

Methods for Reconstructing Paleo Food Webs

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Abstract: TODO.

Keywords: food web, network construction

1 Why build paleo food webs?

- Because its interesting?
- Value in using hindcasting to aid in forecasting. *e.g.*, the Toarcian ms (Dunhill et al., 2024) shows how we can use these paleo communities to understand trophic-level responses to extinctions.

2 How do we do it?

- There is an evolving body of work that focuses on developing tools specifically for the task of predicting food webs.
- There are a handful that have been developed specifically in the context of paleo settings *e.g.*, TODO but we can also talk about those that might have been developed/tested in contemporary settings but still have applicability in paleo ones.
- Different underlying theory though
 - Focus here on the idea of different ‘currencies’ but also aggregations - energy vs compatibility.
- Insert brief overview of the different methods as they pertain to approach (so the T4T triangle)
- Challenges we face (even in contemporary settings)?
 - keep high level - I think the argument here should fall more in the data trade offs...

3 Understanding how networks are different

It is important to be aware that networks can be configured in different ways depending on how the interactions are defined (Strydom, in prep). Basically we have metawebs, which represent *potential* interactions, and realised networks, which represent the subset of potential that are realised as a result of community and environmental context.

4 Challenges specific to paleo communities/networks

Although there are a suite of tools and methods that have been developed to predict species interactions and networks they will not all be suitable for the prediction of paleo communities. Some of these include the fact that the fossil record is incomplete/preservation is biased [REF] which means that we have an incomplete picture of the entire community. Fossils are 2D and only represent specific ‘parts’ of an individual (hard and

bone-y bits), this means we don't have a complete picture of the physical traits of species *e.g.*, no body mass (but yes size), behaviours, or ability to construct well resolved phylogenetic trees the deeper we go back in time. Also owing to the patchy nature of fossils one often has to aggregate over large spatial scales, and also fossils are preserved in 2D so no *real* idea of spatial arrangements, compounded that fossils aren't necessarily conserved/found 'in situ' but can be moved (*e.g.*, alluvial deposits). 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)).

5 Dataset Overview

- Species
- Time/space
- And probably some other paleo things that will be relevant...

6 Methods to use

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

Model	Predicts	Notes
Allometric diet breadth model	Realised network	
Body size ratio model	Metaweb (?)	
Niche model	Structural network	Is not species specific - cannot apply species metadata
Paleo food web inference model	Realised network (if downsampling)	

Paleo food web inference model (PFIM; Shaw et al. (2024)): uses a series of rules for a set of trait categories (such as habitat and body size) to determine if an interaction can feasibly occur between a species pair. If all conditions are met for the different rule classes then an interaction is deemed to be feasible. The original work put forward in Shaw et al. (2024) also includes a 'downsampling' step developed by Roopnarine (2006) that uses a power law, defined by the link distribution, to 'prune' down some of the links. It is worth

44 mentioning that this approach is similar to that developed by Roopnarine (2017) with the exception that
 45 Shaw does not specifically bin species into guilds, and so we choose to use the method developed by Shaw
 46 since both methods should produce extremely similar networks as they are built on the same underlying
 47 philosophy.

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

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

53 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
 54 energy content of the resource and H_{ij} is the ratio handling time, with the relationship being dependent on
 55 the ratio of predator and prey bodymass as follows:

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

56 OR

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

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

58 **Body size ratio model** (Rohr et al., 2010): Determines feeding interactions using the ratio between
 59 consumer and resource body sizes - which supposedly stems from niche theory (still trying to reconcile that
 60 myself). The probability of a link existing between a consumer and resource (in its most basic form) is defined
 61 as follows:

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

62 where

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

63 The original latent-trait model developed by Rohr et al. (2010) also included an additional latent trait term
64 $v_i \delta f_j$ however for simplicity we will use Equation 2 as per Yeakel et al. (2014) Based on Rohr et al. (2010) it
65 is possible to estimate the parameters α , δ , and γ using a GLM but we will use the parameters from Yeakel
66 et al. (2014), which was ‘trained’ on the Serengeti food web data and are as follows: $\alpha = 1.41$, $\delta = 3.75$, and
67 $\gamma = 1.87$.

68 **Niche model** (Williams & Martinez, 2000): The niche model introduces the idea that species interactions
69 are based on the ‘feeding niche’ of a species. Broadly, all species are randomly assigned a ‘feeding niche’ range
70 and all species that fall in this range can be consumed by that species (thereby allowing for cannibalism).
71 The niche of each species is randomly assigned and the range of each species’ niche is (in part) constrained by
72 the specified connectance of the network. The niche model has also been modified, although it appears that
73 adding to the ‘complexity’ of the niche model does not improve on its ability to generate a more ecologically
74 ‘correct’ network (Williams & Martinez, 2008).

75 **7 Results**

76 **7.1 Comparing predicted networks**

77 [Figure 1 about here.]

78 **7.2 Comparing inference**

79 **7.3 Extinctions**

80 [Figure 2 about here.]

81 [Figure 3 about here.]

82 **References**

- 83 Caron, D., Maiorano, L., Thuiller, W., & Pollock, L. J. (2022). Addressing the Eltonian shortfall with
84 trait-based interaction models. *Ecology Letters*, 25(4), 889–899. <https://doi.org/10.1111/ele.13966>
- 85 Dunhill, A. M., Zarzychny, K., Shaw, J. O., Atkinson, J. W., Little, C. T. S., & Beckerman, A. P. (2024).
86 Extinction cascades, community collapse, and recovery across a Mesozoic hyperthermal event. *Nature*

87 *Communications*, 15(1), 8599. <https://doi.org/10.1038/s41467-024-53000-2>

88 Fricke, E. C., Hsieh, C., Middleton, O., Gorczynski, D., Cappello, C. D., Sanisidro, O., Rowan, J., Svenning,
89 J.-C., & Beaudrot, L. (2022). Collapse of terrestrial mammal food webs since the Late Pleistocene.
90 *Science*, 377(6609), 1008–1011. <https://doi.org/10.1126/science.abn4012>

91 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2008). Size, foraging, and food web
92 structure. *Proceedings of the National Academy of Sciences*, 105(11), 4191–4196. <https://doi.org/10.1073/pnas.0710672105>

93

94 Rohr, R., Scherer, H., Kehrl, P., Mazza, C., & Bersier, L.-F. (2010). Modeling food webs: Exploring
95 unexplained structure using latent traits. *The American Naturalist*, 176(2), 170–177. <https://doi.org/10.1086/653667>

96

97 Roopnarine, P. D. (2006). Extinction cascades and catastrophe in ancient food webs. *Paleobiology*, 32(1),
98 1–19. <https://www.jstor.org/stable/4096814>

99 Roopnarine, P. D. (2017). *Ecological Modelling of Paleocommunity Food Webs* (pp. 201–226). University of
100 Chicago Press.

101 Shaw, J. O., Dunhill, A. M., Beckerman, A. P., Dunne, J. A., & Hull, P. M. (2024). *A framework for*
102 *reconstructing ancient food webs using functional trait data* (p. 2024.01.30.578036). bioRxiv. <https://doi.org/10.1101/2024.01.30.578036>

103

104 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Mercier, B.,
105 Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2023). Graph embedding and transfer
106 learning can help predict potential species interaction networks despite data limitations. *Methods in*
107 *Ecology and Evolution*, 14(12), 2917–2930. <https://doi.org/10.1111/2041-210X.14228>

108 Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404(6774), 180–183.
109 <https://doi.org/10.1038/35004572>

110 Williams, R. J., & Martinez, N. D. (2008). Success and its limits among structural models of complex food
111 webs. *The Journal of Animal Ecology*, 77(3), 512–519. <https://doi.org/10.1111/j.1365-2656.2008.01362.x>

112 Yeakel, J. D., Pires, M. M., Rudolf, L., Dominy, N. J., Koch, P. L., Guimarães, P. R., & Gross, T. (2014).
113 Collapse of an ecological network in ancient Egypt. *PNAS*, 111(40), 14472–14477. <https://doi.org/10.1073/pnas.1408471111>

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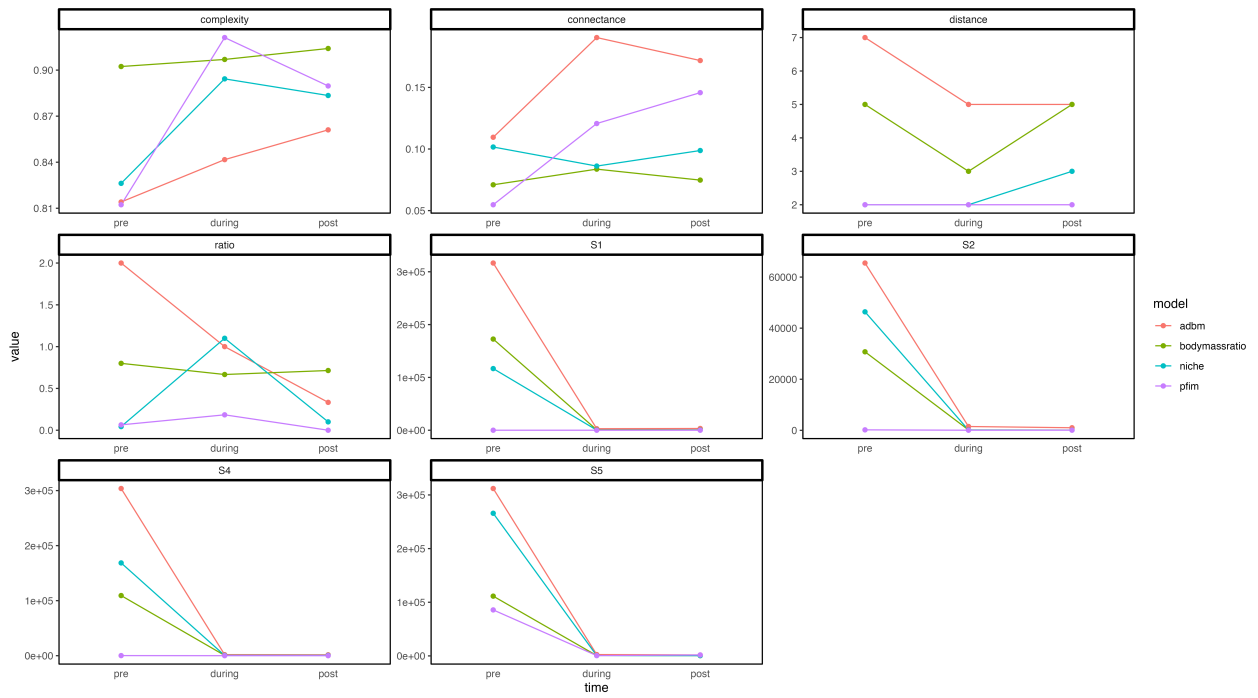


Figure 1: stuff

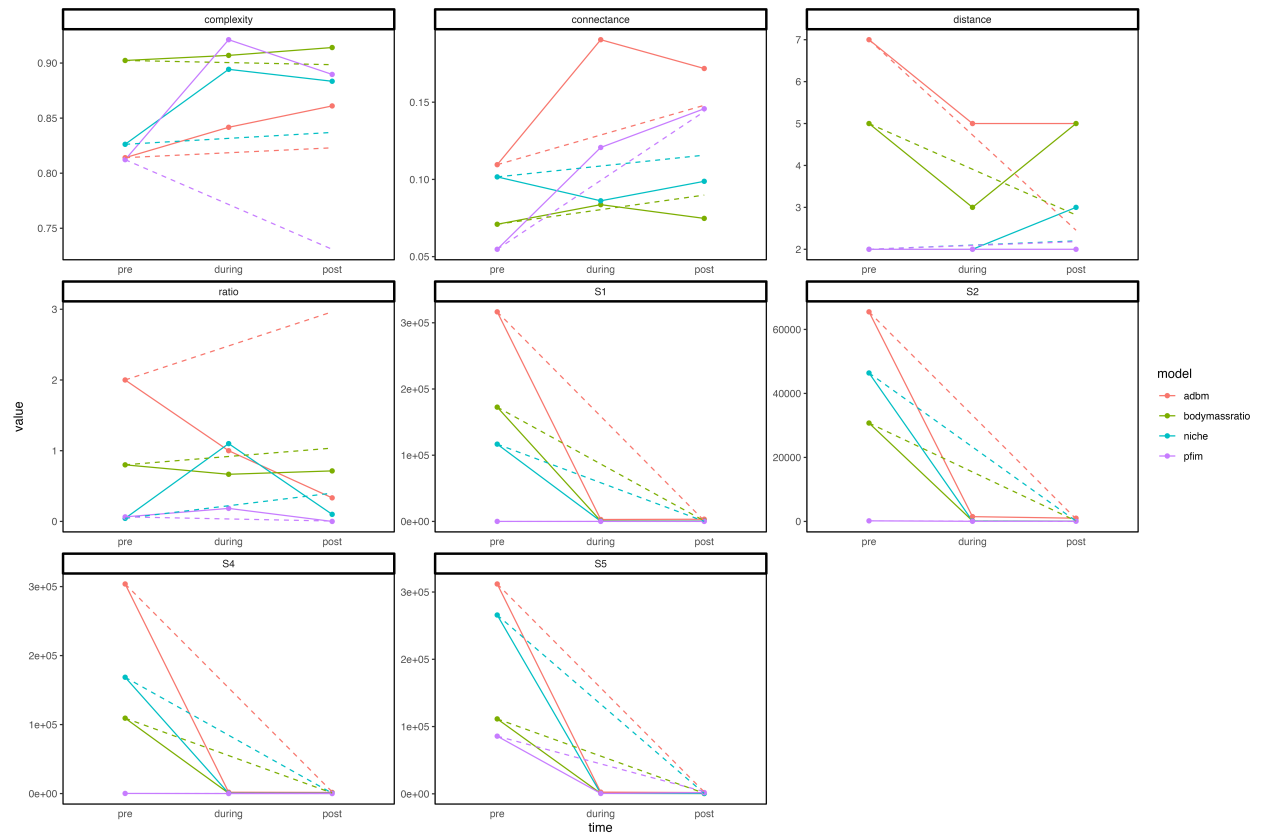


Figure 2: Dashed line indicates the (mean) extinction simulation results (post value, start values are those estimated by the relevant model)

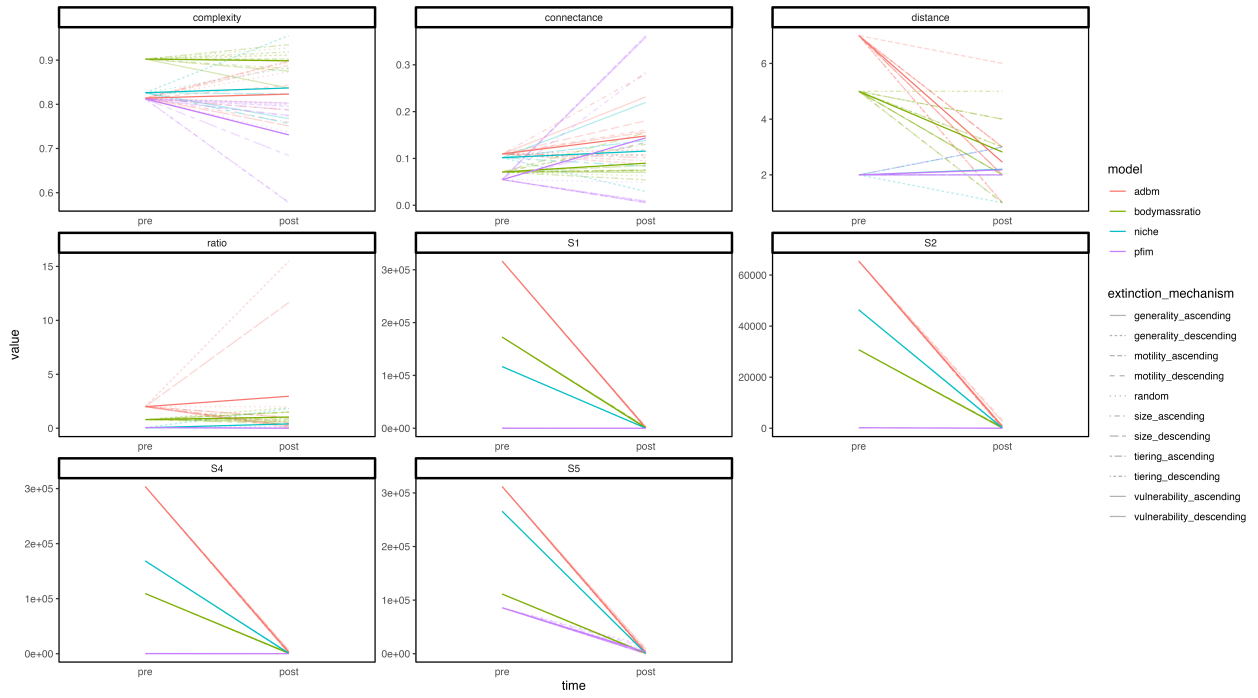


Figure 3: Dark line indicates mean extinction simulation results the lighter lines show each model individually, which is also denoted by linetype