

Predicting metawebs: graph embeddings can help alleviate spatial data deficiencies

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1. Metawebs, i.e. networks of potential interactions within a species pool, are a powerful abstraction to understand how large-scales 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 the predictive ability is to maximize the information used for prediction, by using graph embeddings rather than 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; furthermore, because metawebs are inherently spatial objects, we 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 Having a general solution for inferring *potential* interactions (despite the unavailability of interaction data)
2 could be the catalyst for significant breakthroughs in our ability to start thinking about species interaction
3 networks over large spatial scales (Hortal et al., 2015). In a recent overview of the field of ecological
4 network prediction, Strydom et al. (2021) identified two challenges of interest to the prediction of
5 interactions at large scales. First, there is a relative scarcity of relevant data in most places globally –
6 paradoxically, this restricts our ability to infer interactions to locations where inference is perhaps the least
7 required; second, accurate predictions often demand accurate predictors, and the lack of methods that can
8 leverage small amount of data is a serious impediment to our predictive ability globally.

9 Following the definition of Dunne (2006), a metaweb is a network analogue to the regional species pool;
10 specifically, it is an inventory of all *potential* interactions between species from a spatially delimited area
11 (and so captures the γ diversity of interactions). The metaweb is, therefore, *not* a prediction of the food
12 web at a specific locale within the spatial area it covers, and will have a different structure (notably by
13 having a larger connectance; see e.g. Wood et al., 2015). These local food webs (which captures the α
14 diversity of interactions) are a subset of the metaweb’s species and interactions, and have been called
15 “metaweb realizations” (Poisot et al., 2015). Differences between local food web and their metaweb are
16 due to chance, species abundance and co-occurrence, local environmental conditions, and local
17 distribution of functional traits, among others.

18 Because the metaweb represents the joint effect of functional, phylogenetic, and macroecological
19 processes (Morales-Castilla et al., 2015), it holds valuable ecological information. Specifically, it is the
20 “upper bounds” on what the composition of the local networks can be (see e.g. McLeod et al., 2021). These
21 local networks, in turn, can be reconstructed given appropriate knowledge of local species composition,
22 providing information on structure of food webs at finer spatial scales. This has been done for example for
23 tree-galler-parasitoid systems (Gravel et al., 2018), fish trophic interactions (Albouy et al., 2019), tetrapod
24 trophic interactions (O’Connor et al., 2020), and crop-pest networks (Grünig et al., 2020). Whereas the
25 original metaweb definition, and indeed most past uses of metawebs, was based on the presence/absence
26 of interactions, we focus on *probabilistic* metawebs where interactions are represented as the chance of
27 success of a Bernoulli trial (see e.g. Poisot et al., 2016); therefore, not only does our method recommend
28 interactions that may exist, it gives each interaction a score, allowing us to properly weigh them.

29 **The metaweb is an inherently probabilistic object**

30 Yet, owing to the inherent plasticity of interactions, there have been documented instances of food webs
31 undergoing rapid collapse/recovery cycles over short periods of time (Pedersen et al., 2017). The
32 embedding of a network, in a sense, embeds its macro-evolutionary history, especially as RDPG captures
33 ecological signal (Dalla Riva & Stouffer, 2016); at this point, it is important to recall that a metaweb is
34 intended as a catalogue of all potential interactions, which should then be filtered (Morales-Castilla et al.,
35 2015). In practice (and in this instance) the reconstructed metaweb will predict interactions that are
36 plausible based on the species' evolutionary history, however some interactions would/would not be
37 realized due to human impact.

38 Dallas et al. (2017) suggested that most links in ecological networks may be cryptic, *i.e.* uncommon or
39 otherwise hard to observe. This argument essentially echoes Jordano (2016): the sampling of ecological
40 interactions is difficult because it requires first the joint observation of two species, and then the
41 observation of their interaction. In addition, it is generally expected that weak or rare links would be more
42 common in networks (Csermely, 2004), compared to strong, persistent links; this is notably the case in
43 food chains, wherein many weaker links are key to the stability of a system (Neutel et al., 2002). In the
44 light of these observations, the results in fig. ?? are not particularly surprising: we expect to see a surge in
45 these low-probability interactions under a model that has a good predictive accuracy. Because the
46 predictions we generate are by design probabilistic, then one can weigh these rare links appropriately. In a
47 sense, that most ecological interactions are elusive can call for a slightly different approach to sampling:
48 once the common interactions are documented, the effort required in documenting each rare interaction
49 may increase exponentially. Recent proposals suggest that machine learning algorithms, in these
50 situations, can act as data generators (Hoffmann et al., 2019): in this perspective, high quality
51 observational data can be supplemented with synthetic data coming from predictive models, which
52 increases the volume of information available for inference. Indeed, Strydom et al. (2021) suggested that
53 knowing the metaweb may render the prediction of local networks easier, because it fixes an “upper
54 bound” on which interactions can exist; indeed, with a probabilistic metaweb, we can consider that the
55 metaweb represents an aggregation of informative priors on the interactions.

56 Graph embedding offers promises for the inference of potential 57 interactions

58 Graph embedding is a varied family of machine learning techniques aiming to transform nodes and edges
59 into a vector space, usually of a lower dimension, whilst maximally retaining key properties of the graph
60 (Yan et al., 2005). Ecological networks are an interesting candidate for the widespread application of
61 embeddings, as they tend to possess a shared structural backbone (Mora et al., 2018), which hints at
62 structural invariants that can be revealed at lower dimensions. Indeed, previous work by Eklöf et al. (2013)
63 suggests that food webs are inherently low-dimensional objects, and can be adequately represented with
64 less than ten dimensions. Simulation results by Botella et al. (2022) suggest that there is no best method to
65 identify architectural similarities between networks, and that multiple approaches need to be tested and
66 compared to the network descriptor of interest.

67 But the popularity of graph embedding techniques in machine learning is rather more intuitive than the
68 search for structural invariants: while graphs are discrete objects, machine learning techniques tend to
69 handle continuous data better. Therefore, bringing a discrete graph into a continuous vector space opens
70 up a broader variety of predictive algorithms.

Table 1: Overview of some common graph embedding approaches, by time of publication, alongside examples of their use in the prediction of species interactions. Surprisingly, these methods have not yet been used routinely to predict species interactions; most of the examples we identified were either statistical associations, or analogues to joint species distribution models. ^a: statistical interactions; ^b: joint-SDM-like approach.

Method	Embedding approach	Reference	Species interactions
			application
RDPG	graphs through SVD	Young & Scheinerman (2007)	Poisot et al. (2021)
tSNE	nodes through statistical divergence	Hinton & Roweis (2002)	Cieslak et al. (2020) ^a
DeepWalk	graph walk	Perozzi et al. (2014)	Wardeh et al. (2021)

Method	Embedding approach	Reference	Species interactions
			application
FastEmbed	graph through PCA/SVD analogue	Ramasamy & Madhow (2015)	
LINE	nodes through statistical divergence	Tang et al. (2015)	
SDNE	nodes through auto-encoding	D. Wang et al. (2016)	
node2vec	node embedding	Grover & Leskovec (2016)	
graph2vec	sub-graph embedding	Narayanan et al. (2017)	
DMSE	joint node embedding	D. Chen et al. (2017)	D. Chen et al. (2017) ^b
HARP	nodes through a meta-strategy	H. Chen et al. (2017)	
GraphKKE	graph embedding	Melnyk et al. (2020)	Melnyk et al. (2020) ^a
Joint methods	multiple graphs	S. Wang et al. (2021)	

⁷¹ **TK** Transfer + embedding graf

⁷² **The metaweb embeds hypotheses about which spatial boundaries are**
⁷³ **meaningful**

⁷⁴ As Herbert (1965) rightfully pointed out, “[y]ou can’t draw neat lines around planet-wide problems”; in
⁷⁵ this regard, any inference of a metaweb at large scales must contend with several interesting and
⁷⁶ interwoven families of problems.

77 The first is the spatial and taxonomic limit of the metaweb to embed and transfer. If the initial metaweb is
78 too narrow in scope, notably from a taxonomic point of view, the chances of finding another area with
79 enough related species (through phylogenetic relatedness or similarity of functional traits) to make a
80 reliable inference decreases; this would likely be indicated by large confidence intervals during estimation
81 of the values in the low-rank space, but the lack of well documented metawebs is currently preventing the
82 development of more concrete guidelines. The question of phylogenetic relatedness and dispersal is
83 notably true if the metaweb is assembled in an area with mostly endemic species, and as with every
84 predictive algorithm, there is room for the application of our best ecological judgement. Conversely, the
85 metaweb should be reliably filled, which assumes that the S^2 interactions in a pool of S species have been
86 examined, either through literature surveys or expert elicitation.

87 **TK** Supp. Mat. 1 provides some guidance as to the type of sampling effort that should be prioritized.
88 While RDPG was able to maintain very high predictive power when interactions were missing, the
89 addition of false positive interactions was immediately detected; this suggests that it may be appropriate to
90 err on the side of “too many” interactions when constructing the initial metaweb to be transferred.

91 The second series of problems are related to determining which area should be used to infer the new
92 metaweb in, as this determines the species pool that must be used.

93 **TK** In our application, we focused on the mammals of Canada. The upside of this approach is that
94 information at the country level is likely to be required by policy makers and stakeholders for their
95 biodiversity assessment, as each country tends to set goals at the national level (Buxton et al., 2021) for
96 which quantitative instruments are designed (Turak et al., 2017), with specific strategies often enacted at
97 smaller scales (Ray et al., 2021). And yet, we do not really have a satisfying answer to the question of
98 “where does a food web stop?”; the current most satisfying solutions involve examining the spatial
99 consistency of network area relationships (Fortin et al., 2021; see e.g. Galiana et al., 2018, 2019, 2021),
100 which is of course impossible in the absence of enough information about the network itself. This suggests
101 that an *a posteriori* refinement of the results may be required, based on a downscaling of the metaweb.

102 The final family of problems relates less to the availability of data or quantitative tools, and more to the
103 praxis of spatial ecology. Operating under the context of national divisions, in large parts of the world,
104 reflects nothing more than the legacy of settler colonialism. Indeed, the use of ecological data is not an
105 apolitical act (Nost & Goldstein, 2021), as data infrastructures tend to be designed to answer questions
106 within national boundaries, and their use both draws upon and reinforces territorial statecraft; as per

107 Machen & Nost (2021), this is particularly true when the output of “algorithmic thinking” (e.g. relying on
108 machine learning to generate knowledge) can be re-used for governance (e.g. enacting conservation
109 decisions at the national scale). We therefore recognize that methods such as we propose operate under
110 the framework that contributed to the ongoing biodiversity crisis (Adam, 2014), reinforced environmental
111 injustice (Choudry, 2013; Domínguez & Luoma, 2020), and on Turtle Island especially, should be replaced
112 by Indigenous principles of land management (Eichhorn et al., 2019; No’kmaq et al., 2021). As we see
113 AI/ML being increasingly mobilized to generate knowledge that is lacking for conservation decisions (e.g.
114 Lamba et al., 2019; Mosebo Fernandes et al., 2020), our discussion of these tools need to go beyond the
115 technical, and into the governance consequences they can have.

116 **Acknowledgements:** We acknowledge that this study was conducted on land within the traditional
117 unceded territory of the Saint Lawrence Iroquoian, Anishinabewaki, Mohawk, Huron-Wendat, and
118 Omàmiwininiwak nations. TP, TS, DC, and LP received funding from the Canadian Institute for Ecology &
119 Evolution. FB is funded by the Institute for Data Valorization (IVADO). TS, SB, and TP are funded by a
120 donation from the Courtois Foundation. CB was awarded a Mitacs Elevate Fellowship no. IT12391, in
121 partnership with fRI Research, and also acknowledges funding from Alberta Innovates and the Forest
122 Resources Improvement Association of Alberta. M-JF acknowledges funding from NSERC Discovery
123 Grant and NSERC CRC. RR is funded by New Zealand’s Biological Heritage Ngā Koiora Tuku Iho
124 National Science Challenge, administered by New Zealand Ministry of Business, Innovation, and
125 Employment. BM is funded by the NSERC Alexander Graham Bell Canada Graduate Scholarship and the
126 FRQNT master’s scholarship. LP acknowledges funding from NSERC Discovery Grant (NSERC
127 RGPIN-2019-05771). TP acknowledges financial support from NSERC through the Discovery Grants and
128 Discovery Accelerator Supplement programs.

129 References

- 130 Adam, R. (2014). *Elephant treaties: The Colonial legacy of the biodiversity crisis*. UPNE.
- 131 Albouy, C., Archambault, P., Appeltans, W., Araújo, M. B., Beauchesne, D., Cazelles, K., Cirtwill, A. R.,
132 Fortin, M.-J., Galiana, N., Leroux, S. J., Pellissier, L., Poisot, T., Stouffer, D. B., Wood, S. A., & Gravel, D.
133 (2019). The marine fish food web is globally connected. *Nature Ecology & Evolution*, 3(8, 8),
134 1153–1161. <https://doi.org/10.1038/s41559-019-0950-y>

135 Botella, C., Dray, S., Matias, C., Miele, V., & Thuiller, W. (2022). An appraisal of graph embeddings for
 136 comparing trophic network architectures. *Methods in Ecology and Evolution*, 13(1), 203–216.
 137 <https://doi.org/10.1111/2041-210X.13738>

138 Buxton, R. T., Bennett, J. R., Reid, A. J., Shulman, C., Cooke, S. J., Francis, C. M., Nyboer, E. A., Pritchard,
 139 G., Binley, A. D., Avery-Gomm, S., Ban, N. C., Beazley, K. F., Bennett, E., Blight, L. K., Bortolotti, L. E.,
 140 Camfield, A. F., Gadallah, F., Jacob, A. L., Naujokaitis-Lewis, I., ... Smith, P. A. (2021). Key
 141 information needs to move from knowledge to action for biodiversity conservation in Canada.
 142 *Biological Conservation*, 256, 108983. <https://doi.org/10.1016/j.biocon.2021.108983>

143 Chen, D., Xue, Y., Fink, D., Chen, S., & Gomes, C. P. (2017). *Deep Multi-species Embedding*. 3639–3646.
 144 <https://www.ijcai.org/proceedings/2017/509>

145 Chen, H., Perozzi, B., Hu, Y., & Skiena, S. (2017, November 16). *HARP: Hierarchical Representation*
 146 *Learning for Networks*. <http://arxiv.org/abs/1706.07845>

147 Choudry, A. (2013). Saving biodiversity, for whom and for what? Conservation NGOs, complicity,
 148 colonialism and conquest in an era of capitalist globalization. In *NGOization: Complicity,*
 149 *contradictions and prospects* (pp. 24–44). Bloomsbury Publishing.

150 Cieslak, M. C., Castelfranco, A. M., Roncalli, V., Lenz, P. H., & Hartline, D. K. (2020). T-Distributed
 151 Stochastic Neighbor Embedding (t-SNE): A tool for eco-physiological transcriptomic analysis. *Marine*
 152 *Genomics*, 51, 100723. <https://doi.org/10.1016/j.margen.2019.100723>

153 Csermely, P. (2004). Strong links are important, but weak links stabilize them. *Trends in Biochemical*
 154 *Sciences*, 29(7), 331–334. <https://doi.org/10.1016/j.tibs.2004.05.004>

155 Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs' backbones
 156 using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>

157 Dallas, T., Park, A. W., & Drake, J. M. (2017). Predicting cryptic links in host-parasite networks. *PLOS*
 158 *Computational Biology*, 13(5), e1005557. <https://doi.org/10.1371/journal.pcbi.1005557>

159 Domínguez, L., & Luoma, C. (2020). Decolonising Conservation Policy: How Colonial Land and
 160 Conservation Ideologies Persist and Perpetuate Indigenous Injustices at the Expense of the
 161 Environment. *Land*, 9(3, 3), 65. <https://doi.org/10.3390/land9030065>

162 Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological*

163 *networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.

164 Eichhorn, M. P., Baker, K., & Griffiths, M. (2019). Steps towards decolonising biogeography. *Frontiers of*
165 *Biogeography*, 12(1), 1–7. <https://doi.org/10.21425/F5FBG44795>

166 Eklöf, A., Jacob, U., Kopp, J., Bosch, J., Castro-Urgal, R., Chacoff, N. P., Dalsgaard, B., de Sassi, C., Galetti,
167 M., Guimarães, P. R., Lomáscolo, S. B., Martín González, A. M., Pizo, M. A., Rader, R., Rodrigo, A.,
168 Tylianakis, J. M., Vázquez, D. P., & Allesina, S. (2013). The dimensionality of ecological networks.
169 *Ecology Letters*, 16(5), 577–583. <https://doi.org/10.1111/ele.12081>

170 Fortin, M.-J., Dale, M. R. T., & Brimacombe, C. (2021). Network ecology in dynamic landscapes.
171 *Proceedings of the Royal Society B: Biological Sciences*, 288(1949), rspb.2020.1889, 20201889.
172 <https://doi.org/10.1098/rspb.2020.1889>

173 Galiana, N., Barros, C., Braga, J., Ficetola, G. F., Maiorano, L., Thuiller, W., Montoya, J. M., & Lurgi, M.
174 (2021). The spatial scaling of food web structure across European biogeographical regions. *Ecography*,
175 *n/a*(n/a). <https://doi.org/10.1111/ecog.05229>

176 Galiana, N., Hawkins, B. A., & Montoya, J. M. (2019). The geographical variation of network structure is
177 scale dependent: Understanding the biotic specialization of host–parasitoid networks. *Ecography*,
178 42(6), 1175–1187. <https://doi.org/10.1111/ecog.03684>

179 Galiana, N., Lurgi, M., Claramunt-López, B., Fortin, M.-J., Leroux, S., Cazelles, K., Gravel, D., & Montoya,
180 J. M. (2018). The spatial scaling of species interaction networks. *Nature Ecology & Evolution*, 2(5),
181 782–790. <https://doi.org/10.1038/s41559-018-0517-3>

182 Gravel, D., Baiser, B., Dunne, J. A., Kopelke, J.-P., Martinez, N. D., Nyman, T., Poisot, T., Stouffer, D. B.,
183 Tylianakis, J. M., Wood, S. A., & Roslin, T. (2018). Bringing Elton and Grinnell together: A quantitative
184 framework to represent the biogeography of ecological interaction networks. *Ecography*, 0(0).
185 <https://doi.org/10.1111/ecog.04006>

186 Grover, A., & Leskovec, J. (2016). Node2vec: Scalable Feature Learning for Networks. *Proceedings of the*
187 *22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, 855–864.
188 <https://doi.org/10.1145/2939672.2939754>

189 Grünig, M., Mazzi, D., Calanca, P., Karger, D. N., & Pellissier, L. (2020). Crop and forest pest metawebs
190 shift towards increased linkage and suitability overlap under climate change. *Communications Biology*,

3(1, 1), 1–10. <https://doi.org/10.1038/s42003-020-0962-9>

Herbert, F. (1965). *Dune* (1st ed.). Chilton Book Company.

Hinton, G., & Roweis, S. T. (2002). Stochastic neighbor embedding. *NIPS*, 15, 833–840.

Hoffmann, J., Bar-Sinai, Y., Lee, L. M., Andrejevic, J., Mishra, S., Rubinstein, S. M., & Rycroft, C. H. (2019). Machine learning in a data-limited regime: Augmenting experiments with synthetic data uncovers order in crumpled sheets. *Science Advances*, 5(4), eaau6792. <https://doi.org/10.1126/sciadv.aau6792>

Hortal, J., de Bello, F., Diniz-Filho, J. A. F., Lewinsohn, T. M., Lobo, J. M., & Ladle, R. J. (2015). Seven Shortfalls that Beset Large-Scale Knowledge of Biodiversity. *Annual Review of Ecology, Evolution, and Systematics*, 46(1), 523–549. <https://doi.org/10.1146/annurev-ecolsys-112414-054400>

Jordano, P. (2016). Sampling networks of ecological interactions. *Functional Ecology*, 30(12), 1883–1893. <https://doi.org/10.1111/1365-2435.12763>

Lamba, A., Cassey, P., Segaran, R. R., & Koh, L. P. (2019). Deep learning for environmental conservation. *Current Biology*, 29(19), R977–R982. <https://doi.org/10.1016/j.cub.2019.08.016>

Machen, R., & Nost, E. (2021). Thinking algorithmically: The making of hegemonic knowledge in climate governance. *Transactions of the Institute of British Geographers*, 46(3), 555–569. <https://doi.org/10.1111/tran.12441>

McLeod, A., Leroux, S. J., Gravel, D., Chu, C., Cirtwill, A. R., Fortin, M.-J., Galiana, N., Poisot, T., & Wood, S. A. (2021). Sampling and asymptotic network properties of spatial multi-trophic networks. *Oikos*, n/a(n/a). <https://doi.org/10.1111/oik.08650>

Melnyk, K., Klus, S., Montavon, G., & Conrad, T. O. F. (2020). GraphKKE: Graph Kernel Koopman embedding for human microbiome analysis. *Applied Network Science*, 5(1), 96. <https://doi.org/10.1007/s41109-020-00339-2>

Mora, B. B., Gravel, D., Gilarranz, L. J., Poisot, T., & Stouffer, D. B. (2018). Identifying a common backbone of interactions underlying food webs from different ecosystems. *Nature Communications*, 9(1), 2603. <https://doi.org/10.1038/s41467-018-05056-0>

Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from proxies. *Trends in Ecology & Evolution*, 30(6), 347–356.

219 <https://doi.org/10.1016/j.tree.2015.03.014>

220 Mosebo Fernandes, A. C., Quintero Gonzalez, R., Lenihan-Clarke, M. A., Leslie Trotter, E. F., & Jokar
 221 Arsanjani, J. (2020). Machine Learning for Conservation Planning in a Changing Climate.
 222 *Sustainability*, 12(18, 18), 7657. <https://doi.org/10.3390/su12187657>

223 Narayanan, A., Chandramohan, M., Venkatesan, R., Chen, L., Liu, Y., & Jaiswal, S. (2017, July 17).
 224 *Graph2vec: Learning Distributed Representations of Graphs*. <http://arxiv.org/abs/1707.05005>

225 Neutel, A.-M., Heesterbeek, J. A. P., & de Ruiter, P. C. (2002). Stability in Real Food Webs: Weak Links in
 226 Long Loops. *Science*, 296(5570), 1120–1123. <https://doi.org/10.1126/science.1068326>

227 No'kmaq, M., Marshall, A., Beazley, K. F., Hum, J., Joudry, shalan, Papadopoulos, A., Pictou, S., Rabesca,
 228 J., Young, L., & Zurba, M. (2021). “Awakening the sleeping giant”: Re-Indigenization principles for
 229 transforming biodiversity conservation in Canada and beyond. *FACETS*, 6(1), 839–869.

230 Nost, E., & Goldstein, J. E. (2021). A political ecology of data. *Environment and Planning E: Nature and*
 231 *Space*, 25148486211043503. <https://doi.org/10.1177/25148486211043503>

232 O'Connor, L. M. J., Pollock, L. J., Braga, J., Ficetola, G. F., Maiorano, L., Martinez-Almoyna, C.,
 233 Montemaggiori, A., Ohlmann, M., & Thuiller, W. (2020). Unveiling the food webs of tetrapods across
 234 Europe through the prism of the Eltonian niche. *Journal of Biogeography*, 47(1), 181–192.
 235 <https://doi.org/10.1111/jbi.13773>

236 Pedersen, E. J., Thompson, P. L., Ball, R. A., Fortin, M.-J., Gouhier, T. C., Link, H., Moritz, C., Nenzen, H.,
 237 Stanley, R. R. E., Taranu, Z. E., Gonzalez, A., Guichard, F., & Pepin, P. (2017). Signatures of the
 238 collapse and incipient recovery of an overexploited marine ecosystem. *Royal Society Open Science*, 4(7),
 239 170215. <https://doi.org/10.1098/rsos.170215>

240 Perozzi, B., Al-Rfou, R., & Skiena, S. (2014). DeepWalk: Online learning of social representations.
 241 *Proceedings of the 20th ACM SIGKDD International Conference on Knowledge Discovery and Data*
 242 *Mining*, 701–710. <https://doi.org/10.1145/2623330.2623732>

243 Poisot, T., Cirtwill, A. R., Cazelles, K., Gravel, D., Fortin, M.-J., & Stouffer, D. B. (2016). The structure of
 244 probabilistic networks. *Methods in Ecology and Evolution*, 7(3), 303–312.
 245 <https://doi.org/10.1111/2041-210X.12468>

246 Poisot, T., Ouellet, M.-A., Mollentze, N., Farrell, M. J., Becker, D. J., Albery, G. F., Gibb, R. J., Seifert, S. N.,

247 & Carlson, C. J. (2021, May 31). *Imputing the mammalian virome with linear filtering and singular*
 248 *value decomposition*. <http://arxiv.org/abs/2105.14973>

249 Poisot, T., Stouffer, D. B., & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary
 250 through space and time. *Oikos*, 124(3), 243–251. <https://doi.org/10.1111/oik.01719>

251 Ramasamy, D., & Madhow, U. (2015). Compressive spectral embedding: Sidestepping the SVD. In C.
 252 Cortes, N. Lawrence, D. Lee, M. Sugiyama, & R. Garnett (Eds.), *Advances in neural information*
 253 *processing systems* (Vol. 28). Curran Associates, Inc. [https:](https://proceedings.neurips.cc/paper/2015/file/4f6ffe13a5d75b2d6a3923922b3922e5-Paper.pdf)
 254 [//proceedings.neurips.cc/paper/2015/file/4f6ffe13a5d75b2d6a3923922b3922e5-Paper.pdf](https://proceedings.neurips.cc/paper/2015/file/4f6ffe13a5d75b2d6a3923922b3922e5-Paper.pdf)

255 Ray, J. C., Grimm, J., & Olive, A. (2021). The biodiversity crisis in Canada: Failures and challenges of
 256 federal and sub-national strategic and legal frameworks. *FACETS*, 6, 1044–1068.
 257 <https://doi.org/10.1139/facets-2020-0075>

258 Strydom, T., Catchen, M. D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., Forero-Muñoz,
 259 N. R., Higino, G., Mercier, B., Gonzalez, A., Gravel, D., Pollock, L., & Poisot, T. (2021). A roadmap
 260 towards predicting species interaction networks (across space and time). *Philosophical Transactions of*
 261 *the Royal Society B: Biological Sciences*, 376(1837), 20210063.
 262 <https://doi.org/10.1098/rstb.2021.0063>

263 Tang, J., Qu, M., Wang, M., Zhang, M., Yan, J., & Mei, Q. (2015). LINE: Large-scale Information Network
 264 Embedding. *Proceedings of the 24th International Conference on World Wide Web*, 1067–1077.
 265 <https://doi.org/10.1145/2736277.2741093>

266 Turak, E., Brazill-Boast, J., Cooney, T., Drielsma, M., DelaCruz, J., Dunkerley, G., Fernandez, M., Ferrier,
 267 S., Gill, M., Jones, H., Koen, T., Leys, J., McGeoch, M., Mihoub, J.-B., Scanes, P., Schmeller, D., &
 268 Williams, K. (2017). Using the essential biodiversity variables framework to measure biodiversity
 269 change at national scale. *Biological Conservation*, 213, 264–271.
 270 <https://doi.org/10.1016/j.biocon.2016.08.019>

271 Wang, D., Cui, P., & Zhu, W. (2016). Structural Deep Network Embedding. *Proceedings of the 22nd ACM*
 272 *SIGKDD International Conference on Knowledge Discovery and Data Mining*, 1225–1234.
 273 <https://doi.org/10.1145/2939672.2939753>

274 Wang, S., Arroyo, J., Vogelstein, J. T., & Priebe, C. E. (2021). Joint Embedding of Graphs. *IEEE*
 275 *Transactions on Pattern Analysis and Machine Intelligence*, 43(4), 1324–1336.

276 <https://doi.org/10.1109/TPAMI.2019.2948619>

277 Wardeh, M., Baylis, M., & Blagrove, M. S. C. (2021). Predicting mammalian hosts in which novel
278 coronaviruses can be generated. *Nature Communications*, 12(1, 1), 780.
279 <https://doi.org/10.1038/s41467-021-21034-5>

280 Wood, S. A., Russell, R., Hanson, D., Williams, R. J., & Dunne, J. A. (2015). Effects of spatial scale of
281 sampling on food web structure. *Ecology and Evolution*, 5(17), 3769–3782.
282 <https://doi.org/10.1002/ece3.1640>

283 Yan, S., Xu, D., Zhang, B., & Zhang, H.-J. (2005). Graph embedding: A general framework for
284 dimensionality reduction. *2005 IEEE Computer Society Conference on Computer Vision and Pattern
285 Recognition (CVPR'05)*, 2, 830–837 vol. 2. <https://doi.org/10.1109/CVPR.2005.170>

286 Young, S. J., & Scheinerman, E. R. (2007). Random Dot Product Graph Models for Social Networks. In A.
287 Bonato & F. R. K. Chung (Eds.), *Algorithms and Models for the Web-Graph* (pp. 138–149). Springer.
288 https://doi.org/10.1007/978-3-540-77004-6_11