

# Graph embedding and transfer learning can help predict species interaction networks despite data limitations

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1. Metawebs, (networks of potential interactions within a species pool) are a powerful abstraction to understand how large-scale species interaction networks are structured.
2. Because metawebs are typically expressed at large spatial and taxonomic scales, assembling them is a tedious and costly process; predictive methods can help circumvent the limitations in data deficiencies, by providing 'draft' metawebs.
3. One way to improve our ability to predict metawebs is to maximize available information by using graph embeddings, instead of the list of species interactions. Graph embedding is an emerging field in machine learning that holds great potential for ecological problems.
4. In this perspective, we outline how the challenges associated with inferring metawebs line-up with the advantages of graph embeddings; as well as discuss how the choice of the species pool has consequences on the reconstructed network, but also embeds hypotheses about which human-made boundaries are ecologically meaningful.

1 Being able to infer *potential* interactions could serve as a significant breakthrough in our ability to start  
2 thinking about species interaction networks over large spatial scales (Hortal et al., 2015). Understanding  
3 species interactions holds enormous potential to not only understand and more rapidly learn about  
4 species interactions and metawebs, but also how changes in management of a single species may impact  
5 non-target species. In a recent overview of the field of ecological network prediction, Strydom, Catchen, et  
6 al. (2021) identified two challenges of interest to the prediction of interactions at large scales. First, there  
7 is a relative scarcity of relevant data in most places globally – paradoxically, this restricts our ability to infer  
8 interactions for locations where inference is perhaps the least required (and leaves us unable to make  
9 inference in regions without interaction data); second, accurate predictors are important for accurate  
10 predictions, and the lack of methods that can leverage a small amount of *accurate* data is a serious  
11 impediment to our predictive ability. In most places, our most reliable biodiversity knowledge is that of a  
12 species pool (*i.e.* a set of potentially interacting species in a given area): through the analysis of databases  
13 like GBIF or IUCN, it is possible to construct a list of species in a region of interest; but inferring the  
14 potential interactions between these species is difficult.

15 Following the definition of Dunne (2006), a metaweb is the ecological network analogue to the species  
16 pool; specifically, it inventories all *potential* interactions between species for a spatially delimited area (and  
17 so captures the  $\gamma$  diversity of interactions). The metaweb is not a prediction of the network at a specific  
18 point within the spatial area it covers: it will have a different structure, notably by having a larger  
19 connectance (see *e.g.* Wood et al., 2015) and complexity (see *e.g.* Galiana et al., 2022), from any of these  
20 local networks. These local networks (which capture the  $\alpha$  diversity of interactions) are a subset of the  
21 metaweb’s species and realized interactions, and have been called “metaweb realizations” (Poisot et al.,  
22 2015). Differences between local networks and their metawebs are due to chance, species abundance and  
23 co-occurrence, local environmental conditions, and local distribution of functional traits, among others.  
24 Yet, recent results by Saravia et al. (2021) strongly suggest that the local (metaweb) realizations only  
25 respond weakly to local conditions: instead, they reflect constraints inherited by the structure of their  
26 metaweb. This establishes the metaweb structure as the core goal of predictive network ecology, as it is a  
27 required information to accurately produce downscaled, local predictions.

28 Because the metaweb represents the joint effect of functional, phylogenetic, and macroecological  
29 processes (Morales-Castilla et al., 2015), it holds valuable ecological information. Specifically, it represents  
30 the “upper bounds” on what the composition of the local networks, given a local species pool, can be (see

31 *e.g.* McLeod et al., 2021); this information can help evaluate the ability of ecological assemblages to  
32 withstand the effects of, for example, climate change (Fricke et al., 2022). These local networks may be  
33 reconstructed given an appropriate knowledge of local species composition and provide information on  
34 the structure of food webs at finer spatial scales. This has been done for example for tree-galler-parasitoid  
35 systems (Gravel et al., 2018), fish trophic interactions (Albouy et al., 2019), tetrapod trophic interactions  
36 (Braga et al., 2019; O'Connor et al., 2020), and crop-pest networks (Grünig et al., 2020). In this  
37 contribution, we highlight the power in viewing (and constructing) metawebs as *probabilistic* objects in  
38 the context of rare interactions, discuss how a family of machine learning tools (graph embeddings and  
39 transfer learning) can be used to overcome data limitations to metaweb inference, and highlight how the  
40 use of metawebs introduces important questions for the field of network ecology.

## 41 **A metaweb is an inherently probabilistic object**

42 Treating interactions as probabilistic (as opposed to binary) events is a more nuanced and realistic way to  
43 represent them. Dallas et al. (2017) suggested that most links in ecological networks are cryptic, *i.e.*  
44 uncommon or hard to observe. This argument echoes Jordano (2016): sampling ecological interactions is  
45 difficult because it requires first the joint observation of two species, and then the observation of their  
46 interaction. In addition, it is generally expected weak or rare links to be more prevalent in networks than  
47 common or strong links (Csermely, 2004), compared to strong, persistent links; this is notably the case in  
48 food chains, wherein many weaker links are key to the stability of a system (Neutel et al., 2002). In the  
49 light of these observations, we expect to see an over-representation of low-probability (rare) interactions  
50 under a model that accurately predicts interaction probabilities. Yet the original metaweb definition, and  
51 indeed most past uses of metawebs, was based on the presence/absence of interactions. Moving towards  
52 *probabilistic* metawebs, by representing interactions as Bernoulli events (see *e.g.* Poisot et al., 2016), offers  
53 the opportunity to weigh these rare interactions appropriately. The inherent plasticity of interactions is  
54 important to capture: there have been documented instances of food webs undergoing rapid  
55 collapse/recovery cycles over short periods of time (*e.g.* Pedersen et al., 2017). These considerations  
56 emphasize why metaweb predictions should focus on quantitative (preferentially probabilistic)  
57 predictions, and this should constrain the suite of appropriate models used to predict them.

58 It is important to recall that a metaweb is intended as a catalogue of all potential interactions, which is

then filtered for a given application (Morales-Castilla et al., 2015). In a sense, that most ecological interactions are elusive can call for a slightly different approach to sampling: once the common interactions are documented, the effort required in documenting each rare interaction will increase exponentially. Recent proposals suggest that machine learning algorithms, in these situations, can act as data generators (Hoffmann et al., 2019): high quality observational data can generate the core rules underpinning the network structure, and be supplemented with synthetic data coming from predictive models, increasing the volume of information available for inference. Indeed, Strydom, Catchen, et al. (2021) suggested that knowing the metaweb may render the prediction of local networks easier, because it fixes an “upper bound” on which interactions can exist. In this context, a probabilistic metaweb represents an aggregation of informative priors on the interactions, elusive information with the potential to boost our predictive ability (Bartomeus et al., 2016).

[Figure 1 about here.]

## **Graph embedding offers promises for the inference of potential interactions**

Graph (or Network) embedding (fig. 1) is a family of machine learning techniques, whose main task is to learn a mapping function from a discrete graph to a continuous domain (Arsov & Mirceva, 2019; Chami et al., 2022). Their main goal is to learn a low dimensional vector representations for the nodes of the graph (embeddings), such that key properties of the graph (e.g. local or global structures) are retained in the embedding space (Yan et al., 2005). Ecological networks are an interesting candidate for the widespread application of embeddings, as they tend to possess a shared structural backbone (Bramon Mora et al., 2018), which hints at structural invariants that can be revealed at lower dimensions. Indeed, food webs are inherently low-dimensional objects, and can be adequately represented with less than ten dimensions (Braga et al., 2019; Eklöf et al., 2013). Simulation results by Botella et al. (2022) suggest that there is no best method to identify architectural similarities between networks, and that multiple approaches need to be tested and compared to the network descriptor of interest. This matches previous, more general results on graph embedding, which suggest that the choice of embedding algorithm matters for the results (Goyal & Ferrara, 2018). In tbl. 1, we present a selection of common graph and node embedding methods,

86 alongside examples of their use to predict species interactions; most of these methods rely either on linear  
87 algebra, or on pseudo-random walks on graphs.

88 One prominent family of approaches we do not discuss in the present manuscript is Graph Neural  
89 Networks (GNN; Zhou et al., 2020). GNN are, in a sense, a method to embed a graph into a dense  
90 subspace, but belong to the family of deep learning methods, which has its own set of practices (see *e.g.*  
91 Goodfellow et al., 2016). An important issue with methods based on deep learning is that, because their  
92 parameter space is immense, the sample size of the data fed into them must be similarly large (typically  
93 thousands of instances). This is a requirement for the model to converge correctly during training, but this  
94 assumption is unlikely to be met given the size of datasets currently available for metawebs (or single  
95 time/location species interaction networks). This data volume requirement is mostly absent from the  
96 techniques we list below. Furthermore, GNN still have some challenges related to their shallow structure,  
97 and concerns related to scalability (see Gupta et al., 2021 for a review), which are mostly absent from the  
98 methods listed in [tbl. 1](#). Assuming that the uptake of next-generation biomonitoring techniques does  
99 indeed deliver larger datasets on species interactions (Bohan et al., 2017), there is a potential for GNN to  
100 become an applicable embedding/predictive technique in the coming years.

101 [Table 1 about here.]

102 The popularity of graph embedding techniques in machine learning is more than the search for structural  
103 invariants: graphs are discrete objects, and machine learning techniques tend to handle continuous data  
104 better. Bringing a sparse graph into a continuous, dense vector space (Xu, 2020) opens up a broader variety  
105 of predictive algorithms, notably of the sort that are able to predict events as probabilities (Murphy, 2022).  
106 Furthermore, the projection of the graph itself is a representation that can be learned; Runghen et al.  
107 (2021), for example, used a neural network to learn the embedding of a network in which not all  
108 interactions were known, based on the nodes' metadata. This example has many parallels in ecology (see  
109 [fig. 1 C](#)), in which node metadata can be given by phylogeny or functional traits. Rather than directly  
110 predicting biological rules (see *e.g.* Pichler et al., 2020 for an overview), which may be confounded by the  
111 sparse nature of graph data, learning embeddings works in the low-dimensional space that maximizes  
112 information about the network structure. This approach is further justified by the observation, for  
113 example, that the macro-evolutionary history of a network is adequately represented by some graph  
114 embeddings (Random dot product graphs (RDPG); see Dalla Riva & Stouffer, 2016). In a recent

publication, Strydom et al. (2022) have used an embedding (based on RDPG) to project a metaweb of trophic interactions between European mammals, and transferred this information to mammals of Canada, using the phylogenetic distance between related clades to infer the values in the latent sub-space into which the European metaweb was projected. By performing the RDPG step on re-constructed values, this approach yields a probabilistic trophic metaweb for mammals of Canada based on knowledge of European species, despite a limited ( $\approx 5\%$ ) taxonomic overlap.

Graph embeddings *can* serve as a dimensionality reduction method. For example, RDPG (Strydom et al., 2022) and t-SVD (truncated Singular Value Decomposition; Poisot et al., 2021) typically embed networks using fewer dimensions than the original network (the original network has as many dimensions as species, and as many informative dimensions as trophically unique species; Strydom, Dalla Riva, et al., 2021). But this is not necessarily the case – indeed, one may perform a PCA (a special case of SVD) to project the raw data into a subspace that improves the efficacy of t-SNE (t-distributed stochastic neighbor embedding; Maaten, 2009). There are many dimensionality reductions (Anowar et al., 2021) that can be applied to an embedded network should the need for dimensionality reduction (for example for data visualisation) arise. In brief, many graph embeddings *can* serve as dimensionality reduction steps, but not all do, neither do all dimensionality reduction methods provide adequate graph embedding capacities. In the next section (and fig. 2), we show how the amount of dimensionality reduction can affect the quality of the embedding.

## **An illustration of metaweb embedding**

In this section, we illustrate the embedding of a collection of bipartite networks collected by Hadfield et al. (2014), using t-SVD and RDPG (see Strydom et al., 2022 for the full details). Briefly, an RDPG decomposes a network into two subspaces (left and right), which are matrices that when multiplied give an approximation of the original network. The code to reproduce this example is available as supplementary material (note, for the sake of comparison, that Strydom, Catchen, et al., 2021 have an example using embedding through PCA followed by prediction using a deep neural network on the same dataset). The resulting (binary) metaweb  $\mathcal{M}$  has 2131 interactions between 206 parasites and 121 hosts, and its adjacency matrix has full rank (*i.e.* it represents a space with 121 dimensions). All analyses were done using Julia (Bezanson et al., 2017) version 1.7.2, *Makie.jl* (Danisch & Krumbiegel, 2021), and

143 *EcologicalNetworks.jl* (Poisot et al., 2019).

144 [Figure 2 about here.]

145 The embedding of the metaweb holds several pieces of information (fig. 2). In panel **A**, we show that the  
146  $L_2$  loss (*i.e.* the sum of squared errors) between the empirical and reconstructed metaweb decreases when  
147 the number of dimensions (rank) of the subspace increases, with an inflection point around 25  
148 dimensions. As discussed by Runghen et al. (2021), there is often a trade-off between the number of  
149 dimensions to use (more dimensions are more computationally demanding) and the quality of the  
150 representation. In this instance, accepting  $L_2 = 500$  as an approximation of the network means that the  
151 error for every position in the metaweb is  $\approx (500/(206 \times 121))^{1/2}$ . In fig. 2, panel **B**, we show the positions  
152 of hosts and parasites on the first two dimensions of the left and right subspaces. Note that these values  
153 largely skew negative, because the first dimensions capture the coarse structure of the network: most pairs  
154 of species do not interact, and therefore have negative values. In fig. 2, panel **C**, we show the predicted  
155 weight (*i.e.* the result of the multiplication of the RDGP subspaces at a rank of 25) as a function of whether  
156 the interactions are observed, not-observed, or unknown due to lack of co-occurrence. This reveals that  
157 the observed interactions have higher predicted weights, although there is some overlap; the usual  
158 approach to identify potential interactions based on this information would be a thresholding analysis,  
159 which is outside the scope of this manuscript (and is done in the papers cited in this illustration). Note  
160 that the values are not bound to the unit interval, which emphasizes the need for either scaling or  
161 clamping (although thresholding analyses are insensitive to this choice). Finally, in fig. 2, panel **D**, we  
162 show that the embedding, as it captures structural information about the network, holds ecological  
163 information; indeed, the position of the parasite on the first dimension of the left sub-space is a linear  
164 predictor of its number of hosts.

## 165 **The metaweb embeds both ecological hypotheses and practices**

166 The goal of metaweb inference is to provide information about the interactions between species at a large  
167 spatial scale. But as Herbert (1965) rightfully pointed out, “[y]ou can’t draw neat lines around planet-wide  
168 problems”; any inference of a metaweb at large scales must contend with several novel, and interwoven,  
169 families of problems. In this section, we list some of the most pressing research priorities (*i.e.* problems



170 that can be addressed with subsequent data analysis or simulations), as well as issues related to the  
171 application of these methods at the science-policy interface.

172 The first open research problem is the taxonomic and spatial limit of the metaweb to embed and transfer.  
173 If the initial metaweb is too narrow in scope, notably from a taxonomic point of view, the chances of  
174 finding another area with enough related species (through phylogenetic relatedness or similarity of  
175 functional traits) to make a reliable inference decreases; this would likely be indicated by large confidence  
176 intervals during estimation of the values in the low-rank space, meaning that the representation of the  
177 original graph is difficult to transfer to the new problem. Alternatively, if the initial metaweb is too large  
178 (taxonomically), then the resulting embeddings would need to represent interactions between taxonomic  
179 groups that are not present in the new location. This would lead to a much higher variance in the starting  
180 dataset, and to under-dispersion in the target dataset, resulting in the potential under or over estimation of  
181 the strength of new predicted interactions. The lack of well documented metawebs is currently preventing  
182 the development of more concrete guidelines. The question of phylogenetic relatedness and distribution is  
183 notably relevant if the metaweb is assembled in an area with mostly endemic species (*e.g.* a system that  
184 has undergone recent radiation or that has remained in isolation for a long period of time might not have  
185 an analogous system with which to draw knowledge from), and as with every predictive algorithm, there  
186 is room for the application of our best ecological judgement. Because this problem relates to distribution  
187 of species in the geographic or phylogenetic space, it can certainly be approached through assessing the  
188 performance of embedding transfer in simulated starting/target species pools.

189 The second series of problems relate to determining which area should be used to infer the new metaweb  
190 in, as this determines the species pool that must be used. Metawebs can be constructed by assigning  
191 interactions in a list of species within geographic boundaries. The upside of this approach is that  
192 information at the country level is likely to be required for biodiversity assessments, as countries set  
193 conservation goals at the national level (Buxton et al., 2021), and as quantitative instruments are designed  
194 to work at these scales (Turak et al., 2017); specific strategies are often enacted at smaller scales, nested  
195 within a specific country (Ray et al., 2021). But there is no guarantee that these boundaries are  
196 meaningful. In fact, we do not have a satisfying answer to the question of “where does a food web stop?”;  
197 the most promising solutions involve examining the spatial consistency of network area relationships  
198 (Fortin et al., 2021; see *e.g.* Galiana et al., 2018, 2019, 2021), which is impossible in the absence of enough  
199 information about the network itself. This suggests that inferred metawebs should be further downscaled

to allow for *a posteriori* analyses. The methodology for metaweb downscaling is currently limited, and it is likely that the sustained effort to characterize the spatial dependency of food web structure will lead to more prescriptive guidelines about the need for prediction downscaling.

The final family of problems relates less to ecological methods than to the praxis of ecological research. Operating under the context of national divisions, in large parts of the world, reflects nothing more than the legacy of settler colonialism, which drives a disparity in available ecological data. Applying any embedding to biased data does not debias them, but instead embeds these very same biases, propagating them to the machine learning models using embeddings to make predictions. Indeed, the use of ecological data is not an apolitical act (Nost & Goldstein, 2021), as data infrastructures tend to be designed to answer questions within national boundaries (therefore placing contingencies on what is available to be embedded), and their use often draws upon and reinforces territorial statecraft. As per Machen & Nost (2021), this is particularly true when the output of “algorithmic thinking” (*e.g.* relying on machine learning to generate knowledge) can be re-used for governance (*e.g.* enacting conservation decisions at the national scale). As information on species interaction networks structure is increasingly leveraged as a tool to guide conservation actions (see *e.g.* recent discussions for food-web based conservation; Eero et al., 2021; Naman et al., 2022; Stier et al., 2017), the need to appraise and correct biases that are unwittingly propagated to algorithms when embedded from the original data is paramount. Predictive approaches deployed at the continental scale, no matter their intent, originate in the framework that contributed to the ongoing biodiversity crisis (Adam, 2014) and reinforced environmental injustice (Choudry, 2013; Domínguez & Luoma, 2020). Particularly on Turtle Island and other territories that were traditionally stewarded by Indigenous people, these approaches should be replaced (or at least guided and framed) by Indigenous principles of land management (Eichhorn et al., 2019; No’kmaq et al., 2021), as part of an “algorithm-in-the-loop” approach. Human-algorithm interactions are notoriously difficult and can yield adverse effect (Green & Chen, 2019; Stevenson & Doleac, 2021), suggesting the need to systematically study them for the specific purpose of biodiversity governance, as well as to improve the algorithmic literacy of decision makers. As we see artificial intelligence/machine learning being increasingly mobilized to generate knowledge that is lacking for conservation decisions (*e.g.* Lamba et al., 2019; Mosebo Fernandes et al., 2020) and drive policy decisions (Weiskopf et al., 2022), our discussion of these tools need to go beyond the technical and statistical, and into the governance consequences they can have.

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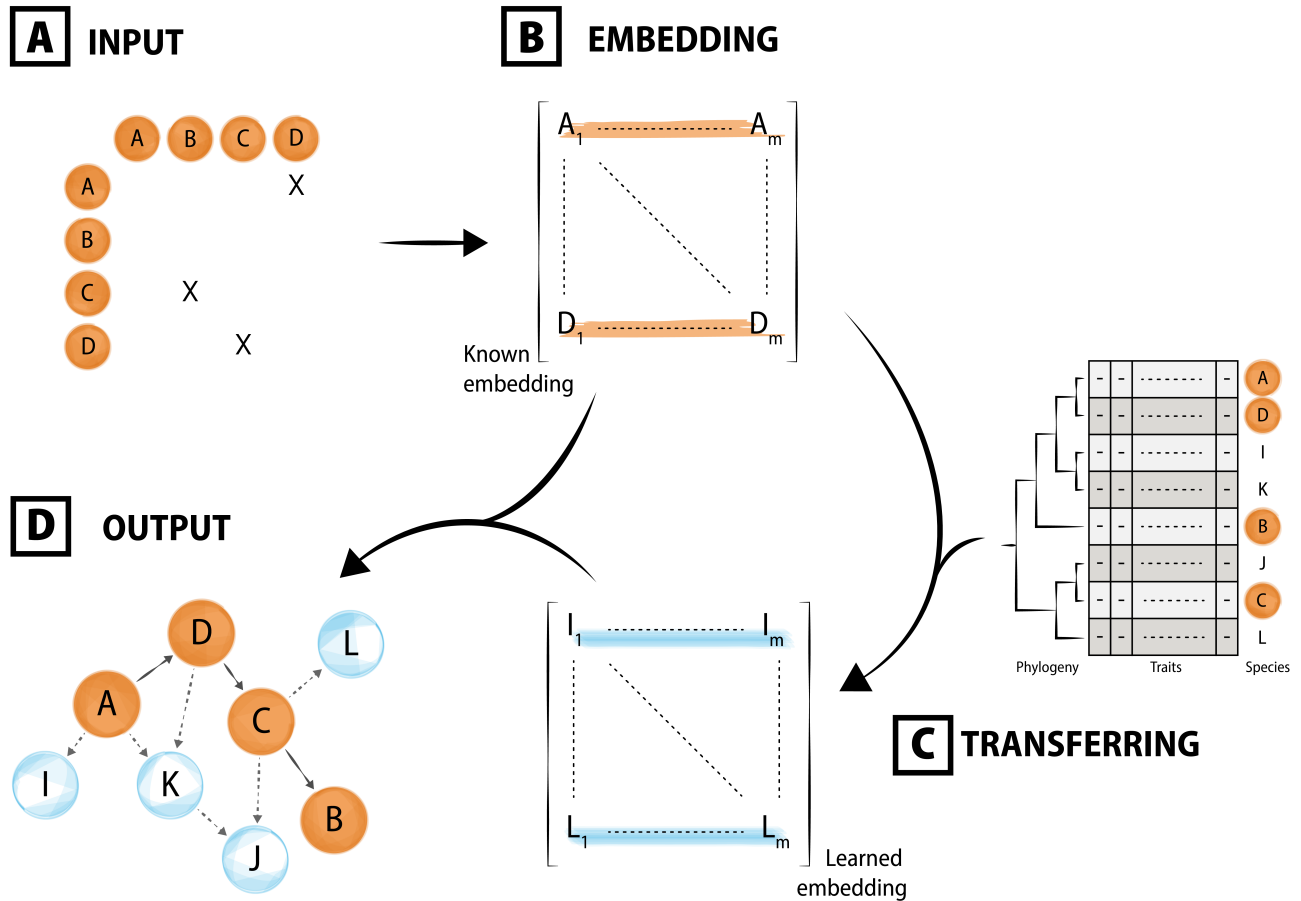


Figure 1: Overview of the embedding process. A network (**A**), represented here as its adjacency matrix, is converted into a lower-dimensional object (**B**) where nodes, subgraphs, or edges have specific values (see [tbl. 1](#) for an overview of methods and their use for species interactions). For the purposes of prediction, this low-dimensional object encodes feature vectors for *e.g.* the nodes. Embedding also allows to visualize the structure in the data differently (see [fig. 2](#)), much like with a principal component analysis. From a low-dimensional feature vector, it is possible to develop predictive approaches. Nodes in an ecological network are usually species (**C**), for which we can leverage phylogenetic relatedness (*e.g.* Strydom et al., 2022) or functional traits to fill the values of additional species we would like to project in this space (here for nodes I, J, K, and L) from the embedding of known species (here, nodes A, B, C, and D). Because embeddings can be projected back to a graph, this allows us to reconstruct a network with these new species (**D**). This entire cycle constitutes an instance of transfer learning, where the transferred information is the representation of graph **A** through its embedding.

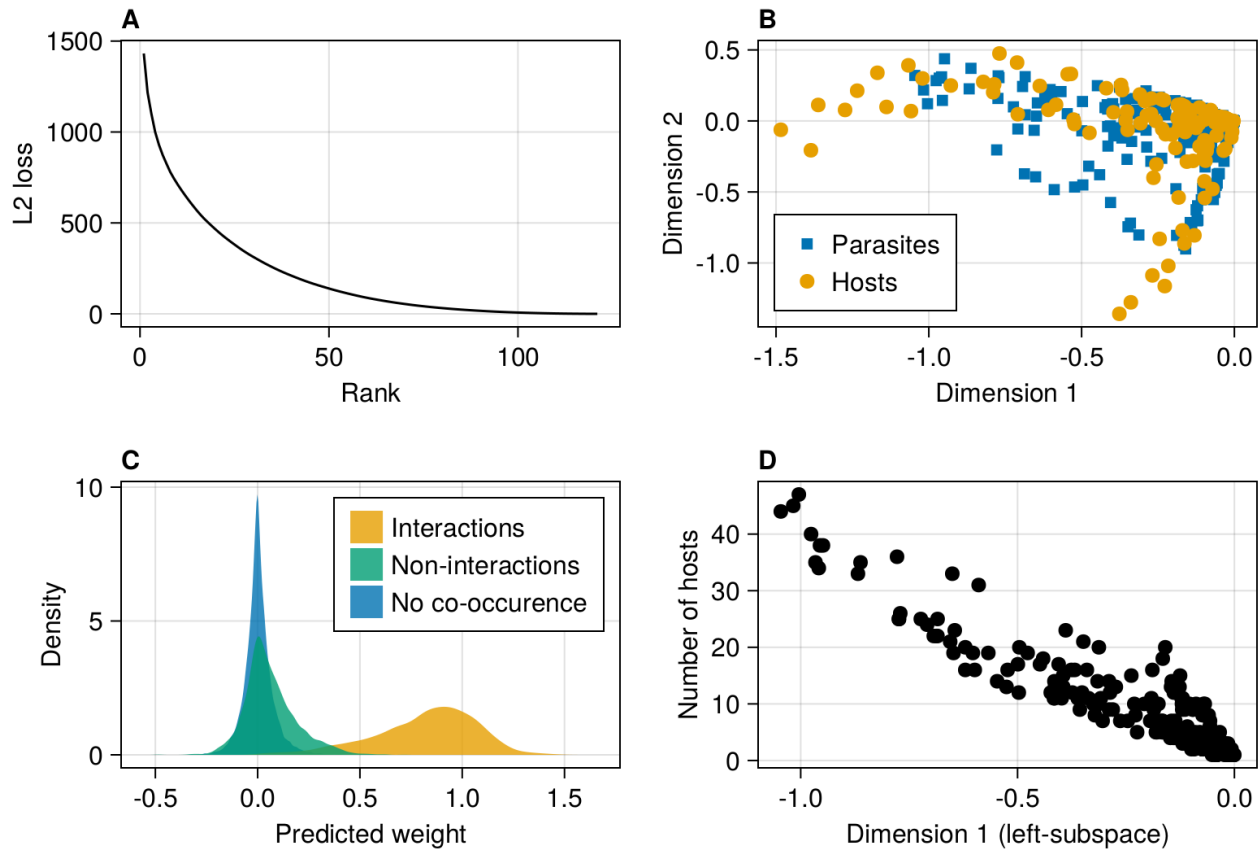


Figure 2: Illustration of an embedding for an host-parasite metaweb, using Random Dot Product Graphs. **A**, decrease in approximation error as the number of dimensions in the subspaces increases. **B**, position of hosts and parasites in the first two dimensions of their respective subspaces. **C**, predicted interaction weight from the RDPG based on the status of the species pair in the metaweb. **D**, relationship between the position on the first dimension and parasite generalism.

Table 1: Overview of some common graph embedding approaches, by type of embedded objects, alongside examples of their use in the prediction of species interactions. These methods have not yet been routinely used to predict species interactions; most examples that we identified were either statistical associations, or analogues to joint species distribution models. <sup>a</sup>: statistical interactions; <sup>b</sup>: joint-SDM-like approach. Note that the row for PCA also applies to kernel/probabilistic PCA, which are variations on the more general method of SVD. Note further that tSNE has been included because it is frequently used to embed graphs, including of species associations/interactions, despite not being strictly speaking, a graph embedding technique (see *e.g.* Chami et al., 2022)

Method	Object	Technique	Reference	Application
tSNE	nodes	statistical divergence	Hinton & Roweis (2002)	Gibb et al. (2021); Cieslak et al. (2020) <sup>a</sup>
LINE	nodes	stochastic gradient descent	Tang et al. (2015)	
SDNE	nodes	gradient descent	D. Wang et al. (2016)	
node2vec	nodes	stochastic gradient descent	Grover & Leskovec (2016)	
HARP	nodes	meta-strategy	H. Chen et al. (2017)	
DMSE	joint nodes	deep neural network	D. Chen et al. (2017)	D. Chen et al. (2017) <sup>b</sup>
graph2vec	sub-graph	skipgram network	Narayanan et al. (2017)	
RDPG	graph	SVD	Young & Scheinerman (2007)	Poisot et al. (2021); Dalla Riva & Stouffer (2016)
GLEE	graph	Laplacian eigenmap	Torres et al. (2020)	
DeepWalk	graph	stochastic gradient descent	Perozzi et al. (2014)	Wardeh et al. (2021)
GraphKKE	graph	stochastic differential equation	Melnyk et al. (2020)	Melnyk et al. (2020) <sup>a</sup>
FastEmbed	graph	eigen decomposition	Ramasamy & Madhow (2015)	
PCA	graph	eigen decomposition	S & Surendran (2013)	Strydom, Catchen, et al. (2021)
Joint methods	multiple graphs	multiple strategies	S. Wang et al. (2021)	