 Trøjelsgaard, K., Jordano, P., Carstensen, D.W. & Olesen, J.M. (2015). Geographical variation in
17 mutualistic networks: similarity, turnover and partner fidelity. *Proc. R. Soc. B*, **282**, 20142925.
18 Retrieved February 1, 2015,
- 19 Tylianakis, J.M., Tscharntke, T. & Lewis, O.T. (2007). Habitat modification alters the structure
20 of tropical hostparasitoid food webs. *Nature*, **445**, 202–205. Retrieved January 28, 2013, from
21 <http://www.nature.com/nature/journal/v445/n7124/abs/nature05429.html>
- 22 [Vizentin-Bugoni, J., Maruyama, P.K. & Sazima, M. \(2014\). Processes entangling interactions in](#)
23 [communities: forbidden links are more important than abundance in a hummingbirdplant network.](#)
24 [Proc. R. Soc. B](#), **281**, 20132397. Retrieved February 28, 2014,

1 Yeakel, J.D., Guimarães, P.R., Novak, M., Fox-Dobbs, K. & Koch, P.L. (2012). Probabilistic patterns
2 of interaction: the effects of link-strength variability on food web structure. *J. R. Soc. Interface*,
3 rsif20120481. Retrieved November 3, 2014,