

Food web reconstruction through phylogenetic transfer of low-rank network representation

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Abstract: Despite their importance in many ecological processes, collecting data and information on ecological interactions, and therefore species interaction networks, is an exceedingly challenging task. For this reason, large parts of the world have a deficit of data of which species interact, and what we can expect the network structure of these interactions to be. As data collection alone is unlikely to be sufficient at filling these global gaps, community ecologists must adopt predictive methods. In this contribution we develop such a method, relying on graph embedding (the extraction of explanatory latent variables from known graph structures) and transfer learning (the application of previous solution to novel problems with limited predictors overlap) in order to assemble a predicted list of trophic interactions between mammals of Canada. This interaction list is derived from extensive knowledge of the mammalian food web of Europe, despite the fact that there are fewer than 5% of common species between the two locations. We provide guidance on how this method can be adapted by substituting some approaches or predictors in order to make it more generally applicable to a broad family of ecological problems.

Keywords:
ecological networks
network embedding
transfer learning
ancestral character estimation
biogeography

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Introduction

There are two core challenges we are faced with in furthering our understanding of ecological networks across space, particularly at macro-ecologically relevant scales (*e.g.* Trøjelsgaard and Olesen 2016). First, networks within a location are difficult to sample properly (Jordano 2016a, 2016b), resulting in a widespread “Eltonian shortfall” (Hortal et al. 2015). This first challenge

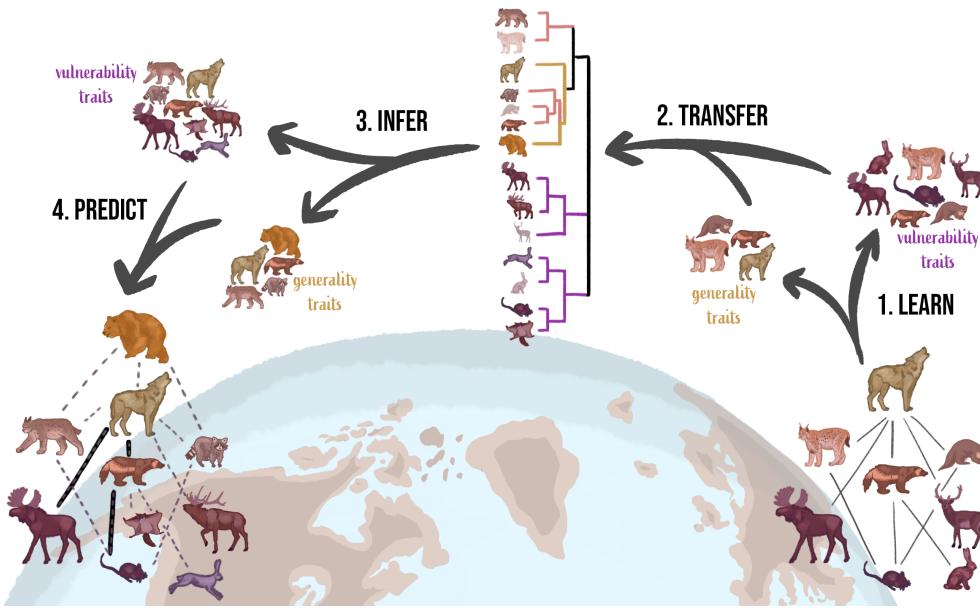


Figure 1 Overview of the phylogenetic transfer learning (and prediction) of species interactions networks. Starting from an initial, known, network, we learn its representation through a graph embedding step (here, a truncated Singular Value Decomposition; Step 1), yielding a series of latent traits (vulnerability traits representing species at the lower trophic-level and generality traits representing species at higher trophic-levels; *sensu* Schoener (1989)); second, for the destination species pool, we perform ancestral character estimation using a phylogeny (here, using a Brownian model for the latent traits; Step 2); we then sample from the reconstructed distribution of latent traits (Step 3) to generate a probabilistic metaweb at the destination (here, assuming a uniform distribution of traits), and threshold it to yield the final list of interactions (Step 4).

(local incompleteness) has been, in large part, addressed by the recent multiplication of methods aiming to predict interactions *within* an *existing* network, a lot of which are reviewed in Strydom et al. (2021). Second, recent analyses based on collected data (Poisot, Bergeron, et al. 2021) or metadata (Cameron et al. 2019) highlight that ecological networks are currently studied in a biased subset of space and bioclimates, which impedes our ability to generalize any local understanding of network structure. Meaning that although the framework to address incompleteness *within* a network exists there would still be regions that, due to a *lack* of local interaction data, we are unable to infer potential species interactions. Having a general solution for the issue of metaweb inference (Morales-Castilla et al. 2015) that, despite situations where minimal knowledge about interactions within a species pool is known, is capable of producing a plausible metaweb could be the catalyst for significant breakthroughs in our ability to start thinking about species interactions networks over large spatial scales.

Here, we present a general method for the transfer learning of network representations, relying on the similarities of species in a biologically/ecologically relevant proxy space (*e.g.* shared morphology or ancestry). Transfer learning is a machine learning methodology that uses the knowledge gained from solving one problem and applying it to a related (destination) problem (Torrey and Shavlik 2010; Pan and Yang 2010). In this instance, we solve the problem of predicting trophic interactions between species, based on knowledge extracted from another species pool for which interactions are known, using phylogenetic structure as a medium for transfer. This allows us to construct a *probabilistic* metaweb for a community for which we have *no* prior interaction data for the desired species pool. Our methodology is outlined in fig. 1, where we provide an illustration based on learning an embedding of a metaweb of trophic interactions for European mammals (known interactions; Maiorano et al. 2020b, 2020a), and based on phylogenetic relationships between mammals globally (Upham, Esselstyn, and Jetz 2019), infer a metaweb for the Canadian mammalian species pool (interactions are treated as unknown in this instance).

There is a plurality of measures of species similarities that can be used for metaweb reconstruction (see *e.g.* Morales-Castilla et al. 2015); however, phylogenetic proximity has several desirable properties when working at large scales. Gerhold et al. (2015) made the point that phylogenetic signal captures diversification of characters (large macro-evolutionary process), but not necessarily community assembly (fine ecological process); Dormann et al. (2010) pre-

viously found very similar conclusions. Interactions tend to conserve a phylogenetic signal that encompasses a wide range of ecological and evolutionary mechanisms (Mouquet et al. 2012; Cavender-Bares et al. 2009), and - most importantly - retain this signal even when it is not detectable at the community scale (Poisot and Stouffer 2018; Hutchinson, Cagua, and Stouffer 2017). Finally, species interactions at macro-ecological scales seem to respond mostly to macro-evolutionary processes (Price 2003); which is evidenced by the presence of conserved backbones in food webs (Dalla Riva and Stouffer 2016), strong evolutionary signature on prey choice (Stouffer et al. 2012), and strong phylogenetic signature in food web intervality (Eklöf and Stouffer 2016). Phylogenetic reconstruction has also previously been used to understand ancestral plant-insect interaction networks (Braga et al. 2021). Taken together, these considerations suggest that phylogenies can reliably be used to transfer knowledge on species interactions.

Our case study shows that phylogenetic transfer learning is indeed an effective approach to predict the Canadian mammalian metaweb. This showcases that although the components (species) that make up the Canadian and European communities may not be *perfectly* shared, if the medium (proxy space) selected in the transfer step is biologically plausible, we can still effectively learn from the known network and make biologically relevant predictions of interactions. It should be reiterated that the framework presented in fig. 1 is amenable to changes; notably, the measure of similarity may not be phylogeny, and can be replaced by information on foraging (Beckerman, Petchey, and Warren 2006), cell-level mechanisms (Boeckaerts et al. 2021), or a combination of traits and phylogenetic structure (Stock 2021).

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Data used for the case study

We use data on the European metaweb assembled by Maiorano et al. (2020b), following the definition of the metaweb first introduced by Dunne (2006), *i.e.* an inventory of all possible interactions within species from a spatially delimited pool. Notably the metaweb is not a prediction of the food web at any specific locale within the frontiers of the species pool – in fact, these local food webs are expected to have a subset of both the species and the interactions of their metaweb (Poisot et al. 2012). This being said, as the metaweb represents the total of functional, phylogenetic, and macroecological processes (Morales-Castilla et al. 2015), it is thus still worthy of ecological attention. We induced the subgraph corresponding to all mammals by matching species names in the original network first to the GBIF taxonomic backbone (GBIF Secretariat 2021) and retaining all those who matched to mammals; all nodes had valid matches to GBIF at this step, and so this backbone is used for all name reconciliation steps as outlined below.

The European metaweb represents the knowledge we want to learn and transfer; the phylogenetic similarity of mammals here represents the support for transfer. We used the mammalian consensus supertree by Upham, Esselstyn, and Jetz (2019), for which all approximatively 6000 names have been similarly matched to their GBIF valid names. This step allows us to place each node of the mammalian European metaweb in the phylogeny.

The destination problem to which we want to transfer knowledge is the trophic interactions between mammals in Canada. We obtained the list of extant species from the IUCN checklist, and selected the terrestrial and semi-aquatic species (this corresponds to the same selection that was applied by Maiorano et al. (2020b) in the European metaweb). The IUCN names were, as previously, reconciled against GBIF to have an exact match to the taxonomy.

After taxonomic cleaning and reconciliation as outlined in the following sections, the mammalian European metaweb had 260 species, and the Canadian species pool has 163; of these, 17 (about 4% of the total) are shared, and 89 species from Canada (54%) had at least one congeneric

species in Europe. The similarity for both species pool predictably increases with higher taxonomic order, with 19% of shared genera, 47% of shared families, and 75% of shared orders; for the last point, Canada and Europe each had a single unique order (*Didelphimorphia* for Canada, *Erinaceomorpha* for Europe).

In the following sections, we describe the representational learning step applied to European data, the transfer step through phylogenetic similarity, and the generation of a probabilistic metaweb for the destination species pool.

3

Method description

The crux of the method is the transfer of knowledge of a known network, in order to predict interactions between species from another location. In fig. 1, we give a high-level overview of the approach; in the example around which this manuscript is built (leveraging detailed knowledge about binary trophic interactions between Mammalia in Europe to predict the less known trophic interactions between closely phylogenetically related Mammalia in Canada), we use a series of specific steps for network embedding, trait inference, network prediction and thresholding.

Specifically, our approach can be summarized as follows: from the known network in Europe, we use a truncated Singular Value Decomposition (t-SVD; Halko, Martinsson, and Tropp 2011) to generate latent traits representing a low-dimensional embedding of the network; these traits give an unbiased estimate of the node's position in the latent feature spaces. Then, we map these latent traits onto a reference phylogeny (other distance-based measures of species proximity that allow for the inference of features in the latent space can be used, for example the dissimilarity in functional traits). Based on the reconstructed latent traits for species in the destination species pool, a Random Dot Product Graph model (hereafter RDPG; S. J. Young and Scheinerman 2007) predicts the interaction between species through a function of the nodes' features through matrix multiplication. Thus, from latent traits and nodes position, we can infer interactions.

3.1. Implementation and code availability The entire pipeline is implemented in *Julia* 1.6 (Bezanson et al. 2017) and is available under the permissive MIT License at <https://osf.io/2zwqm/>. The taxonomic cleanup steps are done using *GBIF.jl* (Dansereau and Poisot 2021). The network embedding and analysis is done using *EcologicalNetworks.jl* (Banville, Vissault, and Poisot 2021; Poisot et al. 2019). The phylogenetic simulations are done using *PhyloNetworks.jl* (Solís-Lemus, Bastide, and Ané 2017) and *Phylo.jl* (Reeve et al. 2016). A complete *Project.toml* file specifying the full tree of dependencies is available alongside the code. This material also includes a fully annotated copy of the entire code required to run this project (describing both the intent of the code and discussing some technical implementation details), a vignette for every step of the process, and a series of Jupyter notebooks with the text and code. The pipeline can be executed on a laptop in a matter of minutes, and therefore does not require extensive computational power.

3.2. Step 1: Learning the origin network representation The first step in transfer learning is to learn the structure of the original dataset. In order to do so, we rely on an approach inspired from representational learning, where we learn a *representation* of the metaweb (in the form of the latent subspaces), rather than a list of interactions (species *a* eats *b*). This approach is conceptually different from other metaweb-scale predictions (*e.g.* Albouy et al. 2019), in that the metaweb representation is easily transferable. Specifically, we use RDPG to create a number of latent variables that can be combined into an approximation of the network adjacency matrix. RDPG results are known to have strong phylogenetic signal, and to capture the evolutionary

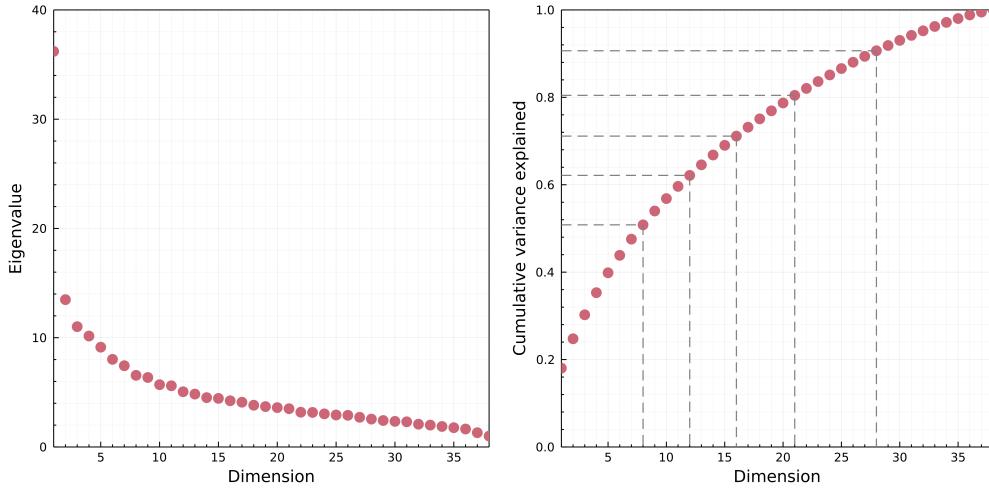


Figure 2 Left: representation of the screeplot of the singular values from the t-SVD on the European metaweb. The screeplot shows no obvious drop in the singular values that may be leveraged to automatically detect a minimal dimension for embedding, after *e.g.* Zhu and Ghodsi (2006). Right: cumulative fraction of variance explained by each dimension up to the rank of the European metaweb. The grey lines represent cutoffs at 50, 60... 90% of variance explained. For the rest of the analysis, we reverted to an arbitrary threshold of 60% of variance explained, which represented a good tradeoff between accuracy and reduced number of features.

backbone of food webs (Dalla Riva and Stouffer 2016). In addition, recent advances show that the latent variables produced this way can be used to predict *de novo* network edges (Runghen, Stouffer, and Dalla Riva 2021).

The latent variables are created by performing a truncated Singular Value Decomposition (t-SVD) on the adjacency matrix. SVD is an appropriate embedding of ecological networks, which has recently been shown to both capture their complex, emerging properties (Strydom, Dalla Riva, and Poisot 2021) and to allow highly accurate prediction of the interactions within a single network (Poisot, Ouellet, et al. 2021). Under SVD, an adjacency matrix \mathbf{A} (where $\mathbf{A}_{m,n} \in \mathbb{B}$ where 1 indicates predation and 0 an absence thereof) is decomposed into three components resulting in $\mathbf{A} = \mathbf{L}\Sigma\mathbf{R}$. Here, Σ is a $m \times n$ diagonal matrix and contains only singular (σ) values along its diagonal, \mathbf{L} is a $m \times m$ unitary matrix, and \mathbf{R}' a $n \times n$ unitary matrix. Truncating the SVD removes additional noise in the dataset by omitting non-zero and/or smaller σ values from Σ using the rank of the matrix. Under a t-SVD $\mathbf{A}_{m,n}$ is decomposed so that Σ is a square $r \times r$ diagonal matrix (where r is the rank of \mathbf{A}) containing only non-zero σ values. Additionally, \mathbf{L} is now a $m \times r$ semi-unitary matrix and \mathbf{R}' a $n \times r$ semi-unitary matrix.

The specific rank at which the SVD ought to be truncated is a difficult question. The purpose of SVD is to remove the noise (expressed at high dimensions) and to focus on the signal, (expressed at low dimensions). In datasets with a clear signal/noise demarcation, a scree plot of Σ can show a sharp drop at the rank where noise starts (Zhu and Ghodsi 2006). Because the European metaweb is almost entirely known, the amount of noise is low; this is reflected in fig. 2 (left), where the scree plot shows no important drop, and in fig. 2 (right) where the proportion of variance explained increases smoothly at higher dimensions. For this reason, we default back to an arbitrary threshold that explains 60% of the variance in the underlying data, corresponding to 12 dimensions.

A RDGP estimates the probability of observing interactions between nodes (species) as a function of the nodes' latent variables. The latent variables used for the RDGP, called the left and right subspaces, are defined as $\mathcal{L} = \mathbf{L}\sqrt{\Sigma}$, and $\mathcal{R} = \sqrt{\Sigma}\mathbf{R}$ – using the full rank of \mathbf{A} , $\mathcal{L}\mathcal{R}' = \mathbf{A}$, and using any smaller rank results in $\mathcal{L}\mathcal{R}' \approx \mathbf{A}$. Using a rank of 1 for the t-SVD provides a first-order approximation of the network.

Because RDGP relies on matrix multiplication, the higher dimensions essentially serve to make specific interactions converge towards 0 or 1; therefore, for reasonably low ranks, there is no guarantee that the values in the reconstructed network will be within the unit range. In order to determine what constitutes an appropriate threshold for probability, we performed the RDGP

approach on the European metaweb, and evaluated the probability threshold by treating this as a binary classification problem, specifically assuming that both 0 and 1 in the European metaweb are all true. Given the methodological details given in Maiorano et al. (2020b) and O'Connor et al. (2020), this seems like a reasonable assumption, although one that does not hold for all metawebs. We used the thresholding approach presented in Poisot, Ouellet, et al. (2021), and picked a cutoff that maximized Youden's J statistic (Youden (1950); a measure of the informedness (trust) of predictions); the resulting cutoff was 0.22, and gave an accuracy above 0.99.

The left and right subspaces for the European metaweb, accompanied by the threshold for prediction, represent the knowledge we seek to transfer. In the next section, we explain how we rely on phylogenetic similarity to do so.

3.3. Steps 2 and 3: Transfer learning through phylogenetic relatedness In order to transfer the knowledge from the European metaweb to the Canadian species pool, we performed ancestral character estimation using a Brownian motion model, which is a conservative approach in the absence of strong hypotheses about the nature of phylogenetic signal in the network decomposition (Litsios and Salamin 2012). This uses the estimated feature vectors for the European mammals to create a state reconstruction for all species (conceptually something akin to a trait-based mammalian phylogeny using generality and vulnerability traits) and allows us to impute the missing (latent) trait data for the Canadian species that are not already in the European network; as we are focused on predicting contemporary interactions, we only retained the values for the tips of the tree. We assumed that all traits (*i.e.* the feature vectors for the left and right subspaces) were independent, which is a reasonable assumption as every trait/dimension added to the t-SVD has an *additive* effect to the one before it. Note that the Upham, Esselstyn, and Jetz (2019) tree itself has some uncertainty associated to inner nodes of the phylogeny. In this case study, we have decided to not propagate this uncertainty, as it would complexify the process. The Brownian motion algorithm returns the *average* value of the trait, and its upper and lower bounds. Because we do not estimate other parameters of the traits' distributions, we considered that every species trait is represented as a uniform distribution between these bounds; in a situation where the algorithm would return point values for all simulations, one could in theory either estimate the parameters of a distribution for each tip, or draw randomly from the outputs. In all cases, the inferred left and right sub-spaces for the Canadian species pool ($\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$) have entries that are distributions, representing the range of values for a given species at a given dimension.

These objects represent the transferred knowledge, which we can use for prediction of the Canadian metaweb.

3.4. Step 4: Probabilistic prediction of the destination network The phylogenetic reconstruction of $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$ has an associated uncertainty, represented by the breadth of the uniform distribution associated to each of their entries. Therefore, we can use this information to assemble a *probabilistic* metaweb in the sense of Poisot et al. (2016), *i.e.* in which every interaction is represented as a single, independent, Bernoulli event of probability p .

Specifically, we have adopted the following approach. For every entry in $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$, we draw a value from its distribution. This results in one instance of the possible left () and right () subspaces for the Canadian metaweb. These can be multiplied, to produce one matrix of real values. Because the entries in $\hat{\mathcal{L}}$ and $\hat{\mathcal{R}}$ are in the same space where \mathcal{L} and \mathcal{R} were originally predicted, it follows that the threshold ρ estimated for the European metaweb also applies. We use this information to produce one random Canadian metaweb, $N = \hat{\mathcal{L}}\hat{\mathcal{R}}' \geq \rho$. As we can see in (fig. 3) the European and Canadian metawebs are structurally similar (as would be expected given the biogeographic similarities) and that the two (left and right) subspaces are distinct *i.e.* capturing predation (generality) and prey (vulnerability) traits.

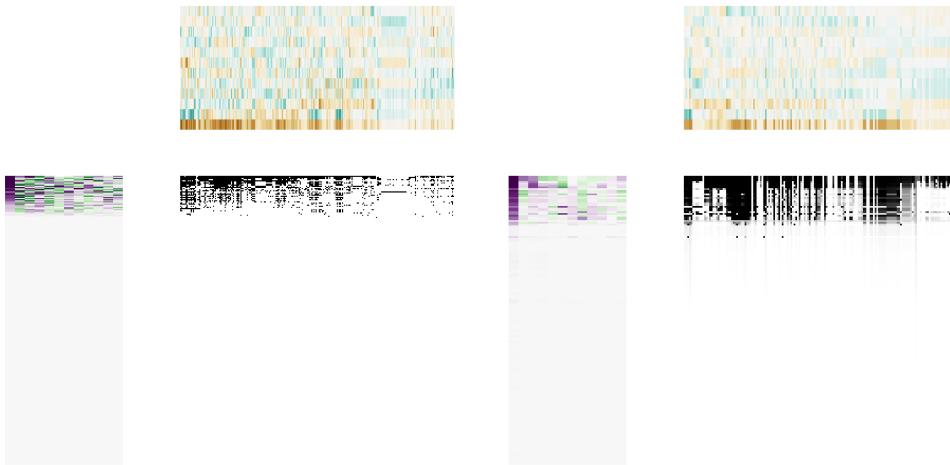


Figure 3 Visual representation of the left (green/purple) and right (green/brown) subspaces, alongside the adjacency matrix of the food web they encode (greyscale). The European metaweb is on the left, and the imputed Canadian metaweb (before data inflation) on the right. This figure illustrates how much structure the left sub-space captures. As we show in fig. 6, the species with a value of 0 in the left subspace are species without any prey.

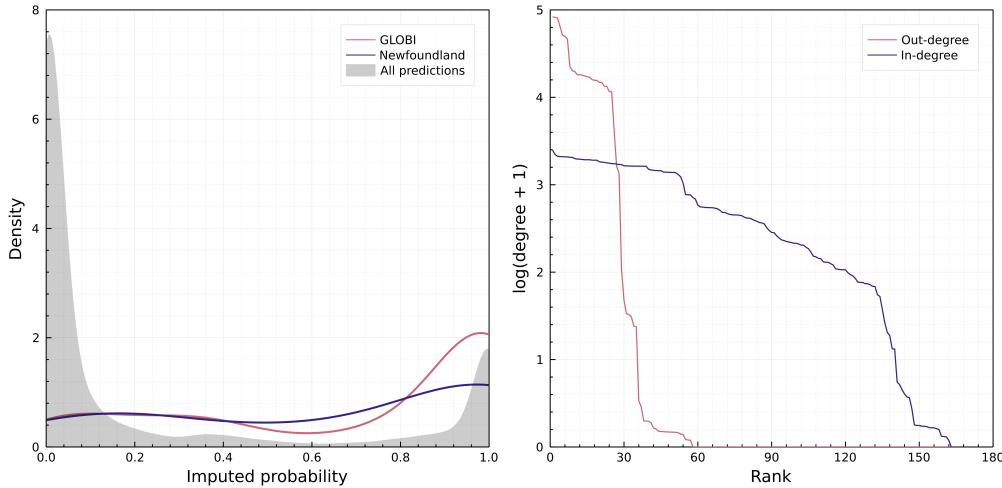


Figure 4 Left, comparison of the probabilities of interactions assigned by the model to all interactions (grey curve), the subset of interactions found in GLOBI (red), and in the Strong and Leroux (2014) Newfoundland dataset (blue). The model recovers more interaction with a low probability compared to data mining, which can suggest that collected datasets are biased towards more common or easy to identify interactions. Right, distribution of the in-degree and out-degree of the mammals from Canada in the reconstructed metaweb. This figure describes a flat, relatively short food web, in which there are few predators but a large number of preys.

Because the intervals around some trait values can be broad (in fact, probably broader than what they would actually be, see *e.g.* Garland, Midford, and Ives 1999), we repeat the above process 2×10^5 times, which results in a probabilistic metaweb P , where the probability of an interaction (here conveying our degree of trust that it exists given the inferred trait distributions) is given by the number of times where it appears across all random draws N , divided by the number of samples. An interaction with $P_{i,j} = 1$ means that these two species were predicted to interact in all 2×10^5 random draws, etc..

3.5. Data cleanup, discovery, validation, and thresholding

Once the probabilistic metaweb for Canada has been produced, we followed a number of data inflation steps to finalize it.

First, we extracted the subgraph corresponding to the 17 species shared between the European and Canadian pools and replaced these interactions with a probability of 0 (non-interaction) or 1 (interaction). This represents a minute modification of the inferred network (about 0.8% of all species pairs from the Canadian web), but ensures that we are directly re-using knowledge from Europe.

Second, we looked for all species in the Canadian pool known to the Global Biotic Interactions (GLoBI) database (Poelen, Simons, and Mungall 2014), and extracted their known interactions.

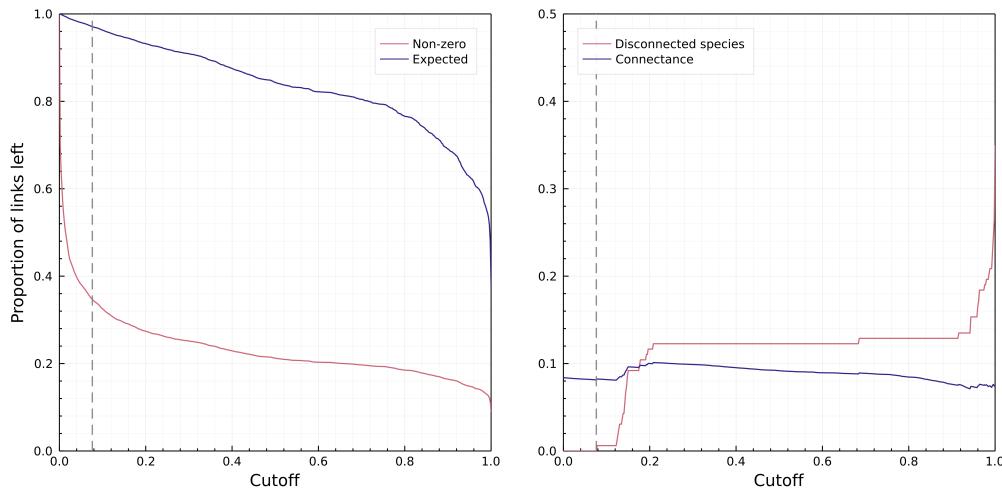


Figure 5 Left: effect of varying the cutoff for probabilities to be considered non-zero on the number of unique links and on \hat{L} , the probabilistic estimate of the number of links assuming that all interactions are independent. Right: effect of varying the cutoff on the number of disconnected species, and on network connectance. In both panels, the grey line indicates the cutoff $P(i \rightarrow j) \approx 0.08$ that resulted in the first species losing all of its interactions.

Because GLOBI aggregates observed interactions, it is not a *networks* data source, and therefore the only information we can reliably extract from it is that a species pair *was reported to interact at least once*. This last statement should yet be taken with caution, as some sources in GLOBI (e.g. Thessen and Parr 2014) are produced through text analysis, and therefore may not document direct evidence of the interaction. Nevertheless, should the predictive model work, we would expect that a majority of interactions known to GLOBI would also be predicted. After performing this check, we set the probability of all interactions known to GLOBI (366 in total, 33 of which were not predicted by the model, for a success rate of 91%) to 1.

Finally, we downloaded the data from Strong and Leroux (2014), who mined various literature sources to identify trophic interactions in Newfoundland. This dataset documented 25 interactions between mammals, only two of which were not part of our (Canada-level) predictions, resulting in a success rate of 92%. These two interactions were added to our predicted metaweb with a probability of 1.

Because the confidence intervals on the inferred trait space are probably over-estimates, we decided to apply a thresholding step to the interactions after the data inflation (fig. 5). Cirtwill and Hambäck (2021) proposed a number of strategies to threshold probabilistic networks. Their methods assume the underlying data to be tag-based sequencing, which represents interactions as co-occurrences of predator and prey within the same tags; this is conceptually identical to our Bernoulli-trial based reconstruction of a probabilistic network. We performed a full analysis of the effect of various cutoffs, and as they either resulted in removing too few interactions, or removing enough interactions that species started to be disconnected from the network, we set this threshold for a probability equivalent to 0 to the largest possible value that still allowed all species to have at least one interaction with a non-zero probability. The need for this slight deviation from the Cirtwill and Hambäck (2021) method highlights the need for additional development on network thresholding.

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Results and discussion of the case study

In fig. 5, we examine the effect of varying the cutoff on $P(i \rightarrow j)$ on the number of links, species, and connectance. Determining a cutoff using the maximum curvature, or central difference approximation of the second order partial derivative, as suggested by e.g. Cirtwill and Hambäck (2021), results in respectively species being lost, or almost all links being kept. We therefore

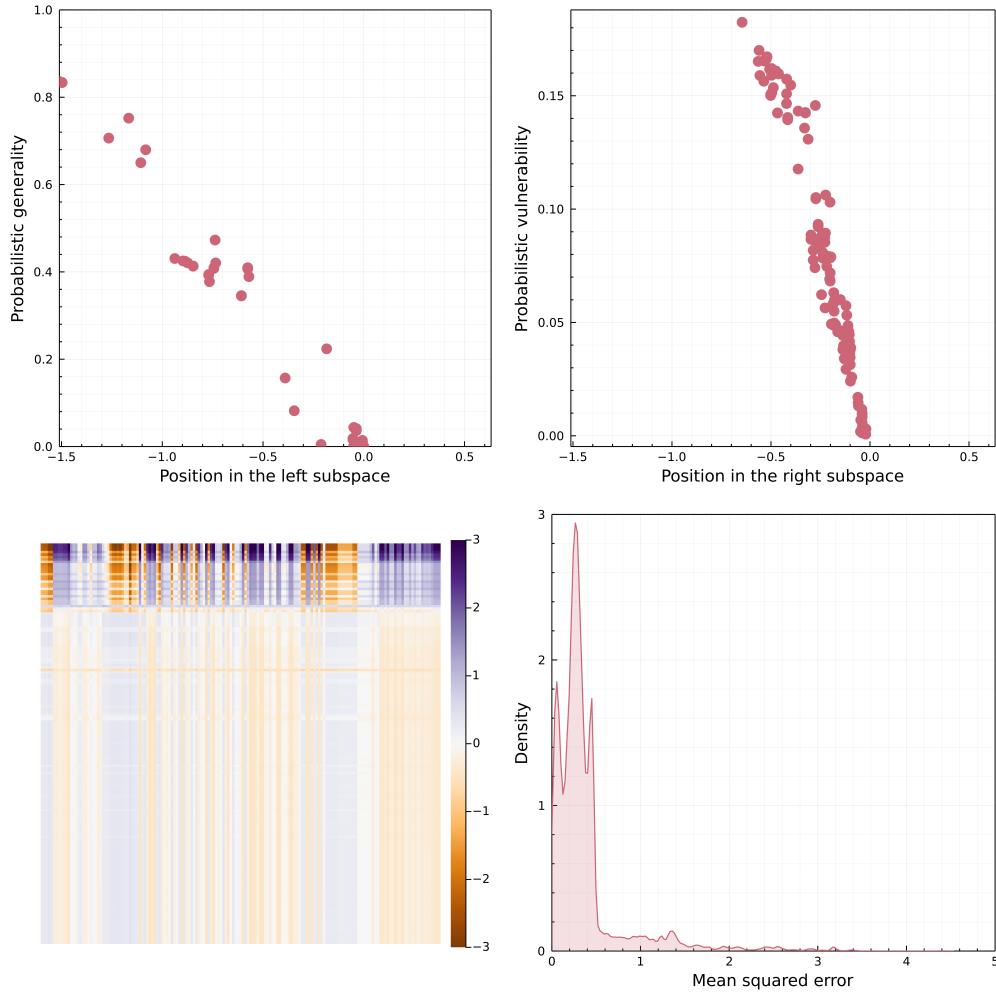


Figure 6 Top: biological significance of the first dimension. Left: there is a linear relationship between the values on the first dimension of the left subspace and the generality, *i.e.* the relative number of preys, *sensu* Schoener (1989). Species with a value of 0 in this subspace are at the bottom-most trophic level. Right: there is, similarly, a linear relationship between the position of a species on the first dimension of the right subspace and its vulnerability, *i.e.* the relative number of predators. Taken together, these two figures show that the first-order representation of this network would capture its degree distribution. Bottom: topological consequences of the first dimension. Left: differences in the z -score of the actual configuration model for the reconstructed network, and the prediction based only on the first dimension. Right: distribution of the differences in the left panel.

settled on the value that allowed all species to remain with at least one interaction. This result, in and of itself, suggests that additional methodological developments for the thresholding of probabilistic networks are required.

The t-SVD embedding is able to learn relevant ecological features for the network. fig. 6 shows that the first rank correlates linearly with generality and vulnerability (Schoener 1989), *i.e.* the number of preys and predators. Importantly, this implies that a rank 1 approximation represents the configuration model for the metaweb, *i.e.* a set of random networks generated from a given degree sequence (Park and Newman 2004). Accounting for the probabilistic nature of the degrees, the rank 1 approximation also represents the *soft* configuration model (van der Hoorn, Lippner, and Krioukov 2018). Both models are maximum entropy graph models (Garlaschelli, Hollander, and Roccaverde 2018), with sharp (all network realizations satisfy the specified degree sequence) and soft (network realizations satisfy the degree sequence on average) local constraints, respectively. The (soft) configuration model is an unbiased random graph model widely used by ecologists in the context of null hypothesis significance testing of network structure (*e.g.* Bascompte et al. 2003) and can provide informative priors for Bayesian inference of network structure (*e.g.* J.-G. Young, Cantwell, and Newman 2021). It is noteworthy that for this metaweb, the relevant information was extracted at the first rank. Because the first rank corresponds to the leading singular value of the system, the results of fig. 6 have a straightforward interpretation: degree-based processes are the most important in structuring the mammalian food web.

Discussion

One important aspect in which Europe and Canada differ (despite their comparable bioclimatic conditions) is the legacy of human impacts, which have been much longer in Europe. Nenzén, Montoya, and Varela (2014) showed that even at small scales (the Iberian peninsula), mammal food webs retain the signal of both climate change and human activity, even when this human activity was orders of magnitude less important than it is now. Similarly, Yeakel et al. (2014) showed that changes in human occupation over several centuries can lead to food web collapse. Megafauna in particular seems to be very sensitive to human arrival (Pires et al. 2015). In short, there is well-substantiated support for the idea that human footprint affects more than the risk of species extinction (Marco et al. 2018), and can lead to changes in interaction structure. Yet, owing to the inherent plasticity of interactions, there have been documented instances of food webs undergoing rapid collapse/recovery cycles over short periods of time (Pedersen et al. 2017). The embedding of a network, in a sense, embeds its macro-evolutionary history, especially as RDPG captures ecological signal (Dalla Riva and Stouffer 2016); at this point, it is important to recall that a metaweb is intended as a catalogue of all possible interactions, which should then be filtered (Morales-Castilla et al. 2015). In practice (and in this instance) the reconstructed metaweb will predict interactions that are plausible based on the species' evolutionary history, however some interactions would not be realized due to human impact.

Cirtwill et al. (2019) previously made the point that network inference techniques based on Bayesian approaches would perform far better in the presence of an interaction-level informative prior; the desirable properties of such a prior would be that it is expressed as a probability, preferably representing a Bernoulli event, the value of which would be representative of relevant biological processes. We argue that the probability returned at the very last step of our framework may serve as this informative prior; indeed, the output of our analysis can be used in subsequent steps, also possibly involving expert elicitation to validate some of the most strongly recommended interactions. One important *caveat* to keep in mind when working with interaction inference is that interactions can never really be true negatives (in the current state of our methodological framework and data collection limitations); this renders the task of validating a model through the usual application of binary classification statistics very difficult (although see Strydom et al. 2021 for a discussion of alternative suggestions).

As Herbert (1965) rightfully pointed out, “[y]ou can't draw neat lines around planet-wide problems”; in this regard, our approach must contend with two interesting problems. The first is the limit of the metaweb to embed and transfer. If the initial metaweb is too narrow in scope, notably from a taxonomic point of view, the chances of finding another area with enough related species to make a reliable inference decrease. This is notably true if the metaweb is assembled in an area with mostly endemic species. Conversely, the metaweb should be reliably filled, which assumes that the S^2 interactions in a pool of S species have been examined, either through literature surveys or expert elicitation. The second problem is to determine which area should be used to infer the new metaweb in, as this determines the species pool that must be used. In our application, we focused on the mammals of Canada. The upside of this approach is that information at the country level is likely to be required by policy makers and stakeholders for their biodiversity assessment, as each country tends to set goals at the national level (Buxton et al. 2021) for which quantitative instruments are designed (Turak et al. 2017), with specific strategies often enacted at smaller scales (Ray, Grimm, and Olive 2021). Yet these national divisions, in large parts of the world, reflect nothing except for the legacy of settler colonialism, and operating under them must be done under the clear realization that they contributed to the ongoing biodiversity crisis (Adam 2014), can reinforce environmental injustice (Choudry 2013; Domínguez and Luoma 2020), and on Turtle Island especially, will probably end up being replaced by Indigenous principles of land management (Eichhorn, Baker, and Griffiths 2019; No'kmaq et al. 2021).

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