

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 is a
8 scarcity of ‘real world’ interaction data (Hortal et al., 2015; Poisot et al., 2021). The difficulty of recording
9 interactions in the field (Jordano, 2016a, 2016b) has necessitated that researchers find and develop alternative
10 means to construct and build food webs using **models** (Morales-Castilla et al., 2015; Strydom et al., 2021).
11 Over the past decade, there has been a proliferation of tools and processes for characterising food webs,
12 these models span a wide range of philosophies that rely on different approaches, data, and definitions, which
13 ultimately determine how the food web is constructed. Although the development of these different models
14 have carved out the path for constructing either synthetic, ecologically plausible networks or providing ‘first
15 draft’ networks that can be utilised in real world settings (Strydom et al., 2022) we are still lacking in
16 discussions that are explicitly comparing and contrasting how the way one chooses to approach the task
17 of constructing a food web is introducing (and ultimately embedding) specific assumptions and hypotheses
18 (Petchey et al., 2008). Most attempts that focus on comparing and contrasting models are focused on the
19 same group of **model families** (Pichler et al., 2020; Williams & Martinez, 2008) and only benchmark the
20 different models as opposed to contextualising them within the bigger framework of understanding the data
21 needs of the different models, as well as how the resulting network is defined and structured. As food webs
22 become a more integrated part of some of the broader fields of ecology (Bhatia et al., 2023; Thuiller et
23 al., 2024) it is critical that we highlight and review these different model families as a whole (and not in
24 isolation), and move away from simply benchmarking the performance of these different model families but
25 also highlight the inherent constraints that these models impose upon themselves and how these will delimit
26 and dictate the potential questions one will be able to ask (Petchey et al., 2011). This will allow us to ensure
27 the right models are being used to answer the right questions, particularly within the context of trying to
28 accelerate cross-cutting research in the face of global change.

29 When navigating the seas of using and constructing food webs the researcher needs to be able to clearly
30 articulate and define the parameters that are used to define their food web(s) of interest. This will aid them
31 in being able to select the correct model to help them to reach their goal. In order to be able to make
32 informed decisions it is important that one has a strong grasp of exactly what it means to ‘code’/define a

food web Section 1, a clear understanding of why one wants to predict a food web Section 2, and ultimately one needs to be able to assess and evaluate which model family is going to best match up with the goal of network prediction Section 3. This body of work sets out to highlight and discuss these three specific points.

[Figure 1 about here.]

1 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 Poisot, Stouffer, et al. (2016) 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. Panel A of 1, 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?).

1.1 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. 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, 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.

1.2 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 (Pringle, 2020) or potential (Dunne, 2006) feeding links, or energy transfer and material flow (Lindeman,

1942). 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, Poisot, Cirtwill, et al., 2016) or continuous measurements (which quantifies the effect of one species on another, Berlow et al., 2004). Although there is a clear argument for moving away from a purely binary way of representing interactions (Banville, in prep) this of course also means that there is an additional layer to the interpretation these links.

1.3 Putting the parts together; what does it mean?

The reality is that feeding interactions between species are the result of the combination of many potential mechanisms (see Box 1 - Mechanisms that determine feeding links) and the way one chooses to represent a food web is a way of capturing one (or a few) of these mechanisms. It is thus beneficial to keep in mind that simply the process of ‘codifying’ a network one is in sense already embedding some sort of hypothesis as to the nature of the feeding links between species (Brimacombe et al., 2023; Proulx et al., 2005). Here it may be meaningful to contextualise the different ‘types’ of food webs within the larger research programmes (or even practical needs) that have been driving the construction of them.

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 Jordano, 2016b)

- As predator and prey we have been co-occurring for a long time and I have found ways to eat you (trying to capture the idea of evolutionary time)

‘Structural’

The ‘energy budget’ for the environment means that only y links are possible between us x number of species and so our interactions reflect that. Or is it more the only way we can all access the energy resource is by arranging ourselves into trophic units...

None

We are interacting because. This is random.

80

2 Why do we want to predict food webs?

81

82 As discussed in Section 1 there are many ways to define a food web, meaning that there are equally as
 83 many reasons one might be interested in predicting a food web. However we may think of two primary
 84 drivers for wanting to predict networks, namely an interest in generating a set of ecologically plausible
 85 networks (*i.e.*, being able to describe networks using a model) or being able to construct a network that has
 86 location specific, ‘realised’ interactions for a specific species community (*i.e.*, being able to predict/infer the
 87 interactions between species). Of course these two categories are not distinct, mutually exclusive, groups
 88 but can rather be viewed as operating on a continuum ranging from a need for generality (*i.e.*, creating a
 89 network that, when taken in aggregate, the distribution of links (interactions) between nodes (species) are
 90 ecologically plausible) to a need for specificity (*i.e.*, local-level predictions between specific species pairs).
 91 Although the ability to predict ‘real-world’ interactions (and the resulting food webs) can have more intuitive
 92 ‘real world’ applications *e.g.*, being able to ‘recover’ food webs that have since gone extinct (Dunne et al.,
 93 2008; Yeakel et al., 2014), using pairwise interactions to understand species distributions [joint SDM ref] or
 94 even co-extinction risk [ref], a more structural approach to network construction affords one an opportunity
 95 to interrogate some of the more high-level mechanisms that are structuring networks (Box 2).

96 It is perhaps more important that when one is talking about ‘why’ they want to predict networks to articulate
 97 exactly what anatomical part of the food web we are interested in scrutinising.

3 How do we predict food webs?

98

99 Selecting a model for the task of network prediction should come down to two things; what *aspect* of a food
 100 web one is interested in predicting, and what data are available. As shown in panel B of Figure 1 (and in more

detail in Table 1) the models that are used to predict a food web tend to focus on only predicting the structure of a network (a **topology generator**) or the interactions for a given species pool (an **interaction predictor**). Although it is possible to construct a food web given a set of interactions interaction predictors themselves lack any sort of parametrisation of the network structure and so the resulting network is a poor reflection of the actual network structure (Caron et al., 2024). These models themselves are a reflection of the different goals and intentions of the research program from which they are developed and are often ‘described’ by a specific mechanism that will determine the resulting structure or interactions (Box 1). Models such as the niche (Williams & Martinez, 2000) or cascade (Cohen et al., 1990) 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 (Cirtwill et al., 2019) or trait hierarchy (Shaw et al., 2024) models have been developed on the basis that the traits of a species are the underlying mechanism in determining the feasibility of interactions (*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). 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 is of interest.

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 B of 1.

Crucially most topology 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, Poisot et al., 2015).

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 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	Williams & Martinez (2008)

Model family	Theory	Network predicted	Nodes represent	Links represent	Interaction	Key reference
generative	Networks are determined by their structural features	structural	agnostic	links	binary	
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	Strydom et al. (2023)
trait matching	Interactions can be inferred by a mechanistic frame-work/relationships	interaction	species	feeding links	binary	Morales-Castilla et al. (2015)

Model		Network	Nodes	Links		Key
family	Theory	predicted	represent	represent	Interaction	reference
binary classifiers	Interactions can be predicted by learning the relationship between interactions and ecologically relevant predictors	interaction	species	feeding links	binary	Pichler et al. (2020)
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	

Model		Network	Nodes	Links		Key
family	Theory	predicted	represent	represent	Interaction	reference
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 2) and linking this back to what aspects of the network (Section 1) 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 (Allesina et al., 2008). 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 (Poisot, 2023).

[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* Dunne (2006)) 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 Poisot et al. (2015) 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 Petchey et al. (2011) - 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).

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4 Concluding remarks

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- As we can see in Figure 3 different models clearly do well in different things...

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• 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 (Pringle, 2020; Pringle & Hutchinson, 2020), 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 Williams & Martinez (2008) 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." - Pringle & Hutchinson (2020) The counter to this is that structural models are often not working at the species level and thus the structure remains 'unchanged' when you increase the resolution - I don't think that people are that concerned with the structure of real world networks barring connectance and since that scales with species richness anyway your final proportion will probably still remain the same...

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

• I think a big take home will (hopefully) be how different approaches do better in different situations

and so you as an end user need to take this into consideration and pick accordingly. I think Petchey et al. (2011) might have (and share) some thoughts on this (thanks Andrew). I feel like I need to look at Berlow et al. (2008) but maybe not exactly in this context but vaguely adjacent.

- An interesting thing to also think about (and arguably it will be addressed based on some of the other thoughts and ideas) is data dependant and data independent ‘parametrisation’ of the models...
- Why do interaction models do so badly at predicting structure? Nuance of metaweb vs realisation but also time? At the core of it interaction models are trained on existing interaction data; this is data that are most likely closer to a metaweb than a local realisation even if they are being inventoried at a small scale.

– I think this is sort of the crux of the argument presented in Brimacombe et al. (2024)

“we highlight an interesting paradox: the models with the best performance measures are not necessarily the models with the closest reconstructed network structure.” - Poisot (2023)

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

– “Another argument for the joint prediction of networks and interactions is to reduce circularity and biases in the predictions. As an example, models like linear filtering generate probabilities of non-observed interactions existing, but do so based on measured network properties.” - Strydom et al. (2021)

– Aligning (dove-tailing) with this the idea of ensemble modelling as presented by Becker et al. (2022)

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

4.1 Downsampling

- Dansereau et al. (2023)
- “That being said, there is a compelling argument for the need to ‘combine’ these smaller functional

units with larger spatial networks (Fortin et al., 2021) and that we should also start thinking about the interplay of time and space (Estay et al., 2023). Although deciding exactly what measure might actually be driving differences between local networks and the regional metaweb might not be that simple (Saravia et al., 2022).”

Glossary

Term	Definition
food web	a representation of feeding links between species
topology 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
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

Term	Definition
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?

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Figure 1: Panel **A** shows the many ways in which a food web can be defined and described at the node, edge, and even network level. Panel **B** (will) shows how the way in which we predict networks also limited and often focuses only on predicting the structure of a network (the final network is parametrised by the expected structure of the network) or the interactions between species (the final network is determined by the behaviour of the nodes). These different models also encode different philosophies/hypotheses not only as to what determines how a network will look but also how the final network itself is encoded *i.e.*, its anatomy. (*aside*: there is the potential to either try and visually summarise how the different model families define a network (so repeating the motifs used in the ANATOMY panel) alternatively it would be cool to try and have a panel C that tries to quantify the different ‘data ingredients’ you would need to try and construct a network, this would probably be very visually overwhelming though...)

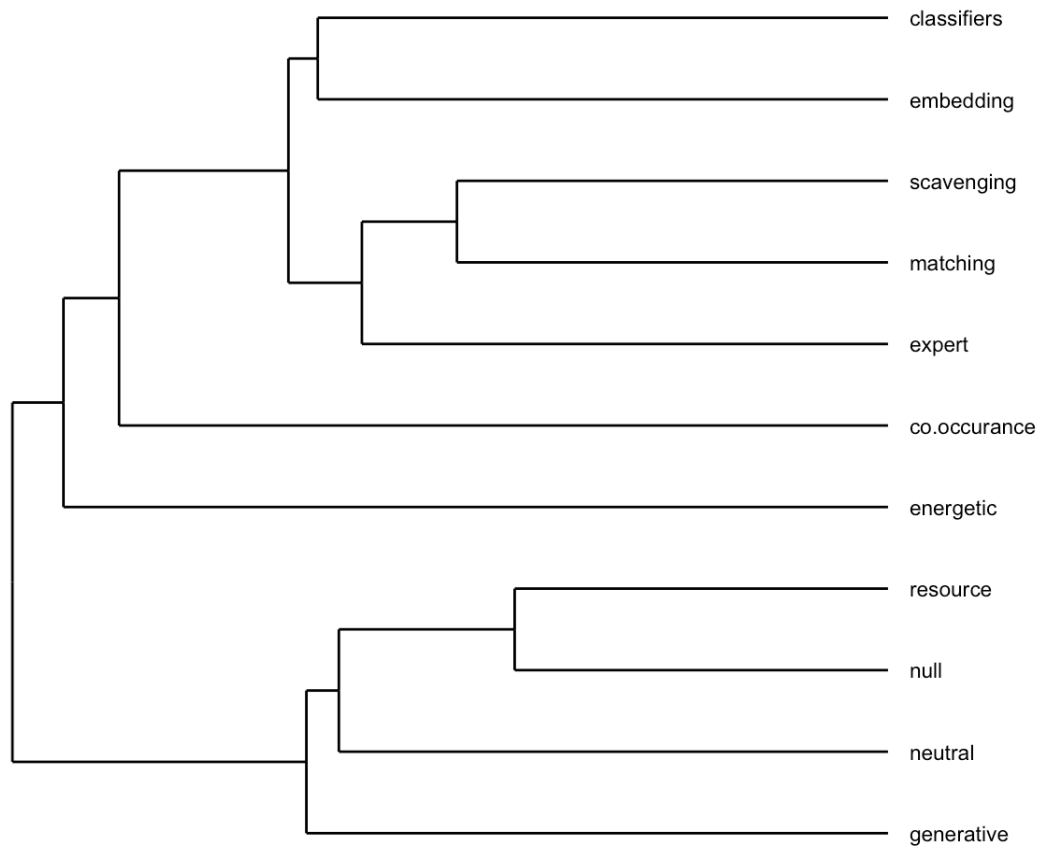


Figure 2: Dendrogram of the trait table

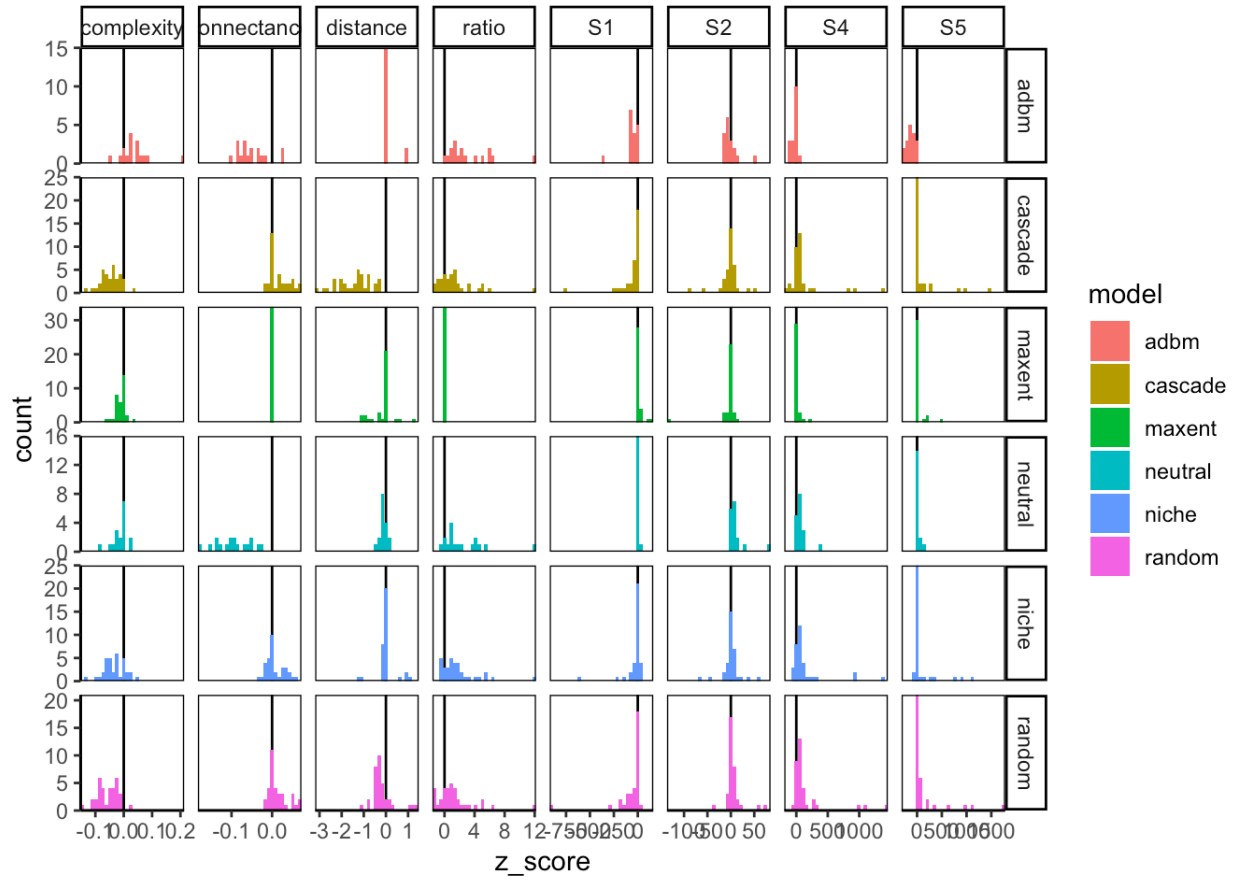


Figure 3: Difference between real and model network property. S1 - S5 represent the different motif structures identified in Stouffer et al. (2007).