

Methods for Reconstructing Paleo Food Webs

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Abstract: Food webs represent the feeding relationships between species and can help infer ecosystem-level processes. Alongside the development of food web theory, methods for constructing food webs have been developed to infer species interactions when empirical data is lacking. Food web construction methods are diverse, each utilising different approaches to infer species interactions —such as the use of traits to infer mechanistic relationships vs using gut content as a proxy for species diets. These methods have distinct theories, mechanisms, and data requirements. In paleoecology, where direct evidence of feeding interactions are rare, food web construction methods are especially valuable and affords us the opportunity to make inferences about paleo communities beyond simply a record of species composition. However, the limitations of paleontological data (e.g., information of species traits is limited to that which can be preserved) restrict which methods can reliably be used. By considering both ecological theory and the constraints of what can be derived from the fossil record, we identify the methods best suited for the construction of paleo food webs. Specifically, we focus on how these methods differ in the networks they produce and what these networks can reveal about species interactions. In doing so we hope to clarify the ecological nuances of network prediction and help prevent the accidental misuse or misinterpretation of paleo food webs.

Keywords: food web, network construction

1 There has been a growing interest in looking at community responses to environmental changes across events in
2 deep time as a means to help understand current and future biodiversity changes (Dillon et al., 2022; Kiessling
3 et al., 2019). The use of species interactions and networks to help us understand aspects of community
4 composition has gained an interest in contemporary settings (eg Thuiller et al. (n.d.) and ??) and so it is
5 perhaps unsurprising that there has been a growing interest in using paleo food webs in a similar manner
6 (*e.g.,* Dunhill et al., 2024 looked at...; Hao et al., 2025 looked at...; Yeakel et al., 2014 looked at...). However,
7 one of the core challenges and limitations of being able to *use* food webs to answer ecological questions is
8 the challenge of *creating* them (Jordano, 2016), a challenge which is compounded when using paleo data as
9 we are limited by that which has been preserved in the fossil record. The challenges with recording species
10 interaction networks has driven the development of a large number of models and tools that can be used to
11 infer either species interactions (see *e.g.*, Morales-Castilla et al., 2015; Pichler & Hartig, 2023; Strydom et al.,
12 2021a for broader reviews) or networks (see *e.g.*, Allesina et al., 2008 (it is one of the more complete review
13 of methods IMO)), each with their own set of nuances and considerations [modify this to organically link
14 to T4T, probably something along the lines of how different network construction approaches are encoding
15 different processes]. Although the paleo food web space has seen its own development of tools that are more
16 tailored to paleo date (Fricke et al., 2022; Roopnarine, 2006; *e.g.,* Shaw et al., 2024) these tools typically
17 only predict the *feasibility* of pairwise interactions and thus the canonical paleo food web models are only
18 occupying a subset of the ‘network construction’ space. Specifically within the paleo space there is a need for
19 models that are able to generate networks that are structurally correct and do not simply represent a collation
20 of pairwise interactions. It is thus useful to identify a broader suite of methods within the contemporary
21 toolbox that can be appropriately scaled/tailored for the constraints of paleo communities (should we include
22 Yeakel et al. (2014) here as an *e.g.*, of how this is ‘possible’).

23 Here we: want to identify the differences between models that predict interactions, and models that predict
24 network structure. Specifically we want to look at 1) the structural difference between all models (*i.e.*, do we
25 see a difference in the distribution of links between networks that have the same number of nodes?) and 2)
26 the identity of pairwise links between species pairs (*i.e.*, do different models differ in which links are present
27 (or absent) between species pairs?) Additionally we want to establish if using networks that are constructed
28 using different models will change the the downstream inferences that are made for this we use the work from
29 Dunhill et al. (2024) as a case study.

30 **1 Contextualising the prediction of paleo webs within the contem-**
31 **porary toolbox**

32 There is an evolving body of work that focuses on developing tools specifically for the task of predicting
33 food webs. However as highlighted in Strydom (T4T in prep) it is important that we understand what
34 assumptions are being embedded within the network as a result of the underlying philosophy which a model
35 was built on. Broadly we can think about models that are nested within two different schools of thought
36 (and thus methodological approaches, Figure 1), models that focus on assessing the *mechanistic* feasibility of
37 an interaction being able to occur between two species or models that are more closely married to specific
38 bodies of ecological *theory* - such as niche theory or foraging ecology. Broadly speaking the difference between
39 these two modelling approaches is that mechanistic models typically asses interactions at a pairwise level
40 by determining if an interaction is feasible between a species *pair* (extended e.g., here about trait-based
41 assumptions), whereas theoretical models typically use some set of assumptions to constrain the distribution
42 of links at the *community* scale (extended e.g., here probably niche model or DBM).

43 [Figure 1 about here.]

44 Models that have specifically been developed in the paleo space tend to be mechanistic models that focus on
45 using a trait-based approach to formalise feeding interactions (e.g., Shaw et al. (2024); Roopnarine (2006)),
46 are assembled by expert opinion (e.g. Dunne et al. (2014)) or make assumptions based on the evolutionary
47 signals of interactions (e.g., Fricke et al. (2022)). However, there is an argument that the theoretical models
48 that have been developed in contemporary settings should hold even for paleo communities as we expect
49 the fundamental ‘currencies of life’ to have remained constant - e.g., the energetic constraints of foraging or
50 foraging niches (is that the right way to phrase it, also I wonder is we can link to some other paleo work that
51 showcases e.g., niche/competition is something present among some of the earliest animals). Somehow close
52 this out by going from we should be able to use contemporary models we need to think about the constraints
53 that are typically placed on us by paleo data as well as the assumptions that some of these models might
54 require us to make (e.g. the niche model makes some heavy assumptions by constraining the connectance -
55 which itself is often used as a metric to understand changes or differences in network structure).

56 Additionally there are models that allow one to construct structurally sound networks that require
57 very little input data. These are methods that are amenable to the data constraints that are
58 prevalent in paleo communities in terms of both the completeness of fossil records as well as how
59 the deeper in time we move the further away we might be moving from contemporary analogs.
60 Secondly it should also be noted that different network construction approaches are encoding

61 different processes (T4T, in prep) and there is value in showcasing how the networks construct
62 models may differ.

63 Introduce here that it is thus important to understand that not all contemporary models may actually be
64 suitable for paleo contexts as the assumptions that they make (or the data that they require) may actually
65 introduce uncertainty/errors into the resulting network rendering them of little use. Similarly not all paleo
66 methods will be suitable for all paleo communities. As a simple example the framework developed by Fricke et
67 al. (2022) uses phylogenetic relatedness as a way to infer interactions of Pleistocene mammals by looking at
68 how their extant relatives interact. Although this approach is ecologically sound (phylogenetic relatedness is
69 also used in other approaches *e.g.*, Strydom et al. (2022)) there is also an argument that the further back in
70 evolutionary time we go (and the greater the phylogenetic distance between extant and extinct communities
71 become) there is more uncertainty introduced by the phylogenetic tree than what is introduced by assuming
72 that interactions will be phylogenetically conserved. On the other side of the coin it can be very challenging
73 to determine traits from the fossil record and so it may be instead by more pragmatic to use models that that
74 are completely agnostic to the identity of the species and are instead concerned with the network structure
75 (*e.g.*, the niche model developed by Williams & Martinez (2008)). Fundamentally this means that there is a
76 trade off between the data that is available and the type of network one is interested in creating.

77 **2 Understanding how networks are different**

78 It is important to be aware that networks can be configured in different ways depending on how the interactions
79 are defined (Strydom, in prep). Basically we have metawebs (which represent *potential* interactions), realised
80 networks (which represent the subset of potential that are realised as a result of community and environmental
81 context), and structural networks (species agnostic networks that are structurally informative). Here also
82 talk about the implications of these different networks types - different uses and capturing different processes.

83 Specifically link this to models - *i.e.*, different models have been developed to construct a *specific* network
84 representation.

85 Think about the axes - trait-based/mechanistic model (metawebs) and then we have the statistical/theoretical
86 models (which have their own mini axis of regression vs full theory models...)

87 Need to link to Gauzens et al. (2025) here.

3 Challenges specific to building paleo networks

Although there has been a push for the development of tools and methods that allow us to predict species interactions and networks [see *e.g.*, XXX for some reviews] they will not all be suitable for the prediction of paleo communities. This is primarily due to limitations that we are faced with in terms of the information that can be inferred from the fossil record (such as species traits abundances, and assemblages), which is needed as input data for the different models. The limited information available from the fossil record is compounded by the incomplete and biased preservation of species [REF], the spatial ambiguity of fossils found in a location [were species conserved *in situ* or were they there owing to geological processes; REF], and an increasing degree of ‘fuzziness’ the further one moves back in geological time [our understanding of both phylogenetic and functional trait space, REF]. Methodologically speaking some tools that ‘learn’ from contemporary communities (*e.g.*, Strydom et al. (2023), Caron et al. (2022)) will become ‘worse’ the further one goes back in time since species then look very different from now but can still be useful for ‘recent’ communities (*e.g.*, Fricke et al. (2022)). This is not to say that it is impossible to construct paleo networks but rather identify that there are a subset of models that are probably not at all suitable for constructing paleo networks (*e.g.*, Null models, since there are fully driven by abundance), other methods will be better suited depending on the community of interest *e.g.*, for more contemporary communities that have modern analogs we can use methods rooted in phylogeny (*e.g.*, Fricke et al. (2022), Strydom et al. (2023)) or traits (*e.g.*, Caron et al. (2022)), and then there is the third axis which is to think about which are the assumptions that are made and there trade off of that. This includes thinking about both assumptions you are making about the actual data *e.g.*, trying to extrapolate body size from fossil data but also assumptions across time *e.g.*, assuming modern trait-feeding modes are the same OR that assumptions about network structure will hold across deep time.

3.1 Approaches to food web prediction

Here we should take the time to go in and just articulate that there are nuance and differences in terms of predicting interactions vs predicting networks. Once it is finally on a preprint server we can obviously link to the T4T stuff...

Here we present six different models (Table 1) that can be used to construct food webs for both this specific community but are also broadly suited to paleo network prediction. These models span all facets of the network representation space (metaweb, realised, and structural network) and are suitable for an array of different paleo communities as the data requirements are ‘paleo friendly’.

Table 1: A summary of the different families of tools that can be used to generate paleo food webs.

Model family	Assumptions	Data needs	'Limitation'	Network type	Key reference
random	Links are randomly distributed within a network	richness, number of links	parameter assumptions, species agnostic	structural network	Erdős & Rényi (1959)
niche	Networks are interval, species can be ordered on a 'niche axis'	richness, connectance	parameter assumptions, species agnostic	structural network	Williams & Martinez (2008)
allometric diet	Interactions are determined by energetic costs (foraging ecology)	body mass, biomass (abundance)	does not account for forbidden links in terms of trait compatibility, assumptions on body size and biomass (abundance) from fossil data	realised network	Petchey et al. (2008)
breadth model (ADBM)					

Model family	Assumptions	Data needs	'Limitation'	Network type	Key reference
l-matrix	Interactions inferred using allometric rules (ratio of body sizes between predator and prey), with links being constrained by a Ricker function	body mass, number of producer species	does not account for forbidden links in terms of trait compatibility, assumptions on body size from fossil data, assumptions as to the number of producer species	realised network	Schneider et al. (2016)
paleo food web inference model (PFIM)	Interactions can be inferred by a mechanistic framework/relationships	feeding traits for taxa, mechanistic feeding rules	Assumption made as to the feeding mechanisms, need to elucidate traits (although this is a way smaller issue)	metaweb	Shaw et al. (2024)

Model family	Assumptions	Data needs	‘Limitation’	Network type	Key reference
body size ratio model	Interactions inferred using allometric rules (ratio of body sizes between predator and prey). :ogit of the linking probability used to further constrain links to an ‘optimal size range’ for prey.	body mass	does not account for forbidden links in terms of evolutionary compatibility, assumptions on body size from fossil data	metaweb??	Rohr et al. (2010)

¹¹⁸ **3.2 Structural models**

¹¹⁹ **3.2.1 Random model**

¹²⁰ The Erdős–Rényi random graph model (Erdős & Rényi, 1959) uniformly at random assigns an L number of ¹²¹ links to an S number of nodes (species richness). From an ecological perspective this model assumes that the ¹²² interactions between species occurs regardless of the identity of the species (*i.e.*, species have no agency) and ¹²³ links are randomly distributed throughout the network. This creates a food web that is as free as possible ¹²⁴ from biological structuring while maintaining the expected richness (S) and connectance (L/S^2)

¹²⁵ We could theoretically use the other ‘null models’ BUT I feel like in the context of constructing ¹²⁶ a network for a given community the Erdős–Rényi is the better choice than the other models ¹²⁷ that (IMO) are more suited to hypothesis testing e.g. do observed networks differ from the null ¹²⁸ network... Whereas Erdős–Rényi really is just a case of here is a truly random network with ¹²⁹ the specified number of links and nodes and anyway one of the Null models is a derivative of ¹³⁰ Erdős–Rényi if I remember correctly.

¹³¹ **3.2.2 Niche model**

¹³² The niche model (Williams & Martinez, 2000) introduces the idea that species interactions are based on the
¹³³ ‘feeding niche’ of a species. Broadly, all species are randomly assigned a ‘feeding niche’ range and all species
¹³⁴ that fall in this range can be consumed by that species (thereby allowing for cannibalism). The niche of each
¹³⁵ species is randomly assigned and the range of each species’ niche is (in part) constrained by the specified
¹³⁶ connectance (Co) of the network. The niche model has also been modified, although it appears that adding
¹³⁷ to the ‘complexity’ of the niche model does not improve on its ability to generate a more ecologically ‘correct’
¹³⁸ network (Williams & Martinez, 2008).

¹³⁹ Each of S species assigned a ‘niche value’ parameter n_i drawn uniformly from the interval [0,1]. Species i
¹⁴⁰ consumes all species falling in a range (r_i) that is placed by uniformly drawing the center of the range (c_i)
¹⁴¹ from $[\frac{r_i}{2}, n_i]$. The size of r_i is assigned by using a beta function to randomly draw values from [0,1] whose
¹⁴² expected value is $2 \times Co$ and then multiplying that value by n_i to obtain the desired Co .

¹⁴³ **3.2.3 Allometric diet breadth model**

¹⁴⁴ The Allometric diet breadth model (ADBM; Petchey et al. (2008)) is rooted in feeding theory and allocates
¹⁴⁵ the links between species based on energetics, which predicts the diet of a consumer based on energy intake.
¹⁴⁶ This means that the model is focused on predicting not only the number of links in a network but also the
¹⁴⁷ arrangement of these links based on the diet breadth of a species, where the diet (K) is defined as follows:

$$K = \frac{\sum_{i=1}^k \lambda_{ij} E_i}{1 + \sum_{i=1}^k \lambda_{ij} H_{ij}}$$

¹⁴⁸ where λ_{ij} is the handling time, which is the product of the attack rate A_i and resource density N_i , E_i is the
¹⁴⁹ energy content of the resource and H_{ij} is the ratio handling time, with the relationship being dependent on
¹⁵⁰ the ratio of predator and prey body mass as follows:

$$H_{ij} = \frac{h}{b - \frac{M_i}{M_j}} \text{ if } \frac{M_i}{M_j} < b$$

¹⁵¹ or

$$H_{ij} = \infty \geq b$$

¹⁵² Refer to Petchey et al. (2008) for more details as to how these different terms are parametrised.

153 **3.2.4 L matrix**

154 For now we can link to the ATNr package (Gauzens et al., 2023) until I can find a more suitable manuscript
155 that breaks down this construction method. Schneider et al. (2016) Interactions are determined by allometric
156 rules (ratio of consumer (M_i) and resource (M_j) body sizes) and a Ricker function as defined by R_{opt} and
157 γ and returns The probability of a link (P_{ij}) existing between a consumer and resource, and is defined as
158 follows:

$$P_{ij} = (L \times \exp(1 - L))^\gamma$$

159 where

$$L = \frac{M_i}{M_j \times R_{opt}}$$

160 It is also possible to apply a threshold value to P_{ij} , whereby any probabilities below that threshold are set to
161 zero.

162 **3.3 Interaction predictions**

163 **3.3.1 Paleo food web inference model**

164 The Paleo food web inference model (PFIM; Shaw et al. (2024)) uses a series of rules for a set of trait
165 categories (such as habitat and body size) to determine if an interaction can feasibly occur between a species
166 pair. If all conditions are met for the different rule classes then an interaction is deemed to be feasible. The
167 original work put forward in Shaw et al. (2024) also includes a ‘downsampling’ step developed by Roopnarine
168 (2006) that uses a power law, defined by the link distribution, to ‘prune’ down some of the links. It is worth
169 mentioning that this approach is similar to that developed by Roopnarine (2017) with the exception that
170 Shaw et al. (2024) does not specifically bin species into guilds, and so we choose to use the method developed
171 by Shaw et al. (2024) since both approaches should produce extremely similar networks as they are built on
172 the same underlying philosophy.

173 **3.3.2 Body size ratio model**

174 The body size ratio model (Rohr et al., 2010) determines the probability of feeding interactions occurring
175 between species by using the ratio between the consumer (M_i) and resource (M_j) body sizes. In order to
176 represent the predator-prey bodymass ratio as a ‘feeding niche’ the ratio is also modified by both a β and γ

₁₇₇ distribution. The probability of a link existing between a consumer and resource (in its most basic form) is
₁₇₈ defined as follows:

$$P_{ij} = \frac{p}{1 + p}$$

₁₇₉ where

$$p = \exp[\alpha + \beta \log(\frac{M_i}{M_j}) + \gamma \log^2(\frac{M_i}{M_j})] \quad (1)$$

₁₈₀ The original latent-trait model developed by Rohr et al. (2010) also included an additional latent trait term
₁₈₁ $v_i \delta f_j$ however for simplicity we will use Equation 1 as per Yeakel et al. (2014). Based on Rohr et al. (2010)
₁₈₂ it is possible to estimate the parameters α , δ , and γ using a GLM but we will use the parameters from Yeakel
₁₈₃ et al. (2014), which was ‘trained’ on the Serengeti food web data and are as follows: $\alpha = 1.41$, $\delta = 3.75$, and
₁₈₄ $\gamma = 1.87$.

₁₈₅ 4 Case study: Toarcian mass extinction event

₁₈₆ 4.1 Dataset overview

₁₈₇ 4.1.1 Species occurrence

₁₈₈ Here we use the fossil occurrence data over an interval extends from the upper Pliensbachian (~185 Ma) to
₁₈₉ the upper Toarcian (~175 Ma) of the Cleveland Basin (see Dunhill et al., 2024 for a more comprehensive
₁₉₀ overview). The data set consists of a subset of four broad time periods (pre-extinction, post-extinction, early
₁₉₁ recovery, and late recovery). The assemblages are treated as communities of interacting organisms. Something
₁₉₂ about the total number of taxa as well as numbers per a time period? Probably also make a comment that
₁₉₃ this is a ‘deep time’ community we are looking at.

₁₉₄ 4.1.2 Defining modes of life (traits)

₁₉₅ We used the modes of life (traits) as identified in Dunhill et al. (2024), who defined four traits: motility (fast,
₁₉₆ slow, facultative, non-motile), tiering (pelagic, erect, surficial, semi-infaunal, shallow infaunal, deep infaunal),
₁₉₇ feeding (predator, suspension feeder, deposit feeder, mining, grazer), and size: gigantic (>500 mm), very large
₁₉₈ (>300–500 mm), large (>100–300 mm), medium (>50–100 mm), small (>10–50 mm), tiny (10 mm), for each
₁₉₉ fossil species based on the ecological traits defined in the Bambach ecospace model (Bambach et al., 2007).

200 4.1.3 Constructing networks

201 For each paleo community (time bin) we constructed **100** networks for each model (so $6 * 100$) networks.
202 These networks were ‘simplified’ to removed any disconnected species. In total 2400 networks were constructed.
203 When a quantitative measure of body size is needed (ADBM, bodymassratio, lmatrix) we drew a body mass
204 for each species from a uniform distribution. The ranges were defined by the different size classes as discussed
205 in insert cross ref to correct subsection here *e.g.*, a species classed as ‘very large’ would have a body mass
206 drawn from $U(300, 500)$. This was repeated for each run in order to add variation to the networks constructed,
207 however the same body sizes were kept consistent for the relevant models (adbm, bodymassratio, l-matrix)
208 *i.e.*, an ADBM and bodymassratio network from the same rep number would have used the same bodysizes.
209 The PFIM networks were downsampled (see relevant section). For both the random and niche model the
210 desired connectance was randomly selected between the range 0.07 - 0.15 for each repetition but kep consistent
211 for both models. For each network we calculated the properties listed in Table 2

212 4.1.4 Simulating Extinctions

213 4.2 Do different models recover different network structures?

214 In terms of wanting to asses and compare across the different models it is beneficial to approach this task by
215 thinking about the different aspects of the network as well as interactions that are being predicted by the
216 different models. It is perhaps beneficial to think of these across different ‘scales’ of organisation within the
217 network, namely macro (the entire network), meso (smaller interacting units within the network), and micro
218 (species-level attributes). Although there are a myriad of possible ways to ‘measure’ and analyse ecological
219 networks (Delmas et al., 2018) we do still lack a clear set of guidelines for assessing how well models recover
220 network structure (Allesina et al., 2008) and it is beneficial to use a small subset of metrics that can clearly
221 be tied to broader aspects of network function or capturing a ecological process.

222 Here we used a Multivariate ANOVA or Multivariate Analysis Of Variance (MANOVA) as it is able to capture
223 model differences based on the combined information of the multiple structural network measures. Model
224 defined as `network structure values ~ model + time period` and Linear Discriminant Analysis (LDA)
225 to determine if different models produced networks with differing structure.

Table 2: An informative caption about the different network properties

Label	Definition	Scale	Reference (for maths), can make footnotes probs
Connectance	L/S^2 , where S is the number of species and L the number of links	Macro	
GenSD	Normalized standard deviation of generality of a species standardized by L/S	Micro	Williams & Martinez (2000)
LinkSD	Normalized standard deviation of links (number of consumers plus resources per taxon)	Micro	
Richness	Number of nodes in the network	Macro	
TL	Prey-weighted trophic level averaged across taxa	Macro	Williams & Martinez (2004)
VulSD	Normalized standard deviation of vulnerability of a species standardized by L/S	Micro	Williams & Martinez (2000)
Diameter	Diameter can also be measured as the average of the distances between each pair of nodes in the network	Macro	Delmas et al. (2018)

Label	Definition	Scale	Reference (for maths), can make footnotes probs
ρ	Spectral radius is a conceptual analog to nestedness (and more appropriate for unipartite networks). It is defined as the absolute value of the largest real part of the eigenvalues of the <i>undirected</i> adjacency matrix	Macro	Staniczenko et al. (2013)
Complexity	SVD complexity of a network, defined as the Pielou entropy of its singular values	Macro	Strydom et al. (2021a)
S1	Number of linear chains	Meso	Milo et al. (2002); Stouffer et al. (2007)
S2	Number of omnivory motifs	Meso	Milo et al. (2002); Stouffer et al. (2007)
S4	Number of apparent competition motifs	Meso	Milo et al. (2002); Stouffer et al. (2007)
S5	Number of direct competition motifs	Meso	Milo et al. (2002); Stouffer et al. (2007)

²²⁶ **4.2.1 Macro network properties**

²²⁷ **Connectance** (Martinez, 1992) has been shown to be the feature of networks that underpin a series of other properties and function (Strydom et al., 2021b) and so it is perhaps the most important structural attribute for a model to be able to retrieve correctly. Additionally we consider the **complexity** of networks by calculating their SVD entropy (this gives us an estimate of the physical as opposed to behavioural complexity of networks; Strydom et al. (2021a)), we could also look at the rank/rank deficiency of networks which (theoretically)

232 represents the number fo unique interaction strategies in the network (Strydom et al., 2021a), which may be
233 specifically interesting in terms of looking at pre and post extinction but also as a way to unpack ‘functional
234 redundancy’ that some models may introduce.

235 **4.2.2 Meso network properties**

236 Motifs represent smaller subset of interactions between three species, and are argued to capture dynamics
237 that are likely to be ecologically relevant (Milo et al., 2002; Stouffer et al., 2007). Here we specifically look at
238 the number of **linear chains**, **omnivory**, **apparent competition**, and **direct competition** motifs. In
239 the broader context the ability of a model in being able to capture these smaller motifs will inform as to its
240 suitability of use understanding the more dynamic component of network ecology.

241 **4.2.3 Micro network properties**

242 The number of interactions established (**generality**) or received (**vulnerability**) by each species (Schoener,
243 1989), are (broadly) indicative of consumer-resource relationships and diet breadth of species [ref]. Although
244 this is usually determined at the species level the standard deviation of the generality and vulnerability of
245 species is often used when benchmarking predicted networks (Petchey et al., 2008; *e.g.*, Williams & Martinez,
246 2008).

247 The **specificity** of species in a network is measured as a function of the proportion of resources they effectively
248 use (Poisot et al., 2012)

249 [Figure 2 about here.]

250 And we can discuss the results and implications here...

251 **4.3 Assessing pairwise interaction differences**

252 **Interaction turnover** (Poisot et al., 2012) tells us which interactions are ‘conserved’ (shared) across the
253 networks from the same period but constructed using different models.

254 [Figure 3 about here.]

255 **4.4 Assessing network inference**

256 Here we will look at extinctions of the different paleo TSS Gupta et al. (2022)

²⁵⁷ **4.4.1 Robustness**

²⁵⁸ R_{50} see Jonsson et al. (2015)

²⁵⁹ [Figure 4 about here.]

²⁶⁰ **Discussion**

²⁶¹ Blah blah blah

²⁶² **References**

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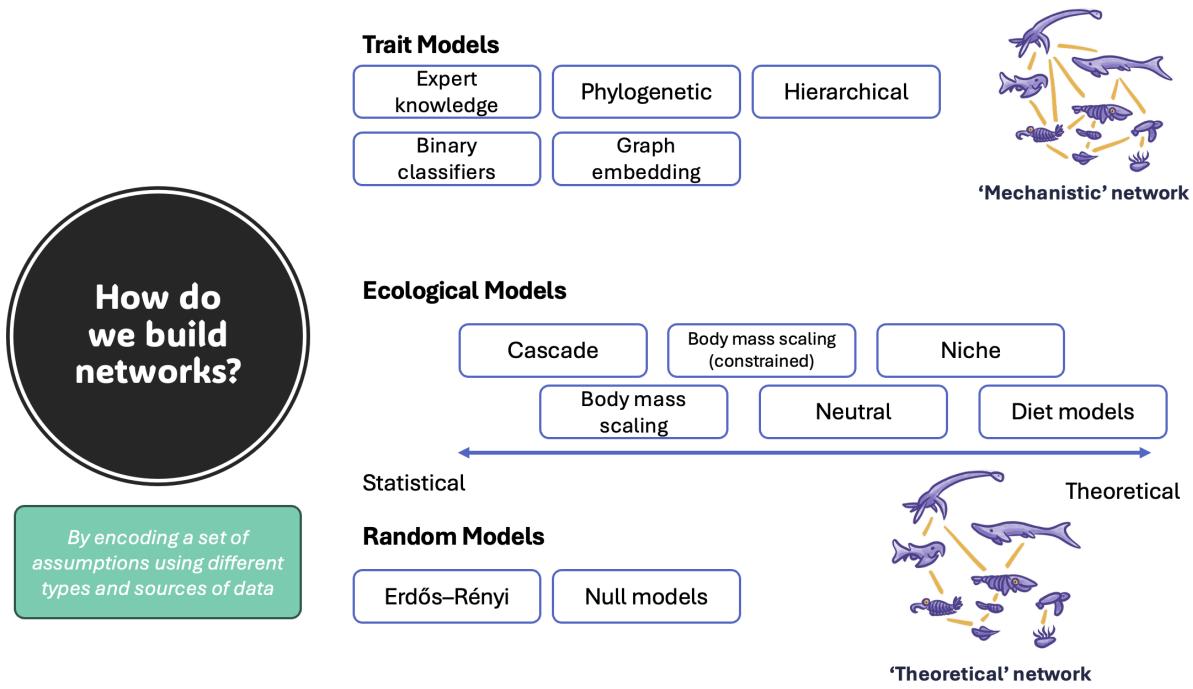


Figure 1: This obviously needs work but a variation on this to try and articulate the different approaches and broadly how they may differ.

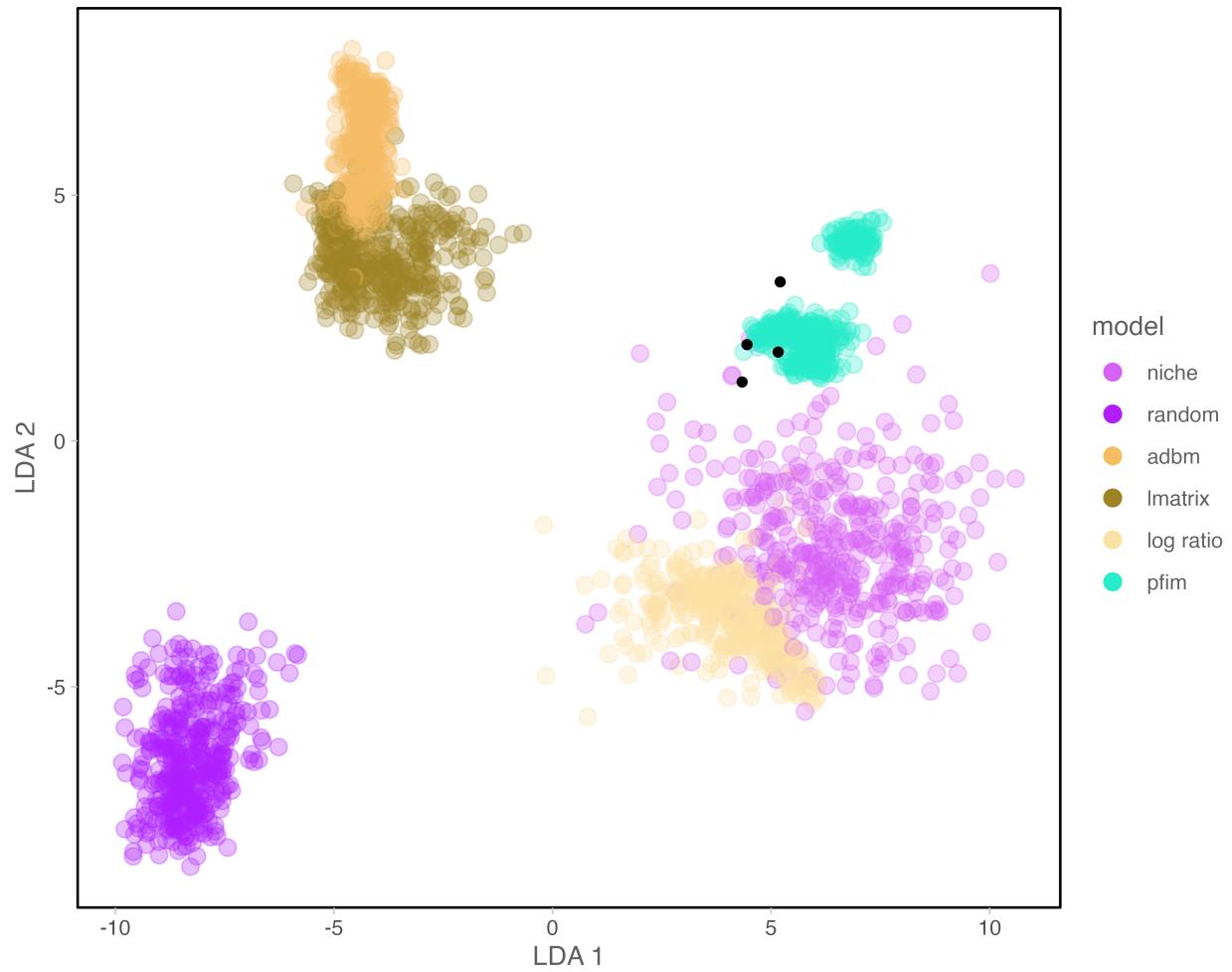


Figure 2: stuff...

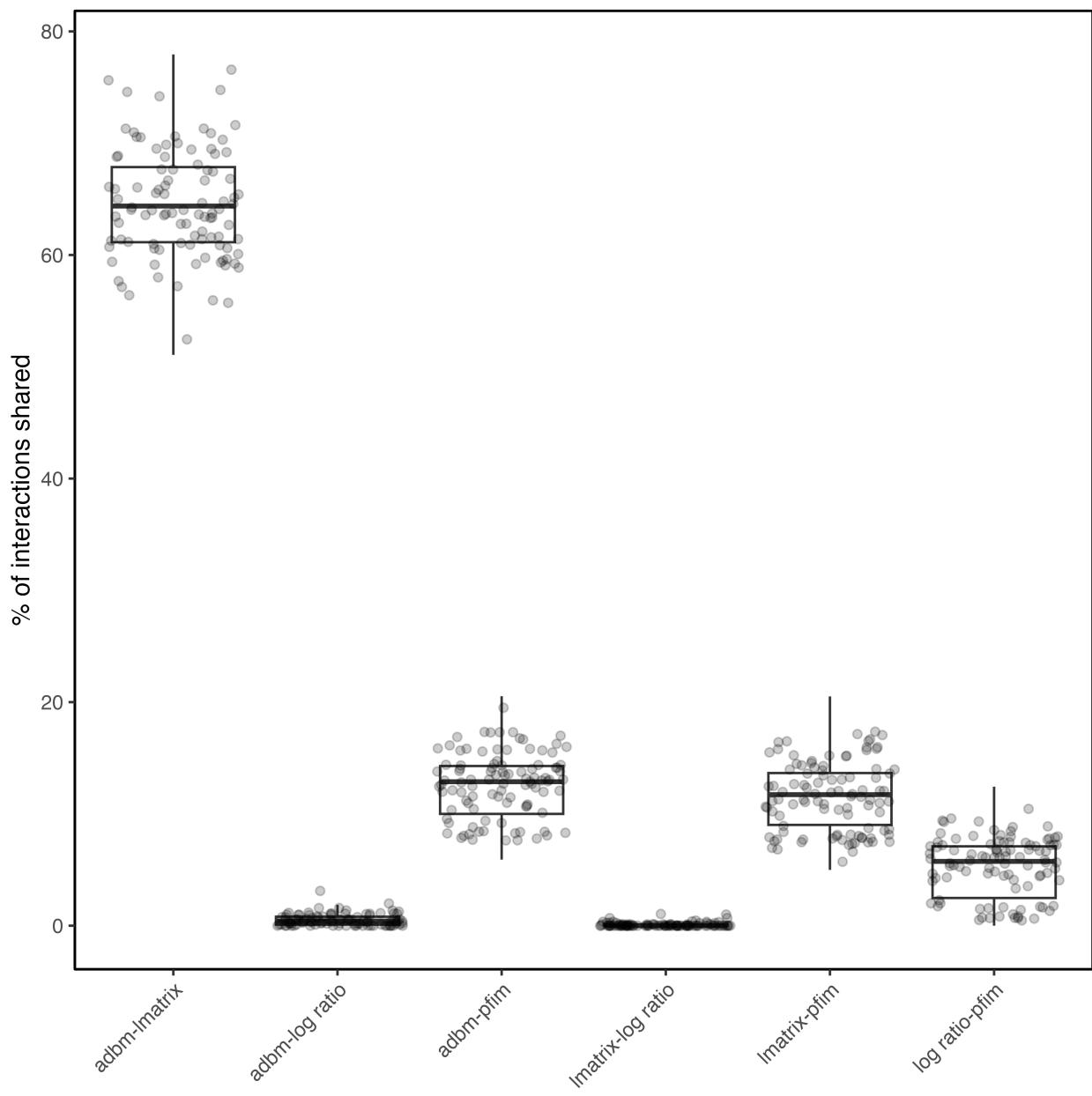


Figure 3: stuff... % interaction shared is calculated as number shared interactions / ((number interactions left - shared interactions) + (number interactions right - shared interactions) + shared interactions). Additionally niche and random models are excluded as it is illogical since both of these models are fundamentally species agnostic

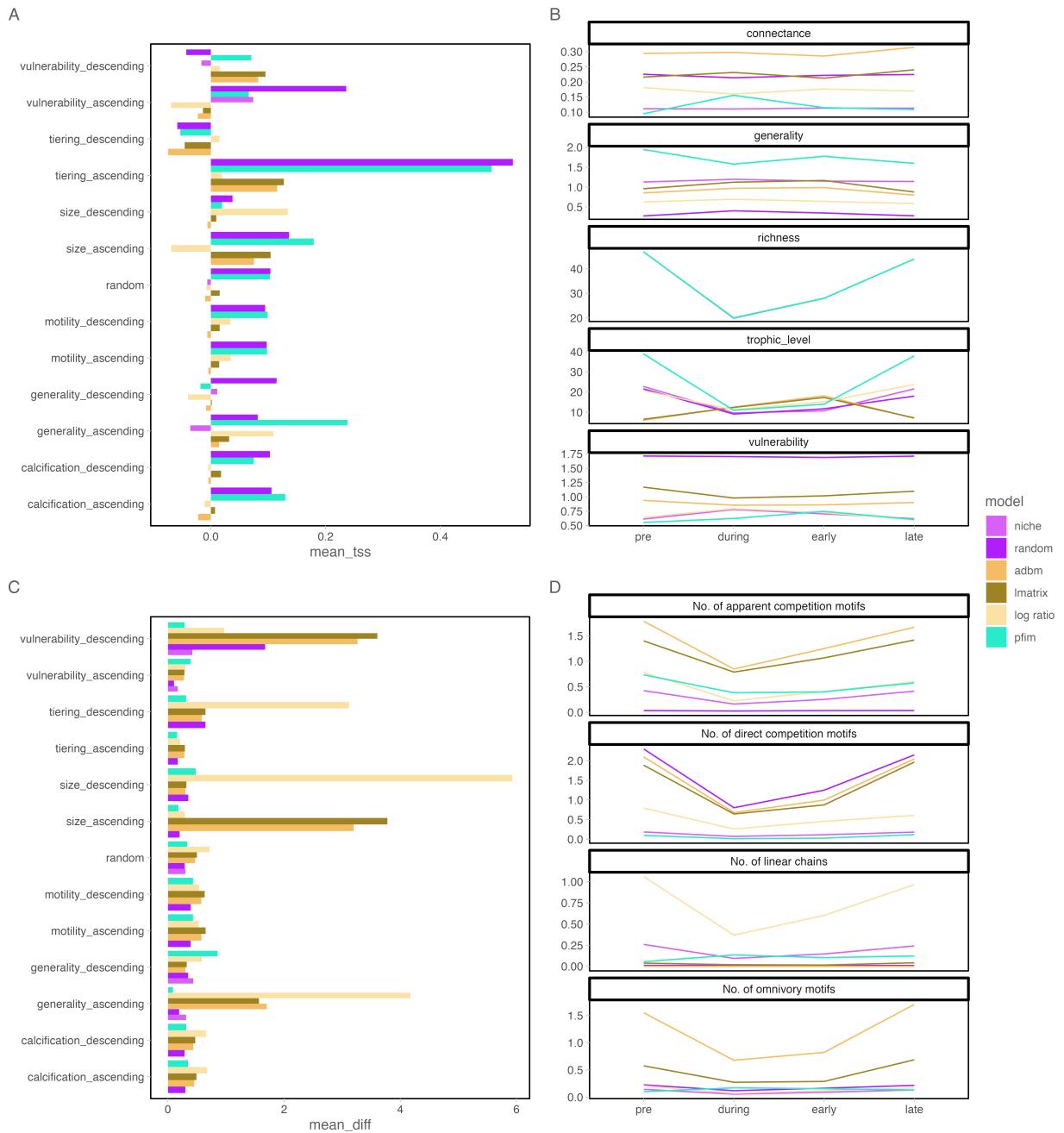


Figure 4: stuff... Recreation of the figure from Dunhill 2024. Note not 100% sold on the TSS and absolute mean calculations...