Model structure conditions ecological inference in food web reconstruction

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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

Early Jurassic (upper Pliensbachian–upper Toarcian, ~183 Ma).

Major taxa studied

Marine invertebrate 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 secondary extinctions, and compared predicted community states using mean absolute differences and rank concordance metrics.

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.

1 Introduction

Ecological networks provide a powerful framework for understanding how communities are structured across space and time. By representing species and their interactions explicitly, food webs allow ecologists to quantify complexity, trophic organization, vulnerability, and the propagation of disturbance through ecosystems (Delmas et al., 2018). Network approaches have therefore become central to comparative ecology, from evaluating latitudinal gradients in interaction structure to assessing how communities reorganize following environmental change (Gravel et al., 2019; Hao et al., 2025; Poisot et al., 2015; Tylianakis & Morris, 2017). However, ecological networks are rarely fully observed (even in modern systems), and interaction data are incomplete, biased, and scale dependent (Catchen et al., 2023; Poisot et al., 2021; Sandra et al., 2025). In most contexts (including historical, biogeographic, and deep-time systems) interactions must be inferred indirectly from traits, co-occurrence, phylogeny, or ecological theory (Morales-Castilla et al., 2015; Strydom et al., 2021). As a result, network construction is not simply a descriptive exercise but an inferential one where models are used to predict links that are plausible, probable, or theoretically consistent with ecological constraints (Strydom et al., 2026). Despite rapid methodological development in interaction inference, few studies have systematically compared alternative reconstruction frameworks within the same empirical system to evaluate how model choice propagates into ecological inference.

This issue is particularly important for comparative studies. While inference from ecological networks regarding structure and complexity is a mathematical task and is therefore relatively independent of biological assumptions (Delmas et al., 2019), their implications for stability and dynamics depend critically on assumptions about the distribution and strength of interaction (Allesina & Tang, 2012; Poisot et al., 2015). Network properties such as connectance, trophic organization, motif frequency, and robustness are often compared across communities to infer ecological differences attributable to environmental gradients, disturbance regimes, or evolutionary history (Dunhill et al., 2024; Michalska-Smith & Allesina, 2019; Poisot & Gravel, 2014; Roopnarine, 2006). However, if network structure depends strongly on the reconstruction model employed, then methodological variation may be conflated with biological signal. Understanding which ecological conclusions are robust to reconstruction assumptions (and which are model-dependent) is therefore essential for reliable cross-system inference. Recent work in network ecology has clarified that reconstruction approaches differ fundamentally in the type of network that they represent (Gauzens et al., 2025; Strydom et al., 2026). Broadly, these include: feasible networks, which map the set of interactions that are biologically possible given trait or phylogenetic compatibility; realised networks, which incorporate energetic or foraging constraints to approximate the subset of interactions likely to occur; and structural networks, which reproduce general topological properties without assigning biologically explicit species identities (Allesina et al., 2008). Each

representation encodes distinct ecological assumptions about how interactions arise and persist. Yet these classes are rarely evaluated comparatively within the same empirical system.

Although modern ecological networks often incorporate direct observations, analyses across historical or biogeographic gradients rely on inferred interactions. In these cases, reconstruction becomes structural hypothesis testing rather than data recovery. Yet most studies adopt a single reconstruction framework without assessing how alternative models might alter inferred ecological patterns, leaving it unclear whether signals such as extinction cascades or stability metrics reflect ecological reality or modelling artefacts. Deep-time ecosystems provide a stringent test of this issue, because interactions are not observed directly (Dunhill et al., 2024; Dunne et al., 2008; Dunne et al., 2014; Roopnarine, 2006), reconstruction assumptions must be explicit, allowing model effects on ecological inference to be isolated.

Here we assess how alternative network reconstruction frameworks influence inferred food web structure and extinction dynamics through a 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 from an identical taxon pool using six contrasting models spanning feasible, realised, and structural network representations. For each community, we compare macro-, meso-, and micro-scale network properties, quantify turnover in inferred interactions, and evaluate extinction dynamics under replicated disturbance simulations. In holding species composition constant while varying reconstruction framework, we isolate the contribution of model structure to ecological inference. This design allows us to distinguish signals that are consistent across models (indicating robust ecological patterns) from those that vary strongly with reconstruction assumptions. In doing so, we provide a general framework for evaluating uncertainty in reconstructed ecological networks and for improving the reliability of comparative network analyses across spatial and temporal scales.

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 (Bambach et al., 2007). 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 (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 family	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
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/biomass	Assumes optimal foraging; does not account for forbidden links	Realised	Petchey et al. (2008)	Predicting realized predator diets; exploring secondary extinctions

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Model family	Assumptions	Data needs	Limitation	Network type	Key reference	Usage examples
Allometric trophic network (ATN)	Links constrained by body-size ratios and functional response	Body mass, number of basal species	Assumes only mechanical/energetic constraints	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
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.

78 The three body mass-based models (ADBM, ATN, Body-size ratio) differ primarily in their underlying
79 ecological assumptions. Although all three models use body mass to infer food web structure, they differ in
80 their ecological assumptions. The ADBM is based on energy maximization under optimal foraging theory,
81 the ATN constrains interactions via mechanically optimal consumer–resource size ratios, and the Body-size
82 ratio model defines links probabilistically within a fixed allometric niche. Together, these approaches span
83 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 community, 100 networks were generated per model (n = 2400) to capture stochastic variation in link assignment. Where models required species body mass or trait values, these were sampled within biologically reasonable ranges to preserve relative differences among species. We adopted uniform sampling by default, as alternative distributions (lognormal, truncated lognormal) have negligible impact on topology (Supplementary Material S2; Figure S1). Structural models were parameterized using connectance values drawn from an empirically realistic range (0.07–0.34), with species richness held constant. Identical parameter draws were applied across comparable models within each replicate to ensure comparability. 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	

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

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. We simulated species loss under multiple scenarios, including trait-based, network-position-based, and random removals, allowing cascading extinctions to propagate. Simulated outcomes were compared to observed or expected community states using mean absolute differences (MAD) and modified true skill statistics (TSS) at node and link levels. Kendall's rank correlation coefficient was used to evaluate concordance in scenario rankings across reconstruction models, providing a measure of robustness in inferred community responses.

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

Across six reconstruction approaches, network structure 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 Inferred pairwise interactions vary widely among models

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

[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 non-linear 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 Figure S2.

[Figure 3 about here.]

To evaluate how model choice affects inferred extinction dynamics, we compared simulated post-extinction

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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 τ 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 τ 0.67 across structural metrics), with little correspondence between ADBM and Body-size ratio model outcomes (mean τ 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 ecological networks from incomplete interaction data (whether in contemporary, historical, or deep-time systems) is fundamentally an exercise in inference under uncertainty. Even in modern ecosystems, interaction networks are rarely fully observed (Poisot et al., 2021), and link prediction often relies on traits, phylogeny, co-occurrence, or mechanistic assumptions (Delmas et al., 2019; Morales-Castilla et al., 2015; Strydom et al., 2026). Theoretical work has long demonstrated that network structure strongly conditions ecological dynamics, including robustness to species loss and the propagation of disturbance (Allesina & Tang, 2012; Dunne et al., 2002; Solé & Montoya, 2001). Our results extend this insight by showing that the reconstruction framework itself functions as a structural prior - in shaping interaction topology, it directly influences inferred food web organisation and community responses to disturbance.

Differences among models arise not from the species pool alone, but from assumptions embedded in each model family (Pichler & Hartig, 2023; Strydom et al., 2021; Strydom et al., 2026). These include how trophic links

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are defined (trait compatibility versus energetic optimisation), how interaction probabilities are parameterised, and whether topology is constrained by macroecological regularities (*e.g.,* niche structure) or mechanistic rules (*e.g.,* body-size scaling). Consequently, network reconstruction is not a neutral technical step; it encodes ecological hypotheses that shape both emergent structure and dynamical predictions. This sensitivity parallels challenges in contemporary network ecology, where model and metric selection influence interpretations of connectance, modularity, motif frequencies, and stability (Michalska-Smith & Allesina, 2019; Poisot & Gravel, 2014).

Multivariate analyses revealed that reconstruction approaches differ along a small number of dominant axes corresponding to horizontal interaction density and vertical trophic organisation. These axes capture systematic, model-specific signatures independent of species composition, indicating that reconstruction framework acts as a major determinant of inferred ecological structure. Although some models converged on global metrics (*e.g.,* ADBM and ATN models), pairwise -turnover revealed disagreements in inferred species-level interactions. Structural similarity therefore does not guarantee concordance in trophic roles. Importantly, extinction scenario inference was scale dependent. Species-level extinction rankings were relatively consistent across models, whereas interaction-level outcomes were highly sensitive to reconstruction assumptions. This asymmetry reflects the dependence of cascade dynamics on link configuration and interaction distribution (Allesina & Tang, 2012; Curtsdotter et al., 2011; Dunne et al., 2002). Thus, while certain aggregate patterns may be robust to modelling choices, fine-grained interaction-level inference remains intrinsically model contingent.

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, researchers 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   Matching ecological questions to network representations

A central implication is that network representations are question specific. Different ecological questions require different classes of network models, a distinction increasingly recognised in contemporary ecology (Gauzens et al., 2025; Gravel et al., 2013; Tylianakis & Morris, 2017).

Feasibility networks: (trait- or phylogeny-based metaweb approaches) delineate the set of biologically plausible interactions. These are well suited for investigating potential dietary breadth, interaction diversity, or assembly constraints across spatial or environmental gradients (Gravel et al., 2019). However, because they maximise compatibility rather than realised foraging dynamics, they may overestimate interaction density when used to infer cascade processes.

Realised networks: (allometric or energetic models such as ADBM and ATN) embed foraging and metabolic rules to approximate likely trophic interactions (Brose et al., 2006; Gauzens et al., 2023; Petchey et al., 2008). In our analyses, these models produced more nonlinear and abrupt disturbance trajectories, consistent with energetic bottlenecks and constraint propagation. They are therefore more appropriate for questions concerning energy flow, trophic stability, and secondary extinction dynamics.

Structural networks: (such as the niche or cascade models) prioritise topological regularities over species identity (Allesina et al., 2008; Williams & Martinez, 2008). These approaches are particularly useful when evaluating macroecological scaling relationships, connectance patterns, motif distributions, or theoretical expectations for network structure. However, because species identity is decoupled from interaction assignment, they are less suitable for species-specific ecological inference.

Rather than asking which model is 'correct', the more productive question is which representation best aligns with the inferential goal. Network reconstruction should therefore be treated as part of hypothesis specification, not merely data preparation.

4.3   Implications for ecological network analysis

Although the present analyses were conducted within a single regional species pool, the implications extend broadly to comparative ecology and biogeography. Networks assembled across environmental gradients, latitudinal bands, disturbance regimes, or temporal intervals often differ in sampling intensity, trait resolution, and reconstruction methodology (Delmas et al., 2018; Poisot et al., 2021; Tylianakis & Morris, 2017). Without explicitly accounting for reconstruction framework, methodological variation may be conflated with ecological signal.

Three general implications follow.

First, reconstruction assumptions should be treated as explicit components of study design. Because network models encode hypotheses about how interactions arise, observed differences in connectance, trophic organisation, or robustness may reflect structural priors rather than ecological processes.

Second, cross-system comparisons should standardise reconstruction framework wherever possible. Comparing networks generated using different model families risks attributing differences in structure or stability to environmental gradients when they may instead arise from modelling choices.

Third, ensemble or sensitivity-based approaches provide a pathway to more robust inference. Evaluating ecological patterns across multiple plausible reconstructions allows identification of signals that are consistent across models and those that are assumption dependent. In this study, species-level vulnerability patterns were comparatively robust, whereas interaction-level cascades were highly variable. Such scale-dependent robustness clarifies where ecological inference is reliable and where it remains uncertain.

These considerations are particularly relevant for global change research. As ecological communities reorganise under climate change, habitat loss, and species invasions, reconstructed or partially observed networks are increasingly used to infer vulnerability, tipping points, and resilience (Michalska-Smith & Allesina, 2019; Tylianakis & Morris, 2017). Recognising reconstruction framework as a structural prior strengthens interpretation of such comparative analyses.

4.4 Toward probabilistic and ensemble reconstruction frameworks

Advances in modern network ecology offer promising directions for explicitly incorporating uncertainty into reconstruction. Probabilistic and Bayesian link-prediction approaches allow interaction probabilities to be estimated rather than assumed deterministic (Baskerville et al., 2011; Elmasri et al., 2020; Poisot et al., 2016). Maximum entropy methods can infer network structure under incomplete information while constraining macroecological properties (Banville et al., 2023). Trait-based and joint species distribution approaches integrate environmental, phylogenetic, and functional information to improve link inference across gradients (Bartomeus et al., 2016; Ovaskainen et al., 2017). Adopting such approaches would allow reconstructed networks to be treated as probabilistic ensembles rather than fixed topologies, improving both transparency and robustness (Banville et al., 2025; Perez-Lamarque et al., 2026; Poisot et al., 2016). In this framework, variation among reconstruction models becomes a quantifiable component of uncertainty rather than a hidden source of bias.

5   Conclusions

Ecological network reconstruction is not merely a technical step but a fundamental component of ecological inference. By comparing six contrasting reconstruction frameworks applied to an identical species pool, we demonstrate that model choice strongly shapes inferred food-web structure, interaction identity, and disturbance dynamics. Broad species-level patterns may be robust across reconstruction approaches, but interaction-level outcomes and cascade pathways are highly contingent on model assumptions. These findings highlight that network reconstruction is inherently hypothesis-driven. Each model encodes distinct ecological assumptions that influence both emergent topology and dynamical predictions. No single representation captures all aspects of ecological reality. However, aligning reconstruction framework with inferential goals, standardising methods across comparisons, and adopting ensemble or sensitivity approaches can distinguish robust ecological signals from model-dependent artefacts. As ecological network analyses continue to expand across spatial, temporal, and environmental gradients, recognising reconstruction framework as a structural prior will be essential for strengthening the reliability and interpretability of comparative ecological research.

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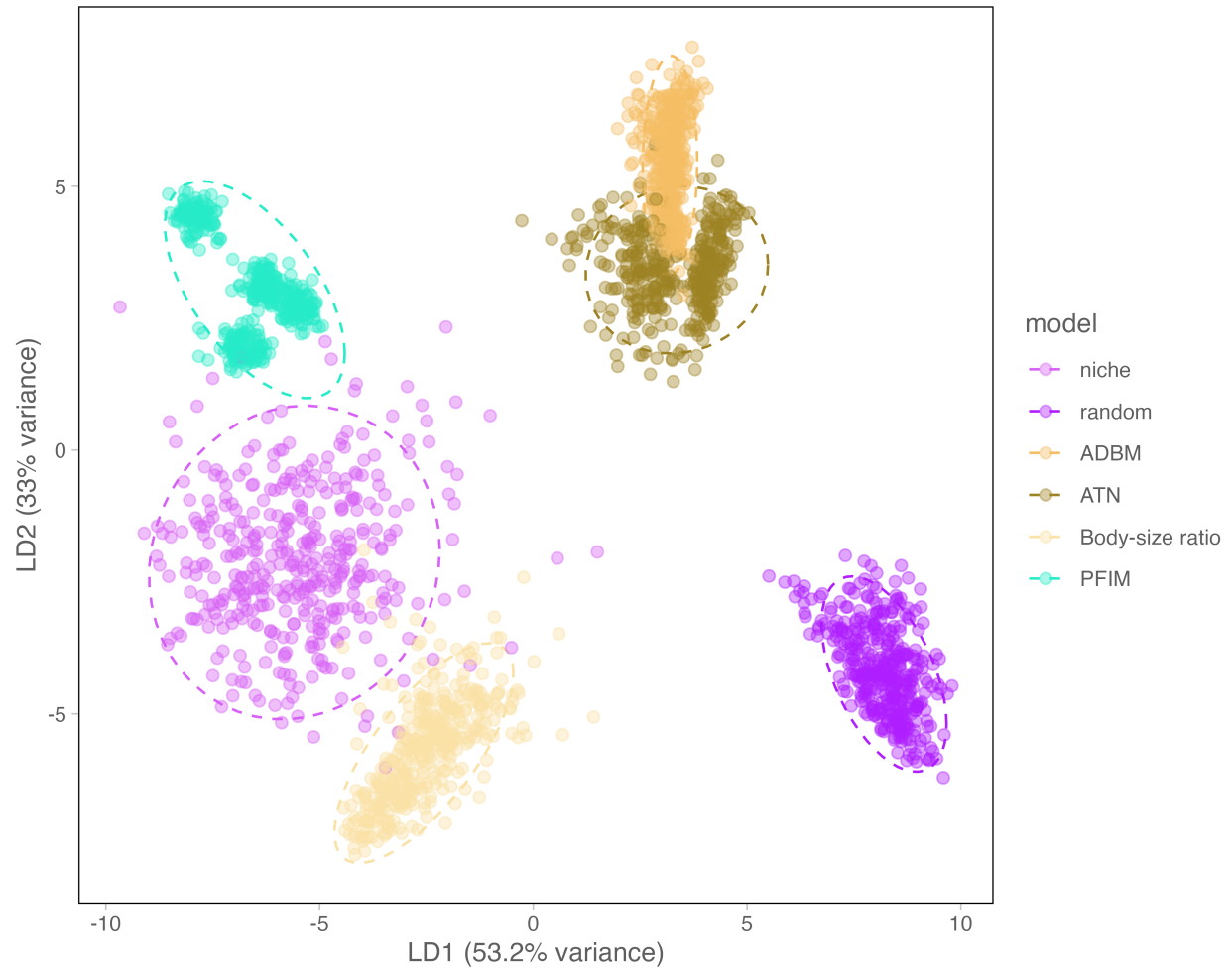
Figure 1: Linear discriminant analysis (LDA) of ecological network metrics for six model types. Each point represents a replicate, and ellipses indicate 95% confidence regions for each model. The second column represents the correlation of the various network metrics with the respective LDA axes.
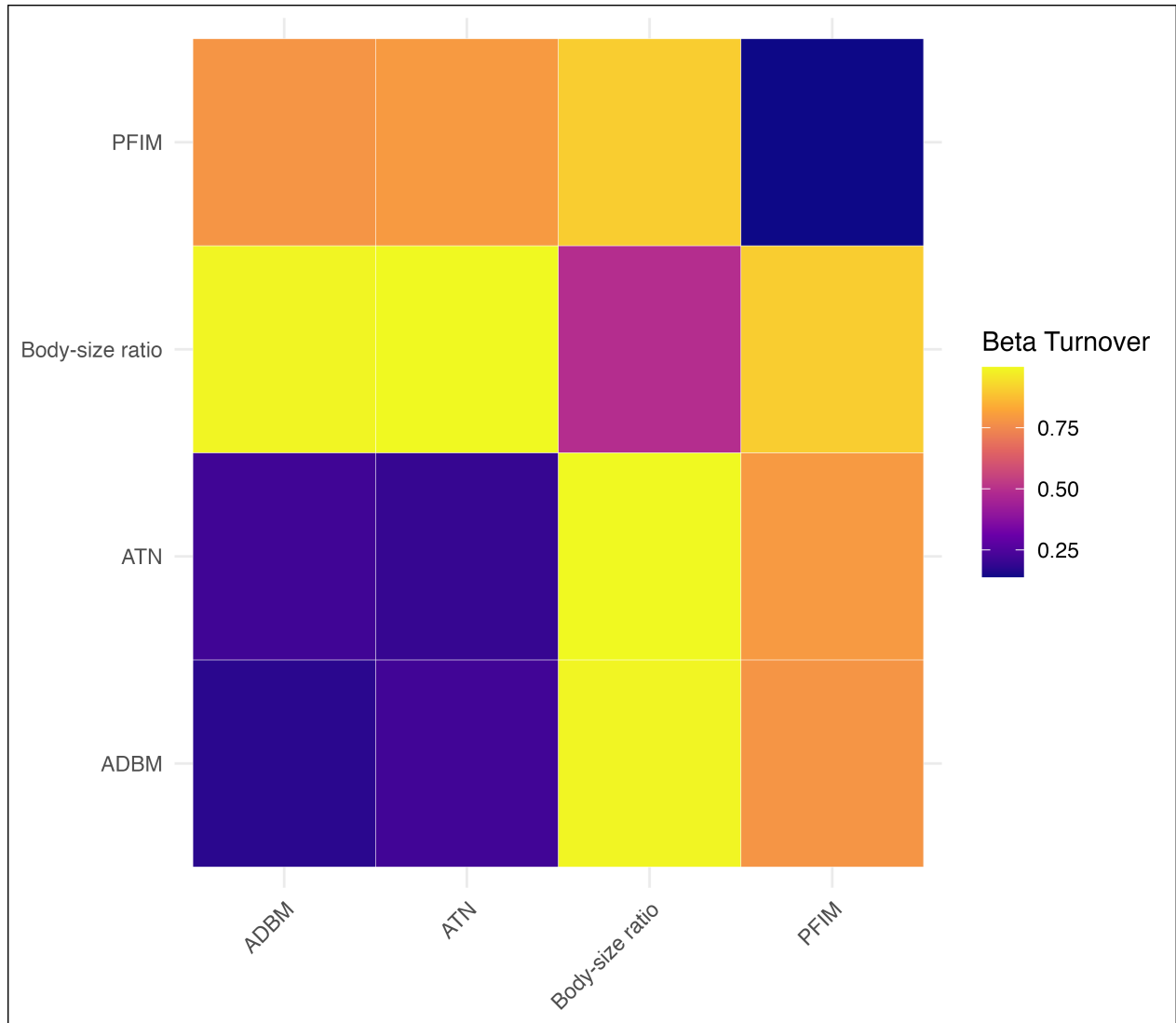
Figure 2: Pairwise -turnover in species interactions among four ecological network models (ADBM, ATN, Body-size ratio, and pfim). Each cell represents the mean turnover value between a pair of models, with warmer colours indicating greater dissimilarity in inferred interactions. The diagonal is omitted. High turnover values (yellow) indicate strong disagreement in network structure between models, whereas lower values (blue–purple) indicate greater similarity.
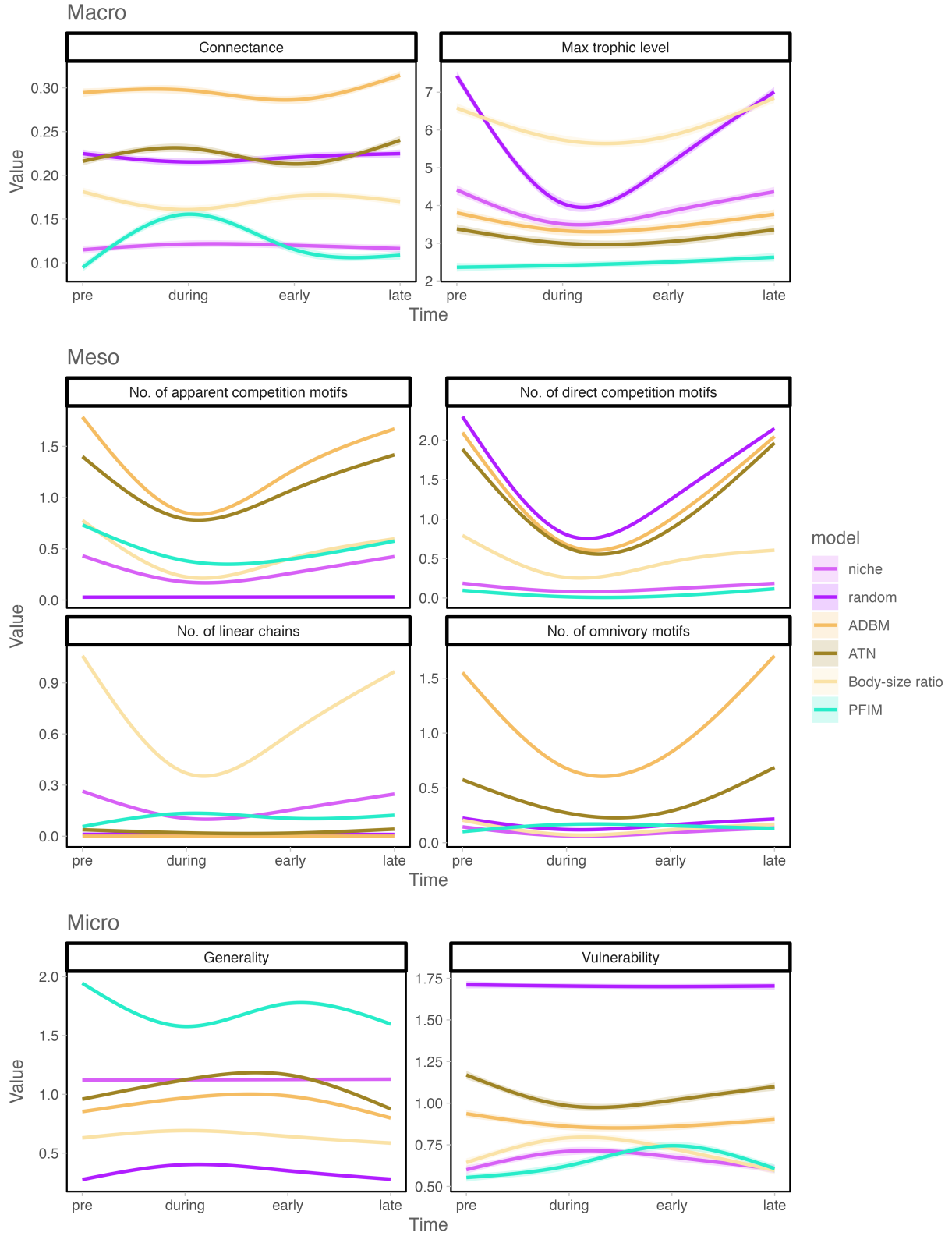
Figure 3: GAM-predicted trajectories of network structure during extinction simulations reveal pronounced differences in the timing and magnitude of change across reconstruction models. Lines show model-specific smooths and shaded areas indicate 95% confidence intervals. Deterministic approaches produce smoother, more consistent dynamics, whereas stochastic models exhibit greater variability, underscoring the sensitivity of inferred collapse pathways to reconstruction assumptions.
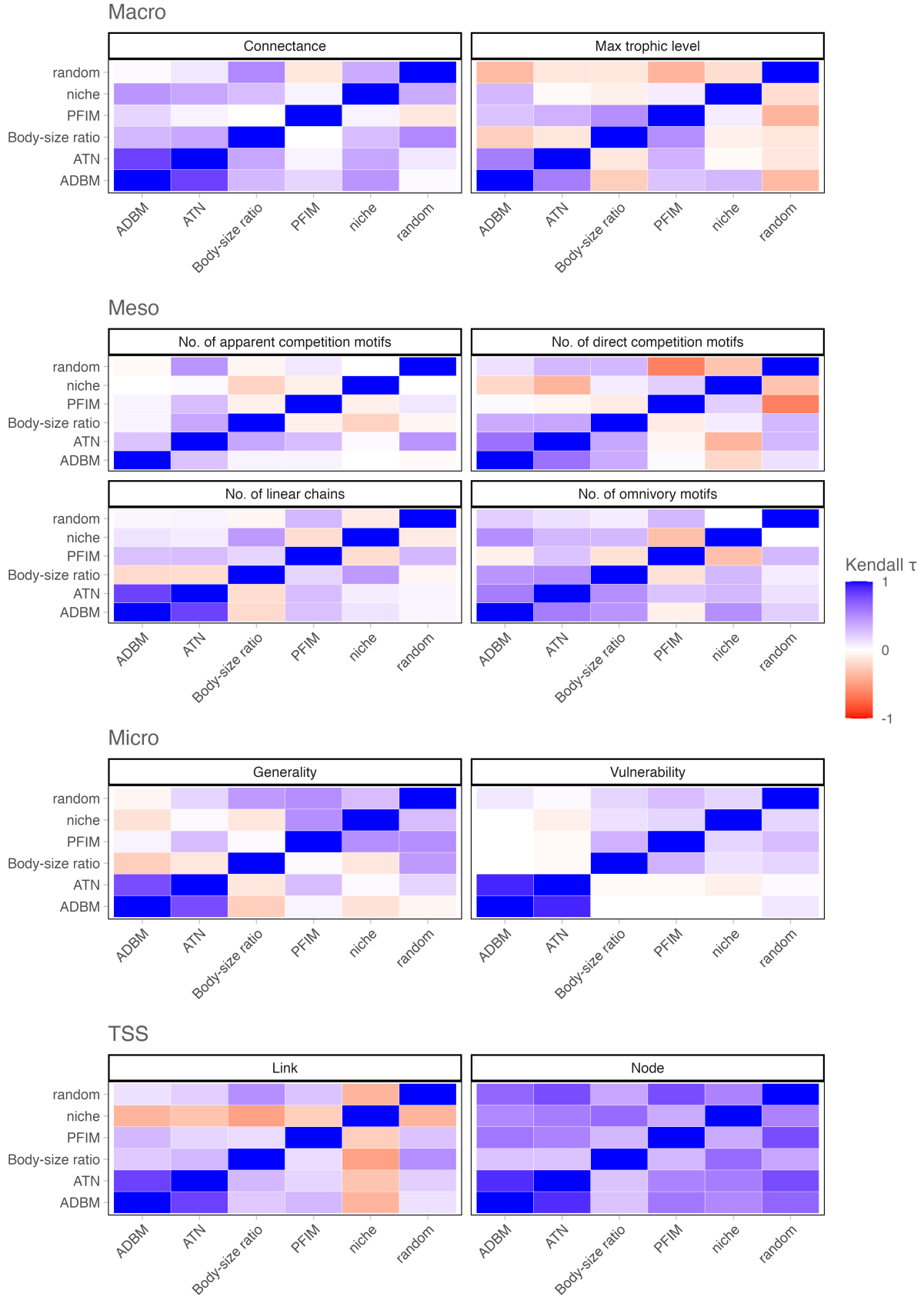
Figure 4: Heatmaps showing pairwise Kendall rank correlation coefficients (τ) between models for each network metric. Each panel corresponds to a different metric and displays the degree of agreement in extinction-scenario rankings across models based on mean absolute differences (MAD) between observed 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