

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

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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 1.1 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 1.2 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).

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

[Figure 1 about here.]

2.1 The processes that determine species interactions

100 Evolutionary compatibility

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

112 (Co)occurrence

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

120 determine the distribution of a species (Higino et al., 2023; Pollock et al., 2014), representing something of
121 a fusion of the the Grinnellian and Eltonian niches (Gravel et al., 2019).

122 Abundance

123 The abundance of different the species within the community is thought to influence the realisation of feeding
124 links primarily in two ways. Firstly there is the argument that that structure of networks (and the interactions
125 that they are composed of) are driven *only* by the abundance of the different species and that interactions
126 are not contingent on there being any compatibility (trait matching) between them, *sensu* neutral processes
127 (Canard et al., 2012; Momal et al., 2020). However, a more ecologically sound assumption would be that
128 the abundance of different prey species will influence which prey are targeted or preferred by the predator
129 as abundance influences factors such as the likelihood of species meeting (Banville et al., 2024; Poisot et al.,
130 2015), or in the dynamic sense will influence the persistence of viable populations.

131 Predator choice (energetic cost)

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

140 Non-trophic interactions

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

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

₁₅₀ It should be self evident that the different processes discussed above are all ultimately going to influence the
₁₅₁ realisation of interactions as well as the structure of a network, however they are acting at different scales
₁₅₂ of organisation. Both the **co-occurrence** and the **evolutionary compatibility** are valid at the scale of
₁₅₃ the species pair of interest, that is the *possibility* of an interaction being present/absent is assessed at the
₁₅₄ pairwise level and one is left with a ‘list’ of interactions that are present/absent. Although it is possible
₁₅₅ to build a network (*i.e.*, metaweb) from this information it is important to be aware that the structure of
₁₅₆ this network is not constrained by real-world dynamics or conditions, and so just because species are able to
₁₅₇ interact does not mean that they will (Poisot et al., 2015). In order to construct a network who’s structure is
₁₅₈ a closer approximation of reality (localised interactions) one needs to take into consideration the properties
₁₅₉ of the community as a whole and information about the individuals it is comprised of (Quintero et al., 2024),
₁₆₀ which requires more data at the community scale, such as the abundance of species.

₁₆₁ **3 Network construction is nuanced**

₁₆₂ The act of constructing a ‘real world’ network will ultimately be delimited by its intended use, however the
₁₆₃ reality is that the empirical collection of interaction data is both costly and challenging to execute (Jordano,
₁₆₄ 2016a, 2016b), especially if one wants to capture *all* aspects of the processes discussed in Section 2 (owing
₁₆₅ to the different time and spatial scales they may be operating at). Thus we often turn to models to either
₁₆₆ predict networks (be that the interaction between two species, or network structure (Strydom et al., 2021)),
₁₆₇ or as a means to identify missing interactions (gap fill) within an existing empirical dataset (Biton et al.,
₁₆₈ 2024; Dallas et al., 2017; Stock, 2021), and so for the purpose of this discussion network construction will be
₁₆₉ synonymous with using a model as a means to represent or predict a network. That is not to say that there is
₁₇₀ no need for empirical data collection but rather that using a model for food web prediction (or reconstruction)
₁₇₁ is a more feasible approach as it allows us to make inferences about interactions that are not happening in
₁₇₂ the ‘observable now’ (Strydom et al., 2021), with the added benefit that one is able to build some uncertainty
₁₇₃ into the resulting network (Banville et al., 2024). Additionally different models have different underlying
₁₇₄ philosophies that allow us to capture one or a few of the processes discussed in Section 2, and although the
₁₇₅ delimits and defines what inferences can be made from the resulting network it also allows us to isolate and
₁₇₆ understand how different processes determine interactions (Song & Levine, 2024; Stouffer, 2019). Here we will
₁₇₇ introduce the three different types of network representations (metawebs, realised networks, and structural
₁₇₈ networks), how they link back to (and encode) the different processes determining interactions Figure 1, and
₁₇₉ broadly discuss some of the modelling approaches that are used to construct these different network types.

180 This is paralleled by a hypothetical case study (Box 1) where we showcase the utility/applicability of the
181 different network representations in the context of trying to understand the feeding dynamics of a seasonal
182 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.]

183

184 **3.1 Models that predict metawebs (feasible interactions)**

185 This is perhaps the most developed group of models; with a variety of approaches having been developed
186 that typically determine the feasibility of an interaction using the trait compatibility between predator and
187 prey (*i.e.* their evolutionary compatibility) to determine 'feeding rules' (Morales-Castilla et al., 2015). These
188 feeding rules are broadly elucidated in two different ways; mechanistic feeding rules can be explicitly defined
189 and applied to a community (Dunne et al., 2008; Roopnarine, 2017; *e.g.*, Shaw et al., 2024) or they are
190 inferred from a community for which there are interaction data and the 'rules' are then applied to a different
191 community (Caron et al., 2022; Cirtwill et al., 2019; Desjardins-Proulx et al., 2017; Eklöf et al., 2013;

192 Llewelyn et al., 2023; Pichler et al., 2020; Strydom et al., 2022; *e.g.*, Strydom et al., 2023). The fundamental
193 difference between these two model groups is that ‘mechanistic models’ rely on expert knowledge and make
194 explicit assumptions on trait-feeding relationships, whereas the ‘pattern finding’ models are dependent on
195 existing datasets from which to elucidate feeding rules. These models are useful for determining all feasible
196 interactions for a specific community, and owing to the availability of empirical interaction datasets (Gray
197 et al., 2015; *e.g.*, Poelen et al., 2014; Poisot, Baiser, et al., 2016), as well as the development of model
198 testing/benchmarking tools (Poisot, 2023), means that these models can be validated and (with relative
199 confidence) be used to construct first draft networks for communities for which we have no interaction data
200 (Strydom et al., 2022), and are valuable not only in data poor regions but also for predicting interactions
201 for ‘unobservable’ communities *e.g.*, prehistoric networks (Fricke et al., 2022; Yeakel et al., 2014) or future,
202 novel community assemblages. Importantly metawebs are inherently ‘static’ in the sense that they are *not*
203 able to capture dynamic processes (since the notion of feasibility is all or nothing), however they provide a
204 bigger picture context (*e.g.*, understanding the *entire* diet breadth of a species) and often require little data
205 to construct.

206 3.2 Models that predict realised networks (realised interactions)

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

223 However, they are ‘costly’ to construct (requiring data about the entire community as it is the behaviour of
224 the system that determines the behaviour of the part) and also lack the larger diet niche context afforded by
225 metawebs.

226 3.3 Models that predict structure (interaction agnostic)

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

241 4 Making Progress with Networks

242 4.1 Further development of models and tools

243 There has been a suite of models that have been developed to predict feeding links, however we are lacking
244 in tools that are explicitly taking into consideration estimating both the feasibility as well as realisation of
245 links, *i.e.*, both interactions and structure simultaneously (Strydom et al., 2021). This could be addressed
246 either through the development of tools that do both (predict both interactions and structure), or to develop
247 an ensemble modelling approach (Becker et al., 2022; Terry & Lewis, 2020) or tools that will allow for the
248 downsampling of metawebs into realised networks (*e.g.*, Roopnarine, 2006). Additionally although realised
249 networks are more closely aligned with capturing interaction strength we lack models that allow us to quantify
250 this (Strydom et al., 2021; Wells & O’Hara, 2013). In addition to the more intentional development of models
251 we also need to consider the validation of these models, there have been developments and discussions for

252 assessing how well a model recovers pairwise interactions (Poisot, 2023; Strydom et al., 2021), although the
253 rate of false-negatives that may be present in the testing data still present a challenge (Catchen et al., 2023),
254 and we still lack clear set of guidelines for benchmarking the ability of models to recover structure (Allesina
255 et al., 2008).

256 **4.2 At what scale should we be predicting and using networks?**

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

268 **5 The future value of networks**

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

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

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

²⁸² Here we can talk about the effects of range shifts and invasions and how this will result in new/novel
²⁸³ community assemblages. And then also the intentional changes of species compositions through rewilding.

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

²⁸⁵ Linking to dynamic networks and how this lets us build spatially/temporally explicit networks which can be
²⁸⁶ used to infer form and function. Also bring in the discussion on the suitable aggregation (and the fact that
²⁸⁷ we don't know)

²⁸⁸ **5.3 How do species persist/co-exist?**

²⁸⁹ Specific sub points to consider here is persistence, especially persistence to perturbation. Again, dynamic
²⁹⁰ networks and network/community assembly and finally extinctions (Dunhill et al., 2024).

²⁹¹ [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

Question (broad)	Question (specific)	Network representation
Species/community persistence	Dynamics over time. Stability/resilience. How does a change in pop <i>A</i> affect pop <i>B</i> ?	Realised networks - but dynamic!
Synthetic networks	Creating ecologically plausible communities for synthetic analyses	Structural networks - data light!
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??

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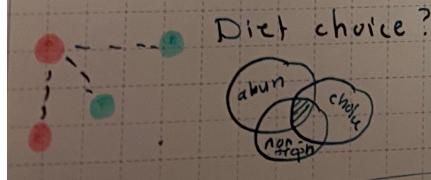
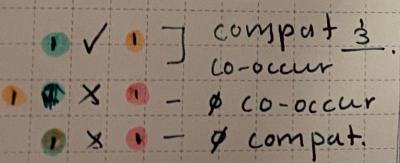
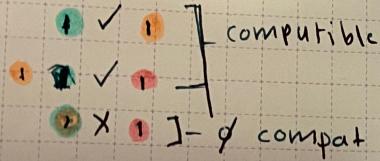
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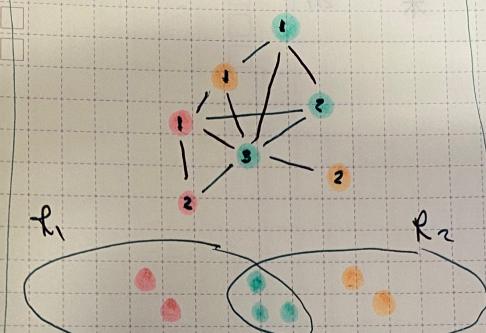
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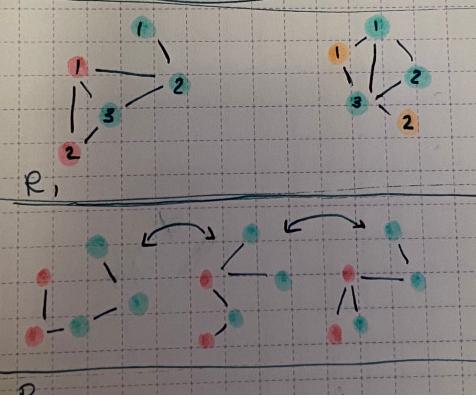
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PROCESS.



REPRESENTATION



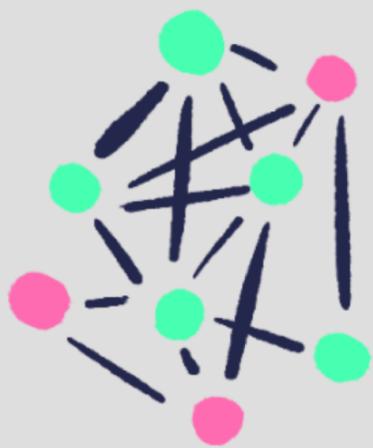
"Global" metaweb.
All possible interactions for collection of spp.



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

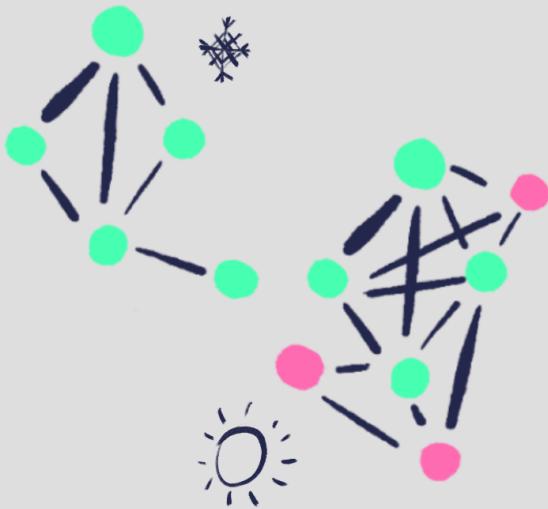
Realised networks.
The dynamic interactions that occur.
Dynamic config.

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.



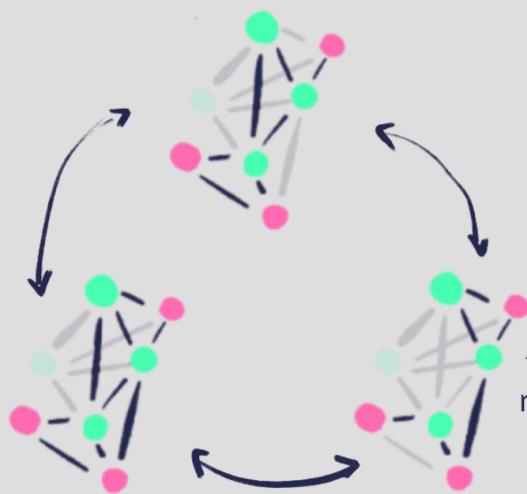
1. A 'global' metaweb

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 metaweb

- 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 (elliptical 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

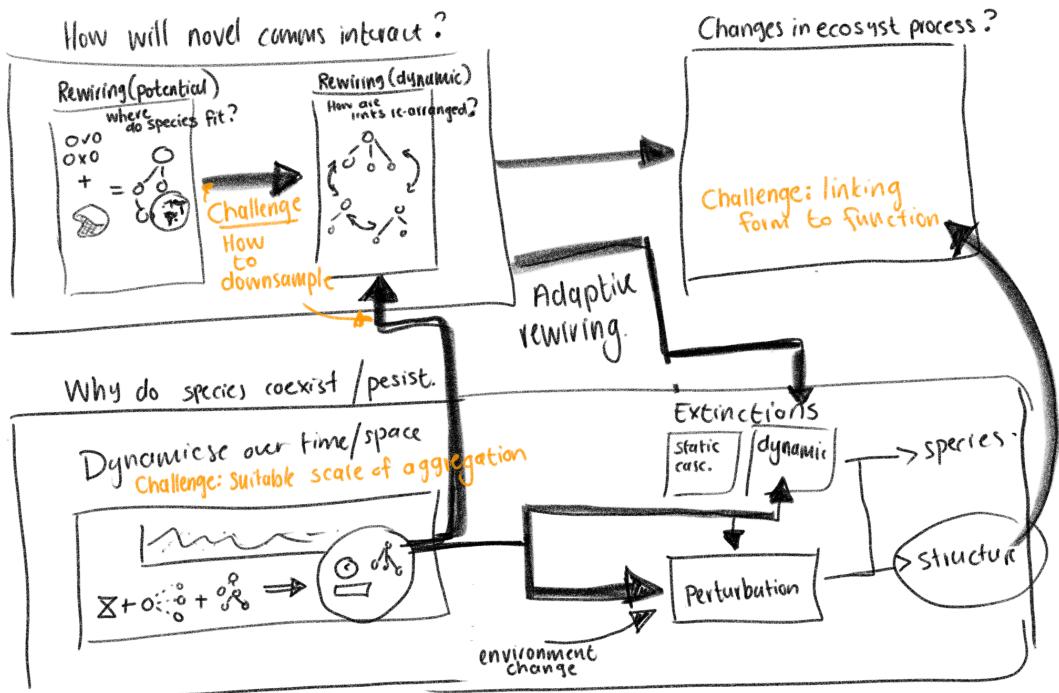


Figure 3: An attempt to try and visualise a way to map the different scales of network representations to the way in which we can interrogate/ask questions about them?