

Reconstructing food webs in deep time: why model choice matters for ecological 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 approaches are most appropriate given the constraints of the fossil record. 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 extinction dynamics, interaction loss, and cascading effects. By framing food-web reconstructions as alternative ecological hypotheses (rather than interchangeable representations) this study bridges paleoecology and modern network theory, and demonstrates how model choice fundamentally conditions inference about extinction dynamics in deep time.

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

¹ 1 Introduction

² There is growing interest in using deep-time fossil data and evidence of species interactions in past ecosystems
³ (*e.g.*, Dunne et al. (2008); Dunne et al. (2014)) as a foundation for understanding how ecological communities
⁴ respond to multi-stressor environmental change, such as temperature increase, ocean acidification, and hypoxia
⁵ (Dillon et al., 2022; Kiessling et al., 2019). Paleoecological networks therefore represent a particularly valuable
⁶ opportunity to investigate community responses to major environmental transitions as they allow for the
⁷ explicit construction of pre- and post-extinction interaction networks and enable the disentangling of extinction
⁸ drivers as well as broader cascading effects (Dunhill et al., 2024; Roopnarine, 2006; Yeakel et al., 2014).
⁹ Insights gained from these deep-time systems provide a critical context for interpreting present day ecological
¹⁰ change and anticipating the impacts of ongoing anthropogenic stressors (Barnosky et al., 2012; Roopnarine &
¹¹ Dineen, 2018).

¹² Inference from ecological networks regarding structure and complexity is (at its core) a mathematical task
¹³ and is therefore relatively independent of biological assumptions (Delmas et al., 2019). While these structural
¹⁴ properties can be analysed independently of biological detail, their implications for stability and dynamics
¹⁵ depend critically on assumptions about the distribution and strength of interaction (Allesina & Tang, 2012;
¹⁶ Poisot et al., 2015). Thus, assumptions become meaningful once network structure and complexity are
¹⁷ interpreted in functional terms or used as templates for simulating community and extinction dynamics. While
¹⁸ there is a well-developed theoretical framework describing what can be inferred from network properties,
¹⁹ a central challenge (particularly in paleoecology) lies in how networks are constructed. Unlike modern
²⁰ systems, paleoecological interactions are rarely directly observed, with only exceptional cases preserving
²¹ explicit evidence of trophic interactions (*e.g.*, Jenny et al. (2019); Vullo (2011)). As a result, paleo food web
²² reconstruction depends on indirect inference, drawing on preserved traits, analogies with modern taxa, and
²³ ecological theory. Simply put, network reconstruction is not a data recovery process, but rather hypothesis
²⁴ generation under constraints.

²⁵ Although numerous tools exist for inferring species interactions (see Morales-Castilla et al., 2015; Pichler
²⁶ & Hartig, 2023; Strydom et al., 2021; Allesina et al., 2008 for reviews), only a subset can be reliably
²⁷ applied in paleo contexts, where data on traits, abundances, and community composition are incomplete
²⁸ and systematically biased. This makes it essential to clearly articulate which reconstruction approaches are
²⁹ appropriate for which inferential purposes. Recent work has shown that reconstruction approaches (*e.g.*,
³⁰ models based on traits, abundances, or co-occurrence) can be categorised by the type of network that they
³¹ predict (Strydom et al., 2026). These include feasible networks (derived from trait matching and phylogenetic
³² inference that produce metawebs of plausible interactions), realised networks, (constrained by ecological rules

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

37 Each of these reconstruction approaches carries distinct assumptions that influence inferred network size,
38 complexity, structure, and node-level properties, with direct consequences for ecological interpretations of
39 extinction dynamics, stability, resilience, and ecosystem function (Dunne et al., 2002; Gravel et al., 2019;
40 Roopnarine, 2006; Solé & Montoya, 2001). Despite this, most paleo food web studies default to constructing
41 networks using expert knowledge (*e.g.*, Dunne et al. (2008)) or mechanistic feeding rules (*e.g.*, Dunhill et al.
42 (2024); Roopnarine (2017); Fricke et al. (2022)), approaches that typically result in metawebs. This raises a
43 critical but underexplored question: to what extent does the choice of network type (and particularly the use
44 of alternatives to metawebs) control not only inferred food web structure but also conclusions about system
45 behaviour, especially with respect to extinction cascades and vulnerability.

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

61 2 Materials and Methods

62 2.1 Study system and fossil data

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

69 2.2 Network reconstruction approaches

70 2.2.1 Conceptual classification of network types

71 Most paleo-specific approaches currently operate within the feasibility space (*e.g.*, Shaw et al., 2024; Fricke et
72 al., 2022; Roopnarine, 2006). Although well suited for reconstructing feasible interactions, these methods
73 represent only a subset of the broader spectrum of network construction approaches. Here, we present a suite
74 of models (Table 1) that enable the construction of a wider range of ecological networks and the exploration
75 of a broader set of ecological questions, provided that their underlying assumptions are compatible with
76 the constraints of fossil data. For example, some tools require quantitative estimates of body size, which
77 must often be inferred from size classes or functional morphology in the fossil record. Structural models,
78 such as the niche model, rely only on species richness and estimates/specification of connectance, but their
79 species-agnostic nature limits their applicability to trait-based or diet-specific questions, although they do still
80 accurately recover network structure (Stouffer et al., 2005) . Mechanistic approaches, by contrast, depend on
81 accurate assignment of feeding traits or robust phylogenetic support. Recognizing how these methodological
82 requirements intersect with the limits of fossil evidence is essential for selecting an appropriate modelling
83 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	structural network	Erdős & Rényi (1959)	
niche	Networks are interval, species can be ordered on a 'niche axis'	richness, connectance	parameter assumptions, species	structural network	Williams & Martinez (2008)	
allometric	Interactions are determined by energetic costs	body mass, biomass	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)	
diet breadth model (ADBM)	(foraging ecology)	(abundance)				

Model family	Assumptions	Data needs	'Limitation'	Network type	Key reference	Usage examples
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)	
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)	Secondary extinctions (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)	Network collapse (Yeakel et al., 2014)

⁸⁴ The three body-mass-based models (ADBM, ATN, body size ratio) differ primarily in their underlying
⁸⁵ ecological assumptions. Although all three models use body mass to infer food web structure, they differ in
⁸⁶ their ecological assumptions. The ADBM is based on energy maximization under optimal foraging theory,
⁸⁷ the ATN constrains interactions via mechanically optimal consumer-resource size ratios, and the body size
⁸⁸ ratio model defines links probabilistically within a fixed allometric niche. Together, these approaches span
⁸⁹ bioenergetic, mechanical, and statistical interpretations of size-structured interactions.

⁹⁰ **2.2.2 Network generation and replication**

⁹¹ We evaluated six models spanning this space Table 1: random and niche models (structural network); allometric
⁹² diet breadth (ADBM), allometric trophic network (ATN), and body-size ratio models (realised network);
⁹³ and a paleo food-web inference model (PFIM; feasibility web). Expanded descriptions of model assumptions,

94 parameterisation, and link-generation rules are provided in Supplementary Material S1. For each of the
 95 four communities, we constructed 100 replicate networks using each of the six models (2400 networks total).
 96 Networks were simplified by removing disconnected species. For size-based models, body masses were drawn
 97 from uniform distributions bounded by size-class limits, allowing for variance between replicates but preserving
 98 relative sizes within replicates. Structural models were parameterised using connectance values drawn from
 99 an empirically realistic range (0.07 – 0.34) while holding richness constant. The same parameter draws were
 100 used across comparable models within each replicate.

101 2.3 Network metrics and structural analyses

102 We quantified network structure using a suite of macro-, meso-, and micro-scale metrics Table 2, capturing
 103 global properties, motif structure, and species-level variability. Differences among models were assessed using
 104 MANOVA, followed by univariate ANOVAs, post-hoc comparisons, and linear discriminant analysis. Pairwise
 105 interaction turnover was quantified using link-based beta diversity, which measures dissimilarity in the identity
 106 of trophic links between networks, capturing differences due to species turnover or changes in interactions
 107 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	
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)

Metric	Definition	Scale	Reference (for maths), can make footnotes probs
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)

¹⁰⁸ **2.4 Extinction simulations and model evaluation**

¹⁰⁹ Following Dunhill et al. (2024) and using the pre-extinction and post-extinction networks, we simulated
¹¹⁰ species loss under multiple extinction scenarios, including trait-based, network-position-based, and random
¹¹¹ removals, allowing for secondary extinctions. Simulated post-extinction networks were compared to empirical
¹¹² post-extinction communities using mean absolute differences (MAD) in network metrics and a modified true
¹¹³ skill statistic (TSS) at both node and link levels. Scenario rankings were compared across models using
¹¹⁴ Kendall's rank correlation coefficient.

115 **3 Results**

116 Across six reconstruction approaches, both global network structure and species-level interactions differed
117 substantially, with implications for interpreting past extinction dynamics. Deterministic models (e.g., PFIM)
118 tended to produce more consistent network-level patterns and smoother extinction trajectories, whereas
119 stochastic or theory-driven models (e.g., ADBM, niche, ATN) showed greater variability in inferred interactions
120 and temporal extinction dynamics. Models with similar macro-level metrics sometimes differed in their
121 specification of pairwise interactions, highlighting that agreement in global structure does not guarantee
122 concordance at the species level. Consequently, inferred extinction pathways and secondary extinctions were
123 highly sensitive to model choice, emphasizing the importance of evaluating multiple network reconstructions
124 when interpreting ecological dynamics in deep time.

125 **3.1 Network structure differs among reconstruction approaches**

126 To test whether network reconstruction approach influences inferred food-web structure, we compared
127 multivariate patterns of network metrics across all six models using a MANOVA. Network structure differed
128 strongly among reconstruction approaches (MANOVA, Pillai's trace = 3.84, approximate $F_{40,11955} = 987.35$,
129 $p < 0.001$). Univariate analyses showed that model choice explained a large proportion of variance in most
130 network metrics, with high partial η^2 values all network structural metrics ($\eta^2 = 0.65\text{--}0.92$). Estimated marginal
131 means and Tukey-adjusted comparisons indicated consistent differences among reconstruction approaches, with
132 PFIM differing significantly from all other models ($p < 0.0001$). Within the allometric frameworks we observed
133 a notable divergence between the ADBM and ATN models ($p < 0.0001$), demonstrating that bioenergetic
134 ranking and mechanical-efficiency rules do not converge on a single structural solution. Interestingly, the only
135 pair to exhibit statistical consensus in multivariate space was the ADBM and the log-ratio model ($p = 0.99$).
136 Linear discriminant analysis (LDA) further helped visualise distinctions among reconstruction approaches in
137 multivariate network space Figure 1, with the first two axes explaining 86% of between-model variance (LD1
138 = 53%, LD2 = 33%). LD1 was most strongly correlated with vulnerability ($r = 0.86$), direct competition
139 motifs ($r = 0.81$), and connectance ($r = 0.75$), whereas LD2 was associated primarily with maximum trophic
140 level ($r = -0.76$) and a positive correlation with apparent competition motifs ($r = 0.73$). Higher-order axes
141 each explained less than 9% of the remaining variance. This demonstrates that the reconstruction approach
142 leaves a strong multivariate signature independent of community composition.

143 [Figure 1 about here.]

¹⁴⁴ **3.1.1 Inferred pairwise interactions vary widely among models**

¹⁴⁵ Building on differences in global network structure, we next examined how reconstruction approach influences
¹⁴⁶ species-level ecological inference by quantifying turnover in inferred pairwise interactions among networks
¹⁴⁷ constructed from the same taxon pool. While models that produced similar global metrics sometimes agreed
¹⁴⁸ broadly on network structure, they often differed sharply in the specific interactions they inferred.

¹⁴⁹ Pairwise -turnover revealed that some model pairs shared very few links despite comparable macro- or
¹⁵⁰ meso-scale properties Figure 2. ADBM and ATN were highly concordant, reflecting similar underlying
¹⁵¹ assumptions despite different generative rules, whereas the body-size ratio model consistently exhibited high
¹⁵² differences in pairwise interactions relative to all other approaches. PFIM showed intermediate overlap with
¹⁵³ size-based theoretical models. These patterns indicate that agreement in global network metrics does not
¹⁵⁴ guarantee agreement in species-level diets or trophic roles, highlighting the importance of evaluating both
¹⁵⁵ network- and species-level outcomes when comparing reconstruction methods.

¹⁵⁶ [Figure 2 about here.]

¹⁵⁷ **3.2 Model choice influences inferred extinction dynamics**

¹⁵⁸ To quantify how network structure changed over time during extinction simulations and whether these
¹⁵⁹ dynamics differed among reconstruction models, we fit generalized additive models (GAMs) to time series of
¹⁶⁰ network-level metrics. GAMs capture nonlinear temporal trajectories, allowing formal tests of whether the
¹⁶¹ shape of these trajectories differs among models. These model-specific temporal trajectories are shown in
¹⁶² Figure 3. For all metrics examined, the inclusion of model-specific smooth terms significantly improved model
¹⁶³ fit (ANOVA model comparison: $p < 0.001$ for all metrics). Deterministic, data-driven approaches (PFIM)
¹⁶⁴ and allometric models (ADBM, ATN) exhibited highly non-linear trajectories, showing structural shifts in
¹⁶⁵ connectivity and motif frequency. In contrast, the Niche model produced the most consistent and gradual
¹⁶⁶ trajectories, effectively smoothing the perceived magnitude of structural change during community collapse.
¹⁶⁷ These results demonstrate that inferred pathways of collapse, trophic bottlenecks, and secondary extinctions
¹⁶⁸ are highly sensitive to model choice. Corresponding raw temporal trajectories are shown in Fig. S3.

¹⁶⁹ [Figure 3 about here.]

¹⁷⁰ To evaluate how model choice affects inferred extinction dynamics, we compared simulated post-extinction
¹⁷¹ networks to observed networks using mean absolute differences (MAD) for network-level metrics and total
¹⁷² sum-of-squares (TSS) for node- and link-level outcomes Figure 4. Overall, models were more consistent in
¹⁷³ ranking extinction scenarios at the network level: Kendall's τ values for MAD-based rankings were generally

¹⁷⁴ positive, with strong agreement between ADBM and ATN models ($\tau = 0.63$). Node-level TSS scores similarly
¹⁷⁵ showed broad consistency across models ($\tau: 0.25 - 0.90$), reflecting comparable species removal sequences. In
¹⁷⁶ contrast, link-level outcomes were more variable ($\tau: -0.48 - 0.29$), reflecting variance in the recovery of specific
¹⁷⁷ pairwise links between real and simulated networks. These results indicate that while different models often
¹⁷⁸ recover similar species-level extinction patterns, inferred interaction loss and cascade dynamics are highly
¹⁷⁹ sensitive to model choice.

¹⁸⁰ [Figure 4 about here.]

¹⁸¹ 4 Discussion

¹⁸² 5 Model choice as a component of ecological inference

¹⁸³ Reconstructing food webs from fossil data is inherently an exercise in inference under uncertainty. It involves
¹⁸⁴ not only assembling data but also making explicit assumptions about how species interact and how those
¹⁸⁵ interactions are represented mathematically (Dunne et al., 2008; Morales-Castilla et al., 2015; Strydom et
¹⁸⁶ al., 2026). This process has parallels in modern ecological network studies, where the tension between data
¹⁸⁷ limitations and the goal of meaningful ecological inference is well recognised (Delmas et al., 2019; Poisot et
¹⁸⁸ al., 2021). Results demonstrate that the choice of network reconstruction model is itself a major ecological
¹⁸⁹ decision, shaping not only the structural properties of inferred networks but also downstream interpretations
¹⁹⁰ of extinction dynamics (Allesina & Tang, 2012; Solé & Montoya, 2001).

¹⁹¹ These differences arise not from the fossil evidence *per se*, but from the assumptions embedded in each model
¹⁹² family (Pichler & Hartig, 2023; Strydom et al., 2021), such as how trophic links are defined (trait compatibility
¹⁹³ versus energetic constraints), how interaction probability is parameterised, and whether network topology is
¹⁹⁴ informed by macroecological theory (*e.g.*, niche structure) or by mechanistic rules (*e.g.*, body-size ratios).
¹⁹⁵ Consequently, network reconstruction is not a neutral methodological step; model choice shapes the ecological
¹⁹⁶ narratives we extract from ancient ecosystems. This sensitivity mirrors challenges faced in modern network
¹⁹⁷ ecology, where the choice of model and metric influences the interpretation of patterns such as connectance,
¹⁹⁸ modularity, or motif distributions (Michalska-Smith & Allesina, 2019; Poisot & Gravel, 2014) .

¹⁹⁹ While previous studies have emphasized the role of model assumptions in metaweb reconstruction (Dunhill
²⁰⁰ et al., 2024; Roopnarine, 2006), our results demonstrate that these assumptions create distinct, predictable
²⁰¹ clusters of network properties. These clusters map directly onto the conceptual divide between feasible,
²⁰² realised, and structural network types (Strydom et al., 2026). Specifically, mechanistic models (PFIM)

identify a broad landscape of trait-compatible interactions, theoretical models (ADBM, ATN, body size ratio) impose energetic filters to approximate realised energy flow, and structural models (niche, random) prioritise topological patterns over species identity.

Pairwise -turnover analysis underscores that disagreements among reconstruction approaches are not merely quantitative differences in metrics, but qualitative differences in the identity of inferred interactions. Models that may produce similar aggregate properties (*e.g.*, connectance) can still disagree strongly on species-level diets and trophic roles. This reinforces concerns raised in both paleoecological and modern studies that metrics alone can mask substantive differences in network structure and function (Fricke et al., 2022; Shaw et al., 2024).

The implications of these differences are most pronounced when interpreting extinction dynamics (Dunne et al., 2002; Sahasrabudhe & Motter, 2011). While broad, trait-driven patterns of species loss are relatively robust across models, the identity of lost interactions, secondary extinctions, and cascade dynamics are sensitive to the type of network reconstructed. Node-level patterns of species loss (such as which taxa are more likely to go extinct under certain scenarios) tend to be relatively robust across models, likely because they reflect consistent trait-based vulnerabilities. However, inferred link-level outcomes vary markedly with reconstruction assumptions as extinctions are determined by network structure, *i.e.*, are emergent properties of model assumptions. This distinction mirrors findings in modern food-web studies, where deterministic and stochastic model assumptions influence the magnitude and timing of secondary extinctions (Allesina & Tang, 2012; Curtsdotter et al., 2011; Dunne et al., 2002; Yeakel et al., 2014).

Taken together, these results highlight that network reconstruction is not neutral. Rather, it is a hypothesis generation process where the chosen model encodes a set of ecological assumptions. Consequently, paleoecologists must carefully consider which ecological signals they aim to recover (potential interactions, realised diets, or macro-scale structural properties) before selecting a reconstruction approach. Importantly, disagreement among models does not imply that any single approach is ‘wrong’, but rather reflects the fact that different models capture different ecological signals (Stouffer, 2019). The challenge therefore lies not in identifying a universally correct model, but rather in aligning model choice with the ecological question being asked. Recognising this is critical for advancing paleoecology beyond descriptive reconstruction toward rigorous comparative inference.

5.1 Aligning ecological questions with model choice

A central insight from our study is that different ecological questions require different network representations. This conclusion parallels broader efforts in network ecology to clarify what various models and metrics

234 can validly infer about ecological systems (Gauzens et al., 2025; Strydom et al., 2026). Here we provide a
235 conceptual divide between feasible, realised, and structural network types and provides a practical framework
236 for matching research goals with appropriate reconstruction approaches.

237 **Feasibility networks:** (*e.g.*, trait- and phylogeny-based metaweb approaches) are best suited for questions
238 about potential trophic links and dietary breadth. These models aim to capture the range of interactions
239 that are biologically plausible given species traits, even if not all are realised in any given context. Such an
240 approach aligns with metaweb concepts in modern ecology, where large pools of potential interactions are
241 used to understand regional species interaction potentials and local assembly processes (Tylianakis & Morris,
242 2017).

243 **Realised networks:** (*e.g.*, models incorporating energetic and foraging constraints such as body-size
244 allometry) are more appropriate when the goal is to infer the most likely realised interactions. These models
245 embed ecological rules that approximate energy transfer and foraging ecology, improving ecological plausibility
246 of predicted links as compared with purely combinatorial approaches (Brose et al., 2006; Petchey et al., 2008).

247 **Structural networks:** (*e.g.*, niche, cascade, and random models) strip away species identities in favour of
248 topological patterns, and are useful when broad questions about connectance or trophic depth are the focus.
249 Structural models have a long history in network ecology for generating null expectations about network
250 topology (Allesina et al., 2008; Williams & Martinez, 2008).

251 Recognising this alignment helps avoid misinterpretation. For example, reconstructing a metaweb and treating
252 predicted links as realised trophic interactions conflates potential with actual diet, potentially exaggerating
253 inferred interaction diversity.

254 5.2 Implications for paleoecological network studies

255 Our findings have three major implications for the field of paleoecological networks:

256 1. **Explicitly acknowledge model assumptions:** Interpretations of ancient food webs must clearly
257 articulate the assumptions underlying reconstruction models. Without this, differences in networks
258 reconstructed from different datasets or by different research groups may be misattributed to ecological
259 differences rather than methodological choices.

260 2. **Standardise comparative frameworks:** When comparing food webs across studies, researchers
261 should ensure that networks are constructed and analysed using comparable model families. Without
262 such standardisation, meta-analyses risk conflating methodological differences with ecological or temporal
263 variation.

264 3. **Leverage modern theory to expand inference:** Integrating modern network ecology frameworks
265 and methods with paleo-specific approaches enriches the inferential toolkit available to paleoecologists
266 (Dunne et al., 2014; Solé & Montoya, 2001). Models developed for modern systems (*e.g.*, allometric or
267 trait-based energy models) can be adapted to the constraints of fossil data (*e.g.*, Perez-Lamarque et al.,
268 2026), enabling novel insights into deep-time dynamics.

269 **5.3 Recommendations for network reconstruction in paleoecology**

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

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

288 **5.4 Future directions**

289 Looking ahead, paleoecological network reconstruction would benefit from deeper integration with advances
290 in modern network ecology. This includes incorporating probabilistic and Bayesian approaches to quantify
291 uncertainty in link prediction, such as Bayesian group models (Baskerville et al., 2011; Elmasri et al., 2020),
292 developing maximum entropy methods to predict network structure under constrained information (Banville

²⁹³ et al., 2023), and exploring multi-layer network representations that integrate trophic interactions with
²⁹⁴ other types of ecological relationships (Pilosof et al., 2017). Such developments, combined with increasing
²⁹⁵ availability of trait and phylogenetic information, can help bridge the gap between fossil constraints and
²⁹⁶ ecological inference, enabling more nuanced and probabilistically grounded reconstructions of deep-time
²⁹⁷ ecosystems (Banville et al., 2025; Perez-Lamarque et al., 2026; Poisot et al., 2016).

²⁹⁸ **6 Conclusions**

²⁹⁹ Ecological network reconstruction in deep time is not merely a technical step but a fundamental component
³⁰⁰ of ecological inference. By explicitly comparing six contrasting reconstruction approaches within a single
³⁰¹ extinction event and location we show that model choice strongly shapes inferred food-web structure, species
³⁰² interactions, and extinction dynamics, even when underlying fossil data are identical. While broad, trait-based
³⁰³ patterns of species loss appear relatively robust, conclusions about pairwise interactions, secondary extinctions,
³⁰⁴ and cascading dynamics depend critically on the assumptions embedded in the chosen network reconstruction
³⁰⁵ approach. These results underscore the need for paleoecological studies to align reconstruction methods
³⁰⁶ with specific ecological questions and to evaluate the sensitivity of key conclusions to alternative network
³⁰⁷ representations. More broadly, our findings highlight that understanding past ecosystem collapse requires not
³⁰⁸ only better fossil data, but also transparent, question-driven modelling frameworks that make explicit the
³⁰⁹ assumptions underlying ecological inference.

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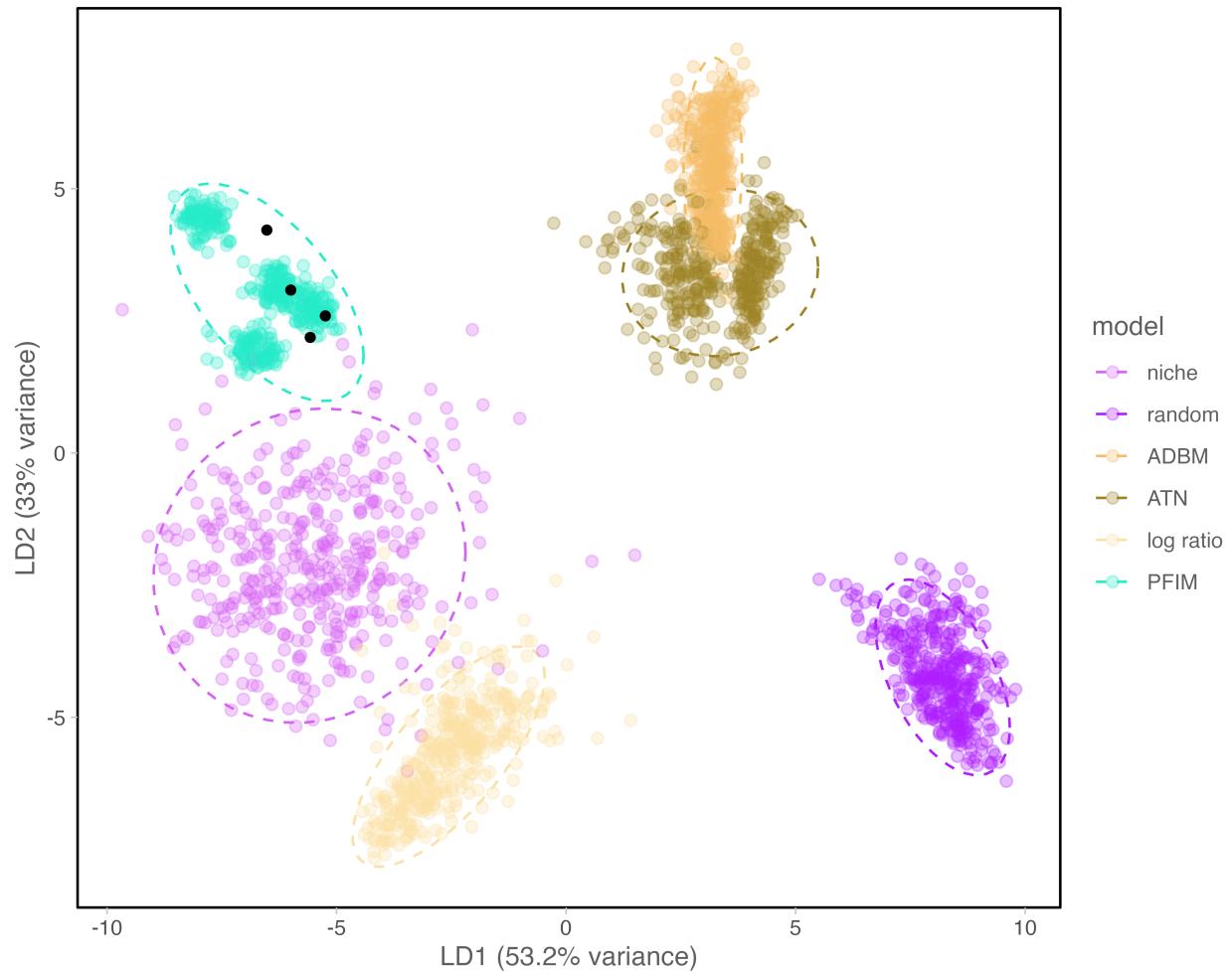


Figure 1: Linear discriminant analysis (LDA) of ecological network metrics for six model types. Each point represents a replicate, and ellipses indicate 95% confidence regions for each model. The second column represents the correlation of the various network metrics with the respective LDA axes.

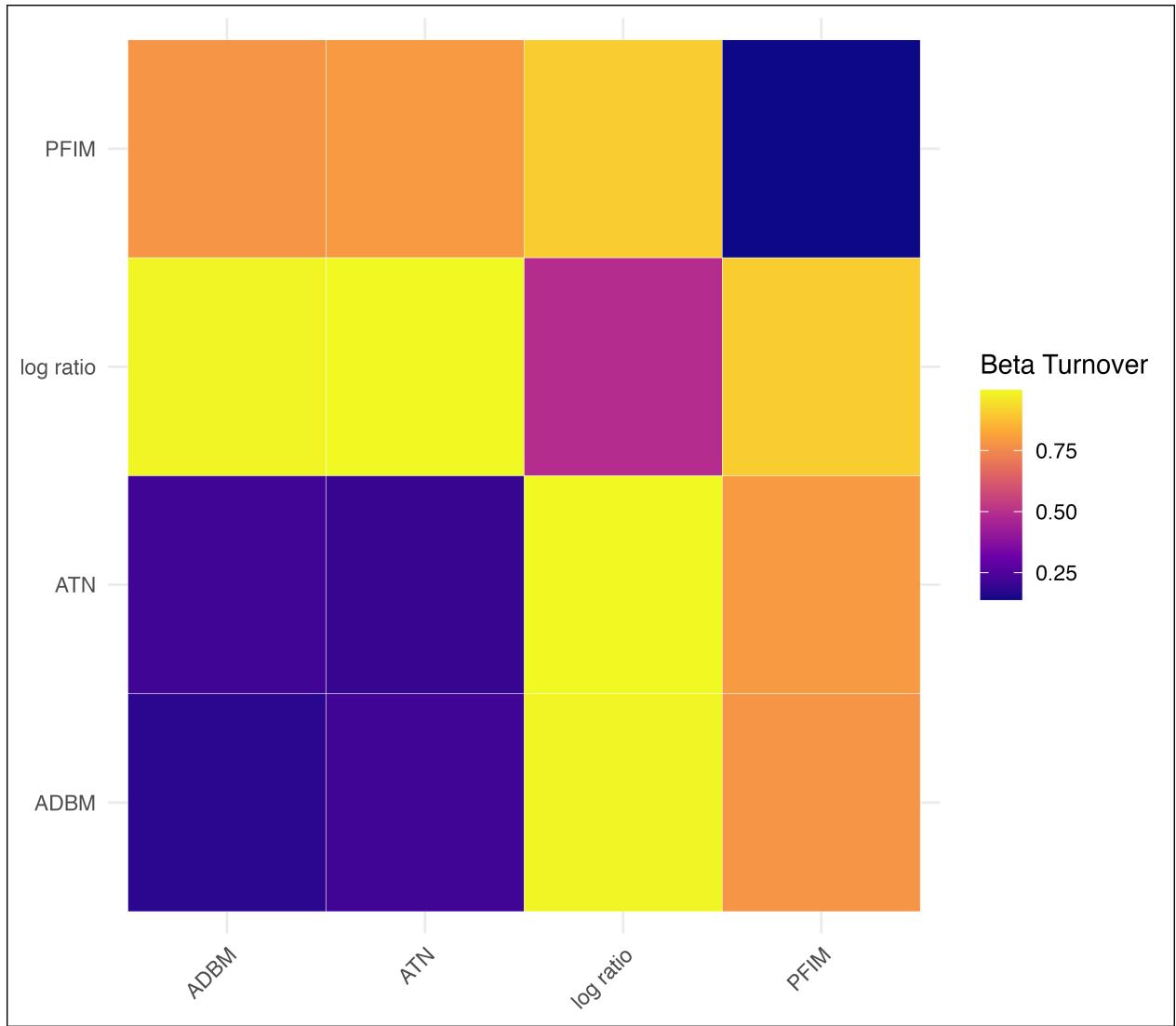


Figure 2: Pairwise beta turnover in species interactions among four ecological network models (ADBM, lmatrix, body-size ratio, and pfim). Each cell represents the mean turnover value between a pair of models, with warmer colors indicating greater dissimilarity in inferred interactions. The diagonal is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

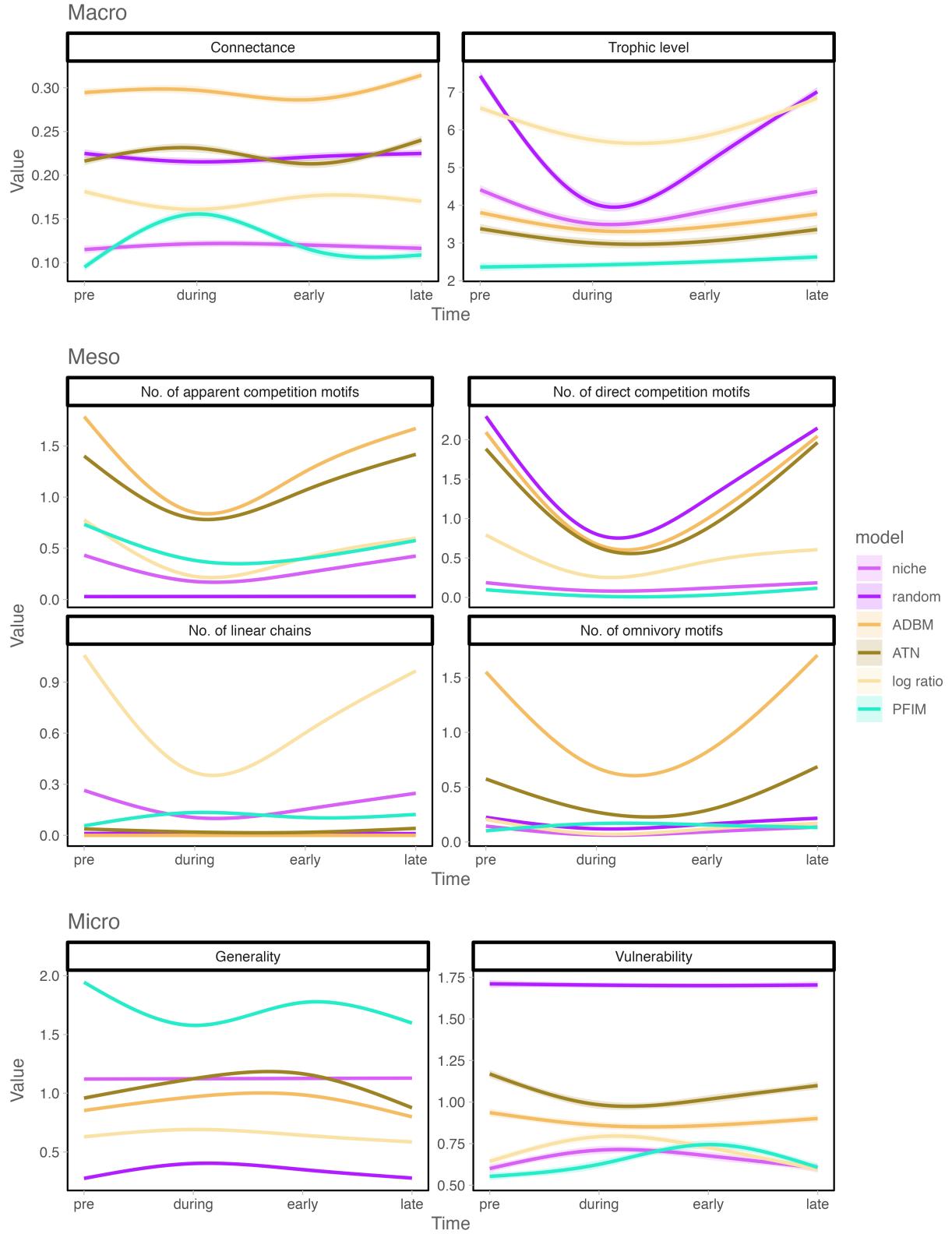
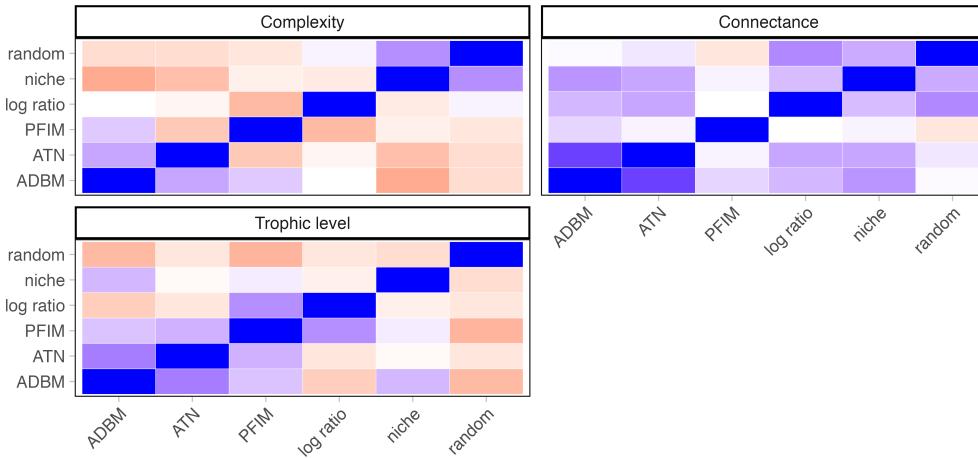
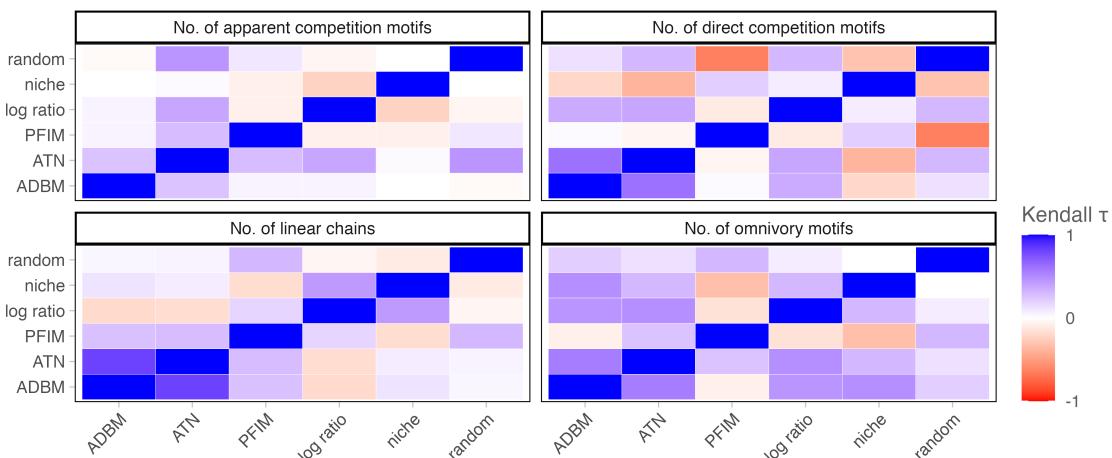


Figure 3: GAM-predicted trajectories of network structure during extinction simulations reveal pronounced differences in the timing and magnitude of change across reconstruction models. Lines show model-specific smooths and shaded areas indicate 95% confidence intervals. Deterministic approaches produce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

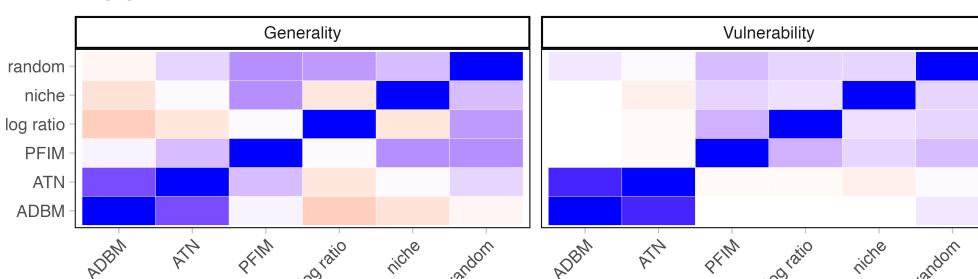
Macro



Meso



Micro



TSS

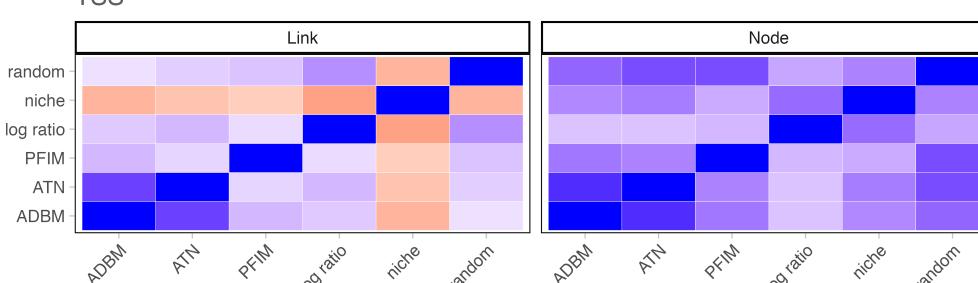


Figure 4: Heatmaps showing pairwise Kendall rank correlation coefficients (τ) between models for each network metric. Each panel corresponds to a different metric and displays the degree of agreement in extinction-scenario rankings across models based on mean absolute differences (MAD) between observed 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