

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 1.0.1 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), representing a fusion of the

120 the Grinnellian and Eltonian niches (Gravel et al., 2019).

121 **Abundance**

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

130 **Predator choice (energetic cost)**

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

139 **Non-trophic interactions**

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

148 **2.2 Contextualising the processes that determine species interactions**

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

160 **3 Network construction is nuanced**

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

¹⁷⁹ This is paralleled by a hypothetical case study (Box 1) where we showcase the utility/applicability of the
¹⁸⁰ different network representations in the context of trying to understand the feeding dynamics of a seasonal
¹⁸¹ 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.]

¹⁸²

¹⁸³ 3.1 Models that predict metawebs (feasible interactions)

¹⁸⁴ This is perhaps the most developed group of models; with a variety of approaches having been developed
¹⁸⁵ that typically determine the feasibility of an interaction using the trait compatibility between predator and
¹⁸⁶ prey (*i.e.* their evolutionary compatibility) to determine 'feeding rules' (Morales-Castilla et al., 2015). These
¹⁸⁷ feeding rules are broadly elucidated in two different ways; mechanistic feeding rules can be explicitly defined
¹⁸⁸ and applied to a community (Dunne et al., 2008; *e.g.*, Shaw et al., 2024) or they are inferred from a community
¹⁸⁹ for which there are interaction data and the 'rules' are then applied to a different community (Caron et al.,
¹⁹⁰ 2022; Cirtwill et al., 2019; Desjardins-Proulx et al., 2017; Eklöf et al., 2013; Llewelyn et al., 2023; Pichler et al.,

¹⁹¹ 2020; Strydom et al., 2022; *e.g.*, Strydom et al., 2023). The fundamental difference between these two model
¹⁹² groups is that ‘mechanistic models’ rely on expert knowledge and make explicit assumptions on trait-feeding
¹⁹³ relationships, whereas the ‘pattern finding’ models are dependent on existing datasets from which to elucidate
¹⁹⁴ feeding rules. These models are useful for determining all feasible interactions for a specific community, and
¹⁹⁵ owing to the availability of empirical interaction datasets (Gray et al., 2015; *e.g.*, Poelen et al., 2014; Poisot,
¹⁹⁶ Baiser, et al., 2016), as well as the development of model testing/benchmarking tools (Poisot, 2023), means
¹⁹⁷ that these models can be validated and (with relative confidence) be used to construct first draft networks for
¹⁹⁸ communities for which we have no interaction data (Strydom et al., 2022), and are valuable not only in data
¹⁹⁹ poor regions but also for predicting interactions for ‘unobservable’ communities *e.g.*, prehistoric networks
²⁰⁰ (Fricke et al., 2022; Yeakel et al., 2014) or future, novel community assemblages. Importantly metawebs
²⁰¹ are inherently ‘static’ in the sense that they are *not* able to capture dynamic processes (since the notion of
²⁰² feasibility is all or nothing), however they provide a bigger picture context (*e.g.*, understanding the *entire*
²⁰³ diet breadth of a species) and often require little data to construct.

²⁰⁴ 3.2 Models that predict realised networks (realised interactions)

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

222 the system that determines the behaviour of the part) and also lack the larger diet niche context afforded by
223 metawebs.

224 **3.3 Models that predict structure (interaction agnostic)**

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

239 **4 Making Progress with Networks**

240 **4.1 Further development of models and tools**

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

251 rate of false-negatives that may be present in the testing data still present a challenge (Catchen et al., 2023),
252 we still lack clear set of guidelines for benchmarking the ability of models to recover structure (Allesina et
253 al., 2008).

254 **4.2 At what scale should we be predicting and using networks?**

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

266 **5 The future value of networks**

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

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

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

²⁸⁰ Here we can talk about the effects of range shifts and invasions and how this will result in new/novel
²⁸¹ community assemblages. And then also the intentional changes of species compositions through rewilding.

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

²⁸³ Linking to dynamic networks and how this lets us build spatially/temporally explicit networks which can be
²⁸⁴ used to infer form and function. Also bring in the discussion on the suitable aggregation (and the fact that
²⁸⁵ we don't know)

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

²⁸⁷ Specific sub points to consider here is persistence, especially persistence to perturbation. Again, dynamic
²⁸⁸ networks and network/community assembly and finally extinctions (Dunhill et al., 2024).

²⁸⁹ [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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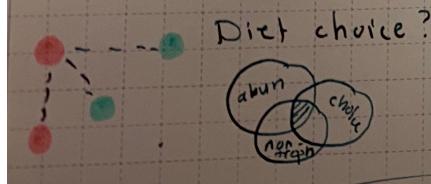
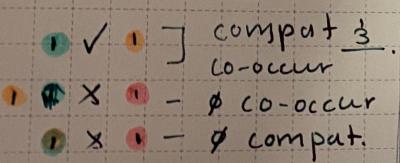
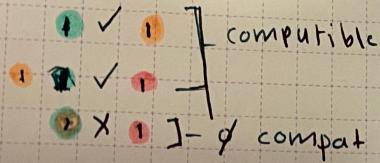
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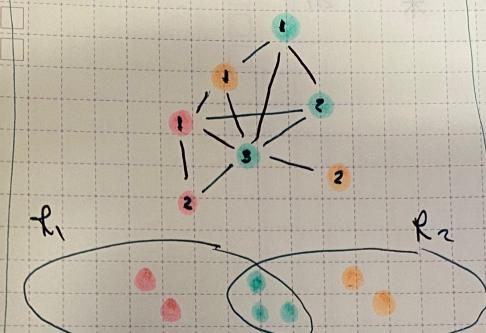
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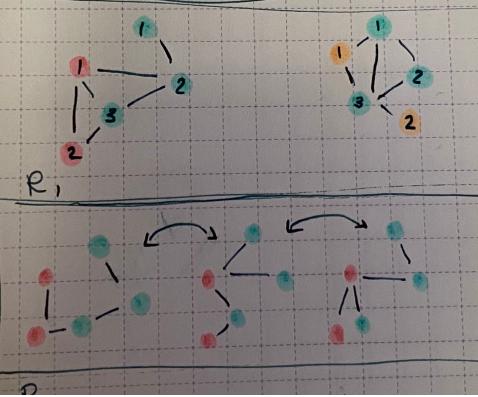
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PROCESS.



REPRESENTATION



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

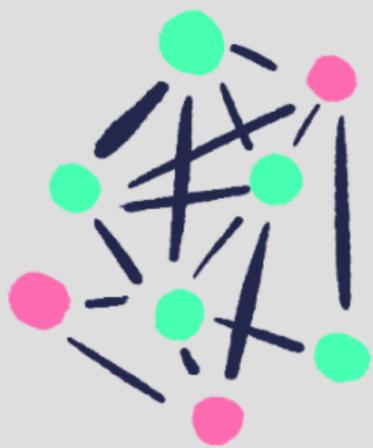


"Regional" metaweb.
All possible interactions for co-occurring species.



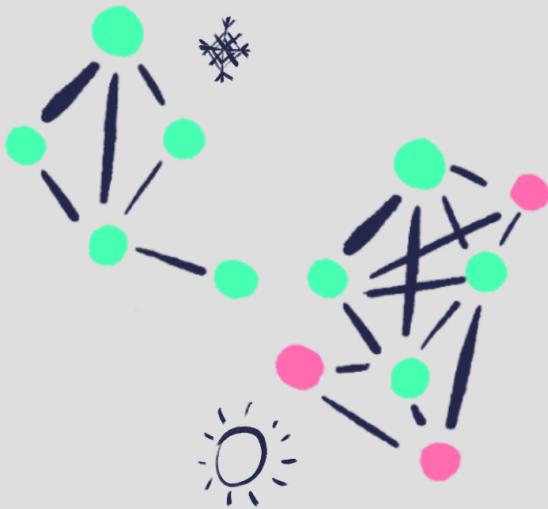
Realized networks.
The dynamic interactions that occur.
Dynamic config.

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.



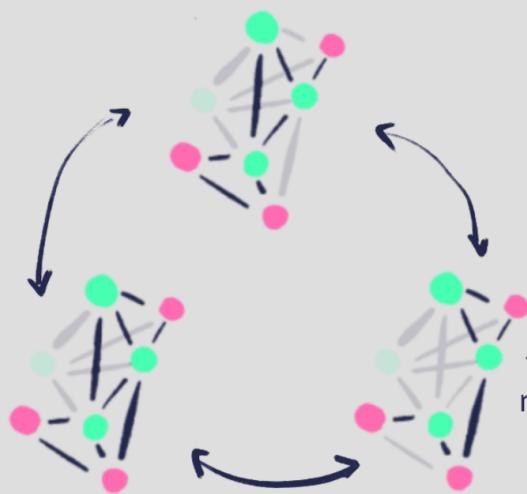
1. A 'global' metaweb

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 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

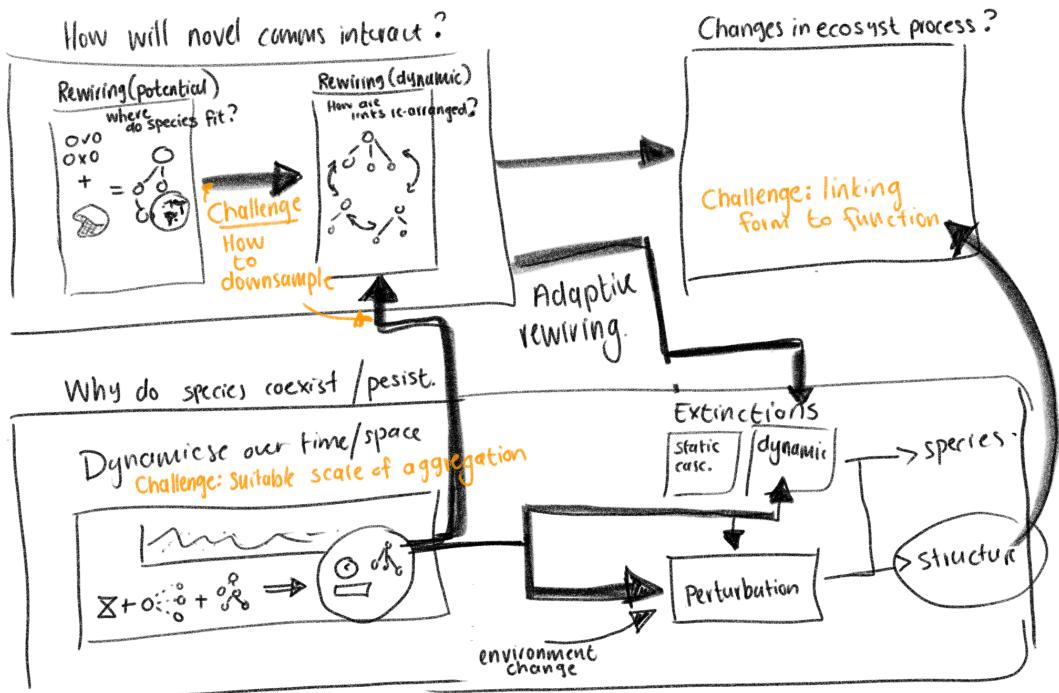


Figure 3: An attempt to try and visualise a way to map the different scales of network representations to the way in which we can interrogate/ask questions about them?