

THE STRUCTURE OF PROBABILISTIC NETWORKS

T. POISOT, A.R. CIRTWILL, K. CAZELLES, D. GRAVEL, M.-J. FORTIN, AND D.B. STOUFFER

ABSTRACT

1. There is a growing realization among community ecologists that interactions between species vary in space and time, and that this variation needs be quantified. Yet, our current numerical framework to analyze the structure of species interactions, largely based on graph-theoretical approaches, is unsuited to probabilistic approaches. Since the variation of species interactions holds valuable ecological 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 us 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 by discussing how the sampling and data representation of ecological networks can be adapted to better allow the application of a fully probabilistic numerical network framework.

Keywords: ecological networks, species interactions, 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 (Bascompte et al. 2003; Jordano 1987). The key result of this line of research was linking network structure to community or ecosystem-level properties such as stability (McCann 2014), coexistence (Bastolla et al. 2009; Haerter, Mitarai, and Sneppen 2014), or ecosystem functioning (Duffy 2002). To a large extent, the description of ecological networks resulted in the emergence of questions about how functions and properties of communities emerged from their structure, and this stimulated the development of a rich methodological literature (see *e.g.* Jordano and Bascompte 2013), 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* (*e.g.* nodes, links, or groups thereof) 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, higher-order moments, or probability distributions.

In the recent years, the interpretation of the properties of network structure (as indicators of the action of ecological or evolutionary processes) has been challenged 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 way (Poisot et al.

1 2012; Trøjelsgaard et al. 2015). Empirical and theoretical studies suggest that the network is not
2 the right unit to understand this variation; rather, network variation is an emergent property of the
3 response of ecological interactions to environmental factors and chance events (see Poisot, Stouffer,
4 and Gravel 2015 for a review). Interactions can vary because of local mismatching in phenology
5 (Olesen et al. 2011; P. K. Maruyama et al. 2014; Vizentin-Bugoni, Maruyama, and Sazima 2014),
6 populations fluctuations preventing the interaction (E. F. Canard et al. 2014), or a combination of
7 both (Olito and Fox 2014; Chamberlain et al. 2014). For example, Olito and Fox (2014) showed that
8 accounting for neutral (population-size driven) and trait-based effects allows the prediction of the
9 cumulative change in network structure, but not of the change at the level of individual interactions.
10 In addition, Carstensen et al. (2014) showed that not all interactions are equally variable within a
11 meta-community: some are highly consistent, whereas others are extremely rare. These empirical
12 results all point to the fact that species interactions cannot always be adequately represented as yes-no
13 events; since it is well established that they do vary, it is necessary to represent them as probabilities.
14 We should therefore replace the question of *Do these two species interact?* by *How likely is it that*
15 *they will interact?*

16 The current way of dealing with probabilistic interactions are either to ignore variability entirely
17 or to generate random networks. Probabilistic measures of network structure are a mathematically
18 rigorous alternative to both. When ignoring the probabilistic nature of interactions (henceforth *binary*
19 networks), every non-zero element of the network is explicitly assumed to occur with probability
20 1. This leads to over-representation of some rare events, and increases the number of interactions;
21 as a result, this changes the estimated value of different network properties, in a way that remains
22 poorly understood. Issues are most likely to arise for the range of connectances where the topological
23 (Chagnon 2015) or permutational (Poisot and Gravel 2014) space of random network is small, leading
24 to over-replication or uncharacterized biases. An alternative is to consider only the interactions above
25 a given threshold, which unfortunately leads to under-representation of rare events and decreases the
26 effective number of interactions (in addition to the problem that there is no robust criterion to decide
27 on a threshold). More importantly, the use of thresholds introduces the risk of removing species
28 that have a lot of interactions that individually have a low probability of occurring. Taken together,

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

8 The elements discussed above requires the considerable methodological adjustment of re-writing
9 measures of network structure to account for the fact that interactions are not consistent; in this
10 paper, we re-develop a unified toolkit of measures to characterize the structure of probabilistic inter-
11 action networks. Several direct and emergent core properties of ecological networks (both bipartite
12 and unipartite) can be re-formulated in a probabilistic context. We conclude by showing how this
13 methodology can be applied to exploit the information contained in the variability of networks, and
14 to reduce the computational burden of current methods in network analysis.

15 SUITE OF PROBABILISTIC NETWORK METRICS

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

1 The unipartite transformation of a bipartite matrix \mathbf{A} is the block matrix \mathbf{A} :

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

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

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

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

11 As all X_i are Bernoulli random variables ,

$$(3) \quad \text{var}(X_1 X_2 \dots X_n) = \prod_i p_i - \prod_i p_i^2$$

12 As a final note, all of the measures described below can be applied on the binary (0/1) versions of the
13 networks in which case they converge on the non-probabilistic version of the measure as usually cal-
14 culated. This property is particularly desirable as it allows our framework to be used on any network,
15 whether they are represented in a probabilistic or binary way. Nonetheless, the approach outlined
16 here differs from using *weighted* networks, in that it answers a completely different question (???).
17 Probabilistic networks describe the probability that any interaction will happen, whereas weighted

networks describe the effect of the interaction when it happens (???). Although there are several measures for *quantitative* networks (Bersier, Banavsek-Richter, and Cattin 2002), in which interactions happen but with different outcomes, these are not relevant for probabilistic networks, which require accounting for the fact that interactions are probabilistic event, *i.e.* they display a variance that will cascade up to the network level. Instead, the weight of each interaction is best viewed as a second modeling step that focuses solely on the non-zero cases (*i.e.* the interactions that are realized); this is similar to the method now frequently used in species distribution models, where the species presence is modeled first, and its abundance second, using a (possibly) different set of predictors (Boulangeat, Gravel, and Thuiller 2012).

10 **Direct network properties.**

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

$$(4) \quad \hat{L} = \sum_{i,j} A_{ij},$$

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

17 *Node degree.* The degree distribution of a network is the distribution of the number of interactions established (number of successors) and received (number of predecessors) by each node. The expected degree of species i is

$$(5) \quad \hat{k}_i = \sum_j (A_{ij} + A_{ji}).$$

1 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
 2 that $\sum \hat{k}_i = 2\hat{L}$, as expected

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

5 **Emergent network properties.**

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

$$(6) \quad n_{ij}^{(k)} = (\mathbf{A}^k)_{ij} ,$$

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

12 It is possible to calculate the probability of having at least one path of length k between the two
 13 species: this can be done by calculating the probability of having no path of length k , then taking
 14 the running product of the resulting array of probabilities. For the example of length 2, species i and
 15 j are connected through g with probability $A_{ig}A_{gj}$, and so this path does not exist with probability
 16 $1 - A_{ig}A_{gj}$. For any pair i, j , let \mathbf{m} be the vector such that $m_g = A_{ig}A_{gj}$ for all $g \notin (i, j)$ (Mirchandani
 17 1976). The probability of not having any path of length 2 is $\prod (1 - \mathbf{m})$. Therefore, the probability of
 18 having a path of length 2 between i and j is

$$(7) \quad \hat{p}_{ij}^{(2)} = 1 - \prod (1 - \mathbf{m}),$$

1 which can also be noted

$$(8) \quad \hat{p}_{ij}^{(2)} = 1 - \prod_g (1 - A_{ig} A_{gj}).$$

2 In most situations, one would be interested in knowing the probability of having a path of length 2
 3 *without* having a path of length 1; this is simply expressed as $\hat{p}_{ij}^{(2)*} = (1 - A_{ij})\hat{p}_{ij}^{(2)}$. These results can
 4 be expanded to any length k in $[2, n - 1]$. First one can, by the same logic, generate the expression
 5 for having at least one path of length k :

$$(9) \quad \hat{p}_{ij}^{(k)} = 1 - \prod_{(g_1, g_2, \dots, g_{k-1})} (1 - A_{ig_1} A_{g_1 g_2} \dots A_{g_{k-1} j})$$

6 where $(g_1, g_2, \dots, g_{k-1})$ are all the $(k - 1)$ -permutations of $1, 2, \dots, n \setminus (i, j)$. Then having a path of length
 7 k without having any smaller path is

$$(10) \quad \hat{p}_{ij}^{(k)*} = (1 - A_{ji})(1 - \hat{p}^{(2)}) \dots (1 - \hat{p}^{(k-1)})\hat{p}^{(k)}.$$

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 (“side” of the network) that are connected through at
 10 least one node of the other mode; for example, two plants are connected if they share at least one
 11 pollinator. It is readily obtained using the formula in the *Path length* section. This yields either the
 12 probability of an edge in the unipartite projection (of the upper or lower nodes), or if using the matrix
 13 multiplication, the 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); this measure is a modification of NODF (Almeida-Neto et al.
 17 2008) for ties in species degree that removes the constraint of decreasing fill. Nestedness for each

1 margin of the matrix is defined as $\eta^{(R)}$ and $\eta^{(C)}$ for, respectively, rows and columns. As per Almeida-
 2 Neto et al. (2008), we define a global statistic for nestedness as $\eta = (\eta^{(R)} + \eta^{(C)})/2$.
 3 Nestedness, in a probabilistic network, is defined as

$$(11) \quad \eta^{(R)} = \sum_{i < j} \frac{\sum_k A_{ik} A_{jk}}{\min(g_i, g_j)},$$

4 where g_i is the expected generality of species i . The reciprocal holds for $\eta^{(C)}$ when using v_i (the
 5 vulnerability) instead of g_i . The values returned are within $[0; 1]$, with $\eta = 1$ indicating complete
 6 nestedness.

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

$$(12) \quad Q = \sum_{m=1}^c (e_{mm} - a_m^2),$$

13 where c is the number of modules,

$$(13) \quad e_{mm} = \sum_{ij} \frac{A_{ij}}{2c} \delta(\mathbf{s}_i, \mathbf{s}_j),$$

14 and

$$(14) \quad a_m = \sum_n e_{mn},$$

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

4 *Centrality.* Although node degree is a rough first order estimate of centrality, other measures are of-
 5 ten needed. Here, we derive the expected value of centrality according to Katz (1953). This measure
 6 generalizes to directed acyclic graphs (whereas other do not). For example, although eigenvector
 7 centrality is often used in ecology, it cannot be measured on probabilistic graphs. Eigenvector cen-
 8 trality requires the matrix's largest eigenvalues to be real, which is not the case for all probabilistic
 9 matrices. The measure proposed by Katz is a useful replacement, because it accounts for the paths
 10 of all length between two species instead of focusing on the shortest path.

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

$$(15) \quad C_i = \sum_{j=1}^n \sum_{k=1}^{n-1} \alpha^k (\mathbf{A}^k)_{ji}.$$

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

$$(16) \quad C_i = \frac{C_i}{\mathbf{C}}.$$

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

19 *Species with no outgoing links.* Estimating the number of species with no outgoing links (successors)
 20 can be useful when predicting whether, *e.g.*, predators will go extinct. Alternatively, when prior

- 1 information about traits are available, this can allows predicting the invasion success of a species in
 2 a novel community.
- 3 A species has no successors if it manages *not* to establish any outgoing interaction, which for species
 4 i happens with probability

$$(17) \quad \prod_j (1 - A_{ij}) .$$

- 5 The number of expected such species is therefore the sum of the above across all species,

$$(18) \quad \hat{P}P = \sum_i \left(\prod_j (1 - A_{ij}) \right) ,$$

- 6 and its variance is

$$(19) \quad \text{var}(\hat{P}P) = \sum_i \left(\prod_j (1 - A_{ij}^2) - \prod_j (1 - A_{ij})^2 \right) .$$

- 7 Note that in a non-probabilistic context, species with no outgoing links would be considered primary
 8 producers. This is not the case here: if interactions are probabilistic events, then even a top predator
 9 may have no preys, and this clearly doesn't imply that it will become a primary producer in the
 10 community. For this reason, the trophic position of the species may be measured better with the
 11 binary version of the matrix.

- 12 *Species with no incoming links.* Using the same approach as for the number of species with no out-
 13 going links, the expected number of species with no incoming links is therefore

$$(20) \quad \hat{T}P = \sum_i \left(\prod_{j \neq i} (1 - A_{ji}) \right) .$$

1 Note that we exclude self-interactions, as top-predators in food webs can, and often do, engage in
2 cannibalism.

3 *Number of species with no interactions.* Predicting the number of species with no interactions (or
4 whether any species will have at least one interaction) is useful when predicting whether species will
5 be able to integrate into an existing network, for example. From a methodological point of view, this
6 can also be a helpful *a priori* measure to determine whether null models of networks will have a lot
7 of species with no interactions, and so will require intensive sampling.

8 A species has no interactions with probability

$$(21) \quad \prod_{j \neq i} (1 - A_{ij})(1 - A_{ji}).$$

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

$$(22) \quad \hat{F}S = \sum_i \prod_{j \neq i} (1 - A_{ij})(1 - A_{ji}).$$

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

$$(23) \quad \text{var}(\hat{F}S) = \sum_i \left(A_{ij}(1 - A_{ij})A_{ji}(1 - A_{ji}) + A_{ij}(1 - A_{ij})A_{ji}^2 + A_{ji}(1 - A_{ji})A_{ij}^2 \right)$$

12 *Self-loops.* Self-loops (the existence of an interaction of a species onto itself) is only meaningful in
13 unipartite networks. The expected proportion of species with self-loops is very simply defined as
14 $\text{Tr}(\mathbf{A})$, that is, the sum of all diagonal elements. The variance is $\text{Tr}(\mathbf{A} \diamond (1 - \mathbf{A}))$, where \diamond is the
15 element-wise product operation (Hadamard product).

1 *Motifs*. Motifs are sets of pre-determined interactions between a fixed number of species (R Milo et
 2 al. 2002; D. B. Stouffer et al. 2007), such as apparent competition with one predator sharing two
 3 prey. As there are an arbitrarily large number of motifs, we will illustrate the approach with only two
 4 examples.

5 The probability that three species form an apparent competition motif where i is the predator, j and
 6 k are the prey, is

$$(24) \quad P(i, j, k \in \text{app. comp}) = A_{ij}(1 - A_{ji})A_{ik}(1 - A_{ki})(1 - A_{jk})(1 - A_{kj}).$$

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

$$(25) \quad P(i, j, k \in \text{omniv.}) = A_{ij}(1 - A_{ji})A_{ik}(1 - A_{ki})A_{jk}(1 - A_{kj}).$$

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

$$(26) \quad \hat{N}_m = \sum_i \sum_{j \neq i} \sum_{k \neq j} P(i, j, k \in m).$$

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

13 **Network comparison.** The dissimilarity of a pair of (ecological) networks can be measured using
 14 the framework set forth by Koleff, Gaston, and Lennon (2003) using β -diversity measures. Measures
 15 of β -diversity compute the dissimilarity between two networks based on the cardinality of three sets,
 16 a , c , and b , which are respectively the shared items, items unique to superset (network) 1, and items

1 unique to superset 2 (the identity of which network is 1 or 2 matters for asymmetric measures). Su-
 2 persets can be the species within each network, or the interactions between species. Following Poisot
 3 et al. (2012), the dissimilarity of two networks can be measured as either β_{WN} (all interactions), or
 4 β_{OS} (interactions involving only common species), with $\beta_{OS} \leq \beta_{WN}$.
 5 Within our framework, these measures can be applied to probabilistic networks. The expected values
 6 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}
 7 is measured requires to alter the matrices \mathbf{A}_1 and \mathbf{A}_2 . To measure β_{OS} , one must remove all unique
 8 species; to measure β_{WN} , one must expand the two matrices so that they have the same species at the
 9 same place, and give a weight of 0 to the added interactions.

10 APPLICATIONS

11 In this section, we contrast the use of probabilistic measures to the current approaches of either using
 12 binary networks, or working with null models through simulations. When generating random net-
 13 works, what we call *Bernoulli trials* from here on, a binary network is generated by doing a Bernoulli
 14 trial with probability A_{ij} , for each element of the matrix. This generates networks that have only 0/1
 15 interactions, and are realizations of the probabilistic network. This is problematic because higher
 16 order structures involving rare events will be under-represented in the sample, and because most
 17 naive approaches (*i.e.* not controlling for species degree) are likely to generate species with no in-
 18 teractions, especially in sparsely connected networks frequently encountered in ecology (R. Milo et
 19 al. 2003; Poisot and Gravel 2014; Chagnon 2015) – on the other hand, non-naive approaches (*e.g.*
 20 based on swaps or quasi-swaps as explained in ???) break the assumption of independence between
 21 interactions.

22 **Comparison of probabilistic networks.** In this sub-section, we apply the above probabilistic mea-
 23 sures to a bacteria–phage interaction network. Poullain et al. (2008) measured the probability that
 24 24 phage can infect 24 strains of bacteria of the *Pseudomonas fluorescens* species (group SBW25).
 25 The (probabilistic) adjacency matrix was constructed by estimating the probability of each phage–
 26 bacteria interaction through 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 results (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
$\eta^{(C)}$	0.75	0.531	0.518
one consumer, two resources motif	4784	2089	2110
two consumers, one resource motif	4718	2116	2120

As these results show, treating all interactions as having the same probability, *i.e.* removing the information about variability, (i) overestimates nestedness by ≈ 0.2 , (ii) overestimates the number of links by 115, and (iii) overestimates the number of motifs (we have limited our analysis to the two following motifs: one consumer sharing two resources, and two consumers competing for one resource). 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). For the number of motifs, the difference was larger, but not overly so. It should be noted that, especially for computationally demanding operations such as motif counting, the difference in runtime between the probabilistic and Bernoulli trials approaches can be extremely important.

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

1 close to the analytical expression of the measures; due to the experimental design of the Poullain
2 et al. (2008) study, probabilities of interactions are bound to be high, and so variance is minimal
3 (most elements of \mathbf{A} have a value of either 0 or 1, and so their individual variance is 0 – though their
4 confidence interval varies as a function of the number of observations from which the probability is
5 derived). Still, despite overall low variance, the binary approach severely mis-represents the structure
6 of the network.

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

12 We use the following null models. First (Type I, Fortuna and Bascompte (2006)), any interaction
13 between plant and animals happens with the fixed probability $P = C\alpha$. This model controls for con-
14 nectance, but removes the effect of degree distribution. Second, (Type II, Bascompte et al. (2003)),
15 the probability of an interaction between animal i and plant j is $(k_i/R + k_j/C)/2$, the average of the
16 richness-standardized degree of both species. In addition, we use the models called Type III in and
17 out (Poisot, Lounnas, and Hochberg 2013), that use the row-wise and column-wise probability of an
18 interaction respectively, as a way to understand the impact of the degree distribution of upper and
19 lower level species.

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

1 We measured the nestedness of the 59 (binary) networks, then generated the random networks under
 2 the four null models, and calculated the expected nestedness using the probabilistic measure. Our
 3 results are presented in [Figure 1](#).

4 There are two striking results. First, empirical data are consistently *more* nested than the null expect-
 5 ation, as evidenced by the fact that all Δ_N values are strictly positive. Second, this underestimation
 6 is *linear* between null models I and II, although null model II is always closer to the nestedness of the
 7 empirical network (which makes sense, since null model II incorporates the higher order constraint
 8 of approximating the degree distribution of both levels). That the nestedness of the null model prob-
 9 ability matrix is so strongly determined by the nestedness of the empirical networks calls for a closer
 10 evaluation of how the results of null models are interpreted (especially since networks generated
 11 using Bernoulli trials revealed a very low variance in their nestedness).

12 There is a strong, and previously unaccounted for, circularity in this approach: empirical networks
 13 are compared to a null model which, as we show, has a systematic bias *and* a low variance (in the
 14 properties of the networks it generates), meaning that differences in nestedness that are small (thus

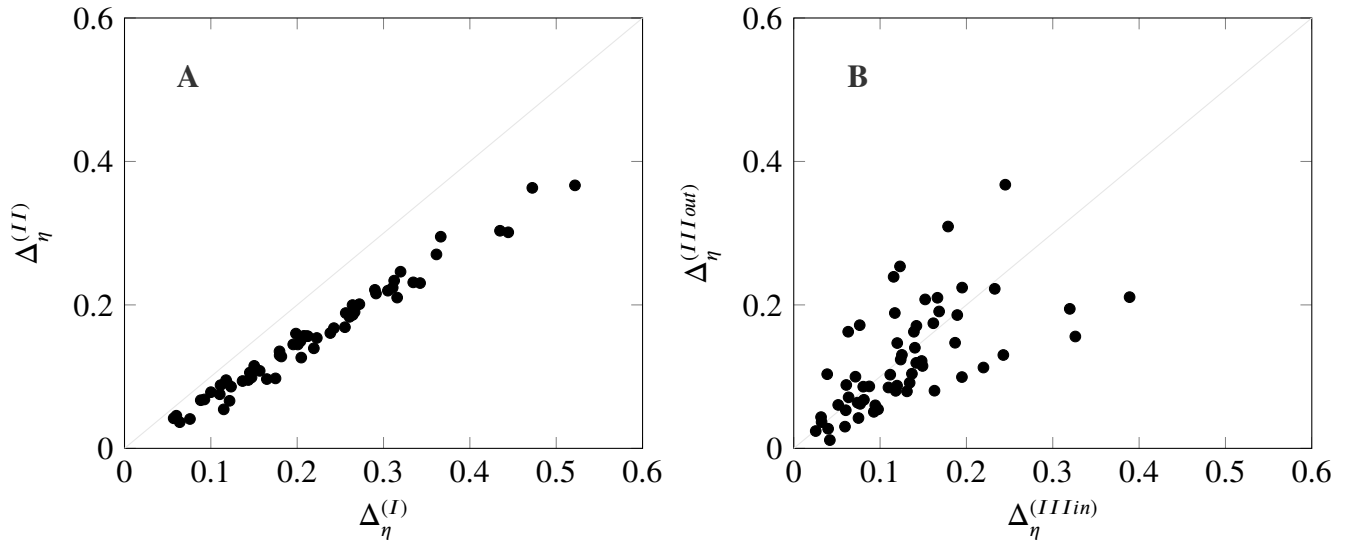


FIGURE 1. Results of the null model analysis of 59 plant-pollination networks. **A.** There is a consistent tendency for (i) both models I and II to estimate less nestedness than in the empirical network, although null model II yields more accurate estimates. **B.** Models III in and III out also estimate less nestedness than the empirical network, but neither has a systematic bias. For each null model i , the difference $\Delta_\eta^{(i)}$ in nestedness η is expressed as $\Delta_\eta^{(i)} = \eta - \mathcal{N}^{(i)}(\eta)$, where $\mathcal{N}^{(i)}(\eta)$ is the nestedness of null model i .

1 potentially ecologically irrelevant) have a good chance of being reported as significant. Interestingly,
2 models III in and III out made overall *fewer* mistakes at estimating nestedness – respectively 0.129
3 and 0.123, compared to resp. 0.219 and 0.156 for model I and II. Although the error is overall
4 sensitive to model type (Kruskal-Wallis $\chi^2 = 35.80$, d.f. = 3, $p \leq 10^{-4}$), the three pairs of models
5 that where significantly different after controlling for multiple comparisons are I and II, I and III in,
6 and I and III out (model II is not different from either models III in or out).

7 In short, this analysis reveals that (i) the null expectation of a network property under randomization
8 scenarios can be obtained through the analysis of the probabilistic matrix, instead of the analysis of
9 simulated Bernoulli networks; (ii) different models have different systematic biases, with models of
10 the type III performing overall better for nestedness than any other models. This can be explained
11 by the fact that nestedness of a network, as expressed by Bastolla et al. (2009), is the average of
12 a row-wise and column-wise nestedness. These depend on the species degree, and as such should
13 be well predicted by models III. The true novelty of the approach outlined here is that, rather than
14 having to calculate the measure for thousands of replicates, an *unbiased* estimate of its mean can be
15 obtained in a fraction of the time using the measures described here. This is particularly important
16 since, as demonstrated by Chagnon (2015), the generation of null randomization is subject to biases
17 in the range of connectance where most ecological networks fall. Our approach aims to provide a
18 bias-free, time-effective way of estimating the expected value of a network property.

19 **Spatial-variation predicts local network structure.** In this final application, we re-analyze data
20 from a previous study by Trøjelsgaard et al. (2015), to investigate how spatial information can be
21 used to derive probability of interactions. In the original dataset, fourteen locations have been sam-
22 pled to describe the local plant-pollination network. This dataset exhibits both species and interaction
23 variability across sampling locations. We define the overall probability of an interaction in the fol-
24 lowing way,

$$(27) \quad P(i \rightarrow j) = \frac{N_{ij}}{O_{ij}},$$

1 where \mathbf{O}_{ij} is the number of sampling locations in which both pollinator i and plant j co-occur, and
2 \mathbf{N}_{ij} is the number of sampling locations in which they interact. This takes values between 0 (no
3 co-occurrence *or* no interactions) and 1 (interaction observed every time there is co-occurrence).
4 This represents a simple probabilistic model, in which it is assumed that our ability to observe the
5 interaction is a proxy of how frequent it is.

6 Based on this information, we compare the connectance, nestedness, and modularity, of each sam-
7 pled network, to the expected values if interactions are well predicted by the probability given above.
8 The results are presented in Figure 2. There is a clear linear, positive correlation (coeff. 0.89 for
9 connectance, 0.76 for η , and 0.92 for modularity) between the observed network properties (binary
10 matrices) and the predictions based on the probabilistic model. This analysis, although simple, sug-
11 gest that the *local* structure of ecological networks can represent the outcome of a filtering of species
12 interactions, the signature of which can be detected at the regional level by a variation in the proba-
13 bilities of interactions.

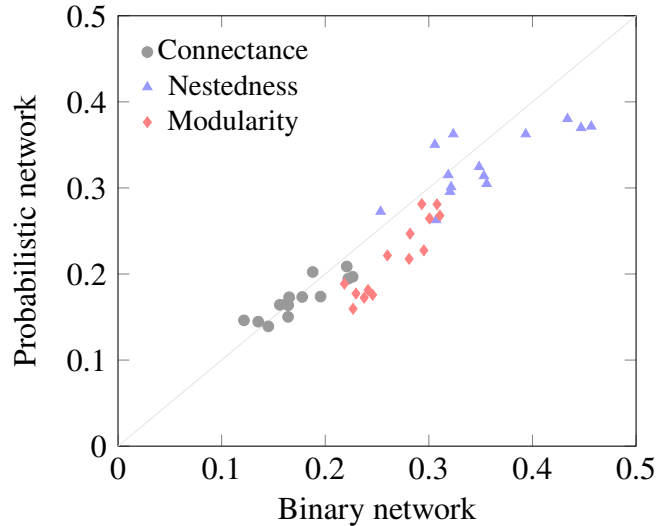


FIGURE 2. Local network structure inferred from the locally observed interactions (x-axis) or the spatial probabilistic model (y-axis) in the Canaria Island dataset. Although the binary networks slightly under-estimate the properties studied here, there is a positive and linear relationship between the empirical structure, and the structure predicted based on probabilities of interactions derived from occurrence information.

Understanding the structure of ecological networks, and whether it relates to emergent ecosystem properties, is 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. Through the suite of measures we present here, we allow future analyses of network structure to account for this phenomenon. There are two main considerations highlighted by this methodological development. First, in what way are probabilistic data are actually independent, and second, what are the implications for data collection.

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

Estimates of interaction probabilities. Estimating interaction probabilities based on species abundances (E. F. Canard et al. 2014; Olito and Fox 2014) do not 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

1 of estimating probability. Using the approach outlined by Poisot, Stouffer, and Gravel (2015), differ-
 2 ent sources of information (species abundance, trait distribution, and the outcome of experiments)
 3 can be combined to estimate the probability that interactions will happen in empirical communities.

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

12 **Implications for data collection.** An important outcome is that, when estimating probabilities from
 13 observational data, it becomes possible to have an estimate of how robust the sampling is. How
 14 completely a network is sampled is a key, yet often-overlooked, driver of some measures of structure
 15 (Nielsen and Bascompte 2007; Chacoff et al. 2011). The probabilistic approach allows to estimate
 16 the *confidence interval* of the interaction probability, knowing the number of samples used for the
 17 estimation. Assuming normally distributed observational error (this can be generalized for other
 18 structure of error), the confidence interval around a probability p estimated from n samples is

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

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

1 poorly when $n < 30$, or when $p \in \{0, 1\}$; it nevertheless provides an *estimate*, in other situations, of
2 how robust the probability estimate is.

3 **Implementation.** We provide these measures of probabilistic network structure in a free and open-
4 source (MIT license) library for the `julia` language, available at <http://github.com/PoisotLab/ProbabilisticNetworks.jl>.
5 The code can be cited using the following DOI: **TODO**. A user guide, and API reference, can be found
6 at <http://probabilisticnetworkjl.readthedocs.org/en/latest/>. The code library under-
7 goes automated testing and coverage analysis, the results of which can be accessed from the *GitHub*
8 page given above.

9 **Acknowledgements:** This work was funded by a CIEE working group grant to TP, DG, and DBS. TP
10 is funded by a starting grant from the Université de Montréal, and a Discovery grant from NSERC.
11 DBS acknowledges support from a Marsden Fund Fast-Start grant (UOC-1101) and Rutherford Dis-
12 covery Fellowship, both administered by the Royal Society of New Zealand. The idea of network
13 measures as direct/emergent properties was first discussed during the *Web of Life* meeting, held in
14 Montpellier in 2012.

15 REFERENCES

- 16 Almeida-Neto, Mário, Paulo Guimarães, Paulo R. Guimarães, Rafael D. Loyola, and Werner Ulrich.
17 2008. “A Consistent Metric for Nestedness Analysis in Ecological Systems: Reconciling Concept
18 and Measurement.” *Oikos* 117 (8): 1227–39. doi:[10.1111/j.0030-1299.2008.16644.x](https://doi.org/10.1111/j.0030-1299.2008.16644.x).
- 19 Bascompte, Jordi, Pedro Jordano, Carlos J Melián, and Jens M Olesen. 2003. “The Nested Assem-
20 bly of Plantanimal Mutualistic Networks.” *Proc. Natl. Acad. Sci. U. S. A.* 100 (16): 9383–87.
21 doi:[10.1073/pnas.1633576100](https://doi.org/10.1073/pnas.1633576100).
- 22 Bastolla, Ugo, Miguel A. Fortuna, Alberto Pascual-García, Antonio Ferrera, Bartolo Luque, and
23 Jordi Bascompte. 2009. “The Architecture of Mutualistic Networks Minimizes Competition and
24 Increases Biodiversity.” *Nature* 458 (7241): 1018–20. doi:[10.1038/nature07950](https://doi.org/10.1038/nature07950).
- 25 Bersier, L F, C Banaśsek-Richter, and M F Cattin. 2002. “Quantitative Descriptors of Food-Web
26 Matrices.” *Ecology* 83 (9): 2394–2407.

- 1 Boulangeat, Isabelle, Dominique Gravel, and Wilfried Thuiller. 2012. "Accounting for Dispersal
2 and Biotic Interactions to Disentangle the Drivers of Species Distributions and Their Abundances."
3 *Ecol. Lett.* 15 (6): 584–93. doi:[10.1111/j.1461-0248.2012.01772.x](https://doi.org/10.1111/j.1461-0248.2012.01772.x).
- 4 Canard, E. F., N. Mouquet, D. Mouillot, M. Stanko, D. Miklisova, and D. Gravel. 2014. "Empirical
5 Evaluation of Neutral Interactions in Host-Parasite Networks." *The American Naturalist* 183 (4):
6 468–79. doi:[10.1086/675363](https://doi.org/10.1086/675363).
- 7 Carstensen, Daniel W., Malena Sabatino, Kristian Trøjelsgaard, and Leonor Patricia C. Morellato.
8 2014. "Beta Diversity of Plant-Pollinator Networks and the Spatial Turnover of Pairwise Interac-
9 tions." *PLoS ONE* 9 (11): e112903. doi:[10.1371/journal.pone.0112903](https://doi.org/10.1371/journal.pone.0112903).
- 10 Chacoff, Natacha P., Diego P. Vázquez, Silvia B. Lomáscolo, Erica L. Stevani, Jimena Dorado, and
11 Benigno Padrón. 2011. "Evaluating Sampling Completeness in a Desert Plant-Pollinator Network."
12 *J. Anim. Ecol.*, August, no–o. doi:[10.1111/j.1365-2656.2011.01883.x](https://doi.org/10.1111/j.1365-2656.2011.01883.x).
- 13 Chagnon, Pierre-Luc. 2015. "Characterizing Topology of Ecological Networks Along Gradients:
14 The Limits of Metrics' Standardization." *Ecological Complexity* 22: 36–39. doi:[10.1016/j.ecocom.2015.01.004](https://doi.org/10.1016/j.ecocom.2015.01.004).
- 15 Chamberlain, Scott A., Ralph V. Cartar, Anne C. Worley, Sarah J. Semmler, Grahame Gielens, Sherri
16 Elwell, Megan E. Evans, Jana C. Vamosi, and Elizabeth Elle. 2014. "Traits and Phylogenetic History
17 Contribute to Network Structure Across Canadian Plantpollinator Communities." *Oecologia*, 1–12.
18 <http://link.springer.com/article/10.1007/s00442-014-3035-2>.
- 19 Duffy, J. Emmett. 2002. "Biodiversity and Ecosystem Function: The Consumer Connection." *Oikos*
20 99 (2): 201–19. doi:[10.1034/j.1600-0706.2002.990201.x](https://doi.org/10.1034/j.1600-0706.2002.990201.x).
- 21 Dunne, Jennifer A. 2006. "The Network Structure of Food Webs." In *Ecological Networks: Link-
22 ing Structure and Dynamics*, edited by Jennifer A Dunne and Mercedes Pascual, 27–86. Oxford
23 University Press.
- 24 Fortuna, Miguel A., and Jordi Bascompte. 2006. "Habitat Loss and the Structure of Plantanimal
25 Mutualistic Networks." *Ecol. Lett.* 9 (3): 281–86. doi:[10.1111/j.1461-0248.2005.00868.x](https://doi.org/10.1111/j.1461-0248.2005.00868.x).
- 26 Gilarranz, Luis J., Malena Sabatino, Marcelo A. Aizen, and Jordi Bascompte. 2014. "Hot Spots of
27 Mutualistic Networks." *J Anim Ecol*, November, n/a–/a. doi:[10.1111/1365-2656.12304](https://doi.org/10.1111/1365-2656.12304).

- 1 Golubski, Antonio J, and Peter A Abrams. 2011. "Modifying Modifiers: What Happens When Inter-
2 specific Interactions Interact?" *J. Anim. Ecol.* 80 (5): 1097–1108. doi:[10.1111/j.1365-2656.2011.01852.x](https://doi.org/10.1111/j.1365-2656.2011.01852.x).
- 3 Haerter, Jan O., Namiko Mitarai, and Kim Sneppen. 2014. "Phage and Bacteria Support Mutual
4 Diversity in a Narrowing Staircase of Coexistence." *ISME Journal*, May. doi:[10.1038/ismej.2014.80](https://doi.org/10.1038/ismej.2014.80).
- 5 Ims, Rolf A., John-André Henden, Anders V. Thingnes, and Siw T. Killengreen. 2013. "Indirect
6 Food Web Interactions Mediated by Predatorrodent Dynamics: Relative Roles of Lemmings and
7 Voles." *Biology Letters* 9 (6): 20130802. doi:[10.1098/rsbl.2013.0802](https://doi.org/10.1098/rsbl.2013.0802).
- 8 Jordano, Pedro. 1987. "Patterns of Mutualistic Interactions in Pollination and Seed Dispersal: Con-
9 nectance, Dependence Asymmetries, and Coevolution." *Am. Nat.* 129 (5): 657–77.
- 10 Jordano, Pedro, and Jordi Bascompte. 2013. *Mutualistic Networks*. Princeton Univ Press. [http:](http://press.princeton.edu/titles/10161.html)
11 [//press.princeton.edu/titles/10161.html](http://press.princeton.edu/titles/10161.html).
- 12 Katz, Leo. 1953. "A New Status Index Derived from Sociometric Analysis." *Psychometrika* 18 (1):
13 39–43. doi:[10.1007/BF02289026](https://doi.org/10.1007/BF02289026).
- 14 Koleff, Patricia, Kevin J Gaston, and Jack J Lennon. 2003. "Measuring Beta Diversity for Presence-
15 Absence Data." *J. Anim. Ecol.* 72 (3): 367–82. doi:[10.1046/j.1365-2656.2003.00710.x](https://doi.org/10.1046/j.1365-2656.2003.00710.x).
- 16 Maruyama, Pietro K., Jeferson Vizentin-Bugoni, Genilda M. Oliveira, Paulo E. Oliveira, and Bo
17 Dalsgaard. 2014. "Morphological and Spatio-Temporal Mismatches Shape a Neotropical Savanna
18 Plant-Hummingbird Network." *Biotropica* 46 (6): 740–47. doi:[10.1111/btp.12170](https://doi.org/10.1111/btp.12170).
- 19 McCann, Kevin S. 2014. "Diversity and Destructive Oscillations: Camerano, Elton, and May." *Bul-*
20 *letin of the Ecological Society of America* 95 (4): 337–40. doi:[10.1890/0012-9623-95.4.337](https://doi.org/10.1890/0012-9623-95.4.337).
- 21 Milo, R, S Shen-Orr, S Itzkovitz, N Kashtan, D Chklovskii, and U Alon. 2002. "Network Motifs:
22 Simple Building Blocks of Complex Networks." *Science* 298 (5594): 824–7. doi:[10.1126/science.298.5594.824](https://doi.org/10.1126/science.298.5594.824).
- 23 Milo, R., N. Kashtan, S. Itzkovitz, M. E. J. Newman, and U. Alon. 2003. "On the Uniform Generation
24 of Random Graphs with Prescribed Degree Sequences." *ArXivcond-Mat0312028*, December. [http:](http://arxiv.org/abs/cond-mat/0312028)
25 [//arxiv.org/abs/cond-mat/0312028](http://arxiv.org/abs/cond-mat/0312028).

- 1 Mirchandani, Pitu B. 1976. "Shortest Distance and Reliability of Probabilistic Networks." *Comput. Oper. Res.* 3 (4): 347–55. <http://www.sciencedirect.com/science/article/pii/0305054876900174>.
- 2
- 3
- 4 Newman, M. E. J. 2004. "Fast Algorithm for Detecting Community Structure in Networks." *Phys. Rev. E* 69 (6): 066133. doi:[10.1103/PhysRevE.69.066133](https://doi.org/10.1103/PhysRevE.69.066133).
- 5
- 6 Nielsen, A, and Jordi Bascompte. 2007. "Ecological Networks, Nestedness and Sampling Effort." *Ecology* 95: 1134–41.
- 7
- 8 Olesen, Jens M., Jordi Bascompte, Yoko L. Dupont, Heidi Elberling, Claus Rasmussen, and Pedro Jordano. 2011. "Missing and Forbidden Links in Mutualistic Networks." *Proc. R. Soc. B* 278 (1706): 725–32. doi:[10.1098/rspb.2010.1371](https://doi.org/10.1098/rspb.2010.1371).
- 9
- 10
- 11 Olito, Colin, and Jeremy W. Fox. 2014. "Species Traits and Abundances Predict Metrics of Plant-pollinator Network Structure, but Not Pairwise Interactions." *Oikos*, n/a–/a. doi:[10.1111/oik.01439](https://doi.org/10.1111/oik.01439).
- 12
- 13 Poisot, Timothée, and Dominique Gravel. 2014. "When Is an Ecological Network Complex? Connectance Drives Degree Distribution and Emerging Network Properties." *PeerJ* 2 (February): e251. doi:[10.7717/peerj.251](https://doi.org/10.7717/peerj.251).
- 14
- 15
- 16 Poisot, Timothée, Elsa Canard, David Mouillot, Nicolas Mouquet, and Dominique Gravel. 2012. "The Dissimilarity of Species Interaction Networks." *Ecol Lett* 15 (12): 1353–61. doi:[10.1111/ele.12002](https://doi.org/10.1111/ele.12002).
- 17
- 18 Poisot, Timothée, Manon Lounnas, and Michael E. Hochberg. 2013. "The Structure of Natural Microbial Enemy-Victim Networks." *Ecol. Process.* 2 (1): 13. doi:[10.1186/2192-1709-2-13](https://doi.org/10.1186/2192-1709-2-13).
- 19
- 20 Poisot, Timothée, Daniel B. Stouffer, and Dominique Gravel. 2015. "Beyond Species: Why Ecological Interaction Networks Vary Through Space and Time." *Oikos* 124 (3): 243–51. doi:[10.1111/oik.01719](https://doi.org/10.1111/oik.01719).
- 21
- 22 Poullain, Virginie, Sylvain Gandon, Michael A. Brockhurst, Angus Buckling, and Michael E. Hochberg. 2008. "The Evolution of Specificity in Evolving and Coevolving Antagonistic Interactions Between a Bacteria and Its Phage." *Evolution* 62 (1): 1–11. doi:[10.1111/j.1558-5646.2007.00260.x](https://doi.org/10.1111/j.1558-5646.2007.00260.x).
- 23
- 24
- 25 Sanders, Dirk, and F J Frank van Veen. 2012. "Indirect Commensalism Promotes Persistence of Secondary Consumer Species." *Biology Letters*, no. August (August): 960–63. doi:[10.1098/rsbl.2012.0572](https://doi.org/10.1098/rsbl.2012.0572).
- 26

- 1 Stouffer, Daniel B, Juan Camacho, Wenxin Jiang, and Luís A Nunes Amaral. 2007. “Evidence for
2 the Existence of a Robust Pattern of Prey Selection in Food Webs.” *Proc. R. Soc. B Biol. Sci.* 274
3 (1621): 1931–40. doi:[10.1098/rspb.2007.0571](https://doi.org/10.1098/rspb.2007.0571).
- 4 Stouffer, Daniel B., and Jordi Bascompte. 2011. “Compartmentalization Increases Food-Web Per-
5 sistence.” *Proc. Natl. Acad. Sci. U.S.A.* 108 (9): 3648–52. doi:[10.1073/pnas.1014353108](https://doi.org/10.1073/pnas.1014353108).
- 6 Trøjelsgaard, Kristian, Pedro Jordano, Daniel W. Carstensen, and Jens M. Olesen. 2015. “Geograph-
7 ical Variation in Mutualistic Networks: Similarity, Turnover and Partner Fidelity.” *Proc. R. Soc. B*
8 282 (1802): 20142925. doi:[10.1098/rspb.2014.2925](https://doi.org/10.1098/rspb.2014.2925).
- 9 Tylianakis, J. M., T. Tscharntke, and O. T. Lewis. 2007. “Habitat Modification Alters the Structure
10 of Tropical Hostparasitoid Food Webs.” *Nature* 445 (7124): 202–5. [http://www.nature.com/
11 nature/journal/v445/n7124/abs/nature05429.html](http://www.nature.com/nature/journal/v445/n7124/abs/nature05429.html).
- 12 Vizentin-Bugoni, Jeferson, Pietro Kiyoshi Maruyama, and Marlies Sazima. 2014. “Processes En-
13 tangling Interactions in Communities: Forbidden Links Are More Important Than Abundance in a
14 Hummingbirdplant Network.” *Proc. R. Soc. B* 281 (1780): 20132397. doi:[10.1098/rspb.2013.2397](https://doi.org/10.1098/rspb.2013.2397).