

Unveiling the Complexity of Food Webs: A Comprehensive Overview of Definitions, Scales, and Mechanisms

Tanya Strydom ¹; Jennifer A. Dunne ²; Timothée Poisot ^{3,4}; Andrew P. Beckerman ¹

Abstract: Food webs are a useful abstraction and representation of the feeding links between species in a community and are used to infer many ecosystem level processes. However, the different theories, mechanisms, and criteria that underpin how a food web is defined and, ultimately, constructed means that not all food webs are representing the same ecological process. Here we present a synthesis of the different assumptions, scales and mechanisms that are used to define different ecological networks ranging from metawebs (an inventory of all potential interactions) to fully realised networks (interactions that occur within a given community over a certain timescale). Illuminating the assumptions, scales, and mechanisms of network inference allows a formal categorisation of how to use networks to answer key ecological and conservation questions and defines guidelines to prevent unintentional misuse or misinterpretation.

Keywords: food web, network construction, scientific ignorance

1 At the heart of modern biodiversity science are a set of concepts and theories about biodiversity, stability
2 and function. These relate to the abundance, distribution and services that biodiversity provides, and how
3 biodiversity – as an interconnected set of species – responds to multiple stressors. The interaction between
4 species is one of the fundamental building blocks of ecological communities, providing a powerful abstraction
5 that can help quantify, conceptualise, and understand biodiversity dynamics, and ultimately, make predic-
6 tions, mitigate change, and manage services. Such network representations of biodiversity (including within
7 species diversity) are increasingly argued to be an asset to predictive ecology, climate change mitigation
8 and resource management. Here, it is argued that characterising biodiversity in a network will allow deeper
9 capacity to understand and predict the abundance, distribution, dynamics and services provided by multiple
10 species facing multiple stressors.

11 A ‘network’ can be defined and conceptualised in a myriad of ways, which means that different networks
12 will be embedding different processes (or determinants) of interactions, ultimately influencing the patterns
13 and mechanisms that are inferred (Brimacombe et al., 2023; Proulx et al., 2005). The different ways in
14 which a network can be represented is the result of *how* the network is constructed, which itself rests on two
15 pillars: the data used to construct the network and the underlying theory as to what drives the interactions
16 between species. The latter represents an expression of mechanism and process that gives rise to the patterns
17 that emerge from collating interactions among species, and will ultimately inform which data are deemed
18 important in the determination of interactions occurring. Each of these pillars carries with it a set of practical,
19 semantic and conceptual constraints that not only influence progress in making network ecology more valuable
20 and potentially predictive, but help define the spatial, temporal, and evolutionary scale of assumptions we
21 make and the predictions we might generate from different network representations.

22 In this perspective we aim to provide an overview of the different **food web** representations, particularly how
23 these relate to the terminology used to define a network, and how this influenced by both the processes that
24 determine networks as well as how this relates to the way in which we construct networks. The provision of
25 this detail ultimately leads to a set of insights and conclusions about whether, when and under what conditions
26 network representations of biodiversity can contribute to the advancement of ecological theory and generate
27 value in predictive ecology. Specifically, we finish this perspective with an overview of fundamental questions
28 in ecology that we think can benefit from network thinking and a proposal that such thinking can accelerate
29 our capacity to predict the impact of multiple stressors on biodiverse communities.

30 1 Setting the Scene: The Not So Basics of Nodes and Edges

31 Defining a food web seems simple; it is the representation of the interactions (edges) between species (nodes),
32 however the definition of ‘edges’ and ‘nodes’, as well as the scale at which they are aggregated can take many
33 forms (Poisot, Stouffer, et al., 2016), which ultimately encodes a series of assumptions and criteria within
34 a network. An awareness of variance in the way a food web can be defined is critical as a network (or its
35 adjacency matrix) is both the ‘object’ from which inferences are made (*e.g.*, the interactions between species,
36 or how the structure influences ecosystem level processes) as well as the ‘product’ of either the data collection
37 (Brimacombe et al., 2023) or prediction process (Banville et al., 2024). One thus needs to be aware of both
38 the criteria that is used to define nodes and edges, and what processes or mechanisms the aggregation of the
39 two represents, as this will determine what the network can be used for.

40 1.0.1 How do we define a node?

41 Although this may seem an elementary question in the context of food webs — a node *should* represent a
42 (taxonomic) species, the reality is that nodes can often represent an aggregation of different species - so called
43 ‘trophic species’ (Williams & Martinez, 2000; Yodzis, 1982) or segregation of species by life stages (Clegg
44 et al., 2018). Practical implications of how we are aggregating the nodes is that the resolution may not
45 always be ‘pixel perfect’, which limits the ability to make (taxonomic) species specific inferences *e.g.*, does
46 species *a* eat species *b*, however there is value in having nodes that represent an aggregation of species, as
47 the distribution of the links between them are more meaningful in terms of understanding energy flow and
48 distribution within the system.

49 1.0.2 What is captured by an edge?

50 At its core, links within food webs can be thought of as a representation of either feeding links between species
51 - be that realised (Pringle, 2020) or potential (Dunne, 2006), alternative links can represent fluxes within the
52 system *e.g.*, energy transfer or material flow as the result of the feeding links between species (Lindeman,
53 1942). Fundamentally this means that the links within a network represent different ‘currencies’ (either the
54 feasibility of a link existing between two species or the energy that is moving through the system) and how the
55 links within a network are specified will influence the resulting structure of the network. For example taking
56 a food web that consists of links representing all *potential* feeding links for a community (*i.e.*, a metaweb)
57 will be meaningless if one is interested in understanding the flow of energy through the network as the links
58 within a metaweb do not represent environmental/energetic constraints, making them poor representations
59 of which interactions are *realised* in a specific location (Caron et al., 2024). In addition to the various ways

of defining the links between species pairs there are also a myriad of ways in which the links themselves can be quantified. Links between species are often treated as being present or absent (*i.e.*, binary) but it is also possible to use probabilities (Banville et al., 2024; which quantifies how likely an interaction is to occur, Poisot, Cirtwill, et al., 2016) or continuous measurements (which quantifies the strength of an interaction, Berlow et al., 2004).

1.0.3 Network representations

Broadly, networks can be thought of to fall into two different ‘types’; namely metawebs; traditionally defined as all of the *potential* interactions for a specific species pool (Dunne, 2006), and realised networks; which is the subset of interactions in a metaweb that are *realised* at a given time and place. The fundamental difference between these two different network representations is that a metaweb provides insight as to the viability of an interaction between two species occurring and is a means to identify links that are not ecologically plausible, *i.e.*, forbidden links (Jordano, 2016b), or provide an idea of the *complete* diet of a species (Strydom et al., 2023). In contrast realised networks are highly localised and links between species are contingent on both the co-occurrence of species as well as the influence of the environment, and population and community dynamics on predator choice. In the context of definitions and semantics the links that are represented by a metaweb and a realised network are different; links that are absent in a metaweb can be treated as being truly absent, however links that are absent in a realised network cannot be considered to be truly absent but are rather as absent due to the broader environmental/community context. Importantly, a realised network is *not* simply the downscaling of a metaweb to a smaller scale (*e.g.*, moving from the country to the 1x1 km² scale based on fine-scale species co-occurrence) but represents a shift towards capturing the higher level processes that determine the *realisation* of an interaction, *i.e.*, the definition of an edges shifts from being determined by interaction feasibility to that of energetic choices/consequences. Thus, different network representations are determined and constrained by different sets of assumptions as to what the processes are that determine the presence/absence of an interaction between two species as well as the resulting network structure.

2 From Nodes and Edges to Scale, Context, and Process

The interplay between network representation and network (node and edge) definition is primarily governed by the process(es) that determine the interaction between species, however these processes are also scale and context dependent. Here we start by introducing the five core processes that determine either the feasibility or the realisation of interactions, namely: evolutionary compatibility, co-occurrence, abundance, predator choice, and non-trophic interactions; while simultaneously contextualising them within, and linking them

90 to the different network representations Figure 1. We can think of the different network representations
91 to be conceptually analogous to the fundamental and realised niche, whereby the metaweb represents the
92 ‘fundamental diet niche’ of a species and a realised network represents the ‘realised diet’ of a species. Of
93 course these processes do not function in a vacuum and do interact with/influence one another, but it is still
94 beneficial to present them in a categorical manner as these different processes are often the underpinning
95 logic in the development of prediction/network models, the criteria for data collection in the field, and the
96 scale of organisation for which they are relevant (species, population, or community).

97 [Figure 1 about here.]

98 2.1 The processes that determine species interactions

99 Evolutionary compatibility

100 There is compelling evidence that an interaction occurring between two species is the result of their shared
101 (co)evolutionary history (Dalla Riva & Stouffer, 2016; Gómez et al., 2010; Segar et al., 2020) which, in the
102 more proximal sense, is manifested as the ‘trait complementarity’ between two species, whereby one species
103 (the predator) has the ‘correct’ set of traits that allow it to chase, capture, kill, and consume the other species
104 (the prey). For species pairs where this condition is not met the link is deemed to be forbidden (Jordano,
105 2016b); *i.e.*, not physically possible and will always be absent within a network. A network constructed on
106 the basis of evolutionary compatible links is most closely aligned with a metaweb, although it would not be
107 required that the species co-occur (as shown in Figure 1), and arguably makes for a good approximation of
108 the ‘Eltonian niche’ of species (Soberón, 2007). Finally, one should be aware that it is possible to represent
109 evolutionary compatible interactions as either binary (possible vs forbidden) or as a probability (Banville et
110 al., 2024), where the probability represents how likely the interaction between two species is to be possible.

111 (Co)occurrence

112 Although the outright assumption that because two species are co-occurring it must mean that they are
113 interacting is flawed (Blanchet et al., 2020), it is of course impossible for two species to interact (at least in
114 terms of feeding links) if they are not co-occurring in time and space. Thus, although co-occurrence data
115 alone is insufficient to build an accurate and ecologically meaningful representation of *feeding links* it is still
116 a critical process that determines the realisation of feeding links and allows us to constrain a global metaweb
117 to only consider ‘realised’ communities (Dansereau et al., 2024) and an understanding of the intersection of
118 species interactions and their co-occurrence is meaningful when one is operating in the space of trying to
119 determine the distribution of a species (Higino et al., 2023; Pollock et al., 2014).

120 **Abundance**

121 The abundance of different species within the community is thought to influence the realisation of feeding
122 links primarily in two ways. Firstly there is the argument that that structure of networks (and the interactions
123 that they are composed of) are driven *only* by the abundance of the different species and that interactions
124 are not contingent on there being any compatibility (trait matching) between them, *sensu* neutral processes
125 (Canard et al., 2012; Momal et al., 2020). However, a more ecologically sound assumption would be that
126 the abundance of different prey species will influence which prey are targeted or preferred by the predator
127 as abundance influences factors such as the likelihood of species meeting (Banville et al., 2024; Poisot et al.,
128 2015), or in the dynamic sense will influence the persistence of viable populations.

129 **Predator choice (energetic cost)**

130 Ultimately, predator choice is underpinned by the energetic cost-benefit of trying to catch, kill, and consume
131 prey (where a predator will optimise energy while minimising handling and search time), and is well described
132 within both optimal foraging (Pyke, 1984) and metabolic theory (Brown et al., 2004). The energetic cost of
133 feeding is itself influenced by the interplay of both the energy content [*i.e.*, body size; Yodzis & Innes (1992)]
134 as well as the density (abundance) of prey (as this influences search time) and as a process will influence which
135 links are realised Figure 1. Additional work on understanding the energetic cost that the environment
136 imposes on an individual (Cherif et al., 2024) as well as the way a predator uses the landscape to search for
137 prey (Pawar et al., 2012) is bringing us closer to accounting for the energetic cost of realising feeding links.

138 **Non-trophic interactions**

139 Perhaps not as intuitive when thinking about the processes that determine feeding links (trophic interac-
140 tions) is thinking about the role of the ability of non-trophic interactions to modify either the realisation or
141 strength of trophic interactions (Golubski & Abrams, 2011; Pilosof et al., 2017). Non-trophic interactions
142 can modify interactions either ‘directly’ *e.g.*, predator *a* outcompetes predator *b* or ‘indirectly’ *e.g.*, mutu-
143 alistic/facilitative interactions will alter the fine-scale distribution and abundance of species as well as their
144 persistence (Buche et al., 2024; Kéfi et al., 2012, 2015). The ‘unobservable’ nature of non-trophic interactions
145 makes them a challenge to quantify, however their importance in network dynamics should not be overlooked
146 (Staniczenko et al., 2010)

147 **2.2 Contextualising the processes that determine species interactions**

148 It should be self evident that the different processes discussed above are all ultimately going to influence the
149 realisation of interactions as well as the structure of a network, however they are acting at different scales of

organisation. Both the **co-occurrence** and the **evolutionary compatibility** are valid at the scale of the species pair of interest, that is the *possibility* of an interaction being present/absent is assessed at the pairwise level and one is left with a ‘list’ of interactions that are present/absent. Although it is possible to build a network (*i.e.*, metaweb) from this information it is important to be aware that the structure of this network is not constrained by real-world dynamics or conditions, and so just because species are able to interact does not mean that they will (Poisot et al., 2015). In order to construct a network who’s structure is a closer approximation of reality (localised interactions) one needs to take into consideration the properties of the community as a whole and not just the two species of interest, which requires more data at the community scale, such as the abundance of species.

3 Network construction is nuanced

The act of constructing a ‘real world’ network will ultimately be delimited by its intended use, however the reality is that the empirical collection of interaction data is both costly and challenging to execute (Jordano, 2016a, 2016b), especially if one wants to capture *all* aspects of the processes discussed in Section 2 (owing to the different time and spatial scales they may be operating at). Thus we often turn to models to either predict networks (be that the interaction between two species, or network structure (Strydom et al., 2021)), or as a means to identify missing interactions (gap fill) within an existing empirical dataset (Biton et al., 2024; Dallas et al., 2017; Stock, 2021), and so for the purpose of this discussion network construction will be synonymous with using a model as a means to represent or predict a network. That is not to say that there is no need for empirical data collection but rather that using a model for food web prediction (or reconstruction) is a more feasible approach as it allows us to make inferences about interactions that are not happening in the ‘observable now’ (Strydom et al., 2021), with the added benefit that one is able to build some uncertainty into the resulting network (Banville et al., 2024). Additionally different models have different underlying philosophies that allow us to capture one or a few of the processes discussed in Section 2, and although the delimits and defines what inferences can be made from the resulting network it also allows us to isolate and understand how different processes determine interactions (Song & Levine, 2024; Stouffer, 2019). Here we will introduce the three different types of network representations (metawebs, realised networks, and structural networks), how they link back to (and encode) the different processes determining interactions Figure 1, and broadly discuss some of the modelling approaches that are used to construct these different network types. This is paralleled by a hypothetical case study (Box 1) where we showcase the utility/applicability of the different network representations in the context of trying to understand the feeding dynamics of a seasonal community.

i Box 1 - Why we need to aggregate networks at different scales: A hypothetical case study

note I am using a figure for layout experimentation purposes

Although it might seem most prudent to be predicting, constructing, and defining networks that are the closest representation of reality there are pros and cons of constructing both realised networks as well as metawebs. Let us take for example a community that experiences a degree of species turnover between seasons. In this community we expect species to be either present or absent depending on the season (*i.e.*, changes in co-occurrence) as well as some species exhibiting seasonal shifts in their diets (be that due to changes in species occurrence or predator choice). If one were to construct a metaweb that disregards these season shifts ('global metaweb') these details would be lost and it would be valuable to construct either smaller metawebs for the different seasonal communities (thereby capturing the changes in community diversity), or realised networks for each season (to capture diet or ecosystem process shifts). However, these small-scale networks lack the context of the bigger picture that is available at the metaweb - that is it gives us a more holistic idea of the entire diet range of a specific species, which is important when one needs to make conservation-based/applied decisions (*e.g.*, conserving the entire diet of a species and not just seasonal prey items) as well as providing information on interactions that may be possible regardless of the environmental/community context (species may have the capacity to consume certain prey items but do not do so due to local conditions). With this in mind let us see how the different network aggregations can be used

[Figure 2 about here.]

181

182 3.1 Models that predict metawebs (feasible interactions)

183 This is perhaps the most developed group of models; with a variety of approaches having been developed
184 that typically determine the feasibility of an interaction using the trait compatibility between predator and
185 prey (*i.e.* their evolutionary compatibility) to determine 'feeding rules' (Morales-Castilla et al., 2015). These
186 feeding rules are broadly elucidated in two different ways; mechanistic feeding rules can be explicitly defined
187 and applied to a community (Dunne et al., 2008; *e.g.*, Shaw et al., 2024) or they are inferred from a community
188 for which there are interaction data and the 'rules' are then applied to a different community (Caron et al.,
189 2022; Cirtwill et al., 2019; Desjardins-Proulx et al., 2017; Eklöf et al., 2013; Llewelyn et al., 2023; Pichler et al.,
190 2020; Strydom et al., 2022; *e.g.*, Strydom et al., 2023). The fundamental difference between these two model
191 groups is that 'mechanistic models' rely on expert knowledge and make explicit assumptions on trait-feeding
192 relationships, whereas the 'pattern finding' models are dependent on existing datasets from which to elucidate

193 feeding rules. These models are useful for determining all feasible interactions for a specific community, and
194 owing to the availability of empirical interaction datasets (Gray et al., 2015; *e.g.*, Poelen et al., 2014; Poisot,
195 Baiser, et al., 2016), as well as the development of model testing/benchmarking tools (Poisot, 2023), means
196 that these models can be validated and (with relative confidence) be used to construct first draft networks for
197 communities for which we have no interaction data (Strydom et al., 2022), and are valuable not only in data
198 poor regions but also for predicting interactions for ‘unobservable’ communities *e.g.*, prehistoric networks
199 (Fricke et al., 2022; Yeakel et al., 2014) or future, novel community assemblages. Importantly metawebs
200 are inherently ‘static’ in the sense that they are *not* able to capture dynamic processes (since the notion of
201 feasibility is all or nothing), however they provide a bigger picture context (*e.g.*, understanding the *entire*
202 diet breadth of a species) and often require little data to construct.

203 3.2 Models that predict realised networks (realised interactions)

204 In order to construct realised networks models need to incorporate *both* the feasibility of interactions (*i.e.*,
205 determine the entire diet breadth of a species) as well as then determine which interactions are realised (*i.e.*,
206 incorporate the ‘cost’ of interactions). As far as we are aware there is no model that explicitly accounts for
207 both of these ‘rules’ and rather *only* account for processes that determine the realisation of an interaction
208 (*i.e.*, abundance, predator choice, or non-trophic interactions). Although the use of allometry *i.e.*, body size
209 (Beckerman et al., 2006; *e.g.*, Valdovinos et al., 2023) may represent a first step in capturing ‘evolutionary
210 compatibility’ alongside more energy (predator choice) driven processes we still need to account for other
211 traits that determine feeding compatibility (*e.g.*, Van De Walle et al., 2023 show how incorporating prey
212 defensive properties alongside body size improves predictions). In terms of constructing realised networks,
213 diet models (Beckerman et al., 2006; Petchey et al., 2008) have been used construct networks based on
214 both predator choice (as determined by the handling time, energy content, and predator attack rate) as well
215 as abundance (prey density) and progress has also been made in understanding the compartmentation of
216 energy in networks and how this influences energy acquisition (Krause et al., 2003; Wootton et al., 2023). As
217 realised networks are build on the concept of dynamic processes (the abundance of species will always be
218 in flux) these networks are valuable for understanding the behaviour of networks over time or their response
219 to change (Curtsdotter et al., 2019; Delmas et al., 2017; Lajaaiati et al., 2024). However, they are ‘costly’ to
220 construct (requiring data about the entire community as it is the behaviour of the system that determines
221 the behaviour of the part) and also lack the larger context afforded by metawebs.

222 **3.3 Models that predict structure (interaction agnostic)**

223 Although we identify mechanisms that determine species interactions in Section 2 not all models that are used
224 to predict networks explicitly operate at the ‘process’ level, but rather represent the *structure* of a network
225 based on a series of *a priori* assumptions as to the distribution of links between species (typically trophic
226 not taxonomic species). These models operate by parametrising an aspect of the network structure, (*e.g.*,
227 the niche model (Williams & Martinez, 2000) makes an assumption as to the expected connectance of the
228 network, although see Allesina & Pascual (2009) for a parameter-free model) or alternatively uses structural
229 features of an existing *realised* network (*e.g.*, stochastic block model, Xie et al. (2017)). Importantly these
230 structural models do not make species specific predictions (they are usually species agnostic and treat nodes
231 as trophic species) and so cannot be used to determine if an interaction is either possible *or* realised between
232 two species (*i.e.*, one cannot use these models to determine if species *a* eats species *b*). Although this means
233 this suite of models are unsuitable as tools for predicting species-specific interactions, they have been shown
234 to be sufficient tools to predict the structure of networks (Williams & Martinez, 2008), and provide a data-
235 light (the models often only require species richness) but assumption heavy (the resulting network structure
236 is determined by an assumption of network structure) way to construct a network.

237 **4 Making Progress with Networks**

238 **4.1 Further development of models and tools**

239 There has been a suite of models that have been developed to predict feeding links, however we are lacking
240 in tools that are explicitly taking into consideration estimating both the feasibility as well as realisation of
241 links, *i.e.*, both interactions and structure simultaneously (Strydom et al., 2021). This could be addressed
242 either through the development of tools that do both (predict both interactions and structure), or to develop
243 an ensemble modelling approach (Becker et al., 2022; Terry & Lewis, 2020) or tools that will allow for the
244 downsampling of metawebs into realised networks (*e.g.*, Roopnarine, 2006). Additionally although realised
245 networks are more closely aligned with capturing interaction strength we lack models that allow us to quantify
246 this (Strydom et al., 2021; Wells & O’Hara, 2013). In addition to the more intentional development of models
247 we also need to consider the validation of these models, there have been developments and discussions for
248 assessing how well a model recovers pairwise interactions (Poisot, 2023; Strydom et al., 2021), although the
249 rate of false-negatives that may be present in the testing data still present a challenge (Catchen et al., 2023),
250 we still lack clear set of guidelines for benchmarking the ability of models to recover structure (Allesina et
251 al., 2008).

252 **4.2 At what scale should we be predicting and using networks?**

253 We lack an understanding of which processes drive the differences between different scales (Saravia et al.,
254 2022), as well as to what the appropriate level of aggregation is for a ‘network’ (Estay et al., 2023). Which
255 presents a challenge both in deciding what the appropriate spatial and time scales are for constructing not only
256 a network but also which type of network representation. Space influences both network properties (Galiana
257 et al., 2018), as well as dynamics (Fortin et al., 2021; Rooney et al., 2008), and time has implications when
258 it comes to accounting for seasonal turnover in communities (Brimacombe et al., 2021; Laender et al., 2010)
259 as well as thinking co-occurrence, particularly the records used to determine it (Brimacombe et al., 2024).
260 Although multilayer networks may allow us to encode the nuances of space and time (Hutchinson et al., 2019)
261 we still need to understand the implications of *e.g.*, constructing networks that are not at ecologically but
262 rather politically relevant scales (Strydom et al., 2022) and what we can learn or infer from networks a these
263 scales.

264 **5 The future value of networks**

265 developing a dictionary of use... that helps navigate between the levels and assumptions

266 It should be clear that there is a high degree of interrelatedness and overlap between the way a network is
267 constructed (modelled or predicted) and the process(es) it captures, these are encoded (embedded) within
268 the network representation and ultimately influences how the network can and should be used (Berlow et al.,
269 2008; Petchey et al., 2011). It is probably both this nuance as well as a lack of clear boundaries and guidelines
270 as to the links between network form and function (although see Delmas et al., 2019) that has stifled the
271 ‘productive use’ of networks beyond inventorying the interactions between species. Although, progress with
272 using networks as a means to address questions within larger bodies of ecological theory *e.g.*, invasion biology
273 (Hui & Richardson, 2019) and co-existence theory (García-Callejas et al., 2023), has been made we still need
274 to have a discussion on what the appropriate network representation for the task at hand would be. This
275 is highlighted in Box 1, and underscores that we need to evaluate exactly what process a specific network
276 representation captures as well as its suitability for the question of interest.

277 **5.1 How will novel communities interact?**

278 Here we can talk about the effects of range shifts and invasions and how this will result in new/novel
279 community assemblages. And then also the intentional changes of species compositions through rewilling.

280 **5.2 How will changes in the community influence ecosystem processes?**

281 Linking to dynamic networks and how this lets us build spatially/temporally explicit networks which can be
282 used to infer form and function. Also bring in the discussion on the suitable aggregation (and the fact that
283 we don't know)

284 **5.3 How/why do species persist and/or co-exist?**

285 Specific sub points to consider here is persistence, especially persistence to perturbation. Again, dynamic
286 networks and network/community assembly and finally extinctions (Dunhill et al., 2024).

287 [Figure 3 about here.]

Table 1: An informative table

Question (broad)	Question (specific)	Network representation
Species invasions	What species will the invading species interact with?	Regional metaweb but need to derive information from a global metaweb since these are interactions that are 'novel'
Species invasions	How does the invading species alter network dynamics and function?	Realised network (after having moved through the global metaweb to understand which interactions are feasible)
Range shifts and novel communities	Under global change how will novel community assemblages interact?	Global metaweb, need context of broader community
Extinctions	Cascading effect of the loss of a species from the network	Regional metaweb - need to account for entire diet, a realised network will exclude the entire diet but will allow to elucidate the final structure
Species/community persistence	Dynamics over time. Stability/resilience. How does a change in pop A affect pop B?	Realised networks - but dynamic!
Synthetic networks	Creating ecologically plausible communities for synthetic analyses	Structural networks - data light!

Question (broad)	Question (specific)	Network representation
Practical use	What is both attainable (data constraints) but also of practical use to ‘real world’ decision making. So moving from theory to applied	??Regional metawebs??

288 References

- 289 Allesina, S., Alonso, D., & Pascual, M. (2008). A General Model for Food Web Structure. *Science*, 320(5876),
 290 658–661. <https://doi.org/10.1126/science.1156269>
- 291 Allesina, S., & Pascual, M. (2009). Food web models: A plea for groups. *Ecology Letters*, 12(7), 652–662.
 292 <https://doi.org/10.1111/j.1461-0248.2009.01321.x>
- 293 Banville, F., Strydom, T., Blyth, P., Brimacombe, C., Catchen, M. D., Dansereau, G., Higino, G., Malpas,
 294 T., Mayall, H., Norman, K., Gravel, D., & Poisot, T. (2024). *Deciphering probabilistic species interaction*
 295 *networks*. EcoEvoRxiv. <https://doi.org/10.32942/X28G8Z>
- 296 Becker, D. J., Albery, G. F., Sjodin, A. R., Poisot, T., Bergner, L. M., Chen, B., Cohen, L. E., Dallas, T.
 297 A., Eskew, E. A., Fagre, A. C., Farrell, M. J., Guth, S., Han, B. A., Simmons, N. B., Stock, M., Teeling,
 298 E. C., & Carlson, C. J. (2022). Optimising predictive models to prioritise viral discovery in zoonotic
 299 reservoirs. *The Lancet Microbe*, 3(8), e625–e637. [https://doi.org/10.1016/S2666-5247\(21\)00245-7](https://doi.org/10.1016/S2666-5247(21)00245-7)
- 300 Beckerman, A. P., Petchey, O. L., & Warren, P. H. (2006). Foraging biology predicts food web complexity.
 301 *Proceedings of the National Academy of Sciences*, 103(37), 13745–13749. <https://doi.org/10.1073/pnas.0603039103>
- 302
- 303 Berlow, E. L., Brose, U., & Martinez, N. D. (2008). The “Goldilocks factor” in food webs. *Proceedings of
 304 the National Academy of Sciences*, 105(11), 4079–4080. <https://doi.org/10.1073/pnas.0800967105>
- 305 Berlow, E. L., Neutel, A.-M., Cohen, J. E., de Ruiter, P. C., Ebenman, B., Emmerson, M., Fox, J. W., Jansen,
 306 V. A. A., Iwan Jones, J., Kokkoris, G. D., Logofet, D. O., McKane, A. J., Montoya, J. M., & Petchey, O.
 307 (2004). Interaction strengths in food webs: Issues and opportunities. *Journal of Animal Ecology*, 73(3),
 308 585–598. <https://doi.org/10.1111/j.0021-8790.2004.00833.x>
- 309 Biton, B., Puzis, R., & Pilosof, S. (2024). *Inductive link prediction boosts data availability and enables
 310 cross-community link prediction in ecological networks*.
- 311 Blanchet, F. G., Cazelles, K., & Gravel, D. (2020). Co-occurrence is not evidence of ecological interactions.
 312 *Ecology Letters*, 23(7), 1050–1063. <https://doi.org/10.1111/ele.13525>

- 313 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2021). Inferred seasonal interaction rewiring of a freshwater
314 stream fish network. *Ecography*, 44(2), 219–230. <https://doi.org/10.1111/ecog.05452>
- 315 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2024). *Applying a method before its proof-of-concept: A
316 cautionary tale using inferred food webs.* <https://doi.org/10.13140/RG.2.2.22076.65927>
- 317 Brimacombe, C., Bodner, K., Michalska-Smith, M., Poisot, T., & Fortin, M.-J. (2023). Shortcomings
318 of reusing species interaction networks created by different sets of researchers. *PLOS Biology*, 21(4),
319 e3002068. <https://doi.org/10.1371/journal.pbio.3002068>
- 320 Brown, J. H., Gillooly, J. F., Allen, A. P., Savage, V. M., & West, G. B. (2004). Toward a Metabolic Theory
321 of Ecology. *Ecology*, 85(7), 1771–1789. <https://doi.org/10.1890/03-9000>
- 322 Buche, L., Bartomeus, I., & Godoy, O. (2024). Multitrophic Higher-Order Interactions Modulate Species
323 Persistence. *The American Naturalist*, 203(4), 458–472. <https://doi.org/10.1086/729222>
- 324 Canard, E., Mouquet, N., Marescot, L., Gaston, K. J., Gravel, D., & Mouillot, D. (2012). Emergence of
325 Structural Patterns in Neutral Trophic Networks. *PLOS ONE*, 7(8), e38295. <https://doi.org/10.1371/journal.pone.0038295>
- 327 Caron, D., Brose, U., Lurgi, M., Blanchet, F. G., Gravel, D., & Pollock, L. J. (2024). Trait-matching models
328 predict pairwise interactions across regions, not food web properties. *Global Ecology and Biogeography*,
329 33(4), e13807. <https://doi.org/10.1111/geb.13807>
- 330 Caron, D., Maiorano, L., Thuiller, W., & Pollock, L. J. (2022). Addressing the Eltonian shortfall with
331 trait-based interaction models. *Ecology Letters*, 25(4), 889–899. <https://doi.org/10.1111/ele.13966>
- 332 Catchen, M. D., Poisot, T., Pollock, L. J., & Gonzalez, A. (2023). *The missing link: Discerning true from
333 false negatives when sampling species interaction networks.*
- 334 Cherif, M., Brose, U., Hirt, M. R., Ryser, R., Silve, V., Albert, G., Arnott, R., Berti, E., Cirtwill, A.,
335 Dyer, A., Gauzens, B., Gupta, A., Ho, H.-C., Portalier, S. M. J., Wain, D., & Wootton, K. (2024). The
336 environment to the rescue: Can physics help predict predator–prey interactions? *Biological Reviews*,
337 n/a(n/a). <https://doi.org/10.1111/brv.13105>
- 338 Cirtwill, A. R., Ekkl, A., Roslin, T., Wootton, K., & Gravel, D. (2019). A quantitative framework for
339 investigating the reliability of empirical network construction. *Methods in Ecology and Evolution*, 10(6),
340 902–911. <https://doi.org/10.1111/2041-210X.13180>
- 341 Clegg, T., Ali, M., & Beckerman, A. P. (2018). The impact of intraspecific variation on food web structure.
342 *Ecology*, 99(12), 2712–2720. <https://doi.org/10.1002/ecy.2523>
- 343 Curtsdotter, A., Banks, H. T., Banks, J. E., Jonsson, M., Jonsson, T., Laubmeier, A. N., Traugott, M., &
344 Bommarco, R. (2019). Ecosystem function in predator–prey food webs—confronting dynamic models with
345 empirical data. *Journal of Animal Ecology*, 88(2), 196–210. <https://doi.org/10.1111/1365-2656.12892>

- 346 Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs' backbones
347 using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>
- 348 Dallas, T., Park, A. W., & Drake, J. M. (2017). Predicting cryptic links in host-parasite networks. *PLOS
349 Computational Biology*, 13(5), e1005557. <https://doi.org/10.1371/journal.pcbi.1005557>
- 350 Dansereau, G., Barros, C., & Poisot, T. (2024). Spatially explicit predictions of food web structure from
351 regional-level data. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 379(1909).
352 <https://doi.org/10.1098/rstb.2023.0166>
- 353 Delmas, E., Besson, M., Brice, M.-H., Burkle, L. A., Riva, G. V. D., Fortin, M.-J., Gravel, D., Guimarães,
354 P. R., Hembry, D. H., Newman, E. A., Olesen, J. M., Pires, M. M., Yeakel, J. D., & Poisot, T. (2019).
355 Analysing ecological networks of species interactions. *Biological Reviews*, 94(1), 16–36. <https://doi.org/10.1111/brv.12433>
- 356 Delmas, E., Brose, U., Gravel, D., Stouffer, D. B., & Poisot, T. (2017). Simulations of biomass dynamics in
357 community food webs. *Methods in Ecology and Evolution*, 8(7), 881–886. <https://doi.org/10.1111/2041-210X.12713>
- 358 Desjardins-Proulx, P., Laigle, I., Poisot, T., & Gravel, D. (2017). Ecological interactions and the Netflix
359 problem. *PeerJ*, 5, e3644. <https://doi.org/10.7717/peerj.3644>
- 360 Dunhill, A. M., Zarzyczny, K., Shaw, J. O., Atkinson, J. W., Little, C. T. S., & Beckerman, A. P. (2024).
361 Extinction cascades, community collapse, and recovery across a Mesozoic hyperthermal event. *Nature
362 Communications*, 15(1), 8599. <https://doi.org/10.1038/s41467-024-53000-2>
- 363 Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological
364 networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.
- 365 Dunne, J. A., Williams, R. J., Martinez, N. D., Wood, R. A., & Erwin, D. H. (2008). Compilation and
366 Network Analyses of Cambrian Food Webs. *PLOS Biology*, 6(4), e102. [https://doi.org/10.1371/journal.pbio.0060102](https://doi.org/10.1371/journal.
367 pbio.0060102)
- 368 Eklöf, A., Tang, S., & Allesina, S. (2013). Secondary extinctions in food webs: A Bayesian network approach.
369 *Methods in Ecology and Evolution*, 4(8), 760–770. <https://doi.org/10.1111/2041-210X.12062>
- 370 Estay, S. A., Fortin, M.-J., & López, D. N. (2023). Editorial: Patterns and processes in ecological networks
371 over space. *Frontiers in Ecology and Evolution*, 11.
- 372 Fortin, M.-J., Dale, M. R. T., & Brimacombe, C. (2021). Network ecology in dynamic landscapes. *Proceedings
373 of the Royal Society B: Biological Sciences*, 288(1949), rspb.2020.1889, 20201889. <https://doi.org/10.1098/rspb.2020.1889>
- 374 Fricke, E. C., Hsieh, C., Middleton, O., Gorczynski, D., Cappello, C. D., Sanisidro, O., Rowan, J., Svenning,
375 J.-C., & Beaudrot, L. (2022). Collapse of terrestrial mammal food webs since the Late Pleistocene.
376

- 379 *Science*, 377(6609), 1008–1011. <https://doi.org/10.1126/science.abn4012>
- 380 Galiana, N., Lurgi, M., Claramunt-López, B., Fortin, M.-J., Leroux, S., Cazelles, K., Gravel, D., & Montoya,
381 J. M. (2018). The spatial scaling of species interaction networks. *Nature Ecology & Evolution*, 2(5),
382 782–790. <https://doi.org/10.1038/s41559-018-0517-3>
- 383 García-Callejas, D., Godoy, O., Buche, L., Hurtado, M., Lanuza, J. B., Allen-Perkins, A., & Bartomeus, I.
384 (2023). Non-random interactions within and across guilds shape the potential to coexist in multi-trophic
385 ecological communities. *Ecology Letters*, 26(6), 831–842. <https://doi.org/10.1111/ele.14206>
- 386 Golubski, A. J., & Abrams, P. A. (2011). Modifying modifiers: What happens when interspecific interactions
387 interact? *Journal of Animal Ecology*, 80(5), 1097–1108. <https://doi.org/10.1111/j.1365-2656.2011.01852.x>
- 388 [X](#)
- 389 Gómez, J. M., Verdú, M., & Perfectti, F. (2010). Ecological interactions are evolutionarily conserved across
390 the entire tree of life. *Nature*, 465(7300), 918–921. <https://doi.org/10.1038/nature09113>
- 391 Gray, C., Figueroa, D. H., Hudson, L. N., Ma, A., Perkins, D., & Woodward, G. (2015). Joining the dots:
392 An automated method for constructing food webs from compendia of published interactions. *Food Webs*,
393 5, 11–20. <https://doi.org/10.1016/j.fooweb.2015.09.001>
- 394 Higino, G. T., Banville, F., Dansereau, G., Muñoz, N. R. F., Windsor, F., & Poisot, T. (2023). Mismatch
395 between IUCN range maps and species interactions data illustrated using the Serengeti food web. *PeerJ*,
396 11, e14620. <https://doi.org/10.7717/peerj.14620>
- 397 Hui, C., & Richardson, D. M. (2019). How to Invade an Ecological Network. *Trends in Ecology & Evolution*,
398 34(2), 121–131. <https://doi.org/10.1016/j.tree.2018.11.003>
- 399 Hutchinson, M. C., Bramon Mora, B., Pilosof, S., Barner, A. K., Kéfi, S., Thébault, E., Jordano, P., &
400 Stouffer, D. B. (2019). Seeing the forest for the trees: Putting multilayer networks to work for community
401 ecology. *Functional Ecology*, 33(2), 206–217. <https://doi.org/10.1111/1365-2435.13237>
- 402 Jordano, P. (2016a). Chasing Ecological Interactions. *PLOS Biology*, 14(9), e1002559. <https://doi.org/10.1371/journal.pbio.1002559>
- 403 Jordano, P. (2016b). Sampling networks of ecological interactions. *Functional Ecology*. <https://doi.org/10.1111/1365-2435.12763>
- 404 Kéfi, S., Berlow, E. L., Wieters, E. A., Joppa, L. N., Wood, S. A., Brose, U., & Navarrete, S. A. (2015).
405 Network structure beyond food webs: Mapping non-trophic and trophic interactions on Chilean rocky
406 shores. *Ecology*, 96(1), 291–303. <https://doi.org/10.1890/13-1424.1>
- 407 Kéfi, S., Berlow, E. L., Wieters, E. A., Navarrete, S. A., Petchey, O. L., Wood, S. A., Boit, A., Joppa, L. N.,
408 Lafferty, K. D., Williams, R. J., Martinez, N. D., Menge, B. A., Blanchette, C. A., Iles, A. C., & Brose,
409 U. (2012). More than a meal... integrating non-feeding interactions into food webs: More than a meal

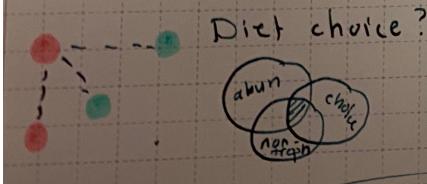
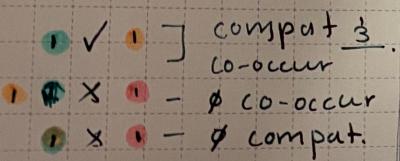
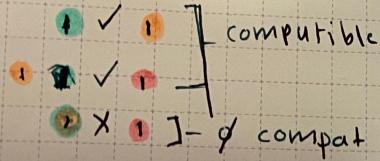
- 412 *Ecology Letters*, 15(4), 291–300. <https://doi.org/10.1111/j.1461-0248.2011.01732.x>
- 413 Krause, A. E., Frank, K. A., Mason, D. M., Ulanowicz, R. E., & Taylor, W. W. (2003). Compartments
414 revealed in food-web structure. *Nature*, 426(6964), 282–285. <https://doi.org/10.1038/nature02115>
- 415 Laender, F. D., Oevelen, D. V., Soetaert, K., & Middelburg, J. J. (2010). Carbon transfer in a herbivore-
416 and microbial loop-dominated pelagic food webs in the southern Barents Sea during spring and summer.
417 *Marine Ecology Progress Series*, 398, 93–107. <https://doi.org/10.3354/meps08335>
- 418 Lajaaiti, I., Bonnici, I., Kéfi, S., Mayall, H., Danet, A., Beckerman, A. P., Malpas, T., & Delmas, E. (2024).
419 *EcologicalNetworksDynamics.jl* A Julia package to simulate the temporal dynamics of complex ecological
420 networks (p. 2024.03.20.585899). bioRxiv. <https://doi.org/10.1101/2024.03.20.585899>
- 421 Lindeman, R. L. (1942). The Trophic-Dynamic Aspect of Ecology. *Ecology*, 23(4), 399–417. <https://doi.org/10.2307/1930126>
- 422 Llewelyn, J., Strona, G., Dickman, C. R., Greenville, A. C., Wardle, G. M., Lee, M. S. Y., Doherty, S.,
423 Shabani, F., Saltré, F., & Bradshaw, C. J. A. (2023). Predicting predator–prey interactions in terrestrial
424 endotherms using random forest. *Ecography*, 2023(9), e06619. <https://doi.org/10.1111/ecog.06619>
- 425 Momal, R., Robin, S., & Ambroise, C. (2020). Tree-based inference of species interaction networks from
426 abundance data. *Methods in Ecology and Evolution*, 11(5), 621–632. <https://doi.org/10.1111/2041-210X.13380>
- 427 Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from
428 proxies. *Trends in Ecology & Evolution*, 30(6), 347–356. <https://doi.org/10.1016/j.tree.2015.03.014>
- 429 Pawar, S., Dell, A. I., & Savage, V. M. (2012). Dimensionality of consumer search space drives trophic
430 interaction strengths. *Nature*, 486(7404), 485–489. <https://doi.org/10.1038/nature11131>
- 431 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2008). Size, foraging, and food web
432 structure. *Proceedings of the National Academy of Sciences*, 105(11), 4191–4196. <https://doi.org/10.1073/pnas.0710672105>
- 433 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2011). Fit, efficiency, and biology: Some
434 thoughts on judging food web models. *Journal of Theoretical Biology*, 279(1), 169–171. <https://doi.org/10.1016/j.jtbi.2011.03.019>
- 435 Pichler, M., Boreux, V., Klein, A.-M., Schleuning, M., & Hartig, F. (2020). Machine learning algorithms
436 to infer trait-matching and predict species interactions in ecological networks. *Methods in Ecology and
437 Evolution*, 11(2), 281–293. <https://doi.org/10.1111/2041-210X.13329>
- 438 Pilosof, S., Porter, M. A., Pascual, M., & Kéfi, S. (2017). The multilayer nature of ecological networks.
439 *Nature Ecology & Evolution*, 1(4), 101. <https://doi.org/10.1038/s41559-017-0101>
- 440 Poelen, J. H., Simons, J. D., & Mungall, C. J. (2014). Global biotic interactions: An open infrastructure to
441 16

- 445 share and analyze species-interaction datasets. *Ecological Informatics*, 24, 148–159. <https://doi.org/10.1016/j.ecoinf.2014.08.005>
- 446
- 447 Poisot, T. (2023). Guidelines for the prediction of species interactions through binary classification. *Methods*
448 in *Ecology and Evolution*, 14(5), 1333–1345. <https://doi.org/10.1111/2041-210X.14071>
- 449 Poisot, T., Baiser, B., Dunne, J., Kéfi, S., Massol, F., Mouquet, N., Romanuk, T. N., Stouffer, D. B., Wood, S.
450 A., & Gravel, D. (2016). Mangal – making ecological network analysis simple. *Ecography*, 39(4), 384–390.
451 <https://doi.org/10.1111/ecog.00976>
- 452 Poisot, T., Cirtwill, A., Cazelles, K., Gravel, D., Fortin, M.-J., & Stouffer, D. (2016). The structure of
453 probabilistic networks. *Methods in Ecology and Evolution*, 7(3), 303–312. <https://doi.org/10.1111/mec.12470>
- 454 Poisot, T., Stouffer, D. B., & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary
455 through space and time. *Oikos*, 124(3), 243–251. <https://doi.org/10.1111/oik.01719>
- 456 Poisot, T., Stouffer, D. B., & Kéfi, S. (2016). Describe, understand and predict: Why do we need networks
457 in ecology? *Functional Ecology*, 30(12), 1878–1882. <https://www.jstor.org/stable/48582345>
- 458 Pollock, L. J., Tingley, R., Morris, W. K., Golding, N., O’Hara, R. B., Parris, K. M., Vesk, P. A., &
459 McCarthy, M. A. (2014). Understanding co-occurrence by modelling species simultaneously with a Joint
460 Species Distribution Model (JSDM). *Methods in Ecology and Evolution*, 5(5), 397–406. <https://doi.org/10.1111/2041-210X.12180>
- 461
- 462 Pringle, R. M. (2020). Untangling Food Webs. In *Unsolved Problems in Ecology* (pp. 225–238). Princeton
463 University Press. <https://doi.org/10.1515/9780691195322-020>
- 464 Proulx, S. R., Promislow, D. E. L., & Phillips, P. C. (2005). Network thinking in ecology and evolution.
465 *Trends in Ecology & Evolution*, 20(6), 345–353. <https://doi.org/10.1016/j.tree.2005.04.004>
- 466 Pyke, G. (1984). Optimal Foraging Theory: A Critical Review. *Annual Review of Ecology, Evolution and*
467 *Systematic*, 15, 523–575. <https://doi.org/10.1146/annurev.ecolsys.15.1.523>
- 468 Rooney, N., McCann, K. S., & Moore, J. C. (2008). A landscape theory for food web architecture. *Ecology*
469 *Letters*, 11(8), 867–881. <https://doi.org/10.1111/j.1461-0248.2008.01193.x>
- 470 Roopnarine, P. D. (2006). Extinction Cascades and Catastrophe in Ancient Food Webs. *Paleobiology*, 32(1),
471 1–19. <https://www.jstor.org/stable/4096814>
- 472 Saravia, L. A., Marina, T. I., Kristensen, N. P., De Troch, M., & Momo, F. R. (2022). Ecological network
473 assembly: How the regional metaweb influences local food webs. *Journal of Animal Ecology*, 91(3),
474 630–642. <https://doi.org/10.1111/1365-2656.13652>
- 475 Segar, S. T., Fayle, T. M., Srivastava, D. S., Lewinson, T. M., Lewis, O. T., Novotny, V., Kitching, R. L.,
476 & Maunsell, S. C. (2020). The Role of Evolution in Shaping Ecological Networks. *Trends in Ecology &*
477 *Evolution*, 35(5), 454–466. <https://doi.org/10.1016/j.tree.2020.01.004>

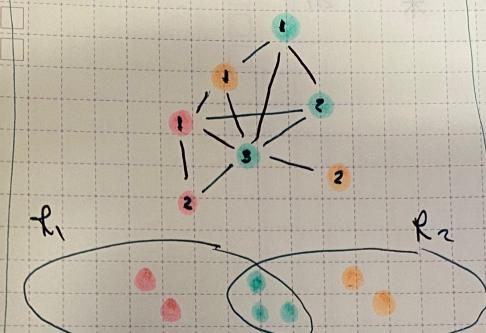
- 478 Shaw, J. O., Dunhill, A. M., Beckerman, A. P., Dunne, J. A., & Hull, P. M. (2024). *A framework for*
479 *reconstructing ancient food webs using functional trait data* (p. 2024.01.30.578036). bioRxiv. <https://doi.org/10.1101/2024.01.30.578036>
- 480
- 481 Soberón, J. (2007). Grinnellian and Eltonian niches and geographic distributions of species. *Ecology Letters*,
482 10(12), 1115–1123. <https://doi.org/10.1111/j.1461-0248.2007.01107.x>
- 483 Song, C., & Levine, J. M. (2024). *Rigorous (in)validation of ecological models* (p. 2024.09.19.613075). bioRxiv.
484 <https://doi.org/10.1101/2024.09.19.613075>
- 485 Staniczenko, P. P. A., Lewis, O. T., Jones, N. S., & Reed-Tsochas, F. (2010). Structural dynamics and
486 robustness of food webs. *Ecology Letters*, 13(7), 891–899. <https://doi.org/10.1111/j.1461-0248.2010.01485.x>
- 487
- 488 Stock, M. (2021). Pairwise learning for predicting pollination interactions based on traits and phylogeny.
489 *Ecological Modelling*, 14.
- 490 Stouffer, D. B. (2019). All ecological models are wrong, but some are useful. *Journal of Animal Ecology*,
491 88(2), 192–195. <https://doi.org/10.1111/1365-2656.12949>
- 492 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Hemming, V.,
493 Mercier, B., Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2022). Food web reconstruction
494 through phylogenetic transfer of low-rank network representation. *Methods in Ecology and Evolution*,
495 13(12), 2838–2849. <https://doi.org/10.1111/2041-210X.13835>
- 496 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Mercier, B.,
497 Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2023). Graph embedding and transfer
498 learning can help predict potential species interaction networks despite data limitations. *Methods in*
499 *Ecology and Evolution*, 14(12), 2917–2930. <https://doi.org/10.1111/2041-210X.14228>
- 500 Strydom, T., Catchen, M. D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., Forero-Muñoz,
501 N. R., Higino, G., Mercier, B., Gonzalez, A., Gravel, D., Pollock, L., & Poisot, T. (2021). A roadmap
502 towards predicting species interaction networks (across space and time). *Philosophical Transactions of*
503 *the Royal Society B: Biological Sciences*, 376(1837), 20210063. <https://doi.org/10.1098/rstb.2021.0063>
- 504 Terry, J. C. D., & Lewis, O. T. (2020). Finding missing links in interaction networks. *Ecology*, 101(7), e03047.
505 <https://doi.org/10.1002/ecy.3047>
- 506 Valdovinos, F. S., Hale, K. R. S., Dritz, S., Glaum, P. R., McCann, K. S., Simon, S. M., Thébault, E., Wetzel,
507 W. C., Wootton, K. L., & Yeakel, J. D. (2023). A bioenergetic framework for aboveground terrestrial
508 food webs. *Trends in Ecology & Evolution*, 38(3), 301–312. <https://doi.org/10.1016/j.tree.2022.11.004>
- 509 Van De Walle, R., Logghe, G., Haas, N., Massol, F., Vandegehuchte, M. L., & Bonte, D. (2023). Arthro-
510 pod food webs predicted from body size ratios are improved by incorporating prey defensive properties.

- 511 *Journal of Animal Ecology*, 92(4), 913–924. <https://doi.org/10.1111/1365-2656.13905>
- 512 Wells, K., & O'Hara, R. B. (2013). Species interactions: Estimating per-individual interaction strength and
513 covariates before simplifying data into per-species ecological networks. *Methods in Ecology and Evolution*,
514 4(1), 1–8. <https://doi.org/10.1111/j.2041-210x.2012.00249.x>
- 515 Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404(6774), 180–183.
516 <https://doi.org/10.1038/35004572>
- 517 Williams, R. J., & Martinez, N. D. (2008). Success and its limits among structural models of complex food
518 webs. *Journal of Animal Ecology*, 77(3), 512–519. <https://doi.org/10.1111/j.1365-2656.2008.01362.x>
- 519 Wootton, K. L., Curtsdotter, A., Roslin, T., Bommarco, R., & Jonsson, T. (2023). Towards a modular theory
520 of trophic interactions. *Functional Ecology*, 37(1), 26–43. <https://doi.org/10.1111/1365-2435.13954>
- 521 Xie, J.-R., Zhang, P., Zhang, H.-F., & Wang, B.-H. (2017). Completeness of Community Structure in
522 Networks. *Scientific Reports*, 7(1), 5269. <https://doi.org/10.1038/s41598-017-05585-6>
- 523 Yeakel, J. D., Pires, M. M., Rudolf, L., Dominy, N. J., Koch, P. L., Guimarães, P. R., & Gross, T. (2014).
524 Collapse of an ecological network in Ancient Egypt. *PNAS*, 111(40), 14472–14477. <https://doi.org/10.1073/pnas.1408471111>
- 525 Yodzis, P. (1982). The Compartmentation of Real and Assembled Ecosystems. *The American Naturalist*,
526 120(5), 551–570. <https://doi.org/10.1086/284013>
- 527 Yodzis, P., & Innes, S. (1992). Body Size and Consumer-Resource Dynamics. *The American Naturalist*,
528 139(6), 1151–1175. <https://doi.org/10.1086/285380>

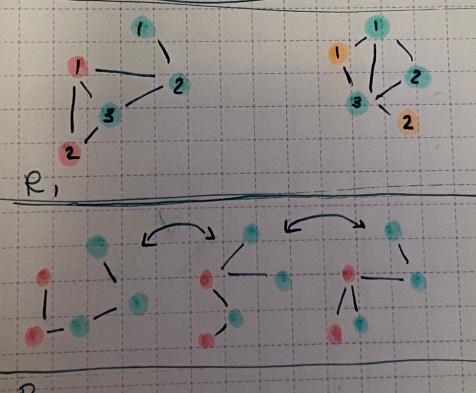
WED
水 276
PROCESS.



REPRESENTATION



"Global" metaweb.
All possible interactions for collection of spp.

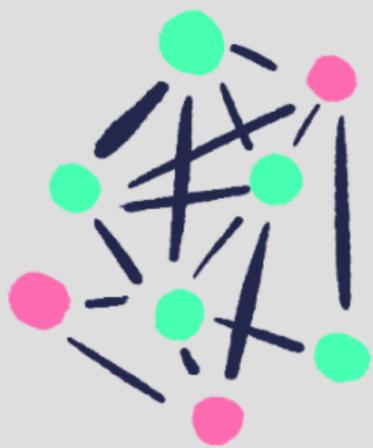


"Regional" metaweb.
All possible interactions for co-occurring species.



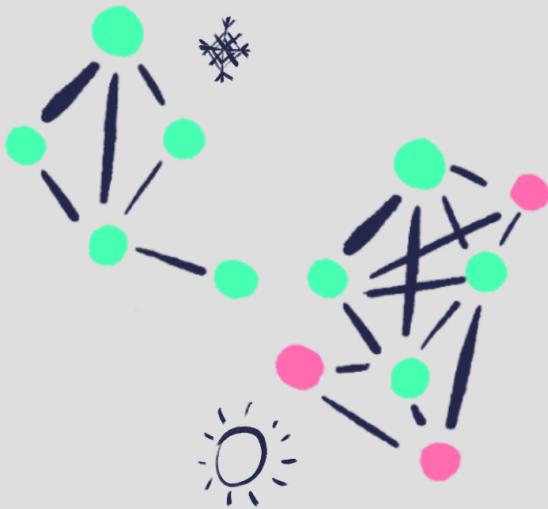
Realized networks.
The dynamic interactions that occur.
Dynamic config.

Figure 1: Aligning the various processes that determine interactions with the different network representations. First we start with a 'global metaweb' this network which captures all possible interactions for an arbitrary collection of species, we can further refine this network by taking in to consideration the co-occurrence of these difference species - as shown here we have two regions with some species (blue) that are found in both regions and others endemic to either region one (pink) or region two (orange). These regional metawebs to capture all possible interactions, however it only considers species that co-occur. However even within a region we do not expect all interactions to be realised but rather that there are multiple configurations of the regional metaweb over both space and time. The 'state' of the different network realisations are ultimately influenced not just by the co-occurrence of a species pair but rather the larger community context such as the abundance of different species, maximising energy gain, or indirect/higher order interactions.



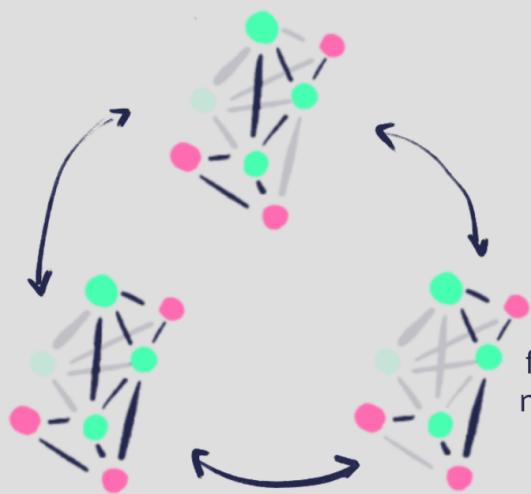
1. A 'global' metaweb

Knowledge of the entire diet breadth of a species is valuable especially in terms of understanding how a species will respond to changes in the community - *e.g.,* invasions/rewilding exercises (where does the new species 'fit' within the network?) as well as potential capacity to shift its diet. Although this might make sense across space and not time but certain species act as links across the landscape.



2. Seasonal metawebs

- Knowledge at the finer scale is also valuable to understand/identify that there are in fact differences between the seasons
- Information of seasonal diet of species



3. Seasonal (re-arranged networks)

Dynamics are useful because they are a representation of the different configurations/energy flows/ecosystem processes. Also to detect more nuanced shifts in diet - *e.g.,* seasonal diet shifts.

- Structurally informative
- can be @ even finer scale & time / space

Figure 2

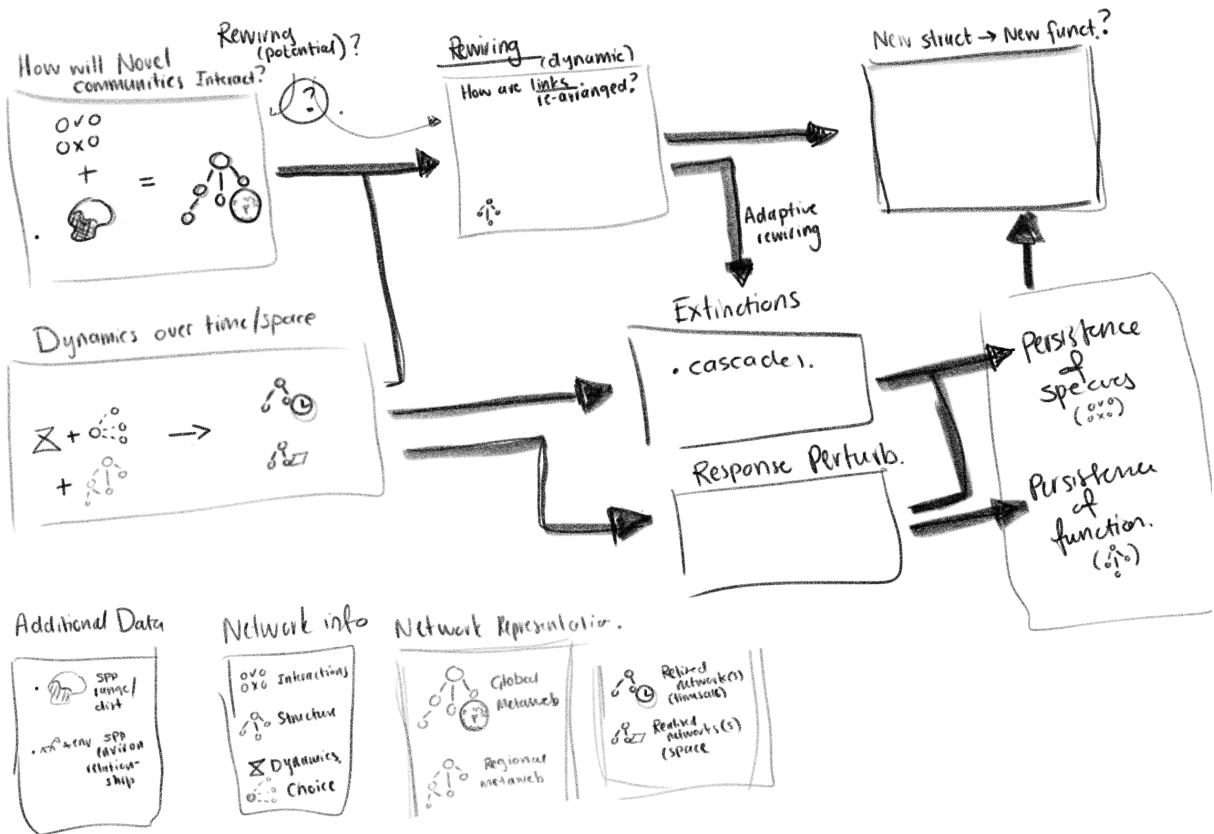


Figure 3: An attempt to try and visualise a way to map the different scales of network representations to the way in which we can interrogate/ask questions about them?