Sampling networks of ecological interactions

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Summary

1. Sampling ecological interactions presents similar challenges, problems, potential biases, and constraints as sampling individuals and species in biodiversity inventories. Interactions are just pairwise relationships among individuals of two unrelated species, such as those among plants and their seed dispersers in frugivory interactions or those among plants and their pollinators. Sampling interactions is a fundamental step to build robustly estimated interaction networks, yet few analyses have attempted a formal approach to their sampling protocols.

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2. Robust estimates of the actual number of interactions (links) within diversified ecological networks require adequate sampling effort that needs to be explicitly gauged. Yet we still lack a sampling theory explicitly focusing on ecological interactions.

3. While the complete inventory of interactions is likely impossible, a robust characterization of its main patterns and metrics is probably realistic. We must acknowledge that a sizable fraction of the maximum number of interactions I_{max} among, say, A animal species and P plant species (i.e., $I_{max} = AP$) is impossible to record due to forbidden links, the restrictions imposed by the organisms life-histories. Thus, the number of observed interactions I in robustly sampled networks is typically $I << I_{max}$, resulting in extremely sparse interaction matrices with low connectance.

4. Reasons for forbidden links are multiple but mainly stem from spatial and temporal uncoupling of partner species encounters and from intrinsically low probabilities of interspecific encounter for many of the potential pairwise interactions. Adequately assessing the completeness of a network of ecological interactions thus needs a deep knowledge of the natural history details embedded, so that forbidden links can be "discounted" when addressing sampling effort.

5. Here I provide a review and outline a conceptual framework for interaction sampling by building an explicit analogue to individuals and species sampling, thus extending diversity-monitoring approaches to the characterization of complex networks of ecological interactions. This is crucial to assess the fast-paced and devastating effects of defaunation-driven loss of key ecological

interactions and the services they provide.

Keywords

complex networks, food webs, frugivory, mutualism, plant-animal interactions, pollination, seed dispersal

Introduction

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Biodiversity sampling is a labour-intensive activity,
and sampling is often not sufficient to detect all or
even most of the species present in an assemblage.
Gotelli & Colwell (2011).
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1 Biodiversity assessment aims at sampling individuals in collections and deter-
2 mining the number of species represented. Given that, by definition, samples are
3 incomplete, these collections enumerate a lower number of the species actually
4 present. The ecological literature dealing with robust estimators of species rich-
5 ness and diversity in collections of individuals is immense, and a number of useful
6 approaches have been used to obtain such estimates (Magurran, 1988; Gotelli &
7 Colwell, 2001; Hortal, Borges & Gaspar, 2006; Colwell, 2009; Gotelli & Colwell,
8 2011). Recent effort has been also focused at defining essential biodiversity vari-
9 ables (EBV) (Pereira *et al.*, 2013) that can be sampled and measured repeatedly
10 to complement biodiversity estimates. Yet sampling species or taxa-specific EBVs
11 is just probing a single component of biodiversity; interactions among species are
12 another fundamental component, the one that supports the existence of species

13   (Memmott *et al.*, 2006). For example, the extinction of interactions represents a

14   dramatic loss of biodiversity because it entails the loss of fundamental ecological

15   functions (Valiente-Banuet *et al.*, 2014). This missed component of biodiversity

16   loss, the extinction of ecological interactions, very often accompanies, or even pre-

17   cedes, species disappearance. Interactions among species are a key component

18   of biodiversity and here I aim to show that most problems associated to sam-

19   pling interactions in natural communities have to do with problems associated to

20   sampling species diversity. I consider pairwise interactions among species at the

21   habitat level, in the context of alpha diversity and the estimation of local interac-

22   tion richness from sampling data (Mao & Colwell, 2005). In the first part I provide

23   a succinct overview of previous work addressing sampling issues for ecological in-

24   teraction networks. In the second part I discuss specific rationales for sampling

25   the biodiversity of ecological interactions.

26   Interactions can be a much better indicator of the richness and diversity of

27   ecosystem functions than a simple list of taxa and their abundances and/or re-

28   lated biodiversity indicator variables (EBVs). Thus, sampling interactions should

29   be a central issue when identifying and diagnosing ecosystem services (e.g., polli-

30   nation, natural seeding by frugivores, etc.). Fortunately, all the whole battery of

31   biodiversity-related tools used by ecologists to sample biodiversity (species, *sensu*

32   *stricto*) can be extended and applied to the sampling of interactions. Analogs

33   are evident between these approaches (Colwell, Dunn & Harris, 2012). Monitor-

34   ing interactions is analogous to any biodiversity sampling [i.e., a species inventory

35   Jordano (1987); Jordano, Vázquez & Bascompte (2009)] and is subject to similar

36   methodological shortcomings, especially under-sampling (Coddington *et al.*, 2009;

37   Vazquez, Chacoff & Cagnolo, 2009; Dorado *et al.*, 2011; Rivera-Hutinel *et al.*,

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2012). For example, when we study mutualistic networks, our goal is to make an inventory of the distinct pairwise interactions that made up the network. We are interested in having a complete list of all the pairwise interactions among species (e.g., all the distinct, species-species interactions, or links, among the pollinators and flowering plants) that can exist in a given community. Sampling these interactions thus entails exactly the same problems, limitations, constraints, and potential biases as sampling individual organisms and species diversity. As Mao & Colwell (Mao & Colwell, 2005) put it, these are the workings of Preston's demon, the moving "veil line" between detected and the undetected interactions as sample size increases (Preston, 1948).

Early efforts to recognize and solve sampling problems in analyses of interactions stem from researchers interested in food web analyses and in determining the biases of undersampled food web metrics (Martinez, 1991; Cohen *et al.*, 1993; Martinez, 1993; Bersier, Banasek-Richter & Cattin, 2002; Brose, Martinez & Williams, 2003; Banasek-Richter, Cattin & Bersier, 2004). In addition, the myriad of classic natural history studies documenting animal diets, host-pathogen infection records, plant herbivory records, etc., represent efforts to document interactions occurring in nature. All of them share the problem of sampling incompleteness influencing the patterns and metrics reported. Yet, despite the early recognition that incomplete sampling may seriously bias the analysis of ecological networks (Jordano, 1987), only recent studies have explicitly acknowledged it and attempted to determine its influence (Ollerton & Cranmer, 2002; Nielsen & Bascompte, 2007; Vazquez, Chacoff & Cagnolo, 2009; Gibson *et al.*, 2011; Olesen *et al.*, 2011; Chacoff *et al.*, 2012; Rivera-Hutinel *et al.*, 2012; Olito & Fox, 2014; Bascompte & Jordano, 2014; Vizentin-Bugoni, Maruyama & Sazima, 2014; Frund, McCann &

Williams, 2015). The sampling approaches have been extended to predict patterns

of coextintions in interaction assemblages (e.g., hosts-parasites) (Colwell, Dunn &

Harris, 2012). Most empirical studies provide no estimate of sampling effort, im-

plicitly assuming that the reported network patterns and metrics are robust. Yet

recent evidences point out that number of partner species detected, number of

actual links, and some aggregate statistics describing network patterns, are prone

to sampling bias (Nielsen & Bascompte, 2007; Dorado *et al.*, 2011; Olesen *et al.*,

2011; Chacoff *et al.*, 2012; Rivera-Hutinel *et al.*, 2012; Olito & Fox, 2014; Frund,

McCann & Williams, 2015). Most of these evidences, however, come from either

theoretical, simulation, studies (Frund, McCann & Williams, 2015) or from rel-

atively species-poor assemblages. Even for species-rich, tropical assemblages it

might be erroneous to conclude that network data routinely come from insuffi-

ciently sampled datasets (Ollerton & Cranmer, 2002; Chacoff *et al.*, 2012), given

the extremely sparse nature of these interaction matrices because of the prevalence

of forbidden links (which, by definition, cannot be documented despite extensive

sampling effort). However, most certainly, sampling limitations pervade biodiver-

sity inventories in tropical areas (Coddington *et al.*, 2009) and we might rightly

expect that frequent interactions may be over-represented and rare interactions

may be missed entirely in studies of mega-diverse assemblages (Bascompte & Jor-

dano, 2014); but, to what extent?

Sampling interactions: methods

When we sample interactions in the field we record the presence of two species

that interact in some way. For example, Snow and Snow(Snow & Snow, 1988)

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86 recorded an interaction whenever they saw a bird "touching" a fruit on a plant. In

87 a similar way, interactions between pollinators and plants are tallied by recording

88 any visit of a pollinator entering a flower and touching the reproductive parts. We

89 observe and record feeding observations, visitation, occupancy, presence in pollen

90 loads or in fecal samples, etc., of *individual* animals or plants and accumulate

91 pairwise interactions, i.e., lists of species partners and the frequencies with which

92 we observe them. Therefore, estimating the sampling completeness of pairwise

93 interactions for a whole network, requires estimating the number (richness) of

94 distinct pairwise interactions accumulated as sampling effort is increased, pooling

95 the data for all partner species. Most, if not all, types of ecological interactions can

96 be illustrated by bipartite graphs, with two or more distinct groups of interacting

97 partners (Bascompte & Jordano, 2014); for illustration purposes I'll focus more

98 specifically on plant-animal interactions.

99   Sampling interactions requires filling the cells of an interaction matrix with

100 data. The matrix, $\Delta = AP$, is a 2D representation of the interactions among,

101 say, A animal species (rows) and P plant species (columns) (Jordano, 1987; Bas-

102 compte & Jordano, 2014). An interaction matrix Δ consists of an array of zeroes

103 or ones, or an array of numeric values (including zeroes)- if the data (interaction

104 frequencies) are quantified. The matrix entries illustrate the values of the pairwise

105 interactions visualized in the Δ matrix, and can be 0 or 1, for presence-absence

106 of a given pairwise interaction, or take a quantitative weight w_{ji} to represent the

107 interaction intensity or unidirectional effect of species j on species i (Bascompte

108 & Jordano, 2014; Vazquez *et al.*, 2015). Given that the outcomes of most eco-

109 logical interactions are dependent on frequency of encounters (e.g., visit rate of

110 pollinators, number of records of ant defenders, frequency of seeds in fecal sam-

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ples), a frequently used proxy for interaction intensities w_{ji} is just how frequent are new interspecific encounters, whether or not appropriately weighted to estimate interaction effectiveness (Vazquez, Morris & Jordano, 2005).

We need to define two basic steps in the sampling of interactions: 1) which type of interactions we sample; and 2) which type of record we get to document the existence of an interaction. In step #1 there are two considerations we need to take into account. First is whether we are sampling the whole community of interactor species (all the animals, all the plants) or we sample just a subset of them, i.e., a sub matrix $\Delta_{m,n}$ of $m < A$ animal species and $n < P$ plant species of the adjacency matrix Δ_{AP}. Subsets can be: a) all the potential plants interacting with a subset of the animals (Fig. 1a); b) all the potential animal species interacting with a subset of the plant species (Fig. 1b); c) a subset of all the potential animal species interacting with a subset of all the plant species (Fig. 1c). While some discussion has considered how to establish the limits of what represents a network (Strogatz, 2001) (in analogy to discussion on food-web limits (Cohen, 1978)), it must be noted that situations a-c in Fig. 1 do not represent complete interaction networks. As vividly stated by Cohen et al. (1993): "*As more comprehensive, more detailed, more explicit webs become available, smaller, highly aggregated, incompletely described webs may progressively be dropped from analyses of web structure (though such webs may remain useful for other purposes, such as pedagogy)*". Subnet sampling is generalized in studies of biological networks (e.g., protein interactions, gene regulation), yet it is important to recognize that most properties of subnetworks (even random subsamples) do not represent properties of whole networks (Stumpf, Wiuf & May, 2005).

In step #2 above we face the problem of the type of record we take to sample

interactions. This is important because it defines whether we approach the problem of filling up the interaction matrix in a "zoo-centric" way or in a "phyto-centric" way. Zoo-centric studies directly sample animal activity and document the plants 'touched' by the animal. For example, analysis of pollen samples recovered from the body of pollinators, analysis of fecal samples of frugivores, radio-tracking data, etc. Phyto-centric studies take samples of focal individual plant species and document which animals 'arrive' or 'touch' the plants. Examples include focal watches of fruiting or flowering plants to record visitation by animals, raising insect herbivores from seed samples, identifying herbivory marks in samples of leaves, etc.

Most recent analyses of plant-animal interaction networks are phyto-centric; just 3.5% of available plant-pollinator ($N = 58$) or 36.6% plant-frugivore ($N = 22$) interaction datasets are zoo-centric (see (Schleuning *et al.*, 2012)). Moreover, most available datasets on host-parasite or plant-herbivore interactions are "host-centric" or phyto-centric (e.g., (Thébault & Fontaine, 2010; Eklöf *et al.*, 2013)). This maybe related to a variety of causes, like preferred methodologies by researchers working with a particular group or system, logistic limitations, or inherent taxonomic focus of the research questions. A likely result of phyto-centric sampling would be adjacency matrices with large $A : P$ ratios. In any case we don't have a clear view of the potential biases that taxa-focused sampling may generate in observed network patterns, for example by generating consistently asymmetric interaction matrices (Dormann *et al.*, 2009). System symmetry has been suggested to influence estimations of generalization levels in plants and animals when measured as I_A and I_P (Elberling & Olesen, 1999); thus, differences in I_A and I_P between networks may arise from different $A : P$ ratios rather than other ecological factors (Olesen & Jordano, 2002).

Interestingly enough, quite complete analyses of interaction networks can be obtained when combining both phyto-centric and zoo-centric sampling. For example, Bosch et al. (Bosch *et al.*, 2009) showed that the addition of pollen load data on top of focal-plant sampling of pollinators unveiled a significant number of interactions, resulting in important network structural changes. Connectance increased 1.43-fold, mean plant connectivity went from 18.5 to 26.4, and mean pollinator connectivity from 2.9 to 4.1; moreover, extreme specialist pollinator species (singletons in the adjacency matrix) decreased 0.6-fold. Zoo-centric sampling has recently been extended with the use of DNA-barcoding, for example with plant-herbivore (Jurado-Rivera *et al.*, 2009) and plant-frugivore interactions (González-Varo, Arroyo & Jordano, 2014). For mutualistic networks we would expect that zoo-centric sampling could help unveiling interactions for rare species or for relatively common species which are difficult to sample by direct observation. Future methodological work may provide significant advances showing how mixing different sampling strategies strengthens the completeness of network data. These mixed strategies may combine, for instance, focal analyses, pollen load or seed contents, camera traps, and DNA barcoding records. We might expect increased power of these mixed sampling approaches when combining different methods from both phyto- and zoo-centric perspectives (Bosch *et al.*, 2009; Bluthgen, 2010).

Sampling interactions: rationale

The number of distinct pairwise interactions that we can record in a landscape (an area of relatively homogeneous vegetation, analogous to the one we would use to monitor species diversity) is equivalent to the number of distinct classes in which

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184 we can classify the recorded encounters among individuals of two different species.

185 Yet, individual-based plant-animal interaction networks have been only recently

186 studied (Dupont, Trøjelsgaard & Olesen, 2011). We walk in the forest and see

187 a blackbird Tm picking an ivy Hh fruit and ingesting it: we have a record for

188 $Tm - Hh$ interaction. We keep advancing and record again a blackbird feeding

189 on hawthorn Cm fruits so we record a $Tm - Cm$ interaction; as we advance we

190 encounter another ivy plant and record a blackcap swallowing a fruit so we now

191 have a new $Sa - Hh$ interaction, and so on. At the end we have a series of classes

192 (e.g., $Sa - Hh, Tm - Hh, Tm - Cm$, etc.), along with their observed frequencies.

193 Bunge & Fitzpatrick (Bunge & Fitzpatrick, 1993) review the main aspects and

194 approaches to estimate the number of distinct classes C in a sample of observations.

195 The sampling of interactions in nature, as the sampling of species, is a cumulative

196 process. In our analysis, we are not re-sampling individuals, but interactions, so we

197 made interaction-based accumulation curves. If an interaction-based curve points

198 towards a robust sampling, it does mean that no new interactions are likely to be

199 recorded, irrespectively of the species, as it is a whole-network sampling approach

200 (N. Gotelli, pers. com.). We add new, distinct, interactions recorded as we increase

201 sampling effort (Fig. 2). We can obtain an Interaction Accumulation Curve (IAC)

202 analogous to a Species cumulating Curve (SAC): the observed number of distinct

203 pairwise interactions in a survey or collection as a function of the accumulated

204 number of observations or samples(Colwell, 2009).

205   Our sampling above would have resulted in a vector $n = [n_1...n_C]'$ where n_i

206 is the number of records in the ith class. As stressed by Bunge & Fitzpatrick

207 (Bunge & Fitzpatrick, 1993), however, the ith class would appear in the sample if

208 and only if $n_i > 0$, and we don't know *a priori* which n_i are zero. So, n is not

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209 observable. Rather, what we get is a vector $c = [c_1 ... c_n]'$ where c_j is the number

210 of classes represented j times in our sampling: c_1 is the number of singletons, c_2 is

211 the number of twin pairs, c_3 the number of triplets, etc. The problem thus turns

212 to be estimating the number of distinct classes C from the vector of c_j values.

213   Estimating the number of interactions with resulting robust estimates of net-

214 work parameters is a central issue in the study of ecological interaction networks

215 (Jordano, 1987; Bascompte & Jordano, 2014). In contrast with traditional species

216 diversity estimates, sampling networks has the paradox that despite the poten-

217 tially interacting species being present in the sampled assemblage (i.e., included

218 in the A and P species lists), some of their pairwise interactions are impossible to

219 be recorded. The reason is forbidden links. Independently of whether we sample

220 full communities of subset communities we face a problem: some of the interac-

221 tions that we can visualize in the empty adjacency matrix Δ with size AP will

222 simply not occur. Thus, independently of the sampling effort we put, we'll never

223 document these pairwise interactions. With a total of AP "potential" interac-

224 tions , a fraction of them are impossible to record, because they are forbidden

225 (Jordano, Bascompte & Olesen, 2003; Olesen *et al.*, 2011). Forbidden links are

226 constraints for the establishment of new links, and mainly arise from the biolog-

227 ical attributes of the species: no link can be established between a plant and an

228 animal mutualist differing in phenology, i.e. the seeds of a winter-ripening plant

229 cannot be dispersed by a frugivore that is a summer stopover migrant (Jordano,

230 1987). Or, for instance, short-tongued pollinators cannot successfully reach the

231 nectar in long-corolla flowers and pollinate them efficiently (Moré *et al.*, 2012).

232 Forbidden links are thus represented as structural zeroes in the interaction matrix,

233 i.e., matrix cells that cannot get a non-zero value. So, we need to account for the

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234 frequency of these structural zeros in our matrix before proceeding. For example,

235 most measurements of connectance ($C = I/(AP)$) implicitly ignore the fact that

236 by taking the full product AP in the denominator they are underestimating the

237 actual connectance value, i.e., the fraction of actual interactions I relative to the

238 *biologically possible* ones, not to the total maximum $I_{max} = AP$.

239 Adjacency matrices are frequently sparse, i.e., they are densely populated with

240 zeroes, with a fraction of them being structural (i.e., unobservable interactions)

241 (Bascompte & Jordano, 2014). It would be thus a serious interpretation error to

242 attribute the sparseness of adjacency matrices for bipartite networks to under-

243 sampling. The actual typology of link types in ecological interaction networks is

244 thus more complex than just the two categories of observed and unobserved inter-

245 actions (Table 1). Unobserved interactions are represented by zeroes and belong

246 to two categories. Missing interactions may actually exist but require additional

247 sampling or a variety of methods to be observed. Forbidden links, on the other

248 hand, arise due to biological constraints limiting interactions and remain unobserv-

249 able in nature, irrespectively of sampling effort (Jordano, Bascompte & Olesen,

250 2003; Olesen *et al.*, 2011). Forbidden links are non-occurrences of pairwise interac-

251 tions that can be accounted for by biological constraints, such as spatio-temporal

252 uncoupling, size or reward mismatching, foraging constraints (e.g., accessibility),

253 and physiological-biochemical constraints (Jordano, 1987). We still have extremely

254 reduced information about the frequency of forbidden links in natural communi-

255 ties (Jordano, Bascompte & Olesen, 2003; Stang *et al.*, 2009; Vazquez, Chacoff &

256 Cagnolo, 2009; Olesen *et al.*, 2011; Ibanez, 2012; Maruyama *et al.*, 2014; Vizentin-

257 Bugoni, Maruyama & Sazima, 2014) (Table 1). Forbidden links FL may actually

258 account for a relatively large fraction of unobserved interactions UL when sam-

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259 pling taxonomically-restricted subnetworks (e.g., plant-hummingbird pollination

260 networks) (Table 1). Phenological unmatching is also prevalent in most networks,

261 and may add up to explain ca. 25–40% of the forbidden links, especially in highly

262 seasonal habitats, and up to 20% when estimated relative to the total number of

263 unobserved interactions (Table 2). In any case, we might expect that a fraction of

264 the missing links ML would be eventually explained by further biological reasons,

265 depending on the knowledge of natural details of the particular systems. Our goal

266 as naturalists would be to reduce the fraction of UL which remain as missing links;

267 to this end we might search for additional biological constraints or added sampling

268 effort. For instance, habitat use patterns by hummingbirds in the Aroma Valley

269 network (Table 2; (Snow & Snow, 1972)) impose a marked pattern of microhab-

270 itat mismatches causing up to 44.5% of the forbidden links. There are a myriad

271 of biological causes beyond those included as FL in Table 2 that may contribute

272 explanations for UL: limits of color perception and or partial preferences, pres-

273 ence of secondary metabolites in fruit pulp and leaves, toxins and combinations of

274 monosaccharides in nectar, etc. However, it is surprising that just the limited set

275 of forbidden link types in Table 1 explain between 24.6–77.2% of the unobserved

276 links. Notably, the Arima Valley, Santa Virgńia, and Hato Ratón networks have

277 > 60% of the unobserved links explained, which might be related to the fact that

278 they are subnetworks (Arima Valley, Santa Virgínia) or relatively small networks

279 (Hato Ratón). All this means that empirical networks may have sizable fractions

280 of structural zeroes. Ignoring this biological fact may contribute to wrongly infer

281 undersampling of interactions in real-world assemblages.

282   To sum up, two elements of inference are required in the analysis of unobserved

283 interactions in ecological interaction networks: first, detailed natural history infor-

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mation on the participant species that allows the inference of biological constraints imposing forbidden links, so that structural zeroes can by identified in the adjacency matrix; second, a critical analysis of sampling robustness a robust estimate of the actual fraction of missing links, M, and thus, a robust estimate of I.

Asymptotic diversity estimates

Let's assume a sampling of the diversity in a specific locality, over relatively homogeneous landscape where we aim at determining the number of species present for a particular group of organisms. To do that we carry out transects or plot samplings across the landscape, adequately replicated so we obtain a number of samples. Briefly, S_{obs} is the total number of species observed in a sample, or in a set of samples. S_{est} is the estimated number of species in the community represented by the sample, or by the set of samples, where est indicates an estimator. With abundance data, let S_k be the number of species each represented by exactly k individuals in a single sample. Thus, S_0 is the number of undetected species (species present in the community but not included in the sample), S_1 is the number of singleton species, S_2 is the number of doubleton species, etc. The total number of individuals in the sample would be:

$$n = \sum_{k=1}^{S_{obs}} S_k$$

A frequently used asymptotic, bias corrected, non-parametric estimator is S_{Chao} (Hortal, Borges & Gaspar, 2006; Chao, 2005; Colwell, 2013):

$$S_{Chao} = S_{obs} + \frac{S_1(S_1 - 1)}{2(S_2 + 1)}$$

[292] Another frequently used alternative is the Chao2 estimator, S_{Chao2} (Gotelli &

[293] Colwell, 2001), which has been reported to have a limited bias for small sample

[294] sizes (Colwell & Coddington, 1994; Chao, 2005):

$$S_{Chao2} = S_{obs} + \frac{S_1^2}{2S_2}$$

[295] A plot of the cumulative number of species recorded, S_n, as a function of

[296] some measure of sampling effort (say, n samples taken) yields the species accu-

[297] mulation curve (SAC) or collector's curve (Colwell & Coddington, 1994). Such a

[298] curve eventually reaches an asymptote converging with S_{est}. In an analogous way,

[299] interaction accumulation curves (IAC), analogous to SACs, can be used to as-

[300] sess the robustness of interactions sampling for plant-animal community datasets

[301] (Jordano, 1987; Jordano, Vázquez & Bascompte, 2009; Olesen *et al.*, 2011). For

[302] instance, a random accumulator function (e.g., library vegan in the R Package (R

[303] Development Core Team, 2010)) which finds the mean IAC and its standard devi-

[304] ation from random permutations of the data, or subsampling without replacement

[305] (Gotelli & Colwell, 2001) can be used to estimate the expected number of distinct

[306] pairwise interactions included in a given sampling of records (Jordano, Vázquez

[307] & Bascompte, 2009; Olesen *et al.*, 2011). We start with a vectorized interaction

[308] matrix representing the pairwise interactions (rows) recorded during a cumulative

[309] number of censuses or sampling periods (columns) (Table 3) , in a way analogous

[310] to a biodiversity sampling matrix with species as rows and sampling units (e.g.,

[311] quadrats) as columns (Jordano, Vázquez & Bascompte, 2009). In this way we

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312 effectively extend sampling theory developed for species diversity to the sampling
313 of ecological interactions. Yet future theoretical work will be needed to formally
314 assess the similarities and differences in the two approaches and developing biolog-
315 ically meaningful null models of expected interaction richness with added sampling
316 effort.

Assessing sampling effort when recording interactions

319 The basic method we can propose to estimate sampling effort and explicitly show
320 the analogues with rarefaction analysis in biodiversity research is to vectorize the
321 interaction matrix AP so that we get a vector of all the potential pairwise inter-
322 actions (I_{max}, Table 1) that can occur in a community of A animal species and
323 P plant species. The new "species" we aim to sample are the pairwise interac-
324 tions (Table 3). So, if we have in our community *Turdus merula* (Tm) and *Rosa*
325 *canina* (Rc) and *Prunus mahaleb* (Pm), our problem will be to sample 2 new
326 "species": $Tm - Rc$ and $Tm - Pm$. In general, if we have $A = 1...i$, animal
327 species and $P = 1...j$ plant species, we'll have a vector of "new" species to sample:
328 $A_1P_1, A_1P_2, ...A_2P_1, A_2P_2, ...A_iP_j$. We can represent the successive samples where
329 we can potentially get records of these interactions in a matrix with the vectorized
330 interaction matrix and columns representing the successive samples we take (Table
331 3). This is simply a vectorized version of the interaction matrix.

332 For example, mixture models incorporating detectabilities have been proposed
333 to effectively account for rare species (Mao & Colwell, 2005). In an analogous line,

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mixture models could be extended to samples of pairwise interactions, also with

specific detectability values. These detection rate/odds could be variable among

groups of interactions, depending on their specific detectability. For example,

detectability of flower-pollinator interactions involving bumblebees could have a

higher detectability than flower-pollinator pairwise interactions involving, say, ni-

tidulid beetles. These more homogeneous groupings of pairwise interactions within

a network define modules (Bascompte & Jordano, 2014), so we might expect that

interactions of a given module (e.g., plants and their hummingbird pollinators; Fig.

1a) may share similar detectability values, in an analogous way to species groups

receiving homogeneous detectability values in mixture models (Mao & Colwell,

2005). Such sampling, in its simplest form, would result in a sample with multiple

pairwise interactions detected, in which the number of interaction events recorded

for each distinct interaction found in the sample is recorded (i.e., a column vector

in Table 3, corresponding to, say, a sampling day). The number of interactions

recorded for the i_{th} pairwise interaction (i.e., A_iP_j in Table 3), Y_i could be treated

as a Poisson random variable with a mean parameter λ_i, its detection rate. Mix-

ture models (Mao & Colwell, 2005) include estimates for abundance-based data

(their analogous in interaction sampling would be weighted data), where Y_i is a

Poisson random variable with detection rate λ_i. This is combined with

the incidence-based model, where Y_i is a binomial random variable (their analo-

gous in interaction sampling would be presence/absence records of interactions)

with detection odds λ_i. Let T be the number of samples in an incidence-based

data set. A Poisson/binomial density can be written as (Mao & Colwell, 2005):

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$$g(y; \lambda) = \begin{cases} \frac{\lambda^y}{y!e^{\lambda}} & [1] \\ \binom{T}{y} \frac{\lambda^y}{(1+\lambda)^T} & [2] \end{cases}$$

357   where [1] corresponds to a weighted network, and [2] to a qualitative network.

358   The detection rates λ_i depend on the relative abundances ϕ_i of the interactions,

359 the probability of a pairwise interaction being detected when it is present, and the

360 sample size (the number of interactions recorded), which, in turn, is a function

361 of the sampling effort. Unfortunately, no specific sampling model has been de-

362 veloped along these lines for species interactions and their characteristic features.

363 For example, a complication factor might be that interaction abundances, ϕ_i, in

364 real assemblages are a function of the abundances of interacting species, that de-

365 termine interspecific encounter rates; yet they also depend on biological factors

366 that ultimately determine if the interaction occurs when the partner species are

367 present. It its simplest form, ϕ_i could be estimated from just the product of part-

368 ner species abundances, an approach recently used as a null model to assess the

369 role of biological constraints in generating forbidden links and explaining interac-

370 tion patterns (Vizentin-Bugoni, Maruyama & Sazima, 2014). Yet more complex

371 models should incorporate not only interspecific encounter probabilities, but also

372 phenotypic matching and incidence of forbidden links.

373   Rarefaction analysis and diversity-accumulation analysis (Magurran, 1988; Hor-

374 tal, Borges & Gaspar, 2006) come up immediately with this type of dataset. This

375 procedure plots the accumulation curve for the expected number of distinct pair-

376 wise interactions recorded with increasing sampling effort (Jordano, Vázquez &

377 Bascompte, 2009; Olesen *et al.*, 2011). Asymptotic estimates of interaction rich-

ness and its associated standard errors and confidence intervals can thus be obtained (Hortal, Borges & Gaspar, 2006). It should be noted that the asymptotic estimate of interaction richness implicitly ignores the fact that, due to forbidden links, a number of pairwise interactions among the I_{max} number specified in the adjacency matrix Δ cannot be recorded, irrespective of sampling effort. Therefore, the asymptotic value most likely is an overestimate of the actual maximum number of links that can be present in an assemblage. If forbidden links are taken into account, the asymptotic estimate should be lower. Yet, to the best of my knowledge, there is no theory developed to estimate this "biologically real" asymptotic value. Not unexpectedly, most recent analyses of sampling effort in ecological network studies found evidences of undersampling (Chacoff *et al.*, 2012). This needs not to be true, especially when interaction subwebs are studied (Olesen *et al.*, 2011; Vizentin-Bugoni, Maruyama & Sazima, 2014), and once the issue of structural zeroes in the interaction matrices is effectively incorporated in the estimates.

The *real* missing links

Given that a fraction of unobserved interactions can be accounted for by forbidden links, what about the remaining missing interactions? We have already discussed that some of these could still be related to unaccounted constraints, and still others would be certainly attributable to insufficient sampling. Would this always be the case? Multispecific assemblages of distinct taxonomic relatedness, whose interactions can be represented as bipartite networks (e.g., host-parasite, plant-animal mutualisms, plant-herbivore interactions- with two distinct sets of unrelated higher taxa), are shaped by interspecific encounters among individuals

20

⁴⁰¹ of the partners (Fig. 2). A crucial ecological aspect limiting these interactions is

⁴⁰² the probability of interspecific encounter, i.e., the probability that two individuals

⁴⁰³ of the partner species actually encounter each other in nature.

⁴⁰⁴ Given log-normally distributed abundances of the two species groups, the ex-

⁴⁰⁵ pected "neutral" probabilities of interspecific encounter (PIE) would be simply

⁴⁰⁶ the product of the two lognormal distributions. Thus, we might expect that for

⁴⁰⁷ low PIE values, pairwise interactions would be either extremely difficult to sam-

⁴⁰⁸ ple, or just simply non-occurring in nature. Consider the Nava de las Correhuelas

⁴⁰⁹ interaction web (NCH, Table 2), with $A = nnn$, $P = nnn$, $I = nnn$, and almost

⁴¹⁰ half of the unobserved interactions not accounted for by forbidden links missing

⁴¹¹ links, $M = 53.1\%$. Given the robust sampling of this network (Jordano, Vázquez

⁴¹² & Bascompte, 2009), a sizable fraction of these possible but missing links would

⁴¹³ be simply not occurring in nature, most likely by extremely low PIE, in fact

⁴¹⁴ asymptotically zero. Given the vectorized list of pairwise interactions for NCH, I

⁴¹⁵ computed the PIE values for each one by multiplying element wise the two species

⁴¹⁶ abundance distributions. The $PIE_{max} = 0.0597$, being a neutral estimate, based

⁴¹⁷ on the assumption that interactions occur in proportion to the species-specific local

⁴¹⁸ abundances. With $PIE_{median} < 1.4\ 10^{-4}$ we may safely expect (note the quantile

⁴¹⁹ estimate $Q_{75\%} = 3.27\ 10^{-4}$) that a sizable fraction of these missing interactions

⁴²⁰ may simply not occur according to this neutral expectation (Jordano, 1987) (Ole-

⁴²¹ sen *et al.*, 2011) (neutral forbidden links, *sensu* (Canard *et al.*, 2012)). Which is

⁴²² the expected frequency for pairwise interactions? and, which is the expected prob-

⁴²³ ability for unobserved interactions? More specifically, which is the probability of

⁴²⁴ missing interactions, M (i.e., the unobserved ones that cannot be accounted for as

⁴²⁵ forbidden links)?

₄₂₆ When we consider the vectorized interaction matrix, enumerating all pairwise

₄₂₇ interactions for the AP combinations, the expected probabilities of finding a given

₄₂₈ interaction can be estimated with a Good-Turing approximation (Good, 1953).

₄₂₉ The technique, developed by Alan Turing and I.J. Good with applications to lin-

₄₃₀ guistics and word analysis (Gale & Sampson, 1995) has been recently applied in

₄₃₁ ecology (Chao *et al.*, 2015), estimates the probability of recording an interaction

₄₃₂ of a hitherto unseen pair of partners, given a set of past records of interactions

₄₃₃ between other species pairs. Let a sample of N interactions so that n_r distinct

₄₃₄ pairwise interactions have exactly r records. All Good-Turing estimators obtain

₄₃₅ the underlying frequencies of events as:

$$P(X) = \frac{(N_X + 1)}{T} \left(1 - \frac{E(1)}{T}\right) \tag{1}$$

₄₃₆ where X is the pairwise interaction, N_X is the number of times interaction X

₄₃₇ is recorded, T is the sample size (number of distinct interactions recorded) and

₄₃₈ $E(1)$ is an estimate of how many different interactions were recorded exactly once.

₄₃₉ Strictly speaking Equation (1) gives the probability that the next interaction type

₄₄₀ recorded will be X, after sampling a given assemblage of interacting species. In

₄₄₁ other words, we scale down the maximum-likelihood estimator $\frac{n}{T}$ by a factor of

₄₄₂ $\frac{1-E(1)}{T}$. This reduces all the probabilities for interactions we have recorded, and

₄₄₃ makes room for interactions we haven't seen. If we sum over the interactions we

₄₄₄ have seen, then the sum of $P(X)$ is $1 - \frac{1-E(1)}{T}$. Because probabilities sum to one,

₄₄₅ we have the left-over probability of $P_{new} = \frac{E(1)}{T}$ of seeing something new, where

₄₄₆ new means that we sample a new pairwise interaction.

₄₄₇ Note, however, that Good-Turing estimators, as the traditional asymptotic

22

estimators, do not account in our case for the forbidden interactions. To account for these FL I re-scaled the asymptotic estimates, so that a more meaningful estimate could be obtained (Table 4). The scaling was calculated as $Chao1 * (I + ML)/AP$, just correcting for the FL frequency, given that $I + ML$ represent the total *feasible* interactions when discounting the forbidden links (Table 1). After scaling, observed I values (Table 2) are within the $Chao1$ and ACE asymptotic estimates but below the ACE estimates for Hato Ratón and Zackenberg (Table 4). Thus, even after re-scaling for FL, it is likely that adequate characterization of most interaction networks will require intensive sampling effort.

Discussion

Recent work has inferred that most data available for interaction networks are incomplete due to undersampling, resulting in a variety of biased parameters and network patterns (Chacoff *et al.*, 2012). It is important to note, however, that in practice, many surveyed networks to date have been subnets of much larger networks. This is true for protein interaction, gene regulation, and metabolic networks, where only a subset of the molecular entities in a cell have been sampled (Stumpf, Wiuf & May, 2005). Despite recent attempts to document whole ecosystem meta-networks (Pocock, Evans & Memmott, 2012), it is likely that most ecological interaction networks will illustrate just major ecosystem compartments. Due to their high generalization, high temporal and spatial turnover, and high complexity of association patterns, adequate sampling of ecological interaction networks requires extremely large sampling effort. Undersampling of ecological networks may originate from the analysis of assemblage subsets (e.g., taxonomi-

23

cally or functionally defined), and/or from logistically-limited sampling effort. It is extremely hard to robustly sample the set of biotic interactions even for relatively simple, species-poor assemblages; yet, concluding that all ecological network datasets are undersampled would be unrealistic. The reason stems form a biological fact: a sizeable fraction of the maximum, potential links that can be recorded among two distinct sets of species is simply unobservable, irrespective of sampling effort (Jordano, 1987).

Missing links are a characteristic feature of all plant-animal interaction networks, and likely pervade other ecological interactions. Important natural history details explain a fraction of them, resulting in unobservable interactions (i.e., forbidden interactions) that define structural zeroes in the interaction matrices and contribute to their extreme sparseness. Sampling interactions is a way to monitor biodiversity beyond the simple enumeration of component species and to develop efficient and robust inventories of functional interactions. Yet no sampling theory for interactions is available. Some key components of this sampling are analogous to species sampling and traditional biodiversity inventories; however, there are important differences. Focusing just on the realized interactions or treating missing interactions as the expected unique result of sampling bias would miss important components to understand how mutualisms coevolve within complex webs of interdependence among species.

Contrary to species inventories, a sizable fraction of non-observed pairwise interactions cannot be sampled, due to biological constraints that forbid their occurrence. A re-scaling of traditional asymptotic estimates for interaction richness can be applied whenever the knowledge of natural history details about the study system is sufficient to estimate at least the main causes of forbidden links. More-

over, recent implementations of inference methods for unobserved species (Chao *et al.*, 2015) can be combined with the forbidden link approach, yet they do not account either for the existence of these ecological constraints.

Ecological interactions provide the wireframe supporting the lives of species, and they also embed crucial ecosystem functions which are fundamental for supporting the Earth system. Yet we still have a limited knowledge of the biodiversity of ecological interactions, but they are being lost (extinct) at a very fast pace, frequently preceding species extinctions (Valiente-Banuet *et al.*, 2014). We urgently need robust techniques to assess the completeness of ecological interactions networks because this knowledge will allow the identification of the minimal components of ecological complexity that need to be restored after perturbations to rebuild functional ecosystems.

Acknowledgements

Data accessiblity

Please state where you have deposited the raw data underlying your analyses. It will need to include the name of the repository (e.g. Dryad, figshare, GenBank etc.) and location of the data (i.e DOI). For authors archiving at Dryad, we can facilitate the process when your paper is accepted.

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34

Table captions

Table 1. A taxonomy of link types for ecological interactions (Olesen et al. 2011). A, number of animal species; P, number of plant species; I, number of observed links; $C = 100I/(AP)$, connectance; FL, number of forbidden links; and ML, number of missing links. As natural scientists, our ultimate goal is to eliminate ML from the equation $FL = AP - I - ML$, which probably is not feasible given logistic sampling limitations. When we, during our study, estimate ML to be negligible, we cease observing and estimate I and FL.

Table 2. Frequencies of different type of forbidden links in natural plant-animal interaction assemblages. AP, maximum potential links, I_{max}; I, number of observed links; UL, number of unobserved links; FL, number of forbidden links; FL_P, phenology; FL_S, size restrictions; FL_A, accessibility; FL_O, other types of restrictions; ML, unknown causes (missing links). Relative frequencies (in parentheses) calculated over $I_{max} = AP$ for I, ML, and FL; for all forbidden links types, calculated over FL. References, from left to right: Olesen et al. 2008; Olesen & Myrthue unpubl.; Snow & Snow 1972 and Jordano et al. 2006; Vizentin-Bugoni et al. 2014; Jordano et al. 2009; Olesen et al. 2011.

Table 3. A vectorized interaction matrix.

Table 4. Sampling statistics for three plant-animal interaction networks (Olesen et al. 2011). Symbols as in Table 1; N, number of records; $Chao1$ and ACE are asymptotic estimators for the number of distinct pairwise interactions I (Hortal

734 et al. 2006), and their standard errors; C, sample coverage for rare interactions

735 (Chao & Jost 2012). Scaled asymptotic estimators and their confidence intervals

736 (CI) were calculated by weighting $Chao1$ and ACE with the observed frequencies

737 of forbidden links.

738

Table 1:

Link type	Formulation	Definition
Potential links	$I_{max} = AP$	Size of network matrix, i.e. maximum number of potentially observable interactions; A and P, numbers of interacting animal and plant species, respectively.
Observed links	I	Total number of observed links in the network given a sufficient sampling effort. Number of ones in the adjacency matrix.
Unobserved links	$UL = I_{max} - I$	Number of zeroes in the adjacency matrix.
Forbidden links	FL	Number of links, which remain unobserved because of linkage constraints, irrespectively of sufficient sampling effort.
Missing links	$ML = AP - I - FL$	Number of links, which may exist in nature but need more sampling effort and/or additional sampling methods to be observed.

Figure captions

Figure 1. Sampling ecological interaction networks (e.g., plant-animal interactions) usually focus on different types of subsampling the full network, yielding submatrices $\Delta[m, n]$ of the full interaction matrix Δ with A and P animal and plant species. a) all the potential plants interacting with a subset of the animals (e.g., studying just the hummingbird-pollinated flower species in a community); b) all the potential animal species interacting with a subset of the plant species (e.g., studying the frugivore species feeding on figs *Ficus* in a community); and c) sampling a subset of all the potential animal species interacting with a subset of all the plant species (e.g., studying the plant-frugivore interactions of the rainforest understory).

Figure 2. Sampling species interactions in natural communities. Suppose an assemblage with $A = 3$ animal species (red, species 1–3 with three, two, and 1 individuals, respectively) and $P = 3$ plant species (green, species a-c with three individuals each) (colored balls), sampled with increasing effort in steps 1 to 6 (panels). In Step 1 we record animal species 1 and plant species 1 and 2 with a total of three interactions (black lines) represented as two distinct interactions: $1 - a$ and $1 - b$. As we advance our sampling (panels 1 to 6, illustrating e.g., additional sampling days) we record new distinct interactions. Note that we actually sample and record interactions among individuals, yet we pool the data across species to get a species by species interaction matrix. Few network analyses have been carried out on individual data(Dupont *et al.*, 2014).
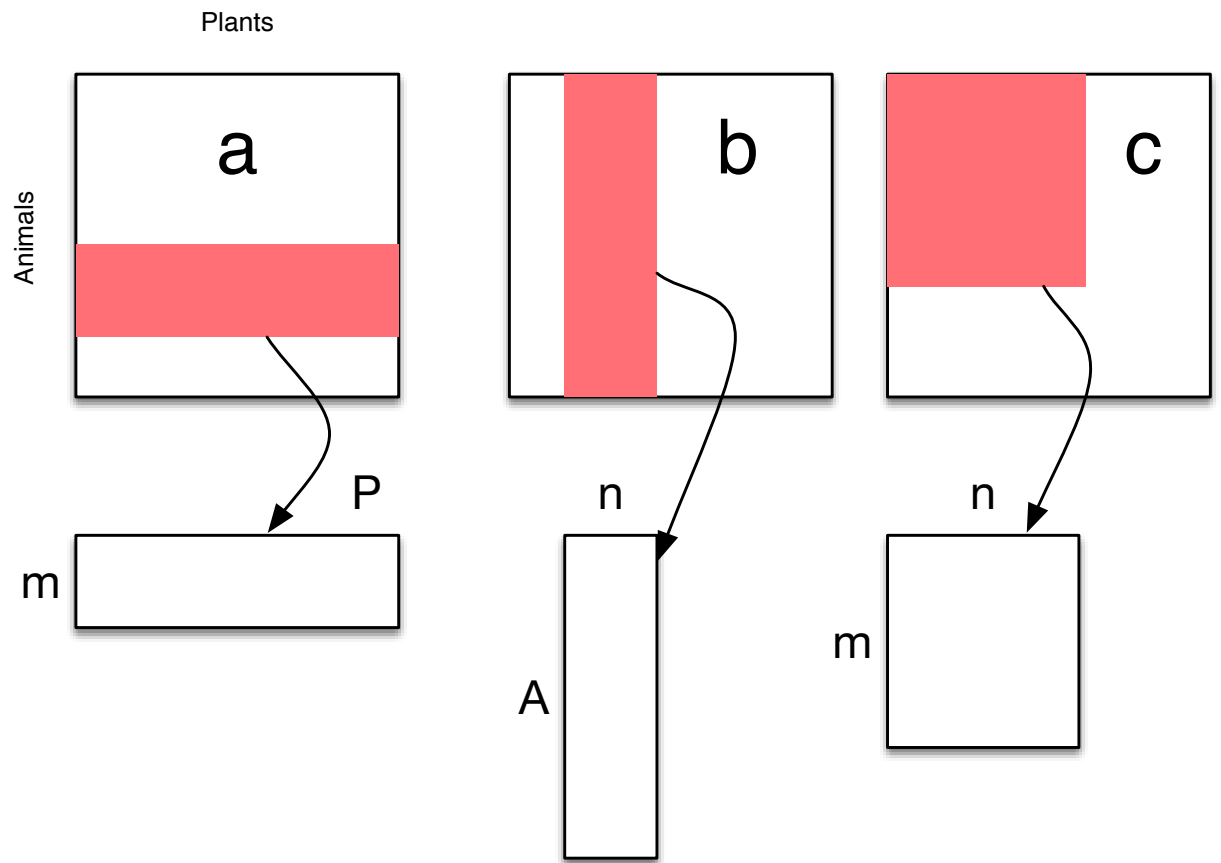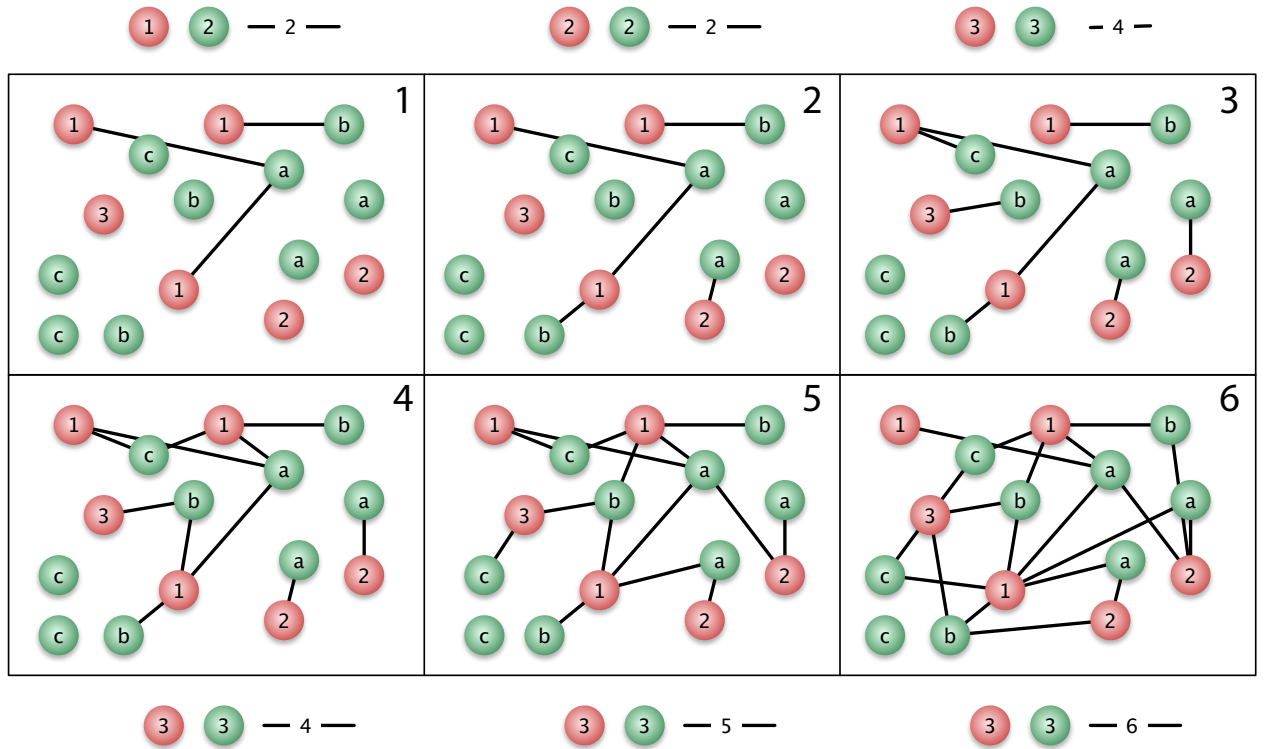
Figure 1:

Figure 2:

Jordano – Figure 1

Table 2:

Link type	Pollination				Seed dispersal	
	Zackenberg	Grundvad	Arima Valley	Sta. Virginia	Hato Ratón	Nava Correhuelas
I_{max}	1891	646	522	423	272	825
I	268 (0.1417)	212 (0.3282)	185 (0.3544)	86 (0.1042)	151 (0.4719)	181 (0.2194)
UL	1507 (0.7969)	434 (0.6718)	337 (0.6456)	337 (0.4085)	169 (0.5281)	644 (0.7806)
FL	530 (0.3517)	107 (0.2465)	218 (0.6469)	260 (0.7715)	118 (0.6982)	302 (0.4689)
FL_P	530 (1.0000)	94 (0.2166)	0 (0.0000)	120 (0.1624)	67 (0.3964)	195 (0.3028)
FL_S	$\cdots(\cdots)$	8 (0.0184)	30 (0.0890)	140 (0.1894)	31 (0.1834)	46 (0.0714)
FL_A	$\cdots(\cdots)$	5 (0.0115)	150 (0.445)[a]	$\cdots(\cdots)$	20 (0.1183)	61 (0.0947)
FL_O	$\cdots(\cdots)$	$\cdots(\cdots)$	38 (0.1128)[b]	$\cdots(\cdots)$	$\cdots(\cdots)$	363 (0.5637)
ML	977 (0.6483)	327 (0.7535)	119 (0.3531)	77 (0.1042)	51 (0.3018)	342 (0.5311)

[a], Lack of accessibility due to habitat uncoupling, i.e., canopy-foraging species vs. understory species.
[b], Colour restrictions, and reward per flower too small relative to the size of the bird.

Table 3:

Interaction	Sample 1	Sample 2	Sample 3	...	Sample i
A1 - P2	12	2	0	...	6
A1 - P2	0	0	0	...	1
...	...	...	...	...	...
A5 - P3	5	0	1	...	18
A5 - P4	1	0	1	...	3
...	...	...	...	...	...
A_i - P_i	1	0	1	...	2

Table 4:

	Hato Ratón	Nava Correhuelas	Zackenberg
A	17	33	65
P	16	25	31
I_{max}	272	825	1891
N	3340	8378	1245
I	151	181	268
C	0.917	0.886	0.707
$Chao1$	263.1 ± 70.9	231.4 ± 14.2	509.6 ± 54.7
ACE	240.3 ± 8.9	241.3 ± 7.9	566.1 ± 14.8
$Scaled\ Chao$	195.4	162.7	308.4
CI	[124.5–266.3]	[148.5–176.9]	[253.6–363.1]
$Scaled\ ACE$	178.5	169.7	342.6
CI	[169.5–187.4]	[161.8–177.6]	[327.8–357.4]
$\%\ unobserved^a$	8.33	15.38	47.8

[a], estimated with library Jade (R Core Development Team 2010,Chao et al. 2015)