

Reconstructing food webs in deep time: Network models as explicit hypotheses for paleoecological inference

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Abstract: Food webs provide a powerful framework for understanding ecosystem structure and function, yet reconstructing them in paleoecological contexts remains challenging because direct evidence of species interactions is rarely preserved. A growing array of models exists for predicting interactions and inferring network structure, but these approaches differ markedly in their assumptions, mechanisms, and data requirements. Here, we evaluate how network reconstruction model choice shapes ecological inference in deep time, and which aspects of inference are robust to alternative assumptions. Using the Toarcian Oceanic Anoxic Event (Early Jurassic, ~183 Ma) as a case study, we reconstruct food webs for four successive community states using six contrasting modelling approaches spanning mechanistic, trait-based, and structural network representations. Despite identical taxon pools, models produced strikingly different network structures and species-level interactions, and these differences propagated into divergent inferences about interaction loss, cascade dynamics, and temporal pathways of collapse. At the same time, models converged on similar species-level extinction patterns and dominant drivers, indicating that some ecological signals are robust across reconstruction assumptions. By framing food-web reconstructions as alternative ecological hypotheses rather than interchangeable representations, this study demonstrates how model choice conditions both the accuracy and precision of paleoecological inference, and provides a framework for identifying which conclusions about extinction dynamics in deep time are robust and which remain model dependent.

Keywords: Paleoecological networks, Food-web reconstruction, Ecological networks, Extinction dynamics, Trophic interactions, Toarcian Oceanic Anoxic Event

1 Introduction

There is growing interest in using deep-time fossil data and evidence of species interactions in past ecosystems (*e.g.*, Dunne et al. (2008); Dunne et al. (2014)) as a foundation for understanding how ecological communities respond to multi-stressor environmental change, such as temperature increase, ocean acidification, and hypoxia (Dillon et al., 2022; Kiessling et al., 2019). Paleoecological networks therefore represent a particularly valuable opportunity to investigate community responses to major environmental transitions as they allow for the explicit construction of pre- and post-extinction interaction networks and enable the disentangling of extinction drivers as well as broader cascading effects (Dunhill et al., 2024; Roopnarine, 2006; Yeakel et al., 2014). Insights gained from these deep-time systems provide a critical context for interpreting present day ecological change and anticipating the impacts of ongoing anthropogenic stressors (Barnosky et al., 2012; Roopnarine & Dineen, 2018).

Inference from ecological networks regarding structure and complexity is (at its core) a mathematical task and is therefore relatively independent of biological assumptions (Delmas et al., 2019). While these structural properties can be analysed independently of biological detail, their implications for stability and dynamics depend critically on assumptions about the distribution and strength of interaction (Allesina & Tang, 2012; Poisot et al., 2015). Thus, assumptions become meaningful once network structure and complexity are interpreted in functional terms or used as templates for simulating community and extinction dynamics. While there is a well-developed theoretical framework describing what can be inferred from network properties, a central challenge (particularly in paleoecology) lies in how networks are constructed. Unlike modern systems, paleoecological interactions are rarely directly observed, with only exceptional cases preserving explicit evidence of trophic interactions (*e.g.*, Jenny et al. (2019); Vullo (2011)). As a result, paleo food web reconstruction depends on indirect inference, drawing on preserved traits, analogies with modern taxa, and ecological theory. Simply put, network reconstruction is not a data recovery process, but rather hypothesis generation under constraints.

Although numerous tools exist for inferring species interactions (see Morales-Castilla et al., 2015; Pichler & Hartig, 2023; Strydom et al., 2021; Allesina et al., 2008 for reviews), only a subset can be reliably applied in paleo contexts, where data on traits, abundances, and community composition are incomplete and systematically biased. This makes it essential to clearly articulate which reconstruction approaches are appropriate for which inferential purposes. Recent work has shown that reconstruction approaches (*e.g.*, models based on traits, abundances, or co-occurrence) can be categorised by the type of network that they predict (Strydom et al., 2026). These include feasible networks (derived from trait matching and phylogenetic inference that produce metawebs of plausible interactions), realised networks, (constrained by ecological rules

and evidence of actual feeding relationships), and purely structural networks (which reproduce ecologically plausible topologies but lack species-level node identities). In this sense, food-web reconstructions are not empirical recoveries of a single past ecosystem, but rather represent alternative, model-based, hypotheses about interaction structure constrained by the fossil record.

Each of these reconstruction approaches carries distinct assumptions that influence inferred network size, complexity, structure, and node-level properties, with direct consequences for ecological interpretations of extinction dynamics, stability, resilience, and ecosystem function (Dunne et al., 2002; Gravel et al., 2019; Roopnarine, 2006; Solé & Montoya, 2001). Despite this, most paleo food web studies default to constructing networks using expert knowledge (*e.g.*, Dunne et al. (2008)) or mechanistic feeding rules (*e.g.*, Dunhill et al. (2024); Roopnarine (2017); Fricke et al. (2022)), approaches that typically result in metawebs. This raises a critical but underexplored question: to what extent does the choice of network type (and particularly the use of alternatives to metawebs) control not only inferred food web structure but also conclusions about system behaviour, especially with respect to extinction cascades and vulnerability.

In this study, we address this question by explicitly evaluating how network reconstruction model choice shapes ecological inference in deep time. We link recent advances in food-web reconstruction methods to a comparative re-evaluation of primary and secondary, trait-based extinction dynamics during the early Toarcian extinction event, a volcanic-driven hyperthermal and marine crisis in the Early Jurassic (~183 Ma) (Dunhill et al., 2024). We reconstruct four successive communities (pre-extinction, post-extinction, early recovery, and late recovery) from the Cleveland Basin of North Yorkshire, UK, using six contrasting network reconstruction approaches spanning feasible, realised, and structural network representations - as recognised in recent network inference frameworks (Morales-Castilla et al., 2015; Strydom et al., 2026). For each community, we compare network-level structure, species-level properties, and inferred interactions across models, allowing us to assess how reconstruction assumptions propagate into ecological interpretations. Finally, we replicate the secondary extinction analyses of Dunhill et al. across all six reconstruction methods to explicitly test how model choice influences inference about extinction drivers, interaction loss, and cascading dynamics. By explicitly comparing multiple reconstruction approaches within a single paleoecological system, this study provides a framework for evaluating how methodological assumptions shape interpretations of ancient food-web structure and dynamics.

2 Materials and Methods

2.1 Study system and fossil data

We used fossil occurrence data from the Cleveland Basin spanning the upper Pliensbachian to the upper Toarcian, following Dunhill et al. (2024). Four paleo-communities were defined: pre-extinction, post-extinction, early recovery, and late recovery. Each assemblage was treated as a community of potentially interacting taxa. Modes of life were assigned following Dunhill et al. (2024) using the Bambach ecospace framework. Traits included motility, tiering, feeding mode, and size class, with size defined categorically based on maximum linear dimensions.

2.2 Network reconstruction approaches

2.2.1 Conceptual classification of network types

Most paleo-specific approaches currently operate within the feasibility space (*e.g.*, Shaw et al., 2024; Fricke et al., 2022; Roopnarine, 2006). Although well suited for reconstructing feasible interactions, these methods represent only a subset of the broader spectrum of network construction approaches. Here, we present a suite of models (Table 1) that enable the construction of a wider range of ecological networks and the exploration of a broader set of ecological questions, provided that their underlying assumptions are compatible with the constraints of fossil data. For example, some tools require quantitative estimates of body size, which must often be inferred from size classes or functional morphology in the fossil record. Structural models, such as the niche model, rely only on species richness and estimates/specification of connectance, but their species-agnostic nature limits their applicability to trait-based or diet-specific questions, although they do still accurately recover network structure (Stouffer et al., 2005). Mechanistic approaches, by contrast, depend on accurate assignment of feeding traits or robust phylogenetic support. Recognizing how these methodological requirements intersect with the limits of fossil evidence is essential for selecting an appropriate modelling framework.

Table 1: Six different models 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 fall within the limitations set by the fossil record.

Model family	Assumptions	Data needs	‘Limitation’	Network type	Key reference	Usage examples
Random	Links are randomly distributed within a network	richness, number of links	parameter assumptions, species agnostic	structural network	Erdős & Rényi (1959)	Null-model comparisons; testing whether observed network structure (connectance, motifs) deviates from random expectations
Niche	Networks are interval, species can be ordered on a ‘niche axis’	richness, connectance	parameter assumptions, species agnostic	structural network	Williams & Martinez (2008)	Evaluating the influence of trophic hierarchy or intervality on network topology; generating baseline predictions for motifs and connectance

Model family	Assumptions	Data needs	‘Limitation’	Network type	Key reference	Usage examples
Allometric diet breadth model (ADBM)	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)	Predicting realised predator diets under energy-maximization rules; exploring secondary extinctions and trophic bottlenecks
Allometric trophic network (ATN)	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	Brose et al. (2006); Gauzens et al. (2023)	Simulating effects of species loss on network structure; examining consequences of mechanical constraints on predator–prey interactions

Model family	Assumptions	Data needs	‘Limitation’	Network type	Key reference	Usage examples
Paleo food web inference model (PFIM)	Interactions can be inferred by a mechanistic frame-work/relationships	feeding traits for taxa, mechanistic feeding rules	Assumption made as to the feeding mechanisms, need to elucidate traits from models (although this is a way smaller issue)	feasibility web	Shaw et al. (2024)	Mapping feasible trophic interactions based on trait compatibility; assessing vulnerability and secondary extinctions in paleo-communities (Dunhill et al., 2024).

Model family	Assumptions	Data needs	‘Limitation’	Network type	Key reference	Usage examples
Body-size ratio model	Interactions inferred using allometric rules (ratio of body sizes between predator and prey). Logit 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	realised network	Rohr et al. (2010)	Estimating likely interaction networks from body-size constraints; evaluating cascading effects and network collapse under extinction scenarios (Yeakel et al., 2014).

The three body mass-based models (ADBM, ATN, Body-size ratio) differ primarily in their underlying ecological assumptions. Although all three models use body mass to infer food web structure, they differ in their ecological assumptions. The ADBM is based on energy maximization under optimal foraging theory, the ATN constrains interactions via mechanically optimal consumer–resource size ratios, and the Body-size ratio model defines links probabilistically within a fixed allometric niche. Together, these approaches span bioenergetic, mechanical, and statistical interpretations of size-structured interactions.

2.2.2 Network generation and replication

We evaluated six models spanning this space Table 1: random and niche models (structural network); allometric diet breadth (ADBM), allometric trophic network (ATN), and Body-size ratio models (realised network); and a paleo food-web inference model (PFIM; feasibility web). Expanded descriptions of model assumptions,

parameterisation, and link-generation rules are provided in Supplementary Material S1. For each of the four communities, we constructed 100 replicate networks using each of the six models (2400 networks total). Networks were simplified by removing disconnected species. For size-based models, body masses were drawn from uniform distributions bounded by size-class limits, allowing for variance between replicates but preserves relative sizes within replicates. We adopt uniform sampling by default, as alternative distributions (lognormal, truncated lognormal) have negligible impact on topology (Supplementary Material S2; Figure S1). Structural models were parameterised using connectance values drawn from an empirically realistic range (0.07 – 0.34) while holding richness constant. The same parameter draws were used across comparable models within each replicate. For the Body-size ratio model, we followed the approach of Yeakel et al. (2014) and excluded latent trait terms as opposed fitting the full model, which introduces additional inference and assumptions.

2.3 Network metrics and structural analyses

We quantified network structure using a suite of macro-, meso-, and micro-scale metrics Table 2, capturing global properties, motif structure, and species-level variability. Differences among reconstruction approaches were assessed using a multivariate analysis of variance (MANOVA), with model identity as a fixed factor and the full set of network metrics as response variables. Pairwise interaction turnover was quantified using link-based beta diversity, which measures dissimilarity in the identity of trophic links between networks, capturing differences due to species turnover or changes in interactions among shared species (Poisot et al., 2012).

Table 2: Network properties used for analysis.

Metric	Definition	Scale	Reference (for maths), can make footnotes probs
Richness	Number of nodes in the network	Macro	
Links	Normalized standard deviation of links (number of consumers plus resources per taxon)	Micro	

Metric	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	
Max trophic level	Prey-weighted trophic level averaged across taxa	Macro	Williams & Martinez (2004)
S1	Number of linear chains, normalised	Meso	Milo et al. (2002); Stouffer et al. (2007)
S2	Number of omnivory motifs, normalised	Meso	Milo et al. (2002); Stouffer et al. (2007)
S4	Number of apparent competition motifs, normalised	Meso	Milo et al. (2002); Stouffer et al. (2007)
S5	Number of direct competition motifs, normalised	Meso	Milo et al. (2002); Stouffer et al. (2007)
Generality	Normalized standard deviation of generality of a species standardized by L/S	Micro	Williams & Martinez (2000)
Vulnerability	Normalized standard deviation of vulnerability of a species standardized by L/S	Micro	Williams & Martinez (2000)

2.4 Extinction simulations and model evaluation

Following Dunhill et al. (2024) and using the pre-extinction and post-extinction networks, we simulated species loss under multiple extinction scenarios, including trait-based, network-position-based, and random removals, allowing for secondary extinctions. Simulated post-extinction networks were compared to empirical post-extinction communities using mean absolute differences (MAD) in network metrics and a modified true

skill statistic (TSS) at both node and link levels. Scenario rankings were compared across models using Kendall's rank correlation coefficient.

3 Results

Across six network reconstruction approaches, inferred food-web structure, species interactions, and extinction dynamics differed consistently. Multivariate analyses showed pronounced separation among models in network metric space. Reconstruction approach explained most of the variance in structural properties, leaving a distinct signature independent of community composition. Notably, agreement among models depended on scale - approaches that were statistically similar in multivariate structural space often diverged in inferred interactions or extinction dynamics. This demonstrates that structural similarity does not guarantee concordance in species-level diets or trophic roles. Model choice also substantially influenced inferred extinction dynamics. Temporal trajectories of network collapse, interaction loss, and motif reorganization differed among approaches. Although species-level extinction rankings were often broadly consistent, link-level outcomes and extinction inferences were highly sensitive to reconstruction assumptions. Together, these results show that ecological inferences drawn from paleo networks depend critically on the reconstruction framework employed. Importantly, agreement among models was not consistent across analytical scales - models that were statistically indistinguishable in multivariate structural space often diverged in inferred interactions or extinction dynamics. Together these results show that reconstruction approaches that appear similar when evaluated using global network metrics can yield fundamentally different ecological narratives when interrogated at the level of interactions and extinction dynamics.

3.1 Network structure differs among reconstruction approaches

To test whether network reconstruction approach influences inferred food-web structure, we compared multivariate patterns of network metrics across all six models using a MANOVA. Network structure differed strongly among reconstruction approaches (MANOVA, Pillai's trace = 3.84, approximate $F_{40,11955} = 987.35$, $p < 0.001$), indicating that model choice systematically alters inferred food-web topology. Canonical discriminant analysis revealed two dominant axes of multivariate network structure, with the first two canonical variates explaining approximately 86% of the total between-model variance (CV1 = 53%, CV2 = 33%; Table S1, Figure S1). All higher-order canonical variates each explained less than 9% of the remaining variance.

Linear discriminant analysis (LDA) visualized distinctions among reconstruction approaches in multivariate network space Figure 1. The first two axes explained 86% of between-model variance (LD1 = 53%, LD2 =

33%). LD1 correlated most strongly with vulnerability ($r = 0.86$), direct competition motifs ($r = 0.81$), and connectance ($r = 0.75$). LD2 correlated primarily with maximum trophic level ($r = -0.76$) and, positively, with apparent competition motifs ($r = 0.73$). These loadings suggest that the primary axis separates models by predation pressure and competitive overlap, while the secondary axis distinguishes models by vertical trophic structure. All higher-order axes explained less than 9% of the remaining variance (Tables S4–S5).

[Figure 1 about here.]

3.1.1 Inferred pairwise interactions vary widely among models

Building on differences in global network structure, we next examined how reconstruction approach influences species-level ecological inference by quantifying turnover in inferred pairwise interactions among networks constructed from the same taxon pool. While models that produced similar global metrics sometimes agreed broadly on network structure, they often differed in the specific interactions they inferred. In some cases, networks with comparable connectance and motif frequencies assigned fundamentally different consumer diets to the same taxa.

Pairwise β -turnover revealed that some model pairs shared very few links despite comparable macro- or meso-scale properties Figure 2. ADBM and ATN were similar and likely reflects their shared reliance on ranked size-based constraints, which strongly shape realised diets even when emergent network structure differs. The Body-size ratio model consistently exhibited high differences in pairwise interactions relative to all other approaches. PFIM showed intermediate overlap with size-based theoretical models. These patterns indicate that agreement in global network metrics does not guarantee agreement in species-level diets or trophic roles, highlighting the importance of evaluating both network- and species-level outcomes when comparing reconstruction methods. Consequently, agreement in global network properties does not guarantee concordance in inferred trophic roles, vulnerability, or competitive relationships among taxa.

[Figure 2 about here.]

3.2 Model choice influences inferred extinction dynamics

To quantify how network structure changed over time during extinction simulations and whether these dynamics differed among reconstruction models, we fit generalized additive models (GAMs) to time series of network-level metrics. GAMs capture nonlinear temporal trajectories, allowing formal tests of whether the shape of these trajectories differs among models. These model-specific temporal trajectories are shown in Figure 3. For all metrics examined, the inclusion of model-specific smooth terms significantly improved model fit (ANOVA model comparison: $p < 0.001$ for all metrics). Model-specific smooths differed not only

in magnitude but also in the timing and abruptness of change, indicating distinct modes of collapse across reconstruction approaches (Tables S3–S4). Deterministic, data-driven approaches (PFIM) and allometric models (ADBM, ATN) exhibited highly non-linear trajectories, showing structural shifts in connectivity and motif frequency. In contrast, the Niche model produced the most consistent and gradual trajectories, effectively smoothing the perceived magnitude of structural change during community collapse. These results demonstrate that inferred pathways of collapse, trophic bottlenecks, and secondary extinctions are highly sensitive to model choice. Corresponding raw temporal trajectories are shown in Fig. S2.

[Figure 3 about here.]

To evaluate how model choice affects inferred extinction dynamics, we compared simulated post-extinction networks to observed networks using mean absolute differences (MAD) for network-level metrics and total sum-of-squares (TSS) for node- and link-level outcomes Figure 4. Across models, MAD-based rankings were generally positively correlated (Kendall’s $\tau = 0.13$ across structural metrics), indicating broad agreement on the relative importance of extinction drivers despite substantial differences in reconstructed network structure. However, agreement within the allometric models differed from patterns observed for reconstructed network structure. Whereas earlier multivariate analyses showed strongest structural similarity between the ADBM and Body-size ratio models, extinction-driven network responses aligned most closely between the ADBM and ATN models (mean $\tau = 0.67$ across structural metrics), with little correspondence between ADBM and Body-size ratio model outcomes (mean $\tau = 0.05$). This reversal relative to structural similarity analyses demonstrates that model concordance is context dependent, with emergent topology and extinction dynamics emphasizing different aspects of model assumptions. Node-level TSS rankings were similarly consistent across models ($\tau = 0.26$ – 0.90), reflecting broadly comparable species removal sequences. In contrast, link-level outcomes were far more variable ($\tau = -0.48$ – 0.29), highlighting that inferences about which interactions are lost, retained, or re-established during collapse and recovery are highly model contingent. Together, these results suggest that while alternative models converge on similar species-level extinction patterns, the inferred pathways of interaction loss and cascading dynamics depend strongly on both reconstruction approach.

[Figure 4 about here.]

4 Discussion

4.1 Model choice as a component of ecological inference

Reconstructing food webs from fossil data is inherently an exercise in inference under uncertainty. It requires not only assembling paleontological data but also making explicit assumptions about how species interact

and how those interactions are represented mathematically (Dunne et al., 2008; Morales-Castilla et al., 2015; Strydom et al., 2026). This process parallels modern ecological network studies, where the tension between data limitations and meaningful ecological inference is well recognised (Delmas et al., 2019; Poisot et al., 2021). Here we demonstrate that the choice of network reconstruction model is itself a major ecological decision, shaping both the structural properties of inferred networks and downstream interpretations of extinction dynamics (Allesina & Tang, 2012; Solé & Montoya, 2001). Results show that the choice of reconstruction approach exerts an influence on inferred food-web structure, shaping multivariate network properties, and inferred interactions and extinction dynamics.

Differences among models do not arise from the fossil evidence itself, but from assumptions embedded in each model family (Pichler & Hartig, 2023; Strydom et al., 2021). These assumptions include how trophic links are defined (trait compatibility versus energetic constraints), how interaction probabilities are parameterised, and whether network topology is guided by macroecological theory (*e.g.*, niche structure) or mechanistic rules (*e.g.*, Body-size ratios). Consequently, network reconstruction is not neutral and it explicitly encodes ecological assumptions that shape inferred structure and downstream dynamical narratives. This sensitivity parallels challenges in modern network ecology, where model and metric selection influence interpretations of connectance, modularity, and motif distributions (Michalska-Smith & Allesina, 2019; Poisot & Gravel, 2014).

Multivariate analyses of network metrics revealed that differences among reconstruction approaches are structured along a small number of dominant multivariate axes rather than dispersed across many weakly informative dimensions. Although some reconstruction approaches converged in multivariate space along one canonical dimension, divergence along the orthogonal axis often persisted. For example, allometric models showed partial overlap along CV1, reflecting similar assumptions about interaction density, yet separated along CV2, indicating contrasting trophic organisation despite shared energetic constraints. The first canonical variate (CV1) captured variation in interaction density and competitive structure. The second canonical variate (CV2) distinguished models based on vertical trophic organisation, omnivory and apparent competition. Together, these axes explain the majority of between-model variance, indicating that reconstruction approaches encode fundamentally different assumptions about both horizontal and vertical dimensions of food-web structure. These patterns demonstrate a strong, model-specific signature independent of community composition.

While some models occasionally converged on some global metrics (*e.g.*, ADBM and ATN models), pairwise -turnover revealed disagreements in inferred species-level interactions. Thus, structural similarity does not guarantee concordance in trophic roles, highlighting that uncertainty in reconstructed networks follows structured, predictable patterns rather than random noise. For example, allometric models tended to

converge on similar species removal sequences while diverging in inferred interaction loss, whereas structural models dampened the apparent magnitude and variability of collapse. Comparing multiple reconstruction approaches provides a means to identify robust ecological signals while delineating areas where inference remains model-dependent.

Mechanistic models (PFIM) typically identify a broad landscape of trait-compatible interactions, theoretical size-based models (ADBM, ATN, Body-size ratio) impose energetic filters to approximate realised diets, and structural models (niche, random) prioritise topological patterns over species identity. Temporal trajectories of network collapse, interaction loss, and motif reorganization varied markedly among approaches. Species-level extinction rankings were often broadly consistent across models. In contrast, link-level outcomes and secondary extinctions were highly sensitive to reconstruction assumptions. This reflects how extinction pathways depend on the specification of interactions, demonstrating that interaction-level inferences about cascade dynamics are inherently model dependent (Allesina & Tang, 2012; Curtsdotter et al., 2011; Dunne et al., 2002).

Taken together, these results underscore that network reconstruction is a hypothesis-generating process where each model encodes a distinct set of ecological assumptions, and the inferred structure and dynamics reflect these assumptions. Accordingly, paleoecologists should carefully align reconstruction approaches with the specific ecological signals of interest, whether potential interactions, realised diets, or macro scale structural properties. Disagreement among models does not imply that any single approach is ‘wrong’, but rather that different models capture different facets of ecological reality (Stouffer, 2019). Viewed through the lens of accuracy (here referring to model convergence/robustness) and precision, our results suggest that some paleoecological inferences are robust across reconstruction assumptions, while others remain intrinsically uncertain. Models consistently recover similar high-level extinction patterns, implying relative accuracy, but disagree on interaction-level details and temporal dynamics, indicating limited precision in reconstructing the fine structure of collapse. Recognizing and explicitly accounting for these differences is essential for advancing paleoecology beyond descriptive reconstruction toward rigorous comparative inference.

4.2 Aligning ecological questions with model choice

A central insight from this study is that different ecological questions require different network representations, echoing broader efforts in network ecology to clarify what models and metrics can validly infer about ecological systems (Gauzens et al., 2025; Strydom et al., 2026). Here we identify a conceptual divide among feasible, realised, and structural networks, providing a practical framework to match research goals with appropriate reconstruction approaches.

Feasibility networks: (*e.g.*, trait- and phylogeny-based metaweb approaches) are most suitable for exploring

potential trophic links and dietary breadth. These models capture the set of interactions that are biologically plausible given species traits, even if not all are realised in a particular community, aligning with metaweb concepts in modern ecology (Tylianakis & Morris, 2017). As reflected in our PFIM results, such approaches maximise interaction diversity but are less suited to inferring realised extinction cascades.

Realised networks: (*e.g.*, allometric or energetic models such as ADBM, ATN, and Body-size ratio approaches) are appropriate when the goal is to infer the most likely interactions. By embedding energetic or foraging rules, these models approximate realised diets and energy transfer, improving ecological plausibility compared to purely combinatorial approaches (Brose et al., 2006; Petchey et al., 2008). In our analyses, these models consistently produced more abrupt and nonlinear collapse trajectories, reflecting the propagation of energetic constraints during extinction.

Structural networks: (*e.g.*, niche, cascade) focus on topological patterns rather than species identity, making them useful when broad questions about connectance, trophic depth, or motif frequency are the focus. Such models have a long history as null frameworks in network ecology (Allesina et al., 2008; Williams & Martinez, 2008).

Recognising this alignment helps avoid misinterpretation; for instance, treating predicted metaweb links as realised interactions conflates potential and actual diets, potentially exaggerating inferred interaction diversity.

4.3 Implications for paleoecological network studies

Findings carry three key implications for paleoecology:

1. **Explicitly acknowledge model assumptions:** Interpretations of ancient food webs must clearly articulate the assumptions underlying reconstruction models. Without this, differences between networks from different datasets or research groups could be misattributed to ecological variation rather than methodological choice.
2. **Standardise comparative frameworks:** When comparing food webs across studies, networks should be constructed and analysed using comparable model families. Failing to do so risks conflating methodological differences with ecological or temporal variation.
3. **Leverage modern theory to expand inference:** Integrating modern network ecology frameworks and methods enriches the paleoecological toolkit (Dunne et al., 2014; Solé & Montoya, 2001). Models developed for modern systems can be adapted to the constraints of fossil data (*e.g.*, Perez-Lamarque et al., 2026), enabling more nuanced insights into deep-time dynamics.

4.4 Recommendations for network reconstruction in paleoecology

Given the sensitivity of ecological inference to reconstruction model choice, we propose the following guidelines to improve consistency, transparency, and ecological relevance:

- 1. Define the Inferential Goal First:** Before reconstructing networks, researchers should articulate whether they aim to infer potential interactions, likely realised diets, or general structural properties. This will inform the selection of an appropriate model family consistent with the ecological question at hand (*e.g.*, metaweb for complete diets, energetic models for trophic energy flows, or structural models for generic topologies)
- 2. Use ensemble and sensitivity frameworks:** Rather than relying on a single model output, researchers should adopt ensemble approaches that generate and compare multiple network reconstructions. This not only quantifies model uncertainty but also reveals which ecological conclusions are robust biological signals and which are methodological artifacts.
- 3. Standardise cross-study comparisons:** Comparisons of networks from different palaeoecological studies should be standardised by model family. When models differ, interpretations about ecological or environmental change should explicitly address how model choice may contribute to observed differences.
- 4. Interpret scale-specific results with caution:** Because robustness to model choice varies by scale (with node-level patterns more consistent than interaction-level outcomes) researchers should prioritise interpretations at the appropriate scale. Structural conclusions about cascade pathways or secondary extinctions should be framed as model-dependent hypotheses rather than definitive historical reconstructions.

4.5 Future directions

Advances in modern network ecology offer several promising directions for paleoecology. These include probabilistic and Bayesian approaches to quantify uncertainty in link prediction (Baskerville et al., 2011; Elmasri et al., 2020), maximum entropy methods to infer network structure under limited data (Banville et al., 2023), and multi-layer network representations that integrate trophic and non-trophic interactions (Pilosof et al., 2017). Combined with increasingly available trait and phylogenetic information, such developments can bridge fossil constraints and ecological inference, enabling more nuanced, probabilistically grounded reconstructions of deep-time ecosystems (Banville et al., 2025; Perez-Lamarque et al., 2026; Poisot et al., 2016).

5 Conclusions

Ecological network reconstruction in deep time is not merely a technical step but a fundamental component of ecological inference. By explicitly comparing six contrasting reconstruction approaches for a single extinction event and location, we show that model choice strongly shapes inferred food-web structure, species interactions, and extinction dynamics (even when the underlying fossil data are identical). While broad, trait-based patterns of species loss are relatively robust, conclusions about pairwise interactions, secondary extinctions, and cascading dynamics depend critically on the assumptions embedded in the chosen network reconstruction approach. By contrast, interaction and extinction based interpretations are far more sensitive to reconstruction assumptions, and should be treated as model-dependent hypotheses rather than definitive historical outcomes. Network reconstruction is inherently hypothesis-driven: each model encodes distinct ecological assumptions that influence both network structure and inferred dynamics. No single approach captures all aspects of past ecosystems, but careful alignment of model choice with research goals, combined with ensemble or comparative frameworks, allows robust inference while quantifying uncertainty. These results underscore the need for paleoecological studies to evaluate the sensitivity of key conclusions to alternative network representations and highlight that understanding past ecosystem collapse requires not only better fossil data, but also transparent, question-driven modelling frameworks that explicitly encode and interrogate the assumptions underlying ecological inference.

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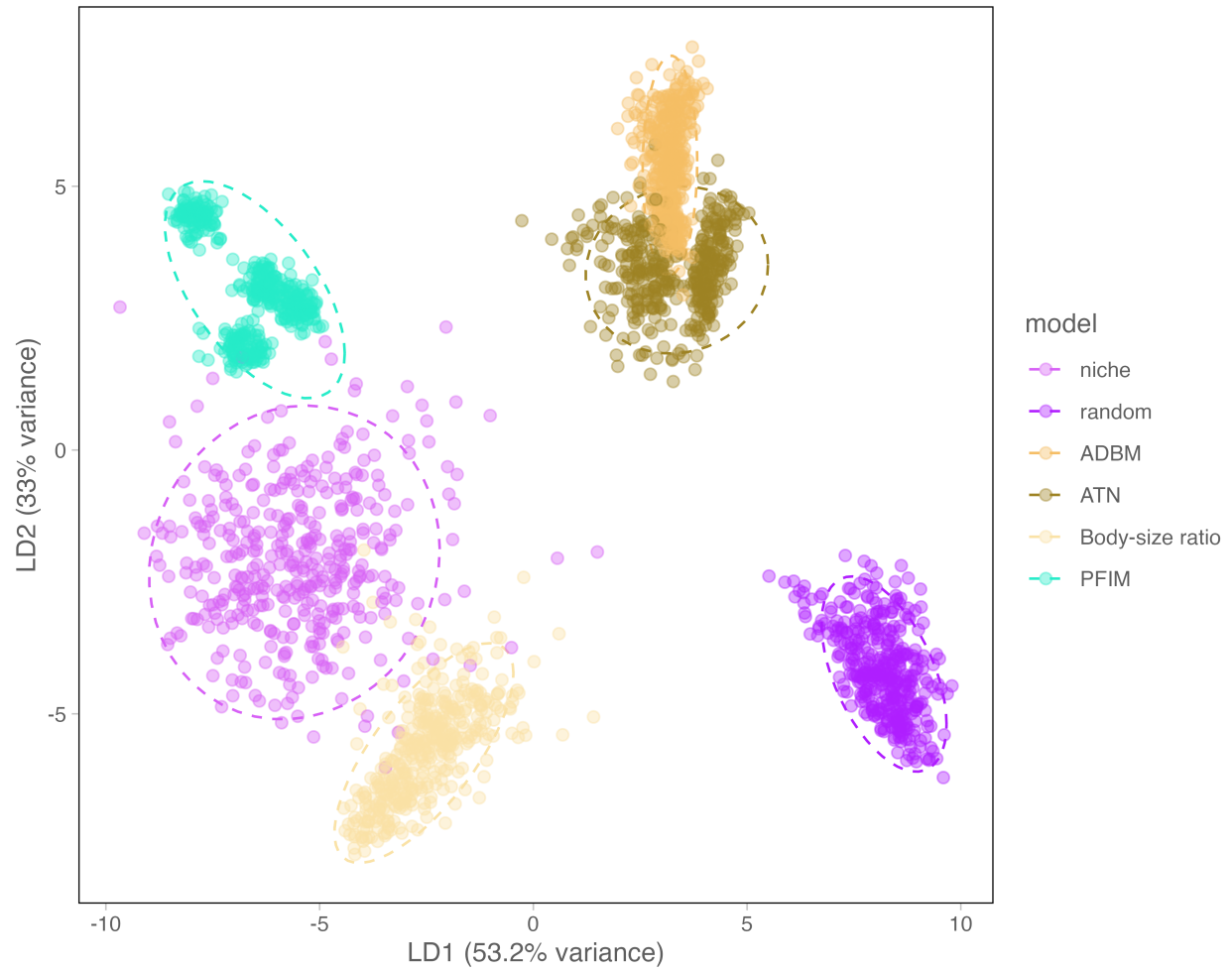


Figure 1: Linear discriminant analysis (LDA) of ecological network metrics for six model types. Each point represents a replicate, and ellipses indicate 95% confidence regions for each model. The second column represents the correlation of the various network metrics with the respective LDA axes.

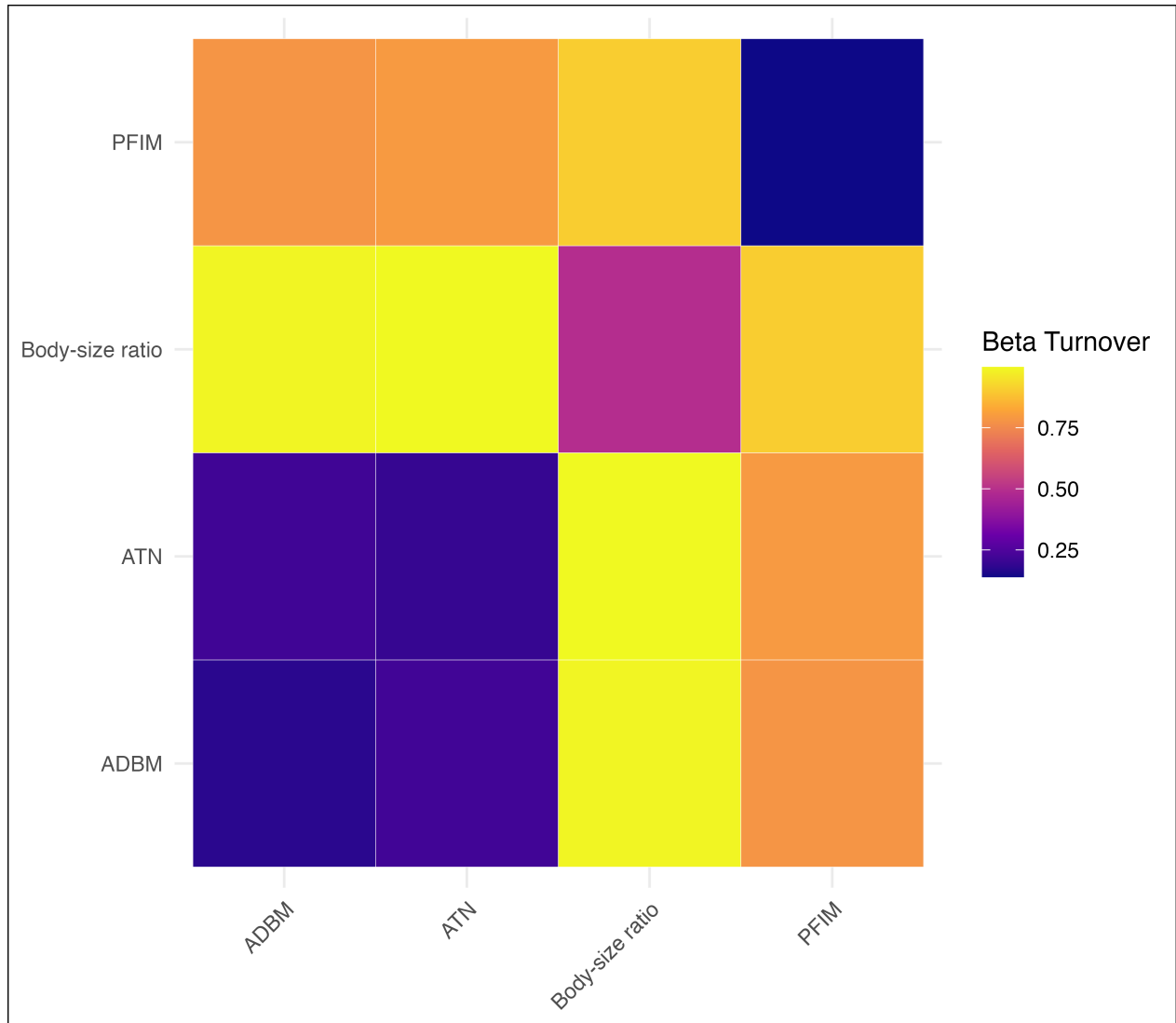


Figure 2: Pairwise β -turnover in species interactions among four ecological network models (ADBM, ATN, Body-size ratio, and pfim). Each cell represents the mean turnover value between a pair of models, with warmer colors indicating greater dissimilarity in inferred interactions. The diagonal is omitted. High turnover values (yellow) indicate strong disagreement in network structure between models, whereas lower values (blue–purple) indicate greater similarity.

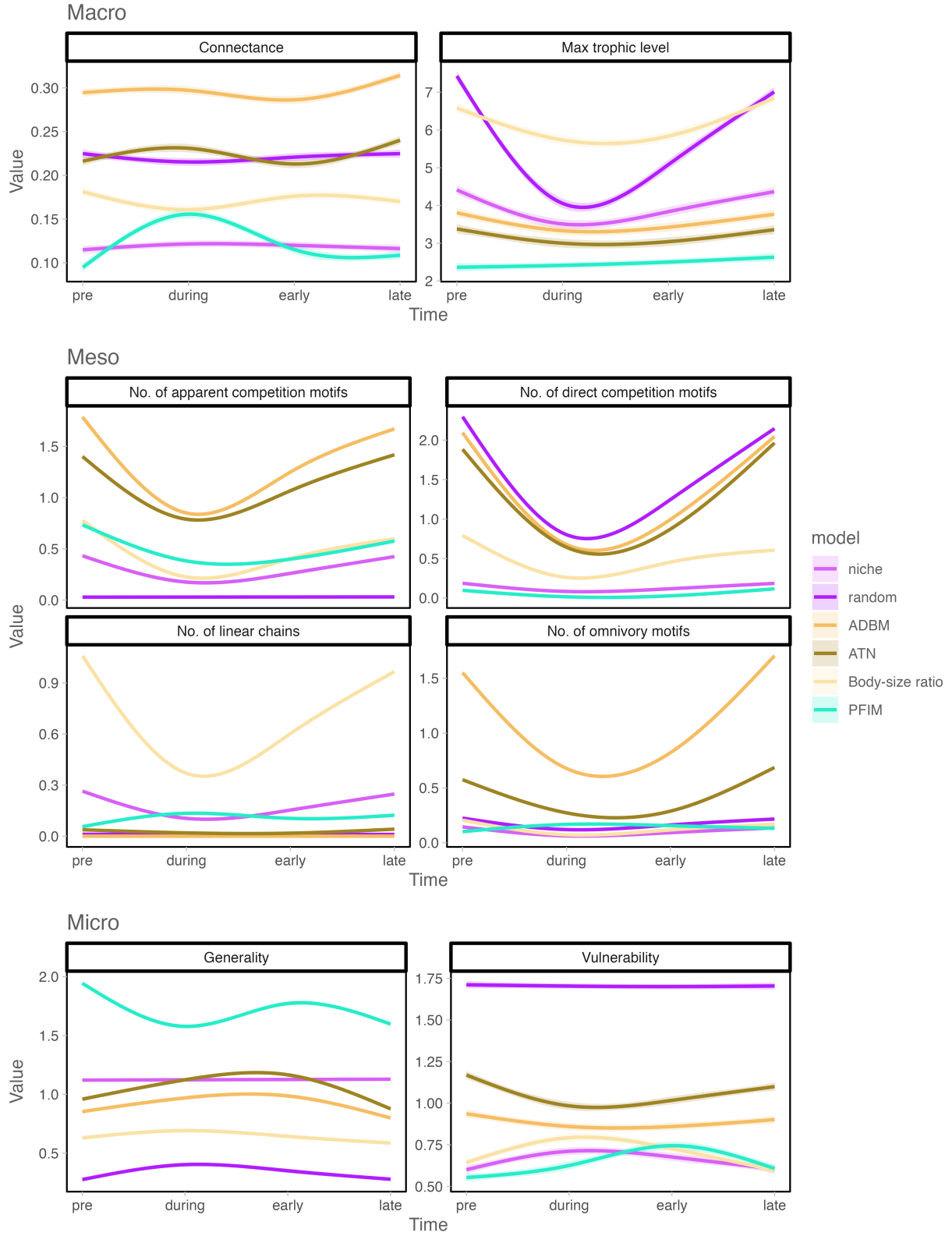


Figure 3: GAM-predicted trajectories of network structure during extinction simulations reveal pronounced differences in the timing and magnitude of change across reconstruction models. Lines show model-specific smooths and shaded areas indicate 95% confidence intervals. Deterministic approaches produce smoother, more consistent dynamics, whereas stochastic models exhibit greater variability, underscoring the sensitivity of inferred collapse pathways to reconstruction assumptions.

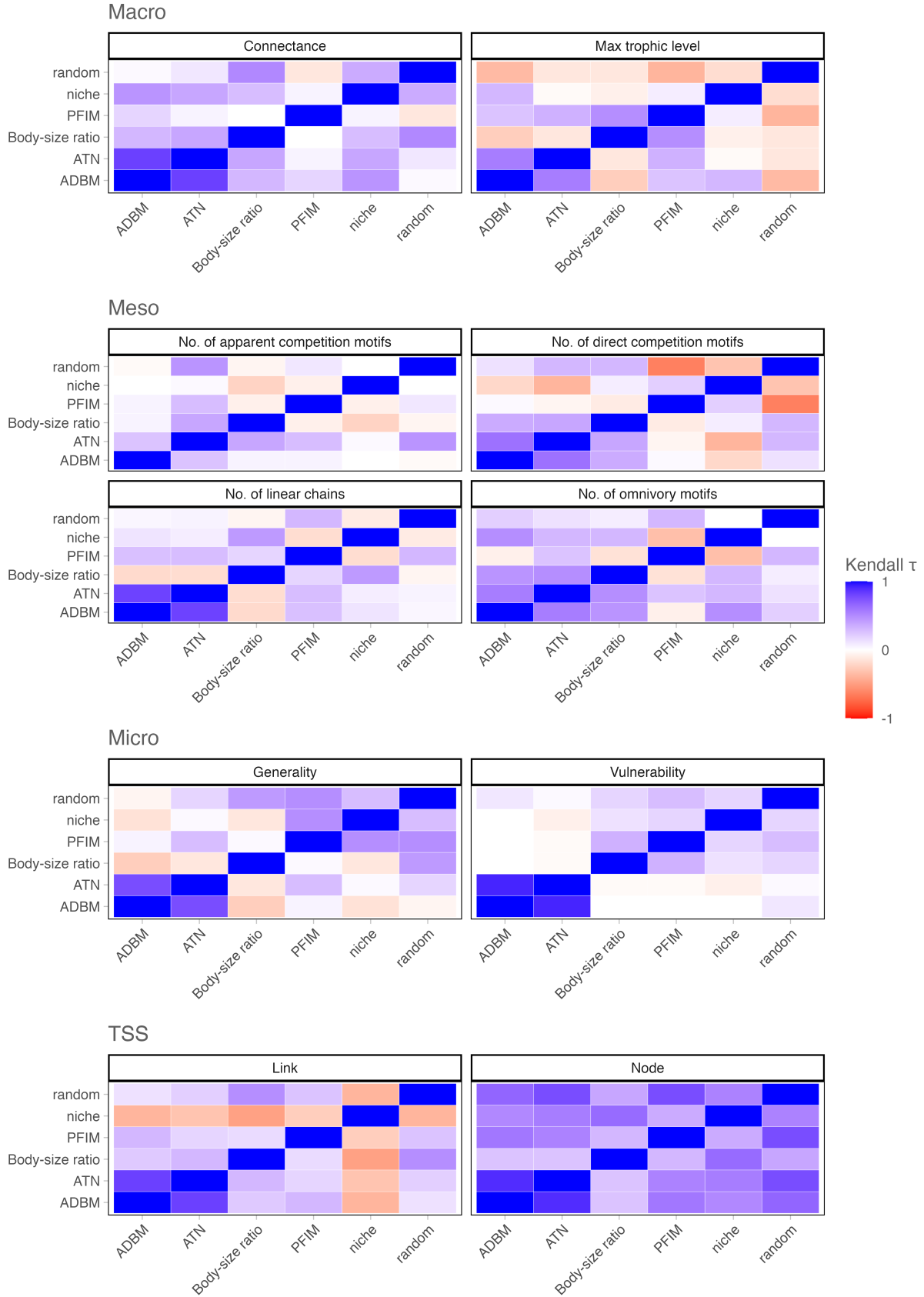


Figure 4: Heatmaps showing pairwise Kendall rank correlation coefficients (τ) between models for each network metric. Each panel corresponds to a different metric and displays the degree of agreement in extinction-scenario rankings across models based on mean absolute differences (MAD) between observed and predicted network values. Positive τ values (blue) indicate concordant rankings between models, whereas negative τ values (red) indicate opposing rankings. Warmer colours approaching zero represent little or no agreement. Panels