

Model structure conditions ecological inference in food web reconstruction

Tanya Strydom ¹; Baran Karapunar ²; Andrew P. Beckerman ¹; Alexander Dunhill ²

Abstract: Aim

Ecological networks are widely used to compare community structure, stability, and responses to disturbance across environmental gradients. However, many networks (particularly those assembled from incomplete interaction data) require model-based reconstruction. We test how alternative reconstruction frameworks condition ecological inference by quantifying their effects on network structure and disturbance dynamics.

Location

Cleveland Basin, United Kingdom.

Time period

Toarcian extinction event (Early Jurassic, late Pliensbachian–late Toarcian, ~183 Ma).

Major taxa studied

Marine animal communities.

Methods

We reconstructed four successive communities from an identical species pool using six contrasting food-web models spanning feasible (trait-based), realised (allometric and energetic), and structural (topological) network representations. For each community and model, 100 replicate networks were generated. We quantified macro-, meso-, and micro-scale network properties and assessed differences among models using multivariate analyses. Pairwise interaction turnover was measured using link-based beta diversity. We then simulated species loss under multiple disturbance scenarios, allowing cascading extinctions, and compared predicted community states using mean absolute differences and rank concordance metrics between models.

Results

Reconstruction framework strongly influenced inferred network topology (MANOVA, $p < 0.001$), generating distinct structural signatures independent of species composition. Models that were similar in global metrics often diverged in species-level interactions, with high -turnover among inferred link sets. During disturbance simulations, species-level vulnerability rankings were broadly consistent across models, but interaction-level outcomes and cascade dynamics varied substantially. Concordance in extinction-scenario rankings was scale dependent, with higher agreement at the species level than at the interaction level.

Main conclusions

Network reconstruction functions as a structural prior that conditions ecological inference. While some aggregate patterns are robust across modelling frameworks, detailed interaction-level dynamics are highly model contingent. Comparative network studies across spatial or environmental gradients should therefore align reconstruction framework with inferential goals and explicitly evaluate sensitivity to modelling assumptions.

Keywords: Ecological networks, Biotic interactions, Community assembly, Environmental gradients, Interaction turnover, Trophic organisation, Ecosystem resilience, Macroecology

¹ 1 Introduction

² Understanding how biodiversity is organised across space and time is a central goal of macroecology and
³ biogeography. While early efforts focused primarily on species richness and composition, there is growing
⁴ recognition that ecological communities are structured not only by which species occur, but by how they
⁵ interact (Thuiller et al., 2024). Interaction networks are increasingly treated as macroecological state variables
⁶ where they are used to compare community organisation across environmental gradients, to quantify -diversity
⁷ in interaction structure, to evaluate stability-complexity relationships, and to infer vulnerability under global
⁸ change (Carstensen et al., 2014; Gravel et al., 2019; Poisot et al., 2015; Trøjelsgaard & Olesen, 2016; Tylianakis
⁹ & Morris, 2017).

¹⁰ As a result, ecological networks now play a central role in comparative analyses spanning latitudinal gradients,
¹¹ disturbance regimes, and deep-time environmental transitions (Dunhill et al., 2024; Hao et al., 2025; Michalska-
¹² Smith & Allesina, 2019; Poisot & Gravel, 2014; Roopnarine, 2006). Implicit in this expansion is the critical
¹³ assumption that network properties estimated across systems are structurally comparable, and that differences
¹⁴ among them reflect ecological signal rather than methodological artefact (Fründ et al., 2016; Jordano, 2016).

¹⁵ Yet most ecological networks are not fully observed as interaction data are incomplete and sampling is
¹⁶ uneven across historical and biogeographic contexts, across both contemporary and deep-time (Catchen et
¹⁷ al., 2023; Poisot et al., 2021; Sandra et al., 2025). Interactions must often be inferred indirectly from traits,
¹⁸ phylogeny, body size, co-occurrence, or theoretical constraints (Morales-Castilla et al., 2015; Strydom et
¹⁹ al., 2021). Network construction therefore constitutes a model-based inference step rather than a purely
²⁰ descriptive exercise. Different reconstruction frameworks encode distinct ecological assumptions about how
²¹ interactions arise - whether as biologically feasible combinations of traits, energetically optimised realised diets,
²² or topological structures constrained by macroecological regularities. These assumptions act as structural
²³ priors over network architecture (Gauzens et al., 2025; Guimarães, 2020; Petchey et al., 2011; Strydom et
²⁴ al., 2026). If alternative reconstruction models systematically generate different trophic configurations, then
²⁵ comparative analyses risk conflating ecological differences among communities with artefacts introduced by
²⁶ modelling choice. The reliability of macroecological inference therefore depends not only on ecological data,
²⁷ but on the structural assumptions embedded in network reconstruction.

²⁸ Despite rapid methodological development in interaction inference, few studies have directly evaluated how
²⁹ alternative reconstruction frameworks condition macroecological conclusions when applied to the same species
³⁰ pool. This gap is particularly consequential for comparative research, where network metrics are routinely
³¹ interpreted as indicators of environmental filtering, disturbance intensity, evolutionary history, or community

stability (Allesina & Tang, 2012; Delmas et al., 2018; Poisot et al., 2015). If reconstruction models encode distinct structural priors over interaction topology, then differences among communities may reflect modelling assumptions rather than ecological processes. We therefore test whether macroecological inference derived from ecological networks is robust to variation in reconstruction framework, asking which aspects of network-based inference are stable across plausible representations of interaction structure and which are intrinsically model dependent.

Deep-time ecosystems provide an especially stringent test of this issue because interactions are not observed directly and must be reconstructed explicitly (Dunhill et al., 2024; Dunne et al., 2008; Dunne et al., 2014; Roopnarine, 2006), rendering modelling assumptions transparent. Against this stringency, here we re-evaluate inferences made by Dunhill et al. (2024) on community structure and extinction dynamics during the early Toarcian extinction event (~183 Ma), a volcanic-driven hyperthermal and marine crisis in the Early Jurassic (Kemp et al., 2024). Using four successive communities drawn from an identical taxon pool, we reconstruct ecological networks under six contrasting model classes spanning feasible, realised, and structural representations. For each reconstruction framework, we quantify emergent topology across scales, measure interaction turnover, and simulate disturbance-driven collapse. By holding species composition constant while varying the food web model used, this design isolates the influence of model constrained structure on inferred food web organisation and extinction dynamics, allowing us to distinguish ecological signals that are robust from those that are reconstruction contingent.

2 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. This interval encompasses a major volcanic-driven hyperthermal and marine extinction event. To capture network dynamics across this transition, we defined four successive paleo-communities: Pre-extinction (Pliensbachian), Post-extinction (Lower Toarcian), Early recovery, and Late recovery (Middle/Upper Toarcian). Each taxon was characterized using their size and Bambach's ecospace framework (Bambach et al., 2007), coding for tiering, motility, and feeding mode as per Dunhill et al. (2024). Each assemblage was treated as a community of potentially interacting taxa. The dataset includes 57 taxa across diverse groups (*e.g.*, cephalopods, bivalves, and gastropods). By restricting our analysis to a single basin with consistent lithofacies, we controlled for biogeographic noise, ensuring that structural shifts across the four time-bins reflect localised ecological responses to environmental stress rather than sampling or facies bias.

62 2.2 Network reconstruction approaches

63 2.2.1 Conceptual classification of network types

64 Most paleo-specific research (*e.g.*, Fricke et al. (2022); Roopnarine (2006); Shaw et al. (2024)) currently uses
65 models from within the feasibility space. That is, the model reconstructions identify and encode the entire
66 feasible diet of a species to build the network. These methods, however, represent only a subset of the broader
67 spectrum of network construction approaches. Here, we present a suite of methods (Table 1) that enable
68 the construction of a wider range of ecological networks and the exploration of a broader set of ecological
69 questions, provided that their underlying assumptions are compatible with the constraints of fossil data. The
70 methods include a) structural models that create species agnostic networks that are structurally ‘correct’ by
71 assigning links between nodes based on assumptions of link distributions; and b) realised models that create
72 networks where links between species are constrained based on some form of ‘species choice’ *e.g.*, maximising
73 energy gain.

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 (feasibility, 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	Assumptions	Data needs	Limitation	Network type	Key reference	Usage examples
Random	Links assigned randomly	Species richness, number of links	Parameter assumptions, species agnostic	Structural	Erdős & Rényi (1959)	Null-model comparisons; testing whether observed network structure (connectance, motifs) deviates from random expectations

Model	Assumptions	Data needs	Limitation	Network type	Key reference	Usage examples
Niche	Species ordered along a ‘niche axis’; interactions interval-constrained	Species richness, connectance	Parameter assumptions, species agnostic	Structural	Williams & Martinez (2008)	Evaluating trophic hierarchy and motif structure; baseline structural predictions
Allometric diet breadth model (ADBM)	Energy-maximizing predator diets	Body mass, abundance/predator dance/biomass foraging; does not account for forbidden links	Assumes optimal foraging; does not account for forbidden links	Realised	Petchey et al. (2008)	Predicting realized predator diets; exploring secondary extinctions
Allometric trophic network (ATN)	Links constrained by body-size ratios and functional response	Body mass, number of basal species	Assumes only basal species	Realised	Brose et al. (2006); Gauzens et al. (2023)	Simulating species loss; evaluating network collapse dynamics
Paleo food web inference model (PFIM)	Interactions inferred using trait-based mechanistic rules	Feeding traits	Assumes feeding mechanisms; trait resolution required	Feasibility	Shaw et al. (2024)	Mapping feasible trophic interactions; assessing secondary extinctions

Model	Assumptions	Data needs	Limitation	Network type	Key reference	Usage examples
Body-size ratio model	Probabilistic assignment of links based on predator-prey size ratios	Body mass	Does not account for forbidden links	Realised	Rohr et al. (2010)	Estimating likely interactions; simulating cascading effects.

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

80 2.2.2 Network generation and replication

81 We evaluated six models spanning this space Table 1: random and niche models (structural networks);
 82 allometric diet breadth (ADBM), allometric trophic network (ATN), and Body-size ratio models (realised
 83 networks); and a paleo food web inference model (PFIM; feasibility network). Expanded descriptions of
 84 model assumptions, parameterisation, and link-generation rules are provided in Supplementary Material
 85 S1. For each community, 100 networks were generated per model per successive community ($n = 2400$) to
 86 capture stochastic variation in link assignment. Where models required species body mass or trait values,
 87 these were sampled within biologically reasonable ranges to preserve relative differences among species. We
 88 adopted uniform sampling by default, as alternative distributions (lognormal, truncated lognormal) have
 89 negligible impact on topology (Supplementary Material S2; Figure S1). Structural models were parameterized
 90 using connectance values drawn from an empirically realistic range (0.07 – 0.34), with species richness held
 91 constant. Identical parameter draws were applied across comparable models within each replicate to ensure
 92 comparability. For the Body-size ratio model, we followed the approach of Yeakel et al. (2014) and excluded
 93 latent trait terms as opposed fitting the full model, which introduces additional inference and assumptions.

94 2.3 Network metrics and structural analyses

95 We quantified network structure using a suite of macro-, meso-, and micro-scale metrics Table 2, capturing
 96 global properties, motif structure, and species-level variability. Differences among reconstruction approaches
 97 were assessed using a multivariate analysis of variance (MANOVA), with model identity as a fixed factor
 98 and the full set of network metrics as response variables. Pairwise interaction turnover was quantified using
 99 link-based beta diversity, which measures dissimilarity in the identity of trophic links between networks,
 100 capturing differences due to species turnover or changes in interactions among shared species (Poisot et al.,
 101 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)
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)

Metric	Definition	Scale	Reference (for maths), can make footnotes probs
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, standardised by L/S	Micro	Williams & Martinez (2000)
Vulnerability	Normalized standard deviation of vulnerability of a species, standardised by L/S	Micro	Williams & Martinez (2000)

102 2.4 Extinction simulations and model evaluation

103 Following Dunhill et al. (2024) and using the pre-extinction and post-extinction networks, we simulated
 104 species loss under multiple extinction scenarios including trait-based, network-position-based, and random
 105 removals, allowing cascading extinctions to propagate (cascading secondary extinctions). Simulated outcomes
 106 were compared to observed or expected community states using mean absolute differences (MAD) of food web
 107 metrics and modified true skill statistics (TSS) at node and link levels. Kendall's rank correlation coefficient
 108 was used to evaluate concordance in scenario rankings across reconstruction models, providing a measure of
 109 robustness in inferred community responses.

110 3 Results

111 Results show that reconstruction approaches that appear similar when evaluated using global network metrics
 112 can yield fundamentally different ecological narratives when interrogated at the level of interactions and
 113 extinction dynamics. Across six network reconstruction approaches, inferred food web structure, species
 114 interactions, and extinction dynamics differed consistently. Multivariate analyses showed pronounced separation
 115 among models in network metric space. Reconstruction approach explained most of the variance in structural
 116 properties, leaving a distinct signature independent of community composition. Notably, agreement among

models depended on the scale at which the comparison was made- approaches that were statistically similar in multivariate structural space (scale 1) often diverged in inferred interactions (scale 2) or extinction dynamics (scale 3). This demonstrates that structural similarity does not guarantee concordance in species-level diets or trophic roles.

Model choice 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 networks depend critically on the reconstruction framework employed.

3.1 Network structure differs among reconstruction approaches

Across six reconstruction approaches, network structure (network properties listed in Table 2) differed significantly (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 identified two dominant axes of variation, explaining 86% of between-model variance. LD1 correlated with vulnerability, direct competition motifs, and connectance. LD2 correlated with maximum trophic level and apparent competition motifs, reflecting vertical trophic structure (Figure 1; Table S1, Figure S1). All higher-order canonical variates each explained less than 9% of the remaining variance.

[Figure 1 about here.]

3.1.1 Variance partitioning of network structure

Permutational multivariate analysis of variance revealed that reconstruction framework accounted for the majority of variation in multivariate network structure ($R^2 = 0.795$, $p < 0.001$), whereas temporal turnover across extinction phases explained a comparatively small proportion of variance ($R^2 = 0.064$, $p < 0.001$). The model \times time interaction contributed a further 7.1% of variance ($R^2 = 0.071$, $p < 0.001$), indicating limited but significant time-dependent divergence among reconstruction frameworks. Thus, differences among modelling approaches were more than an order of magnitude greater than structural differences associated with ecological turnover through the extinction sequence, even if the Toarcian dataset was characterized with a significant community turnover.

To determine whether the dominance of the reconstruction framework reflected absolute mean shifts among time bins, we repeated the analysis after centring network metrics within each extinction phase. This procedure removes between-phase differences while retaining within-phase structural variation. Even after temporal

¹⁴⁷ bin-standardised centring, the reconstruction framework explained 84.8% of multivariate variance ($R^2 = 0.848$,
¹⁴⁸ $p < 0.001$). These results demonstrate that the influence of model choice is not driven by temporal mean
¹⁴⁹ differences, but reflects intrinsic divergence among reconstruction frameworks in how ecological interactions
¹⁵⁰ are organised.

¹⁵¹ **3.1.2 Inferred pairwise interactions vary widely among models**

¹⁵² Despite some models showing similar global metrics, specific pairwise interactions often differed. Pairwise
¹⁵³ -turnover revealed that certain model pairs shared very few links Figure 2. Size-based models (ADBM,
¹⁵⁴ ATN) were broadly similar due to shared sole reliance on body-size constraints, whereas the Body-size ratio
¹⁵⁵ model exhibited consistently higher differences to other models. PFIM showed intermediate overlap with
¹⁵⁶ theoretical models. These results demonstrate that agreement in global network structure does not guarantee
¹⁵⁷ concordance in species-level interactions.

¹⁵⁸ [Figure 2 about here.]

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

¹⁶⁰ To quantify how network structure changed over time during extinction simulations and whether these
¹⁶¹ dynamics differed among reconstruction models, we fit generalized additive models (GAMs) to time series
¹⁶² of network-level metrics. GAMs capture non-linear temporal trajectories, allowing formal tests of whether
¹⁶³ the shape of these trajectories differs among models. These model-specific temporal trajectories are shown
¹⁶⁴ in Figure 3. For all metrics examined, the inclusion of model-specific smooth terms significantly improved
¹⁶⁵ model fit (ANOVA model comparison: $p < 0.001$ for all metrics). Model-specific smooths differed not only
¹⁶⁶ in magnitude but also in the timing and abruptness of change, indicating distinct modes of collapse across
¹⁶⁷ reconstruction approaches (Tables S3–S4). Deterministic, data-driven approaches (PFIM) and allometric
¹⁶⁸ models (ADBM, ATN) exhibited highly non-linear trajectories, showing structural shifts in connectivity
¹⁶⁹ and motif frequency. In contrast, the Niche model produced the most consistent and gradual trajectories,
¹⁷⁰ effectively smoothing the perceived magnitude of structural change during community collapse. These results
¹⁷¹ demonstrate that inferred pathways of collapse, trophic bottlenecks, and secondary extinctions are highly
¹⁷² sensitive to model choice. Corresponding raw temporal trajectories are shown in Figure S2.

¹⁷³ [Figure 3 about here.]

¹⁷⁴ To evaluate how model choice affects inferred extinction dynamics, we compared simulated post-extinction
¹⁷⁵ networks to observed networks using mean absolute differences (MAD) for network-level metrics and true
¹⁷⁶ skills statistics (TSS) for node- and link-level outcomes Figure 4. Across models, MAD-based rankings were

177 generally positively correlated (Kendall's $\tau = 0.13$ across structural metrics), indicating broad agreement on
178 the relative importance of extinction drivers despite substantial differences in reconstructed network structure.
179 However, agreement within the allometric models differed from patterns observed for reconstructed network
180 structure.

181 Node-level TSS rankings were similarly consistent across models ($\tau = 0.26\text{--}0.90$), reflecting broadly comparable
182 species removal sequences. In contrast, link-level outcomes were far more variable ($\tau = -0.48\text{--}0.29$), highlighting
183 that inferences about which interactions are lost, retained, or re-established during collapse and recovery are
184 highly model contingent. Together, these results suggest that while alternative models converge on similar
185 species-level extinction patterns, the inferred pathways of interaction loss and cascading dynamics depend
186 strongly on both reconstruction approaches.

187 [Figure 4 about here.]

188 4 Discussion

189 4.1 Network reconstruction is not neutral: structural priors shape ecological 190 theory

191 Food web ecology has long treated network reconstruction as a technical step preceding ecological analysis.
192 Once a network is assembled (whether from observation, inference, or simulation) its properties are typically
193 analysed as reflections of underlying ecological organisation. Implicit in this workflow is a powerful assumption
194 - that reconstructed networks provide structurally comparable representations of ecological communities, such
195 that differences in connectance, trophic structure, motif composition, or robustness primarily reflect biological
196 variation.

197 Our results challenge this assumption and reveal strong sensitivity of inference about secondary extinction
198 dynamics in paleo-foodwebs. Across an identical species pool, reconstruction frameworks explained the majority
199 of variance among reconstructed network topologies, generating distinct structural signatures independent
200 of community composition. Although some model classes converged on similar global metrics, pairwise
201 interaction turnover revealed substantial divergence in inferred trophic links. Structural similarity at the
202 level of connectance or trophic height therefore does not guarantee concordance in species roles or interaction
203 architecture.

204 Reconstruction framework explained the majority of variance in inferred food web topology, far outweighing
205 the influence of temporal turnover across extinction phases. These patterns demonstrate that the divergence

among reconstruction approaches reflects intrinsic differences in how models organise interactions, not temporal shifts in network structure. In other words, different reconstruction approaches impose distinct structural priors on inference of ecological organisation. These priors are not subtle - they propagate into emergent topology, species roles, and dynamical predictions. Network structure is therefore not solely a property of ecological communities; it is jointly determined by ecological data, modelling assumptions, and level of organisation (Gauzens et al., 2025; Guimarães, 2020; Pichler & Hartig, 2023; Strydom et al., 2021; Strydom et al., 2026).

This has direct implications for the interpretation of comparative network studies. Feasible, realised, and structural models encode different assumptions about constraint, optimisation, and topology, and these assumptions propagate into emergent metrics and dynamical predictions (Allesina & Tang, 2012; Dunne et al., 2002; Michalska-Smith & Allesina, 2019; Poisot & Gravel, 2014; Solé & Montoya, 2001). When networks reconstructed under different model classes are compared across spatial gradients, disturbance regimes, or evolutionary transitions, part of the observed variation may derive from structural priors rather than ecological process. Without explicit standardisation or sensitivity analysis, methodological heterogeneity can be mistaken for biological signal. Food web ecology has devoted substantial effort to understanding how topology shapes dynamics; comparatively less attention has been paid to how reconstruction method shapes topology. Our findings indicate that these two questions cannot be separated.

4.2 Scale-dependent robustness in network-based inference

Importantly, reconstruction sensitivity was not uniform across network scales (macro-, meso-, micro- level properties). Species-level extinction rankings were broadly consistent among model classes, whereas interaction-level outcomes and cascade trajectories were highly contingent on structural prior. The predominance of reconstruction framework over temporal turnover (~80% vs. 6% variance explained) illustrates why coarse-grained patterns like species-level extinction rankings are more robust. Model-imposed structure dominates the overall topology, leaving finer-scale interaction dynamics highly contingent on framework choice. This asymmetry reveals a context-dependent pattern of robustness. Coarse-grained macroecological patterns (such as the vulnerability of a community to collapse) can emerge from multiple plausible interaction architectures. By contrast, fine-grained inferences about which links are lost, retained, or reorganised depend strongly on how interactions are inferred.

This distinction challenges a central ambition of food web ecology - the use of detailed interaction structure to diagnose mechanisms of stability and collapse (*e.g.*, Dunhill et al., 2024). If interaction-level cascade pathways vary substantially across equally plausible reconstructions, then mechanistic narratives derived

²³⁷ from a single inferred topology may overstate their precision (Allesina & Tang, 2012; Curtsdotter et al., 2011;
²³⁸ Dunne et al., 2002). The apparent determinism of extinction cascades or trophic bottlenecks may partly
²³⁹ reflect model-imposed structure rather than ecological inevitability.

²⁴⁰ For macroecology, this metric dependence clarifies where network-based inference is accurate. Aggregate
²⁴¹ properties may be comparatively robust to reconstruction assumptions, whereas conclusions about interaction
²⁴² turnover, motif reorganisation, or fine-scale trophic dynamics are intrinsically uncertain. Recognising this
²⁴³ asymmetry is essential if network analyses are to inform comparative synthesis across space and time.

²⁴⁴ Taken together, these results underscore that network reconstruction is not a neutral preprocessing step but
²⁴⁵ part of a hypothesis-generating process in which each model encodes a distinct set of ecological assumptions.
²⁴⁶ The inferred topology and dynamics of a food web therefore reflect not only ecological data, but the theoretical
²⁴⁷ assumptions embedded in the reconstruction framework. Disagreement among models does not imply that
²⁴⁸ any single approach is ‘wrong’, but rather that different models capture different facets of ecological reality
²⁴⁹ (Petchey et al., 2011; Stouffer, 2019). Disagreement among models does not imply that any single approach
²⁵⁰ is ‘incorrect’. Rather, different models capture different facets of ecological constraint—trait compatibility,
²⁵¹ energetic optimisation, or topological regularity. The critical point is that these facets are not interchangeable.

²⁵² This perspective reframes reconstruction choice as part of hypothesis specification. Researchers must align
²⁵³ reconstruction approaches with the ecological signals of interest (whether potential interactions, realised
²⁵⁴ diets, or macro-scale structural properties) rather than treating model selection as a technical convenience.
²⁵⁵ Viewed through the lens of accuracy and precision, our results indicate that some network-based inferences
²⁵⁶ are relatively robust across reconstruction approaches, whereas others remain intrinsically uncertain. High-
²⁵⁷ level extinction rankings were broadly convergent, suggesting relative accuracy at coarse resolution, but
²⁵⁸ interaction-level details and temporal cascade dynamics diverged substantially, indicating limited precision
²⁵⁹ in reconstructing the fine structure of collapse. Recognising and explicitly accounting for this distinction
²⁶⁰ is essential if food web ecology is to move beyond descriptive reconstruction toward rigorous comparative
²⁶¹ inference.

²⁶² 4.3 Implications for comparative biogeography and global change research

²⁶³ Network approaches are increasingly applied to examine how ecological organisation varies across latitudinal
²⁶⁴ gradients, environmental filters, disturbance regimes, and climate-driven transitions. These studies frequently
²⁶⁵ interpret variation in connectance, trophic height, interaction -diversity, or robustness as indicators of
²⁶⁶ ecological differentiation among regions or time intervals. Yet reconstruction frameworks often differ among
²⁶⁷ systems due to variation in sampling intensity, trait resolution, or modelling preference. Our results show

268 that such differences can systematically alter inferred topology and disturbance dynamics even when species
269 composition is held constant.

270 This finding has consequences for interaction biogeography. Apparent differences in network turnover across
271 spatial gradients may reflect divergence in structural priors rather than genuine ecological reorganisation.
272 Similarly, projected differences in vulnerability under climate change may depend on how realised interactions
273 are modelled, not solely on community composition. Without explicit treatment of reconstruction assumptions,
274 comparative network analyses risk conflating modelling artefact with macroecological process.

275 If ecological networks are to function as reliable macroecological state variables, reconstruction framework must
276 be treated as a formal component of hypothesis specification. Cross-system comparisons should standardise
277 modelling approaches wherever possible, or explicitly evaluate sensitivity to alternative structural priors.
278 Ensemble reconstruction—treating networks as distributions rather than single topologies—offers a principled
279 pathway toward incorporating structural uncertainty into comparative synthesis.

280 4.4 Toward a more explicit modelling paradigm in food web ecology

281 The broader implication is not that any single reconstruction framework is ‘correct’ or ‘incorrect’. Rather, each
282 model class represents a distinct hypothesis about how interactions are constrained—by trait compatibility,
283 energetic optimisation, or topological regularity (Petchey et al., 2011). Food web reconstruction is therefore
284 theory-laden. Making this explicit shifts reconstruction from a preparatory step to a central component of
285 ecological modelling.

286 A mature modelling paradigm in food web ecology would treat structural priors as testable assumptions,
287 incorporate probabilistic link inference where possible, and quantify the sensitivity of macroecological
288 conclusions to alternative representations of interaction structure. Such an approach aligns with recent
289 advances in probabilistic and ensemble network modelling and would strengthen the interpretability of
290 network-based inference under global change (Banville et al., 2025; Baskerville et al., 2011; Elmasri et al.,
291 2020; Perez-Lamarque et al., 2026; Poisot et al., 2016).

292 5 Conclusions

293 Ecological network reconstruction is not a neutral technical procedure but a theoretical act that shapes
294 ecological inference. By applying six contrasting reconstruction frameworks to an identical species pool, we
295 show that structural priors systematically influence inferred food-web topology, interaction identity, and
296 disturbance dynamics. Some coarse-grained patterns, such as relative species vulnerability, are comparatively

297 robust across representations. In contrast, fine-scale interaction structure and cascade pathways are highly
298 contingent on modelling assumptions. The reliability of network-based inference is therefore scale dependent.

299 These results challenge the implicit assumption that reconstructed networks are structurally commensurable
300 across systems. When reconstruction frameworks differ, variation in connectance, trophic organisation,
301 robustness, or interaction turnover may reflect embedded modelling assumptions as much as ecological
302 processes. Network reconstruction should thus be treated as an explicit component of hypothesis specification
303 in comparative macroecology and biogeography.

304 No single model captures the full complexity of ecological organisation, but neither are alternative models
305 interchangeable. Aligning reconstruction framework with inferential goals, standardising approaches across
306 comparative studies, and incorporating ensemble or probabilistic representations will be essential for strength-
307 ening the interpretability of network analyses across spatial and temporal gradients. As ecological networks
308 increasingly inform global change research, recognising structural priors as fundamental determinants of
309 inference is critical for advancing food web ecology from descriptive reconstruction toward rigorous comparative
310 synthesis.

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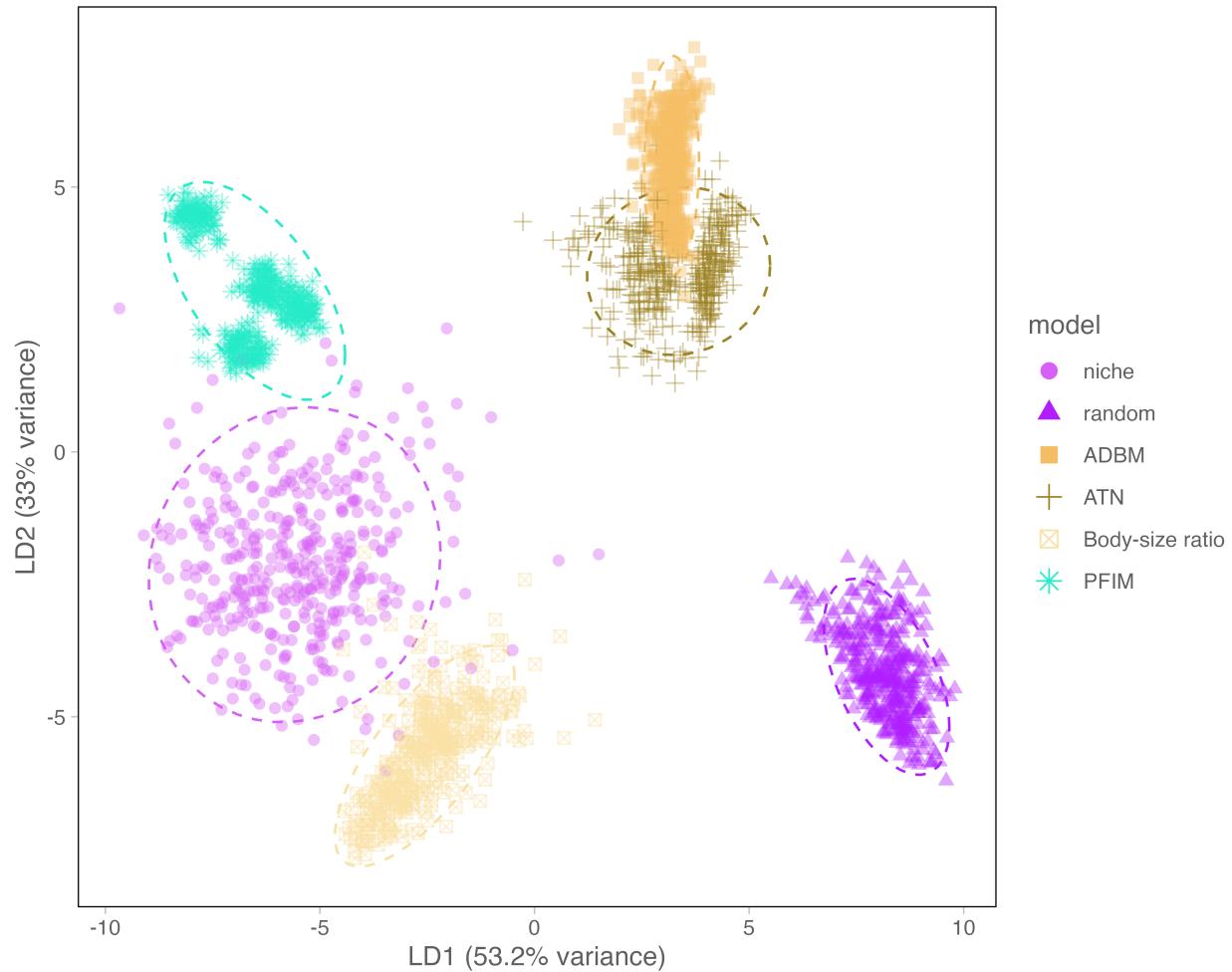


Figure 1: Linear discriminant analysis (LDA) of ecological network metrics for six model types. Each point represents a replicate, and ellipses indicate 95% confidence regions for each model. The second column represents the correlation of the various network metrics with the respective LDA axes.

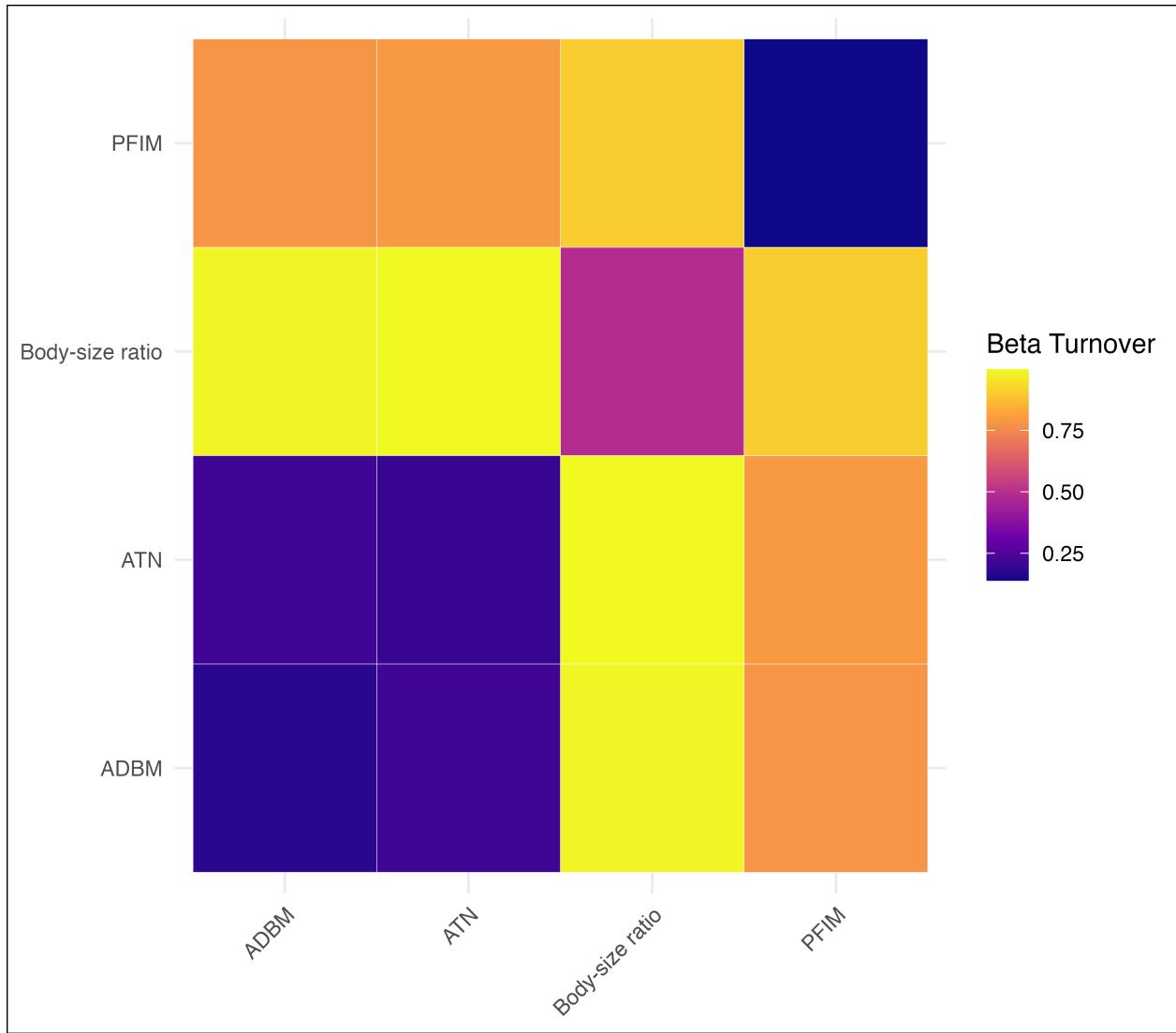


Figure 2: Pairwise β -turnover in species interactions among four ecological network models (ADBM, ATN, Body-size ratio, and PFIM). Each cell represents the mean turnover value between a pair of models, with warmer colours indicating greater dissimilarity in inferred interactions. The diagonal is omitted.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

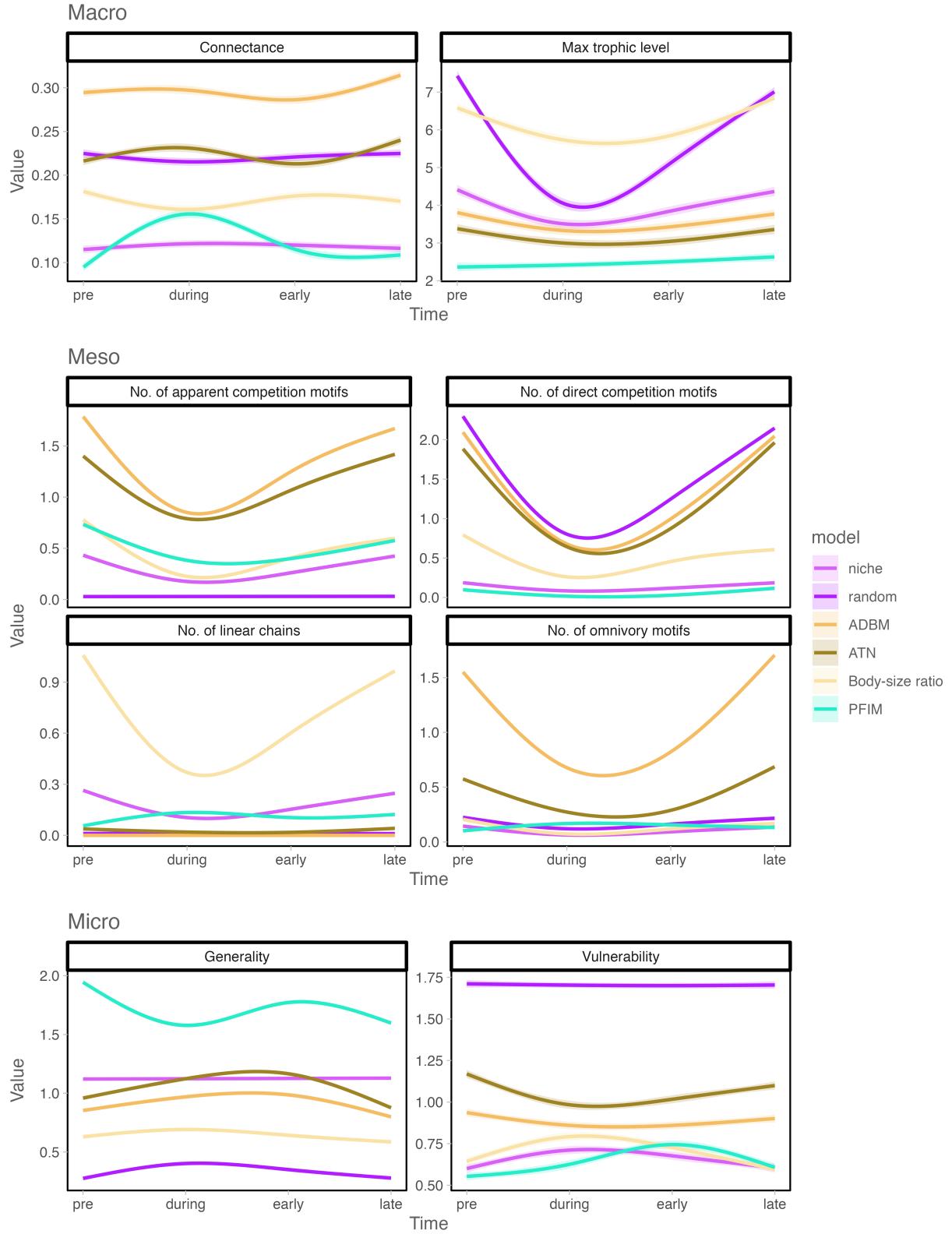


Figure 3: GAM-predicted trajectories of network structure during extinction simulations reveal pronounced differences in the timing and magnitude of change across reconstruction models. Lines show model-specific smooths and shaded areas indicate 95% confidence intervals. Deterministic approaches produce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

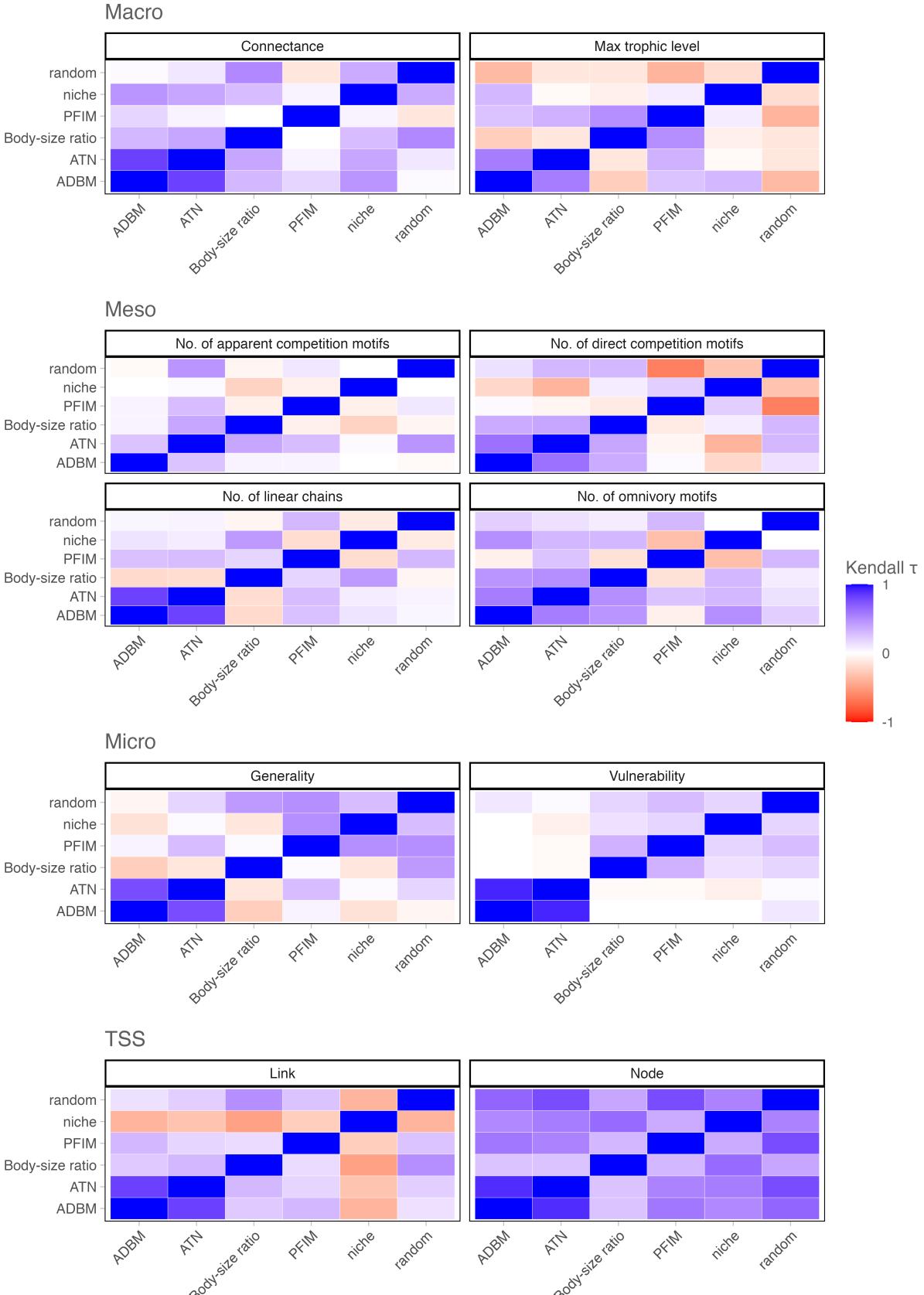


Figure 4: Heatmaps showing pairwise Kendall rank correlation coefficients (τ) between models for each network metric. Each panel corresponds to a different metric and displays the degree of agreement in extinction-scenario rankings across models based on mean absolute differences (MAD) between observed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