T is for Topology

Tanya Strydom

Andrew P. Beckerman

2024-02-06

Abstract

Pending…

## 1 Introduction

The standard run of the mill that we cannot always feasibly make network predictions because 1. hard, 2. time (prehistoric mostly), and 3. probably something else meaningful that’s just slipping my mind at the moment.

Maybe a brief history of the development of predictive tools? Sort of where the theory/body of work was based and how that has changed?

Maybe start here already about discussing the core mechanistic differences that models will work at - some are really concerned (and thus constrained by) structure, others are more mechanistic in nature *i.e.,* species *a* had the capacity to eat species *b*, and then you get Rohr et al. (2010) and Strydom et al. (2022) that sit in the weird latent space…

At some point we are going to need to discuss the key difference and implication between a metaweb and a network realisation.

Do we need to delve into individual-based networks? (*sensu* Tinker 2012, Araújo 2008) I think its probably a step too far and one starts delving into apples and pears type of comparisons. Especially since these work off of already existing networks and its more about about ‘tweaking’ those - so not so much *de novo* predictions. Although this might be useful to keep in mind when it comes to re-wiring… Also on that note do we opn the re-wiring door here in this ms or wait it out a bit.

## 2 Data & Methods

### 2.1 Overview of topology generators

I know table are awful but in this case they may make more sense

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table 1: Lets make a table that gives an overview of the different topology generators that we will look at   | Model | Reference | Core Mechanism | | --- | --- | --- | | Niche model | Cohen, Newman, and Steele (1997) | structural | | Cascade model | Williams and Martinez (2000) | structural | | PFIM | Shaw et al. (2024) | mechanistic | | Log-ratio | Rohr et al. (2010) | latent trait space | | Nested hierarchy | Cattin et al. (2004) |  | | ADBM | Petchey et al. (2008) | mechanistic | | Stochastic | Rossberg et al. (2006) |  | | Transfer learning | Strydom et al. (2022) | latent trait space | | Trait-based | Caron et al. (2022) | mechanistic | |

### 2.2 Datasets used

Here I think we need to span a variety of domains, at minimum aquatic and terrestrial but maybe there should be a ‘scale’ element as well *i.e.,* a regional and local network. I think there is going to be a ‘turning point’ where structural will take over from mechanistic in terms of performance. More specifically at local scales bioenergetic constraints (and co-occurrence) may play a bigger role in structuring a network whereas at the metaweb level then mechanistic may make more (since by default its about who can potentially interact and obviously not constrained by real-world scenarios) *sensu* Caron et al. (2023)

## 3 Results

How we want to compare and contrast. I think there won’t be a ‘winner’ and thus we need to think of ‘tests’ that are going to measure performance in different situations/settings. With that in mind I think some valuable points to consider would be:

* Structural vs pairwise link predictions (graph vs node level)
  + % of links correctly retrieved
  + connectence
  + trophic level
  + generalism vs specialism
  + something related to false positives/negatives
* Data ‘cost’ (some methods might need a lot lot of supporting data vs something very light weight)
* I think it would be remiss to also take into consideration computational cost

## 4 Conclusion

## References

Source: [Article Notebook](https://BecksLab.github.io/ms_t_is_for_topology/index.qmd.html)

Caron, Dominique, Ulrich Brose, Miguel Lurgi, Guillaume Blanchet, Dominique Gravel, and Laura J. Pollock. 2023. “Trophic Interaction Models Predict Interactions Across Space, Not Food Webs,” May.

Caron, Dominique, Luigi Maiorano, Wilfried Thuiller, and Laura J. Pollock. 2022. “Addressing the Eltonian Shortfall with Trait-Based Interaction Models.” *Ecology Letters* 25 (4): 889–99. <https://doi.org/10.1111/ele.13966>.

Cattin, Marie-France, Louis-Félix Bersier, Carolin Banašek-Richter, Richard Baltensperger, and Jean-Pierre Gabriel. 2004. “Phylogenetic Constraints and Adaptation Explain Food-Web Structure.” *Nature* 427 (6977): 835–39. <https://doi.org/10.1038/nature02327>.

Cohen, Joel E., C. M. Newman, and John Hyslop Steele. 1997. “A Stochastic Theory of Community Food Webs I. Models and Aggregated Data.” *Proceedings of the Royal Society of London. Series B. Biological Sciences* 224 (1237): 421–48. <https://doi.org/10.1098/rspb.1985.0042>.

Petchey, Owen L., Andrew P. Beckerman, Jens O. Riede, and Philip H. Warren. 2008. “Size, Foraging, and Food Web Structure.” *Proceedings of the National Academy of Sciences* 105 (11): 4191–96. <https://doi.org/10.1073/pnas.0710672105>.

Rohr, Rudolf Philippe, Heike Scherer, Patrik Kehrli, Christian Mazza, and Louis-Félix Bersier. 2010. “Modeling Food Webs: Exploring Unexplained Structure Using Latent Traits.” *The American Naturalist* 176 (2): 170–77. <https://doi.org/10.1086/653667>.

Rossberg, A. G., H. Matsuda, T. Amemiya, and K. Itoh. 2006. “Food Webs: Experts Consuming Families of Experts.” *Journal of Theoretical Biology* 241 (3): 552–63. <https://doi.org/10.1016/j.jtbi.2005.12.021>.

Shaw, Jack O., Alexander M. Dunhill, Andrew P. Beckerman, Jennifer A. Dunne, and Pincelli M. Hull. 2024. “A Framework for Reconstructing Ancient Food Webs Using Functional Trait Data.” bioRxiv. <https://doi.org/10.1101/2024.01.30.578036>.

Strydom, Tanya, Salomé Bouskila, Francis Banville, Ceres Barros, Dominique Caron, Maxwell J. Farrell, Marie-Josée Fortin, et al. 2022. “Food Web Reconstruction Through Phylogenetic Transfer of Low-Rank Network Representation.” *Methods in Ecology and Evolution* 13 (12): 2838–49. <https://doi.org/10.1111/2041-210X.13835>.

Williams, Richard J., and Neo D. Martinez. 2000. “Simple Rules Yield Complex Food Webs.” *Nature* 404 (6774): 180–83. <https://doi.org/10.1038/35004572>.