**Title:** Bringing Elton and Grinnell together: a quantitative framework to represent the biogeography of ecological interactions

**Authors:** Dominique Gravel, Timothée Poisot, Néo Martinez, Jennifer A. Dunne, Jason Tylianakis, Tomas Roslin, Tommy Nyman, Ben Baiser, Daniel B. Stouffer

1: Canada Research Chair in Integrative Ecology. Département de biologie, Université de Sherbrooke, 2500 Boulevard l’Université, Sherbrooke (Québec). J1K 2R1

2: Québec Centre for Biodiversity Sciences

3: University of Canterbury at Christchurch, School of Biological Sciences,

4:

5:

6:

7:

**Keywords:** networks, spatial ecology, co-occurrence, probability of interaction

**Words in the abstract:**

**Words in the main text:**

**Words in the legends:**

**Figures:**

**Tables:**

**References:**

# Abstract

# Introduction

Community ecology is defined in most textbooks as *the study of the interactions that determine the distribution and abundance of organisms* (Krebs2001). Despite a general concensus on this definition (Scheiner2007), it is surprising that most research on the variation of community structure has focused mostly on the turnover of species composition (Anderson2011), neglecting variation in the way they interact with each other (McGill2006). Not surprisingly given this fact, biogeographers are still struggling to figure out if interactions do impact species distribution (Wisz2012; Kissling2012). There has been a step ahead with recent methodological improvements accounting for interactions in species distribution models (Pollock2014; Pelissier2013), but those remain nonetheless a ’species- based’ approach to communities where interactions are fixed covariates affecting distribution. Here we plea for a more integrated approach of species and interaction distribution.

The problem of community assembly is often formulated as *how do we sample a regional pool of species to constitute a local community?* This question could be rewritten to adress the problem of network assembly, as *how do we sample a regional pool of interactions to constitute a local interaction network?*. An illustration of this problem for a food web is provided at Figure 1. The metaweb represents potential interactions among all species that could be found in a given area. In this particular case, there are 274 nodes, and 1077 links among plants, herbivores and parasitoids from Northern Europe. An instance of a local community is also illustrated, with 44 nodes and 160 interactions. Only of all potential interactions are realized. Our objective here is to provide a conceptual framework to explain the sampling of the regional pool of interactions, along with a quantitative method to predict it. The problem could be formalized by sequentially understanding why only a fraction of the species are locally co-occurring, and after why these species are interacting or not.

There are multiple causes to spatial turnover in community composition. The first and most studied driver is the effect of variation in the abiotic environment on species performance. Combined with specific responses in demography, it generates variation among localities by locally selecting the fittest species (Leibold2004). Stochasticity additionnaly plays a role, either because of the inherently unpredictable nature of colonization and extinction events, or because of strong non-linear feedbacks generating alternative transients and equilibrium (Chase2007; Vellend2014). The analysis of community turnover is usually performed with data represented in a table with rows corresponding to sites (or measurements) and the columns to species. Beta- diversity metrics quantify the variance of this community data (Legendre2005). Traditionnal approaches rely on measures of the dissimilarity between communities, using indices such as the Jaccard or the Bray Curtis measures of dissimilarity. Recent methods decompose the total variation of the community data into species and site contributions to beta diversity (Legendre2013). Even though these methods compare whole list of species between sites, or measurements, they remain fundamentally ’species-based’ since they are all based on the within column variation. None of them consider the variation of associations (pairs or higher order motifs) explicitly.

The niche is by far the dominant concept to explain species distribution and community assembly, from the local to the global scale. Following Hutchinson, the niche is viewed as the set of environmental conditions allowing a population to establish and maintain a population (see also Holt2009). Community turnover arises following successive species replacement along an environmental gradient, in agreement with a Gleasonian view of communities (Gleason). The concept is straighforward to operationalize with species distribution models, as it maps naturally on the available data (both distribution and environmental data) and a vast array of statistical tools representing it (e.g. Biomod, MaxEnt). It is however much harder to account for ecological interactions in this approach (Peterson2011). These are often viewed as externalities, constraining or expanding the range of environmental conditions required for a species to maintain a population (Pulliam2000; Soberon2007).

The network approach proposes a convenient formalism to represent the structure of local communities. Species are represented as nodes and interactions by links. The data could also be represented by matrices, with each species in rows and columns, and the entries representing the occurrence or the intensity of an interaction. Studies of network diversity are mostly concerned by the distribution of the interactions within a location and not so much by the variation among locations (Dunne2005; Bascompte2007; Ings2007; Kefi2012). Network complexity is computed as the number of interactions in the case of binary networks or interaction diversity in the case of quantitative networks (Bersier2002). However, there is now evidence that ecological interactions do also vary in space and time (Poisot2012; Trojelsgaard2015). The variability of community structure in this situation arises from the turnover of species composition, along with the turnover of the interactions among pairs of species. The occurrence and intensity of interactions could vary because of the environment, species abundance and higher order interactions (Poisot2015a). The variation in community composition is often independent of the variation of ecological interactions, suggesting these two components of network variability respond to different drivers (Poisot2012).

Interestingly, the ecological network literature also has its own ’niche model’ to position a species in a community (Williams2000). The niche of a species in this context represents the multidimentional space that could represent all of its interactions. Each species is characterized by a niche position, an optimum and a range over 3 to 5 different niche axes (Williams2000; Eklof2013). The niche model has been successful at explaining the complexity of a variety of networks, from food webs to plant-pollinator systems. The conceptual framework is however limited to local communities and does not provide any explanation to the turnover of network structure along environmental gradients.

Here we adopt the view that a community structure is best represented as an ecological network of interactions and develop a theory to explain its turnover in space and time. We propose a new description of the niche that integrates the effect of the environment on species distribution and on ecological interactions. We first present the conceptual framework and then formalize it mathematically with a probabilistic approach to the sampling of the regional pool of interactions. We apply the framework to study the spatial variation of host-parasite interactions across Europe. We find that the variation of the environment causes both species and interaction turnover. The network structures changes systematically across the latitudinal gradient, with a peak of connectance at intermediate latitudes. At the pairwise level, the statistical approach could be conceived as an interaction distribution model. At the community level, the approach provides a likelihood based method to compare different hypotheses of network turnover.

# The integrated niche

Correctly describing the niche is key to understand turnover in community structure. Despite several attempts to refresh the conceptual basis of what ecological niches are, ecologists have not moved far past the “n-dimensional hypervolume” formalism (Holt2009) introduced by Hutchinson. Despite its intuitive interpretation and translation into species distribution models (Boulangeat2012; Blonder2014), the concept has been constantly criticized (Hardin1960; Peters1991; Chase2003; Silvertown2004; Soberon2007) and several attempts have been made to expand and reinforce it.

Part of the problem surrounding the definition of the niche has been clarified with the distinction between Eltonian and Grinnellian definitions (Chase2003). The Grinnellian dimension of the niche is the set of environmental conditions required for a species to maintain a population in a location. The Grinnellian niche is the most intuitive to apply and is the conceptual backbone of species distribution models. The Eltonian niche on the other hand is the effect of a species on its environment. This aspect of the niche is well known by community ecologists, but is trickier to turn into predictive models. Nonetheless, the development of the niche model of food web structure (Williams2000) and its parameterization (Williams2010; Gravel2013) made it more operational.

These perspectives are rather orthogonal to each other and thus lead to considerable confusion in the literature (McIntyre). Chase2003 attempted to reconcile them in their definition of the niche: *[The niche is] the joint description of the environmental conditions that allow a species to satisfy its minimum requirements so that the birth rate of a local population is equal or greater than its death rate along with the set of per capita effects of that species on these environmental conditions.* Their representation merges zero-net growth isoclines figuring the Grinnelian niche (when do the population persists) with impact vectors figuring the Eltonian niche (what is the per capita impact). While this representation has been very influential in community ecology at the local scale (the resource-ratio theory of coexistence - Tilman1982), it remains impracticable at the large spatial scale because of the difficulties to measure it. The absence of any mathematical representation of the niche that could easily be fit to ecological data perhaps explain why biogeographers are still struggling to develop species distribution models taking into account ecological interactions.

We propose to integrate the two perspectives of the niche with a visual representation of the Eltonian niche into a ’Grinnelian space’ (Fig. 2). The Grinnelian niche is the set of abiotic environmental conditions allowing a sustainable population to occur. It is also more formally defined as the set of conditions with a positive intrinsic rate of increase. By analogy and reference to the niche model (Williams2000), the Eltonian niche of a given species could be defined as the set of traits allowing it to interact with other species and sustain a population. Accordingly, each species could be characterized by a niche position and the range of niches constituing its diet. Doing so, we could project both niches in a plane and find that the integrated niche is hypervolume where interactions could occur and sustain a population. The limits of the niches are independent of each other in the example, but we could figure out situations where they are jointly related. For instance, the optimimal prey body size for predatory fishes could reduce with increasing temperature (Lelong2015), which would make diet boundaries functions of the environment. Alternatively, the growth rate of the predator could change with the body size of the preys it feeds on, thereby altering the environmental boundaries. This approach radically change the representation of the niche, putting species distribution and ecological interactions in the same formalism.

# A probabilistic representation of ecological interactions networks in space

We now formalize the integrated niche with a probabilistic approach to interactions and distribution. We seek to describe the set of conditions for an interaction to occur.

We seek to represent the probability an interaction between species and occurs at location . We consequently define as a stochastic variable and we are thus looking at the probabilty this event occurs, . The occurrence of an interaction is dependent on the co- occurrence of species and . This argument might seem trivial at first, but the explicit consideration of this condition in the probabilistic representation of ecological interactions will prove fundamental to understand their variation. We thus define as a stochastic variable representing the occurrence of a species at location , and similarly the co-occurrence of species and . The quantity we seek to understand is the probability of a joint event:

Or simply said, the probability of observing both species and , and an interaction from to . This probability could be further decomposed in two parts using the product rule of probabilities:

We will refer to the left term as the metaweb. It is a conditional probability, representing the probability that an interaction occurs between species and , given their set of traits and they are co- occurring. It corresponds to the Eltonian dimension of the niche described above. The right term is the probability of observing the two species co- occurring at location . It corresponds to the Grinnelian dimension of the niche. This formalisme could be directly fitted to empirical data, as we will see below. But before turning to an application, we will discuss the interpretation of different variants of these two terms.

## Variants of the metaweb

There are many variants of the metaweb representing different hypotheses about the origin of temporal and spatial variation in network structure (see the explicit formulations at Table 1). First, most documentations of the metaweb thus far considered that ecological interactions are deterministic, not probabilistic. Species are assumed to interact if they are found together in a location, independently of their abundance and the environment. In other words, if , and 0 otherwise. This approach might be a reasonnable approximation when the sampling and inference scales are large enough so that probabilities of observing at least one interaction converges to unity. and that the only variation of networks considered arises from species distribution.

Ecological interactions could also vary with the environment. Although it is not common to see a conditional representation of ecological interactions, experimental studies of pairwise interactions revealing their sensitivity to the environment are common (REF). For instance, it has been documented that the predation risks of shorebirds do vary at the continental scale, from the south to the north (REF). The effect of the environment on interactions propagate up the community and influence network structure (REF).

## Variants of co-occurrence

There are also variants to the co-occurrence matrix. Akin to the metaweb, co- occurrence could be conditional or not. The simplest model relates co- occurrence probability directly to the environment, . In this situation there is no underlying assumption about the ecological processes responsible for co-occurrence. It could arise because of the impact of ecological interactions on distribution (such as in the cases studied by Diamond, Connor, Gotelli etc..) or alternatively because of share environmental requirements. In the former case, species are not independent to each other and the conditional occurrence must be accounted for explicitlty, . In the later case, species are independent only the marginal occurrence must be accounted for, .

Finally, the co-occurrence probability itself could be dependent on ecological interactions. Direct pairwise interactions such as competition, facilitation and predation have long been studied for their impact on co-distribution. Second and higher order interactions (e.g. trophic cascade) could also impact co-occurrence. There is however currently no general theory on the expected co-occurrence in complex ecological networks (Cazelles). For instance, we do not know how far co-occurrence is not-random when going along the chain of indirect interactions. Berlow (2009) shown previously that almost only first and second order interactions do matter in ecological networks, but we don’t know for co-distribution. We neither know what is the sensitivity to species richness: do interactions tend to buffer each other? For now we will focus on the variation of interactions and not on the distribution, and leave this issue for Discussion and future research.

# Application: continental-scale variation of host-parasite community structure

In this section we provide an illustration of the framework with an empirical dataset of host-parasitoid networks sampled throughout continental Europe along a south-north gradient. The analysis targets networks composed of willows (genus Salix), their galling insects, and the natural enemies of these gallers. The questions we adress with the framework and the dataset are: i) how much variation in the network structure is there across the gradient and ii) what is the primary driver of network turnover across the gradient ?

## Data

Communities of both willows and gallers are species-rich and widely distributed, with pronounced variation in community composition across space. The genus Salix includes over 400 species, most of which are shrubs or small trees (ref). The genus is common in most habitats across the Northern Hemisphere (ref). Willows support a highly diverse community of herbivorous insects, and one of the main herbivore groups in this system are gall-inducing sawflies (Hymenoptera: Tenthredinidae: Nematinae: Euurina (ref). Gall formation is induced by sawfly females during oviposition, and gall formation includes marked manipulation of plant chemistry by the galler (ref). The enemy community of the gallers includes nearly 100 species belonging to 17 insect families of four orders. These enemies encompass both inquilines and parasitoids: inquiline larvae (Coleoptera, Lepidoptera, Diptera, and Hymenoptera) feed primarily on gall tissue, but typically kill the galler larva in the process. Parasitoid larvae (representing many families in Hymenoptera) kill the galler larvae by direct feeding (REF). In terms of associations between the trophic levels, phylogeny-based comparative studies have demonstrated that galls represent “extended phenotypes” of the gallers, meaning that gall form, location, and chemistry is determined mainly by the galling insects and not by their host plants [ref]. Because galler parasitoids have to penetrate a protective wall of modified plant tissue in order to gain access to their victims, gall morphology has been inferred to strongly affect the associations between parasitoids and hosts (ref, ref). Thus, the set of parasitoids attacking each host is presumptively constrained by the form, size, and thickness of its gall.

Local realizations of the willow–galler–enemy network were reconstructed from samples collected between 1982 and 2010. Plant galls were collected by J.P. Kopelke during this period at 374 sites across Central and Northern Europe. Sampling was conducted in the summer months of June and/or July, during the latter stages of larval development. Galler species were identified on the basis of willow host species and gall morphology, as these are distinct for each sawfly species. At each site, galls were randomly collected from several willow individuals in an area of about 0.1-0.3 km2. Most sites were visited only once, with a total of 641 site visits across the 374 sites. GPS coordinates were recorded for each location and the annual mean temperature and annual precipitation were obtained from WorldClim. While other covariates could have been considered, we figured that they are representative of the most important axes of the climatic space across Europe, and more easily interpretable than reduced variables obtained by a PCA,

The methods used for rearing natural enemies from the galls have been previously described by e.g. [ref, ref]. In brief, galls were opened to score the presence of galler or parasitoid/inquiline larvae. Enemy larvae were classified to preliminary morphospecies, and the identity of each morphospecies was determined by connecting them to adults emerging after hibernation. The galls were reared by storing single galls in small glass tubes (Kopelke 1985a, 1994a, 1999, 2003a, b). Hibernation of galls containing parasitoids took place either within the glass tubes or between blotting paper in flowerpots filled with clay granulate or a mixture of peat dust and sand. These pots were stored over the winter in a roof garden and/or in a climatic chamber. In most cases, the matching of larval morphospecies with adult individuals emerging from the rearings allowed the identification of the natural enemies to the species level. Nonetehless, in some cases, individuals could only be identified to one of the (super)families Braconidae, Ichneumonidae, and Chalcidoidea. This was particularly the case when only remains of faeces, vacant cocoons of parasitoids, and/or dead host larvae were found, as was the case when parasitoids had already emerged from the gall. As a result, the largest taxon in the data set, “Chalcidoidea indeterminate,” represents a superfamily of very small parasitoids that are hard to distinguish.

In total, the sampling targeted 52 Salix taxa, yielding 146,622 galls for dissection and rearing. These galls represented 96 galler species, and yielded 42,133 individually-identified parasitoids and inquilines. Of these, 25,170 (60%) could be identified to the species level. Overall, 126 parasitoid and inquiline taxa were distinguished in the material. Data on host associations within subsets of this material have been previously reported by (Kopelke ref ref b) and by Nyman et al. 2007, whereas the current study represents the first analysis of the full data set from a spatial food-web perspective.

## Analysis

Computing the probability of observing an interaction is fairly straightforward as it involves fitting a set of binomial models and collecting their estimated probabilities. We considered second-order generalized linear models for the sake of the illustration, but more sophisticated fitting algorithms (e.g. GAM or Random Forest) could be used as well, as long as the algorith can provide a an estimated probability for each observation. The data consists of a simple (albeit large) table with the observation of each species, and , their co-occurrence, , the observation of an interaction , and environmental co-variates (here the first three axes of the PCA on climatic variables). There is one row per ennemy-victim pair of species per site. We considered that an absence of a record of an interaction or of a species at a site means a true absence.

We compared three models for the co-occurrence probability. The first model fits directly fits the co-occurrence probability conditional on the local environmental variables. This model therefore does not make any hypothesis about the mechanisms driving co-occurrence for any given environment and use the information directly available in the data. The second models consider independent co-occurrence of species. In this case, we fit independently and and take their product to derive co-occurrence probability. This model should be viewed as a null hypothesis with respect to the first model since their comparison reveals if there is significant spatial association of the two species once considering the response to the environment (Cazelles2016). Finally the third model considers that co-occurrence probability is independent of the environment and thus constant throughout the landscape. In other words, is obtained by simply counting the number of observed co-occurrences, divided by the total number of observations. The comparison between the first and third model allows testing the hypothesis that co-occurrence is conditional on the environment. Whenever the environment is included as a co-variate in the glm, we considered a second-order polynomial response for both the temperature and precipitations. There are consequently 5 parameters for the first model when fitting a given pair of species, 10 parameters for the second model and only 1 for the third model.

Following the same logic, we compared three models for the interaction probability, given the two species co-occur. Consequently, models were fitted on a subset of the data, when the two species are found co-occurring. Not surprisingly, it was impossible to compute this model for a very large number of pairs of species. The reported likelihood across the entire dataset is therefore summed over all pairs of species that were observed co-occurring at least one time. An interaction probability was set to 0 for pairs of co- occurring species that are never found interacting. The first model fits the interaction probability conditional on the local environmental variables, .The second model fits the interaction probability independently of the local environmental variables, . It corresponds to the number of times the two species were observed interacting when co-occurring, divided by the number of times they co-occurred. The third model is an extreme case performed only to test the hypothesis that if two species are found to interact at least once, then they should interect whenever they co-occur, . While not necessarily realistic, this models model allows to test an hypothesis that is commonly done in the representation of local networks from knowledge of a deterministic metaweb (such as in Havens1992,Piechnik2008). There are consequently 5 parameters for the first model, a single parameter for the second model and no parameter to evaluate for the third model (the interaction probability is fixed by hypothesis).

The different models were fitted to each pair species and the fitted probabilities were recorded. The joint probability was then computed from Eq. 1 and the likelihood of each observation was computed as if an interaction was observed and if no interaction was observed. The log- likelihood was summed over the entire dataset to compare the different models by AIC. We considered separately the salix-gall and the gall-parasitoid interactions. The confidence interval around the estimated interaction probability can be computed using the Clopper-Pearson method.

Finally, we used the full model (both the co-occurrence and the interaction are conditional on the environment) was used to interpolate species distribution and the interaction probability across the entire Europe to reconstruct the expected network for each location in a 1km X 1km grid. We then after computed the probabilistic connectance following Poisot2015b.

All of the data are openly available in the database *mangal* (Poisot2015) and all R scripts for querying and pre-processing the data, along with the analysis are provided in supplementary material.

## Results

We start with an example for a single pair of species that we selected because of a sufficiently large number of times they were found co-occurring (). Despite the extent of the sampling, many pairs of species are found co- occurring only a few times, making it hard to evaluate interaction probabilities. This particular example involves the interaction between *Phyllocolpa plicalapponum* and *Pediobius saulius*, two fairly abundant species, observed respectively and times across the 374 sites. These two species are found interacting with marginal probability , which means they were found interacting at 30 different sites. The model comparaison (Table 1) reveals that the interaction probability conditional on the co-occurrence better explain the distribution (Model 1 vs Model 2). In other words, the probabilistic representation of the metaweb yields a much better fit to the data than the deterministic version. When the two species co-occur, the occurrence of the interaction is insensitive to the environment (Model 2 vs Model 3). Alternatively, climatic variables significantly impact co-occurrence (Model 3 vs Model 4). The neutral model is perform worst than the non-random co-occurrence model (Model 3 vs Model 6). The full model reveals that the greatest interaction probability occurs at intermediate temperature and precipitations, simply because this is where the two species are found co-occurring the most often (Fig. X). The co- occurrence and the interaction probabilities could be represented in space, where we find that the highest interaction probability occurs in central Europe (Fig. X).

We did evaluate each model for all pairs of species in order to better understand the large scale drivers of network turnover. Salix-gallers and gallers-parasitoids were analyzed separately (Table 2). The results are comparable, albeit some very minor details. We do find that across all pairs of species, again the probabilistic representation of interactions does better than the deterministic (Model 1 vs Model 2). Interactions do not happen systematically whenever the two species are found co-occurring. There are 1077 recorded pairs of interactions, with only 224 of them occurring less than 5 times. Out of these 224 interactions, only 77 where found systematically whenever the two species do co-occur. Even though interactions are better represented probabilistically, the two environmental variables that were considered are pretty poor predictors of their occurrence (Model 2 vs Model 3). Not surprisingly, the likelihood increases for both types of interactions when the environment is considered. The extra number of parameters however exceed the gain in likelihood, and therefore the best model exclude the effect of the environment.

According to the likelihood only, the co-occurrence is non-neutral for salix-galler interactions, while it is neutral for the galler-parasitoid interaction. However, the gain in likelihood for the neutral model of galler-parasitoid co-occurrence is inferior to the extra number of parameters (twice as many since two species distribution models are fitted instead of just one), which has for consequence that the best model according to AIC has non-random co-occurrence (Model 3 vs Model 6), for both types of interactions.

The approach we developped not only has implications for understanding the biogeography of pairwise interactions and interaction networks, but also the quality of the evaluation of metawebs. We investigated the reliability of the estimated metaweb across the entire dataset. As mentionned above, across the 32 412 pairs of species, only 1077 were documented interacting with at least a single location, for a connectance of 0.03. However, only 8437 species were found co-occurring at least one across all sites. There are consequently 23 975 gaps of knowledge in the metaweb (74.0% - see Fig. X). Given that we do not know if the non co-occurring species do indeed co-occur, it means that a more appropriate estimate of connectance would be . Given that many network properties are cosntrained by connectance (Poisot2014), their computation across all pairs is susceptible to be strongly biased. The investigation of the quality of network sampling is a problem on its own that worths further attention.

Once we selected the best model (3), we were able to reconstruct the expected species richness across Europe, along with the most likely network for each location, and therefore map the expected distribution of network properties (Fig. X). We simply considered connectance, as it could be easily computed from probablistic networks (Poisot2015b) and is also a good proxy for many other network properties (Poisot2014). The diversity of Salix tends to increase toward boreal areas, and we consequently find a peak in diversity in northern Europe. The distribution of the expected number of interactions follows the distribution of species richness, but not at the same rate. Consequently, connectance is expected to peak in central Europe and in England.

# Discussion

**Summary of the framework**  
 **Toward interaction distribution models**

**What are the drivers of network variation in space?**  
 **Forecasting network structure under global change**

**Investigating the realized niche and the impact of biotic interactions on distribution**

**Guidance for empirical studies**

# Conclusion

**Research agenda on probabilistic interactions**

Need a new type of data

Need to investigate the reliability of interactions

From interaction probabilities to a distribution of network properties

Deeper investigations of the environmental dependence of interactions

Trait-based approach to interactions

The effect of interaction on co-occurrence

# Acknowledgements

This is a contribution to the working groups *Networks over ecological gradients* (Santa Fe Institute) and *Continental-scale variation of ecological networks* (Canadian Institute for Ecology and Evolution).

# Figure legends

## Figure 1

**Non-random sampling of the metaweb**. Network assembly could be viewed as a sampling process of the regional pool of potential interactions. Species are sampled first (indicated by colored nodes) and among the present species in the local network, only some interactions are occurring (indicated by colored links). The challenge we address with the quantitive framework proposed is to adequately characterize this sampling process. The sampling of the metaweb is illustrated with a local interaction network among Salix, gallers and parasitoids. Here, the metaweb was constructed by aggregating observed interactions across 374 local networks. The color nodes represent the species that were found in the most diverse of these 374 local networks.

## Figure 2

**Visual representation of the integrated niche**. We represent visually the integration between two views of the niche. In biogeography, the niche is considered the set of environmental conditions where the intrinsic growth rate is positive. The horizontal axis represents an environmental gradient impacting the growth of the focal species (in red). The location of the different species along this gradient represent their optimum, and the vertical dotted lines represent the limits of the [Grinnelian] niche of the focal species. In food web ecology, the [Eltonian] niche represents the location of a species in the food web, as determined by its preys and its predators. The vertical axis represents a niche gradient, presumably a trait such as body size. The location of each species along this gradient represent their niche position. The focal species will feed on the different preys whose niche location falls within a given interval around the optimum, represented by the horizontal dotted lines. The integrated niche [Grinnelian & Eltonian] corresponds to the square in the middle where an interaction is possible. According to our probabilistic framework, the central square represents the area where the joint probability of observing interactions and co-occurrence is positive.

## Figure 3

**Probabilistic representation of the interaction probability between a leaf galler (*Phyllocolpa plicalapponum*) and a parasitoid (*Pediobius saulius*) across a temperature and a precipitation gradient**. The representation is based on predictions from model 3 (see Table 1). For the left panel: open circles represent the absence of both species or of an interaction, the closed circles represent co-occurrence and other symbols the occurrence of only one of the two species. For the other two panels the open circles represent co-occurrence but an absence of interaction and the closed circles represent the occurrence of an interaction.

## Figure 4

**Probabilistic representation of the interaction probability between a leaf galler (*Phyllocolpa plicalapponum*) and a parasitoid (*Pediobius saulius*) across Europe**.

## Figure 5

**Representation of the A) metaweb and B) gaps of data in the metaweb**. The salix and gallers were regrouped as ’victims’ for the sake of the illustration, as the gallers and the parasitoids were regrouped as ’ennemies’.

## Figure 6

**Mapping the distribution of species richness, the number of links and connectance across Europe**. The representation is based on predictions from model 3 (see Table 2).

## Figure 1

image

## Figure 2

image

## Figure 3

image

## Figure 4

image

## Figure 5

image

## Figure 6

image