

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 strong ecological hypotheses**

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

76 The first is the spatial and taxonomic limit of the metaweb to embed and transfer. If the initial metaweb is
77 too narrow in scope, notably from a taxonomic point of view, the chances of finding another area with

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

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

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

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

103 The final family of problems relates less to the availability of data or quantitative tools, and more to the
104 praxis of spatial ecology. Operating under the context of national divisions, in large parts of the world,
105 reflects nothing more than the legacy of settler colonialism. Indeed, the use of ecological data is not an
106 apolitical act (Nost & Goldstein, 2021), as data infrastructures tend to be designed to answer questions
107 within national boundaries, and their use both draws upon and reinforces territorial statecraft; as per
108 Machen & Nost (2021), this is particularly true when the output of “algorithmic thinking” (e.g. relying on
109 machine learning to generate knowledge) can be re-used for governance (e.g. enacting conservation

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

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128 References

- 129 Adam, R. (2014). *Elephant treaties: The Colonial legacy of the biodiversity crisis*. UPNE.
- 130 Albouy, C., Archambault, P., Appeltans, W., Araújo, M. B., Beauchesne, D., Cazelles, K., Cirtwill, A. R.,
131 Fortin, M.-J., Galiana, N., Leroux, S. J., Pellissier, L., Poisot, T., Stouffer, D. B., Wood, S. A., & Gravel, D.
132 (2019). The marine fish food web is globally connected. *Nature Ecology & Evolution*, 3(8, 8),
133 1153–1161. <https://doi.org/10.1038/s41559-019-0950-y>
- 134 Botella, C., Dray, S., Matias, C., Miele, V., & Thuiller, W. (2022). An appraisal of graph embeddings for
135 comparing trophic network architectures. *Methods in Ecology and Evolution*, 13(1), 203–216.

<https://doi.org/10.1111/2041-210X.13738>

- Buxton, R. T., Bennett, J. R., Reid, A. J., Shulman, C., Cooke, S. J., Francis, C. M., Nyboer, E. A., Pritchard, G., Binley, A. D., Avery-Gomm, S., Ban, N. C., Beazley, K. F., Bennett, E., Blight, L. K., Bortolotti, L. E., Camfield, A. F., Gadallah, F., Jacob, A. L., Naujokaitis-Lewis, I., ... Smith, P. A. (2021). Key information needs to move from knowledge to action for biodiversity conservation in Canada. *Biological Conservation*, 256, 108983. <https://doi.org/10.1016/j.biocon.2021.108983>
- Chen, D., Xue, Y., Fink, D., Chen, S., & Gomes, C. P. (2017). *Deep Multi-species Embedding*. 3639–3646. <https://www.ijcai.org/proceedings/2017/509>
- Chen, H., Perozzi, B., Hu, Y., & Skiena, S. (2017, November 16). *HARP: Hierarchical Representation Learning for Networks*. <http://arxiv.org/abs/1706.07845>
- Choudry, A. (2013). Saving biodiversity, for whom and for what? Conservation NGOs, complicity, colonialism and conquest in an era of capitalist globalization. In *NGOization: Complicity, contradictions and prospects* (pp. 24–44). Bloomsbury Publishing.
- Cieslak, M. C., Castelfranco, A. M., Roncalli, V., Lenz, P. H., & Hartline, D. K. (2020). T-Distributed Stochastic Neighbor Embedding (t-SNE): A tool for eco-physiological transcriptomic analysis. *Marine Genomics*, 51, 100723. <https://doi.org/10.1016/j.margen.2019.100723>
- Csermely, P. (2004). Strong links are important, but weak links stabilize them. *Trends in Biochemical Sciences*, 29(7), 331–334. <https://doi.org/10.1016/j.tibs.2004.05.004>
- Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs' backbones using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>
- Dallas, T., Park, A. W., & Drake, J. M. (2017). Predicting cryptic links in host-parasite networks. *PLOS Computational Biology*, 13(5), e1005557. <https://doi.org/10.1371/journal.pcbi.1005557>
- Domínguez, L., & Luoma, C. (2020). Decolonising Conservation Policy: How Colonial Land and Conservation Ideologies Persist and Perpetuate Indigenous Injustices at the Expense of the Environment. *Land*, 9(3, 3), 65. <https://doi.org/10.3390/land9030065>
- Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.

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

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

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

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

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

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

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

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

188 Grünig, M., Mazzi, D., Calanca, P., Karger, D. N., & Pellissier, L. (2020). Crop and forest pest metawebs
189 shift towards increased linkage and suitability overlap under climate change. *Communications Biology*,
190 3(1, 1), 1–10. <https://doi.org/10.1038/s42003-020-0962-9>

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

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

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

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

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

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

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

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

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

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

216 Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from
 217 proxies. *Trends in Ecology & Evolution*, 30(6), 347–356.
 218 <https://doi.org/10.1016/j.tree.2015.03.014>

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

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

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

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

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

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

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

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

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

245 Poisot, T., Ouellet, M.-A., Mollentze, N., Farrell, M. J., Becker, D. J., Albery, G. F., Gibb, R. J., Seifert, S. N.,
 246 & Carlson, C. J. (2021, May 31). *Imputing the mammalian virome with linear filtering and singular*

value decomposition. <http://arxiv.org/abs/2105.14973>

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

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

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

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

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

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

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

Wang, S., Arroyo, J., Vogelstein, J. T., & Priebe, C. E. (2021). Joint Embedding of Graphs. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 43(4), 1324–1336. <https://doi.org/10.1109/TPAMI.2019.2948619>

- 276 Wardeh, M., Baylis, M., & Blagrove, M. S. C. (2021). Predicting mammalian hosts in which novel
277 coronaviruses can be generated. *Nature Communications*, 12(1, 1), 780.
278 <https://doi.org/10.1038/s41467-021-21034-5>
- 279 Wood, S. A., Russell, R., Hanson, D., Williams, R. J., & Dunne, J. A. (2015). Effects of spatial scale of
280 sampling on food web structure. *Ecology and Evolution*, 5(17), 3769–3782.
281 <https://doi.org/10.1002/ece3.1640>
- 282 Yan, S., Xu, D., Zhang, B., & Zhang, H.-J. (2005). Graph embedding: A general framework for
283 dimensionality reduction. *2005 IEEE Computer Society Conference on Computer Vision and Pattern*
284 *Recognition (CVPR'05)*, 2, 830–837 vol. 2. <https://doi.org/10.1109/CVPR.2005.170>
- 285 Young, S. J., & Scheinerman, E. R. (2007). Random Dot Product Graph Models for Social Networks. In A.
286 Bonato & F. R. K. Chung (Eds.), *Algorithms and Models for the Web-Graph* (pp. 138–149). Springer.
287 https://doi.org/10.1007/978-3-540-77004-6_11