

Navigating food web prediction; assumptions, rationale, and methods

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Abstract: Although it has been acknowledged that communities consist not only of co-occurring species but that they also interact being able to quantify those interactions and assemble them into interaction networks has been a limiting factor in the integration of network ecology into other fields of ecology. As the field of network ecology has matured there has been an accompanying expansion in the development of theory and tools that are centred around generating networks or predicting the interactions between species. Notably many of these tools have been developed with different underlying philosophies, ideas, and mechanisms as to what structures the interactions between species. It is thus critically important that those wanting to adopt these network generating tools be aware of how the the specific questions being asked maps to the underlying assumptions made when generating networks, as well as the limitations of how the networks/interactions are delimited. Here we provide an overview of the canonical network generating models, comparing and contrasting the underlying assumptions, data requirements, and resulting network predictions made by the different families in an attempt to provide guidance for those interested in adopting the generation of networks into their workflow. [R1. a discussion on the underlying assumptions we are making when we delimit a network]. [R2. an overview of how the different model families differ - ordination space/benchmarking]. [R3. identifying the relevant questions/bodies of theory that the networks generated by different families are suited to answer]. When choosing to construct an interaction network the researcher is faced with many assumptions and considerations that should be made and it is important to be aware of these limitations to avoid constructing (something poetic to capture the idea of falsity/false idols). Being aware of these choices is particularly important as the availability of these tools grows and network ecology starts to be adopted into other aspects of ecology and conservation biology.

Keywords: food web, network construction, scientific ignorance

1 At the heart of modern biodiversity science are a set of concepts about how biodiversity, community structure,
2 productivity and asynchrony define the stability, resilience and dynamics of complex communities. Human-
3 ity relies on these complex communities for numerous functions and services and they are under multiple,
4 simultaneous threats. With such formalisation, it is possible to model the relationships among biodiversity,
5 community structure, productivity and asynchrony and how they define the stability, resilience and dynamics
6 of complex communities.

7 One of the fundamental challenges that we are faced with in using and studying food webs is that there
8 is a scarcity of ‘real world’ interaction data [1,2]. The difficulty of recording interactions in the field [3,4]
9 has necessitated that researchers find and develop alternative means to construct and build food webs using
10 **models** [5,6]. Over the past decade, there has been a proliferation of tools and processes for characterising
11 food webs, these models span a wide range of philosophies that rely on different approaches, data, and
12 definitions, which ultimately determine how the food web is constructed. Although the development of these
13 different models have carved out the path for constructing either synthetic, ecologically plausible networks
14 or providing ‘first draft’ networks that can be utilised in real world settings [7] we are lacking in discussions
15 that are explicitly comparing and contrasting how the way one chooses to approach the task of constructing a
16 food web is introducing (and ultimately embedding) specific assumptions and hypotheses [8]. Most attempts
17 that focus on comparing and contrasting models are focused on the same group of **model families** [9,10]
18 and only benchmark the different models as opposed to contextualising them within the bigger framework
19 of understanding the data needs of the different models, as well as how the resulting network is defined and
20 structured. As food webs become a more integrated part of some of the broader fields of ecology [11,12] it
21 is critical that we highlight and review these different model families as a whole (and not in isolation), and
22 move away from simply benchmarking the performance of these different model families but also highlight
23 the inherent constraints that these models impose upon themselves and how these will delimit and dictate the
24 potential questions one will be able to ask [13]. This will allow us to ensure the right models are being used
25 to answer the right questions, particularly within the context of trying to accelerate cross-cutting research
26 in the face of global change.

27 In this (item) we will...

28 [Figure 1 about here.]

1 Why do we want to predict food webs?

Simply put, the prediction of networks comes from a place of need. However, these needs come from two different (but still aligned) places of interest within the field of network ecology.

Crucially most network generators lack some key data on the interaction between species (this can be because of how the model itself defines species or the way in which links are assigned in the network) and interaction predictors lack some sort of parametrisation of network structure [just because two species can interact it does not mean that they will, 14].

In order for a model to formalise a ‘complete’ food web it is necessary to formalise two aspects of the network, ‘who eats whom’ (to determine the links between nodes) as well as the structure of the network (to limit the distribution of links), however most models are inclined to focus on one of the two aspects panel A of 1.

Because measuring in the field is hard and sometimes we need model systems so we don’t have real data. The bigger reason is that we *think* that using a network-based approach is really the answer to helping us address some of the more bending issues we toil and think about in the world. Predicting because we want to get an approximation of the real world but also predicting because we want a model of the real world system

Arguably the need for methods and tools that can be used to construct synthetic food webs arises from two different (but still aligned) places of interest within the field of network ecology. On the one side sits the researcher who is interested in generating a set of ecologically plausible networks for the purpose of understanding some higher-level process/concept (*e.g.*, understanding energy flows) in a more synthetic setting, whereby these networks do not require any level of species specificity *per se* and it is more the arrangement of the nodes and links within the context of network structure that is of value. This researcher is contrasted by one that is interested in constructing real-world, location specific, interaction data for a specific collection of species (community). This is driven by the need for researchers to find alternative ways to infer the interactions between species as a way to overcome the inherent challenges of inventorying interactions in the field (see [5] for a more mechanistic, and [6] for a more statistical overview of ways to approach this specific issue). Of course these two categories are not distinct, mutually exclusive, groups but can rather be viewed as operating on a continuum ranging from a need for generality (*i.e.*, creating a network that, when taken in aggregate, the distribution of links (interactions) between nodes (species) are ecologically plausible) to a need for specificity (*i.e.*, local-level predictions between specific species pairs). It is thus clear that (realistically) there will probably never be a ‘best fit’ tool that is able to construct a food web that will span the entire range of needs, and rather the responsibility lies with the researcher to be aware of not

only the underlying philosophy of the specific toolset (as this could have knock-on effects when using those networks for downstream analyses/simulations; pers. comms. Beckerman, 2024), but also how well the tool is able to retrieve the specific network or interaction properties that they desire.

2 The anatomy of a food web

Defining a food web seems simple, it is the representation of the interactions (edges) between species (nodes), however the definition of ‘edges’ and ‘nodes’, as well as the scale at which they are aggregated can take many forms. As highlighted in [15] networks can be constructed at the population (the links between individuals), community (the links between species), or metacommunity (fluxes between locations) level. Even if one were to limit their scope to thinking of interaction networks only in terms of food webs at the community-level there are still many ways to define the various components of the network, one needs to understand the different intentions/assumptions that are made when a food web is constructed. Although the main intention of a food web is to capture and represent the feeding links between species there are many ways to define the nodes (*e.g.*, species or taxonomic group), edges (*e.g.* potential or realised feeding links), the magnitude of the edges (*e.g.*, binary vs probabilistic), and even how the network itself is delimited (does it represent an aggregation of interactions over time?). It is thus clear that the way that a network is coded (constructed) can influence the resulting observations and conclusions that are made [16,17], and it is important to have a strong grasp of what information a network is attempting to convey.

2.1 How do we define a node?

Although this may seem an elementary question in the context of food webs — a node should represent a species, the reality is that nodes can often represent an aggregate of different (taxonomic) species - so called ‘trophic species’, and it is not uncommon that networks can have nodes that represent both taxonomic and trophic species (*e.g.*, there are many that do the basal ‘plant/phytoplankton’ node but include at least one REF). Practical implications of how we are aggregating the nodes is that the resolution may not always be ‘pixel perfect’ *i.e.*, we may be unable to assess the co-extinction risk of a species pair [mutualism ref, at least there should be one of them], however there is value in having nodes that represent an aggregation of species, as these convey a much more general overview of how the links are distributed within the community.

2.2 What is meant by an edge?

As discussed earlier there are many ways to define the links between species — even feeding links. At its core links within food webs can be thought of as a representation of either the flow of a resource [ref], realised [18]

or potential [19] feeding links, or energy transfer and material flow [20]. How we quantify links will influence the resulting structure of the network - and the inferences we will make thereof. For example taking a food web that consists of links representing *potential* feeding links between species will be meaningless if you are interested in understanding the flow of energy through the system as the links within the network are over connected. In addition to the various ways of defining the links between species pairs there are also a myriad of ways in which the links themselves can be quantified. Links between species are often treated as being present or absent (*i.e.*, binary) but it is also possible to use probabilities [which quantifies how likely an interaction is to occur, 21] or continuous measurements [which quantifies the effect of one species on another, 22]. Although there is a clear argument for moving away from a purely binary way of representing interactions [probabilities preprint] this of course also means that there is an additional layer to the interpretation these links.

[23] states that “[*Their*] approach is more like gross anatomy than like physiology... that is, the gross anatomy is frozen, rather than in motion.”.

2.3 Putting the parts together; what does it mean?

It is clear that there are many ways to define, code, and construct food webs, however what may be less clear is understanding *why* there is such a diversity of thought. Here it may be meaningful to contextualise the different ‘types’ of food webs within the larger questions (or needs) that have been driving them. Some of the earliest work on food webs was linked to the idea of niche space, and more specifically, the idea of trophic niches and how this would influence the dimensionality of a networks [24]. This introduced the idea that a single dimension [the “niche axis,” 25] constrains the interactions between species; in this instance it makes sense to think of species in terms of what they consume and what they are consumed by, as they are occupying the same space in the niche axis. Networks that are defined in this way may be useful for understanding how the flow of energy (resources) are constrained between ‘species’, particularly how it moves through the trophic levels. This ‘niche-based’ way of thinking might be beneficial when thinking about networks at the structural level, and when trying to map large-scale processes [ref?] however there was also a need to develop ways of thinking that were more geared to thinking about why does species *a* predate species *b*, broadly this is the result of two things; a predator needs to have the correct traits to be able to capture, kill, and consume, its prey (a mismatch between predator and prey is termed a forbidden link, [4]) and it needs to be energetically feasible [feeding ecology ref]. When we think of interactions in these terms it makes sense that nodes are defined at the species level (or at least as species that have the same traits and/or energy content), however the links between them can be quantified in different ways... [this is lazy writing]

i Box 1 - Mechanisms that determine feeding links

Proximity

We are co-occurring in space and in time and thus we can interact

Mass-effect

Our (respective and instantaneous) abundance in that time and space is going to influence how we interact

Complementarity

We have a set of ‘traits’ that means we can interact including:

- You as a prey item fit in my gob (I can eat you, ~~even if its small bites~~) [ref]
- You as a prey item are energetically ‘worth it’ [ref foraging ecology]
- As a predator I have the required traits that allow me to ~~kill~~ unalive and eat you [*sensu* forbidden links 4]

3 How do we predict food webs?

Selecting a model for the task of network prediction should come down to two things; what *aspect* of a food web am I interested in predicting, and what data is available. As shown in panel A of Figure 1 the models that are used to predict a food web tend to focus on only predicting the structure of a network (topology generator) or the interactions for a given species pool (interaction predictor). These models themselves are a reflection of the different goals and intentions of the research program from which they are developed. Models such as the niche [26] or cascade [27] were developed with the intent of being used to understand the *structural* aspects of food webs, specifically how links are distributed amongst species in the community, whereas bayesian [28], trait hierarchy [29], and the log-ratio [30] models have been developed so as to be used as a tool to determine if species are able to interact (*i.e.*, species *a* has the capacity to eat species *b*). Along with predicting different anatomical parts of a food web the different models have varying degrees of data that are needed to ‘parametrise’ the network. Once these two limitations are assessed and addressed it is then possible to select the model (or model family) that will best be able to capture food web feature that the researcher is most interested in (see Box 2 - Assessing model outputs).

3.1 Model families

As there are many food web models to choose from it is perhaps useful to think about the models in terms of model families, a summary of these families is presented in Table 1 and highlights the differences and

1 similarities of the philosophies and assumptions that determine a network. Models within model families

Table 1: A summary of the different families of tools that can be used to generate food webs, this includes a brief description of the underlying philosophy of the family as well as how the different elements (nodes and edges) of the generated network represents.

Model		Network	Nodes	Links		Key
family	Theory	predicted	represent	represent	Interaction	reference
null	Links are randomly distributed within a network	structural	agnostic	feeding links	binary	
neutral	Network structure is random, but species abundance determines links between nodes	structural	species	feeding links	binary	
resource	Networks are interval, species can be ordered on a ‘niche axis’	structural	trophic species	subdivision of resource	binary	[9]
generative	Networks are determined by their structural features	structural	agnostic	links	binary	

Model family	Theory	Network predicted	Nodes represent	Links represent	Interaction	Key reference
energetic	Interactions are determined by foraging theory (feeding links)	interaction	species	feeding links	quantitative	
graph embedding	Interactions can be predicted from the latent traits of networks	interaction	species	potential feeding links	probabilistic	[31]
trait matching	Interactions can be inferred by a mechanistic framework/relationships	interaction	species	feeding links	binary	[5]
binary classifiers	Interactions can be predicted by learning the relationship between interactions and ecologically relevant predictors	interaction	species	feeding links	binary	[10]

Model family	Theory	Network predicted	Nodes represent	Links represent	Interaction	Key reference
expert knowledge	‘Boots on the ground’ ecological knowledge and observations	interaction	species	feeding links	binary	
data scavenging	Webscraping to create networks from online databases	interaction	species	feeding links	binary	
co-occurrence	co-occurrence patterns arise from interactions so we can use these patterns to reverse engineer the interactions	co-occurrence patterns	species	association links	binary	

[Figure 2 about here.]

Source: [Model family traits](#)

i Box 2 - Assessing model outputs

Although understanding the underlying philosophy of the different model families is beneficial it is also important to understand in what situations the different families are likely to perform well or poorly. When we are assessing the performance of the different model families it is beneficial to think

of benchmarking these assessments based on a broader basis than just its ability to correctly recover network structure or pairwise interactions. When thinking about how to benchmark models it is perhaps beneficial to take a step back and once again assess what are the needs of the researcher (Section 1) and linking this back to what aspects of the network (Section 2) are of importance and assess the performance of a model within those parameters.

Benchmarking

Benchmarking how well a model is doing to capture the desired elements of a network is also a task that required some thought and contemplation. Even if we think about the predicting the structure of a network it is possible that two networks may have the same number of nodes and links but that those links may be distributed in very different ways. Thus it is important to think critically about the suite of summary statistics that are used to assess a model, since there is no one ‘silver bullet’ summary statistic that will be able to assess if a model is able to fully replicate an empirical network [25]. One of the main challenges when assessing the ability to retrieve pairwise interactions is that food webs are sparse (that means that there are few links given the number of species) and it is important that we are able to discern between a model that is able to correctly predict interactions that do (true positives) and not (true negatives) occur and one that is simply predicting a lack of interactions [32].

[Figure 3 about here.]

Source: [Quantitative approach to topology generators](#)

Data cost

This includes thinking about the need for additional data sources (such as trait or phylogenetic data), the computational cost, as well as the time it might take to generate a network, *e.g.*, binary classifiers require an (often times) extensive list of additional trait data for the model training process, which limits predictions to communities for which you do have the relevant auxiliary data available.

Philosophical constraints

Probably mentioned elsewhere but basically are we constructing networks because we want to make real-world, case-specific predictions *e.g.*, for a conservation area or do we want to just have a set of ecologically plausible networks we can use for theoretical stuffs. Need to discuss the key differences and implications between predicting a metaweb (*sensu* [19]) and a network realisation. (In a way the idea of predicting a metaweb vs realisation is what makes me hesitant to use the Mangal networks to test the structural models because do we even know what the Mangal networks represent and what the structural models are predicting...) Maybe also [14] that discuss how the local factors are going to play a role.

Also need to take into consideration inherent constraints that the model imposes on itself and how it will affect our ability to test hypotheses/ask questions using the *e.g.*, from [13] - models that are constrained by connectance means that we are unable to explain connectance itself and you would need a different approach if understanding connectance is your goal. Another way of phrasing this is thinking about what is needed (input data/parameters), produced (final network characteristics), and desired (end-use).

4 Concluding remarks

- Bring up the fact that delimiting a network is in and of itself fuzzy - we tend to think of them in terms of snapshots but in reality the final (empirical) network is often the result of aggregation over multiple timescales.
- Also the fact that *some* people are concerned about the taxonomic resolution and cascading effects those might have on our understanding of network structure [18,34], we are at risk of losing our ability to distinguish the wood from the tree - are we not (at least at times) concerned more with understanding ecosystem level processes than with needing to understand things *perfectly* at the species level.
 - I don't think these 'rare'/nuanced links (e.g. carnivorous hippos) are going to rock the boat when we think about networks at the structural level.
- In certain situations structure is 'enough' but there may be use cases where we are really interested in the node-level interactions *i.e.*, species identity is a thing we care about and need to be able to retrieve specific interactions at specific nodes correctly.
- What is the purpose of generating a network? Is it an element of a bigger question we are asking, *e.g.*, I want to generate a series of networks to do some extinction simulations/bioenergetic stuff OR are we looking for a 'final product' network that is relevant to a specific location? (this can still be broad in geographic scope).

Interestingly [9] also explicitly talk about *structural* food-web models in their introduction... so how I see it that means that there has always been this inherent acknowledgement that models are functioning at a specific 'network level'.

"The resolution of food-web data is demonic because it can radically change network topology and associated biological inferences in ways that are unknowable in the absence of better data." - [34]

The counter to this is that structural models are often not working at the species level and thus

1 the structure remains ‘unchanged’ when you increase the resolution - I don’t think that people
2 are that concerned with the structure of real world networks barring connectance and since that
3 scales with species richness anyway your final proportion will probably still remain the same...

4 “It makes no sense to describe the interaction structure of nodes which in themselves are poorly
5 defined.” — Roslin et al. (2013, p. 2)

- 6 • I think a big take home will (hopefully) be how different approaches do better in different situations
7 and so you as an end user need to take this into consideration and pick accordingly. I think [13] might
8 have (and share) some thoughts on this (thanks Andrew). I feel like I need to look at [35] but maybe
9 not exactly in this context but vaguely adjacent.
- 10 • An interesting thing to also think about (and arguably it will be addressed based on some of the other
11 thoughts and ideas) is data dependant and data independent ‘parametrisation’ of the models...
- 12 • Why do interaction models do so badly at predicting structure? Nuance of metaweb vs realisation but
13 also time? At the core of it interaction models are trained on existing interaction data; this is data
14 that are most likely closer to a metaweb than a local realisation even if they are being inventoried at a
15 small scale.

16 — I think this is sort of the crux of the argument presented in [36]

17 *“we highlight an interesting paradox: the models with the best performance measures are not*
18 *necessarily the models with the closest reconstructed network structure.” - [32]*

- 19 • *Do we need network models to predict interactions and interaction models to predict structure?* (lets
20 not think about that too hard or I might just have to sit in silence for a while...)

21 — “Another argument for the joint prediction of networks and interactions is to reduce circularity
22 and biases in the predictions. As an example, models like linear filtering generate probabilities of
23 non-observed interactions existing, but do so based on measured network properties.” - [6]

24 — Aligning (dove-tailing) with this the idea of ensemble modelling as presented by [37]

- 25 • It will be interesting to bring up the idea that if a model is missing a specific pairwise link but doing
26 well at the structural level then when does it matter?
- 27 • Close out with a call to action that we have models that predict networks very well and models that
28 predict interactions very well but nothing that is doing well at predicting both - this is where we should
29 be focusing our attention when it comes to furthering model development. (we need models that will

fill the space in the top right quadrant of panel A in Figure 1)

4.1 Downsampling

- [38]
- “That being said, there is a compelling argument for the need to ‘combine’ these smaller functional units with larger spatial networks [39] and that we should also start thinking about the interplay of time and space [40]. Although deciding exactly what measure might actually be driving differences between local networks and the regional metaweb might not be that simple [41].”

Glossary

Term	Definition
food web	a representation of feeding links between species
network generator	a model that predicts a network based on assumptions of structure, this network is species agnostic in the sense that it does not necessarily contain information at the node level
interaction predictor	a model that predicts species interactions, these interactions can be used to construct a network but there are no <i>a priori</i> assumptions as that will constrain the network structure
model	A tool that can be used to construct food webs, where the resulting network is a representation of a real world network. Models typically only capture specific elements of real world networks and are intended to be used in specific settings
model family	A family of models that share an underlying philosophy when it comes to the mapping, pragmatism, and reduction of a network. Families have the same underlying philosophies and assumptions that determine the links between nodes as well as how these may be encoded

Term	Definition
metaweb	A network that represents <i>all</i> the potential links between species. Importantly these links will not necessarily all be realised in a specific location for a specific time
realised network	A network that represents the links between species that are occurring. These networks represent a very localised network...
potential feeding link	links that indicate that an interaction is ecologically feasible but not realised <i>per se</i> (a metaweb would contain potential feeding links)
realised feeding link	links that indicate that the interaction is realised ‘in the field’. (a realised network contains realised feeding links)
confusion matrix	captures the number of true positives (interaction predicted as present when it is present), false negatives (interaction predicted as absent when it is present), false positives (interaction predicted as present when it is absent), and true negatives (interaction predicted as absent when it is absent)

Outstanding questions

- non-consumptive effects
- can we develop a model that is both an topology generator as well as an interaction predictor?

References

- Hortal, J. *et al.* (2015) [Seven Shortfalls that Beset Large-Scale Knowledge of Biodiversity](#). *Annual Review of Ecology, Evolution, and Systematics* 46, 523–549
- Poisot, T. *et al.* (2021) [Global knowledge gaps in species interaction networks data](#). *Journal of Biogeography* n/a

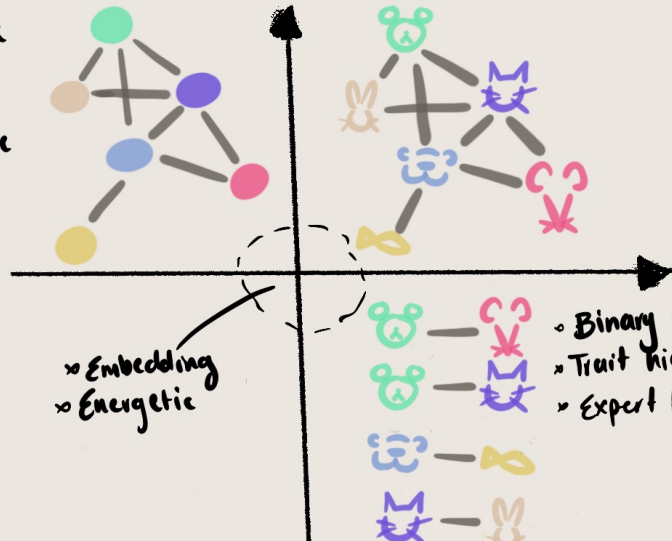
- 1 3. Jordano, P. (2016) [Chasing Ecological Interactions](#). *PLOS Biology* 14, e1002559
- 2 4. Jordano, P. (2016) Sampling networks of ecological interactions. *Functional Ecology* DOI: [10.1111/1365-2435.12763](#)
- 3 5. Morales-Castilla, I. *et al.* (2015) [Inferring biotic interactions from proxies](#). *Trends in Ecology & Evolution* 30, 347–356
- 4 6. Strydom, T. *et al.* (2021) [A roadmap towards predicting species interaction networks \(across space and time\)](#). *Philosophical Transactions of the Royal Society B: Biological Sciences* 376, 20210063
- 5 7. Strydom, T. *et al.* (2022) [Food web reconstruction through phylogenetic transfer of low-rank network representation](#). *Methods in Ecology and Evolution* 13, 2838–2849
- 6 8. Petchey, O.L. *et al.* (2008) [Size, foraging, and food web structure](#). *Proceedings of the National Academy of Sciences* 105, 4191–4196
- 7 9. Williams, R.J. and Martinez, N.D. (2008) [Success and its limits among structural models of complex food webs](#). *Journal of Animal Ecology* 77, 512–519
- 8 10. Pichler, M. *et al.* (2020) [Machine learning algorithms to infer trait-matching and predict species interactions in ecological networks](#). *Methods in Ecology and Evolution* 11, 281–293
- 9 11. Bhatia, U. *et al.* (2023) [Network-based restoration strategies maximize ecosystem recovery](#). *Communications Biology* 6, 1–10
- 10 12. Thuiller, W. *et al.* (2024) [Navigating the integration of biotic interactions in biogeography](#). *Journal of Biogeography* 51, 550–559
- 11 13. Petchey, O.L. *et al.* (2011) [Fit, efficiency, and biology: Some thoughts on judging food web models](#). *Journal of Theoretical Biology* 279, 169–171
- 12 14. Poisot, T. *et al.* (2015) [Beyond species: Why ecological interaction networks vary through space and time](#). *Oikos* 124, 243–251
- 13 15. Poisot, T. *et al.* (2016) [Describe, understand and predict: Why do we need networks in ecology?](#) *Functional Ecology* 30, 1878–1882
- 14 16. Proulx, S.R. *et al.* (2005) [Network thinking in ecology and evolution](#). *Trends in Ecology & Evolution* 20, 345–353
- 15 17. Brimacombe, C. *et al.* (2023) [Shortcomings of reusing species interaction networks created by different sets of researchers](#). *PLOS Biology* 21, e3002068
- 16 18. Pringle, R.M. (2020) [Untangling Food Webs](#). In *Untangling Food Webs*, pp. 225–238, Princeton University Press

19. Dunne, J.A. (2006) The Network Structure of Food Webs. In *Ecological networks: Linking structure and dynamics* (Dunne, J. A. and Pascual, M., eds), pp. 27–86, Oxford University Press
20. Lindeman, R.L. (1942) [The Trophic-Dynamic Aspect of Ecology](#). *Ecology* 23, 399–417
21. Poisot, T. *et al.* (2016) [The structure of probabilistic networks](#). *Methods in Ecology and Evolution* 7, 303–312
22. Berlow, E.L. *et al.* (2004) [Interaction strengths in food webs: Issues and opportunities](#). *Journal of Animal Ecology* 73, 585–598
23. Cohen, J.E. *et al.* (1985) [A stochastic theory of community food webs I. Models and aggregated data](#). *Proceedings of the Royal Society of London. Series B. Biological Sciences* 224, 421–448
24. Cohen, J.E. (1977) [Food webs and the dimensionality of trophic niche space](#). *Proceedings of the National Academy of Sciences* 74, 4533–4536
25. Allesina, S. *et al.* (2008) [A General Model for Food Web Structure](#). *Science* 320, 658–661
26. Williams, R.J. and Martinez, N.D. (2000) [Simple rules yield complex food webs](#). *Nature* 404, 180–183
27. Cohen, J.E. *et al.* (1990) *Community Food Webs: Data and Theory*, Springer-Verlag
28. Cirtwill, A.R. *et al.* (2019) [A quantitative framework for investigating the reliability of empirical network construction](#). *Methods in Ecology and Evolution* 0
29. Shaw, J.O. *et al.* (2024) [A framework for reconstructing ancient food webs using functional trait](#) [databioRxiv](#), 2024.01.30.578036
30. Rohr, R.P. *et al.* (2010) [Modeling Food Webs: Exploring Unexplained Structure Using Latent Traits](#). *The American Naturalist* 176, 170–177
31. Strydom, T. *et al.* (2023) [Graph embedding and transfer learning can help predict potential species interaction networks despite data limitations](#). *Methods in Ecology and Evolution* 14, 2917–2930
32. Poisot, T. (2023) [Guidelines for the prediction of species interactions through binary classification](#). *Methods in Ecology and Evolution* 14, 1333–1345
33. Stouffer, D.B. *et al.* (2007) [Evidence for the existence of a robust pattern of prey selection in food webs](#). *Proceedings of the Royal Society B: Biological Sciences* 274, 1931–1940
34. Pringle, R.M. and Hutchinson, M.C. (2020) [Resolving Food-Web Structure](#). *Annual Review of Ecology, Evolution and Systematics* 51, 55–80
35. Berlow, E.L. *et al.* (2008) [The “Goldilocks factor” in food webs](#). *Proceedings of the National Academy of Sciences* 105, 4079–4080
36. Brimacombe, C. *et al.* (2024) [Applying a method before its proof-of-concept: A cautionary tale using inferred food webs](#)

- 1 37. Becker, D.J. *et al.* (2022) [Optimising predictive models to prioritise viral discovery in zoonotic reservoirs](#). *The Lancet Microbe* 3, e625–e637
- 2 38. Dansereau, G. *et al.* (2023) Spatially explicit predictions of food web structure from regional level data
- 3 39. Fortin, M.-J. *et al.* (2021) [Network ecology in dynamic landscapes](#). *Proceedings of the Royal Society B: Biological Sciences* 288, rspb.2020.1889, 20201889
- 4 40. Estay, S.A. *et al.* (2023) Editorial: Patterns and processes in ecological networks over space. *Frontiers in Ecology and Evolution* 11
- 5 41. Saravia, L.A. *et al.* (2022) [Ecological network assembly: How the regional metaweb influences local food webs](#). *Journal of Animal Ecology* 91, 630–642

A Predicting.

- Resource
- Null
- Neutral
- Generative



B Benchmarking

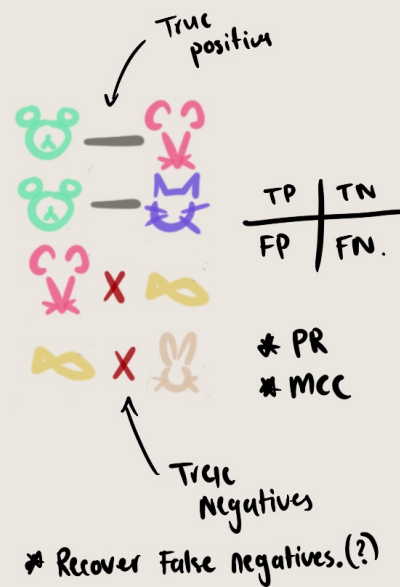
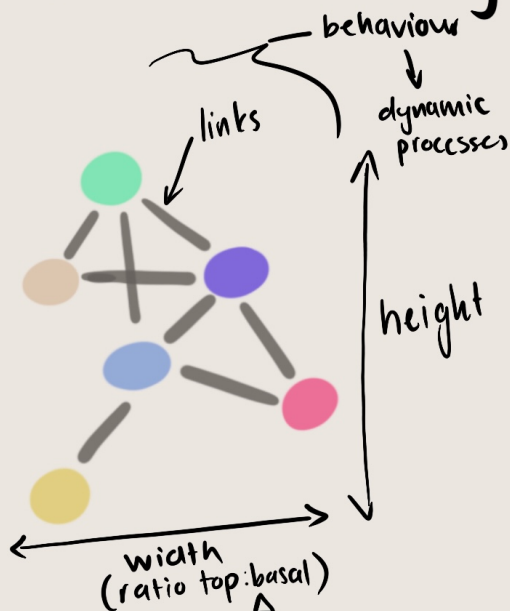


Figure 1: Conceptual figure of the ‘network prediction’. Panel A shows where the model families fall in the the context of being models that predict networks or models that predict interactions space. Panel B serves to highlight the characteristics one might like to ‘test’/benchmark for a model based on it being either a network or interaction predicting model

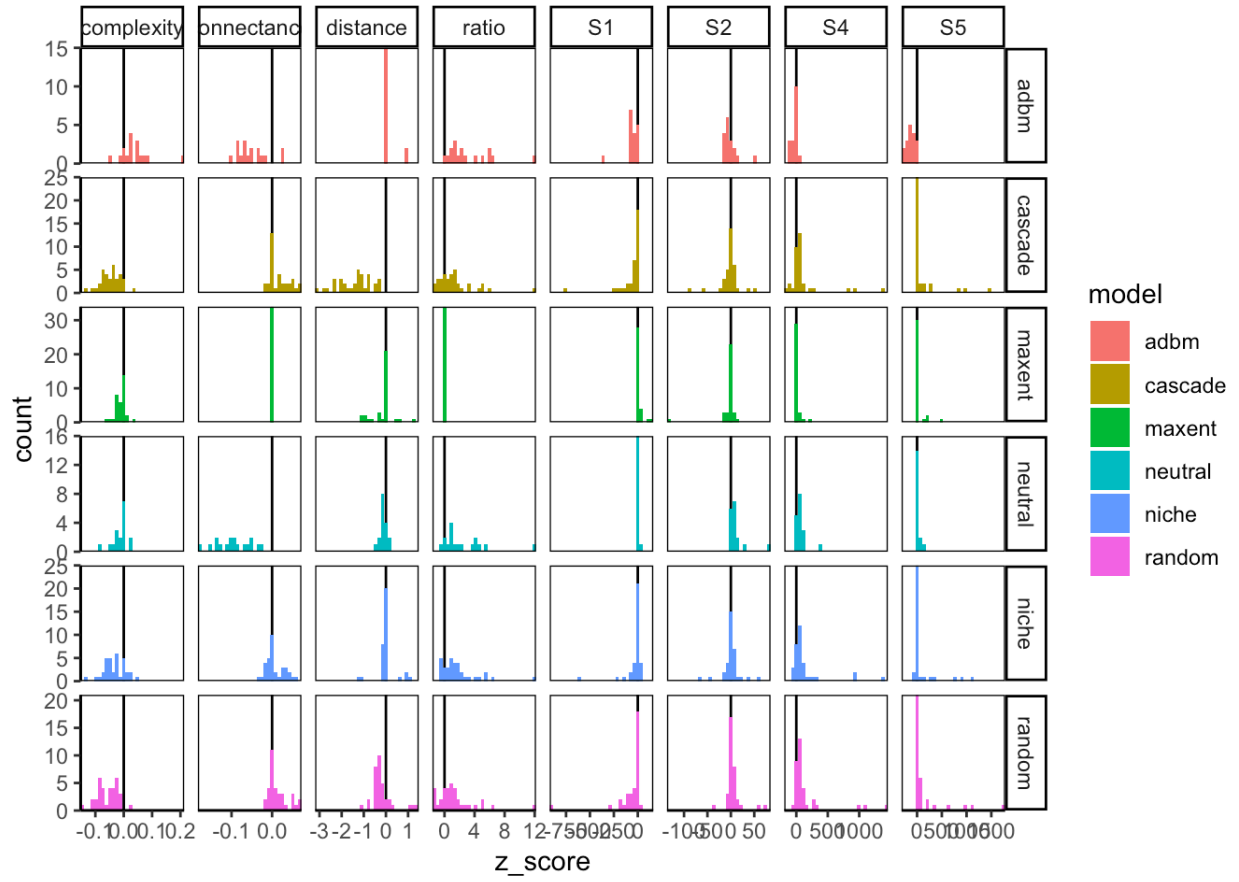


Figure 3: Difference between real and model network property. S1 - S5 represent the different motif structures identified in [33].