

# **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 (or individuals) is one of the fundamental building blocks of ecological communities provide a powerful  
5 abstraction that can help quantify, conceptualise, and understand biodiversity dynamics, and ultimately,  
6 one hopes, make prediction, mitigate change and manage services [ref]. Such network representations of  
7 biodiversity (including within species diversity) are increasingly argued to be an asset to predictive ecology,  
8 climate change mitigation and resource management. Here, it is argued that characterising biodiversity in  
9 a network will allow deeper capacity to understand and predict the abundance, distribution, dynamics and  
10 services provided by multiple species facing multiple stressors.

11 However, the way that a network is constructed (encoded) defines an epistemology of the network concept  
12 which, we argue, can influence the resulting observations and conclusions about pattern and mechanisms  
13 that are made (Brimacombe et al., 2023; Proulx et al., 2005). This process of constructing networks has two  
14 major pillars: the data and theory, the latter representing an expression of mechanism and process giving  
15 rise to patterns that emerge from collating interactions among species. Each of these pillars carries with it  
16 a set of practical, semantic and conceptual constraints that not only influence progress in making network  
17 ecology more valuable and potentially predictive, but help define the spatial, temporal and evolutionary scale  
18 of assumptions we make and predictions we might generate from the networks.

19 With respect to data, it is extremely challenging to actually record species interactions in the field (Jordano,  
20 2016a, 2016b). Despite notable herculean efforts (**Woodward? Benguela?** Maiorano et al. (2020)), actual  
21 coverage of ‘real world’ interaction data remains sparse (Poisot et al., 2021). Against this practical challenge,  
22 there is additionally high variance in the terminology we use to define networks. Finally, the mathematical  
23 and statistical tools we use to construct, conceptualise, analyse and predict with these networks are also  
24 highly variable.

25 1. what are the underlying assumptions about nodes, edges, scale and process that are made when we  
26 attempt to delimit and describe a food webs;

27 2. are there families of commonly used tools that map onto assumptions about scales and processes;

28 The provision of this detail ultimately leads to a set of insights and conclusions about whether, when and  
29 under what conditions network representations of biodiversity can contribute to the advancement of ecological  
30 theory and generate value in predictive ecology. Specifically, we finish this perspective with an overview of  
31 fundamental questions in ecology that we think can benefit from network thinking and a proposal that such

32 thinking can accelerate our capacity to predict the impact of multiple stressors on biodiverse communities.

## 33 1 Setting the Scene: The Not So Basics of Nodes and Edges

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

### 43 1.0.1 How do we define a node?

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

### 52 1.0.2 What is meant by an edge?

53 At its core, links within food webs can be thought of as a representation of either feeding links between  
54 species - be that realised (Pringle, 2020) or potential (Dunne, 2006), or representative of fluxes within  
55 the community/system *e.g.*, energy transfer or material flow (Lindeman, 1942). How we specify links will  
56 influence the resulting structure of the network - and the inferences we will make thereof. For example taking  
57 a food web that consists of links representing all *potential* feeding links for a community (*i.e.*, a metaweb)  
58 will be meaningless if one is interested in understanding the flow of energy through the network as the links  
59 within a metaweb do not represent environmental/energetic constraints, making them poor representations  
60 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* ‘on the ground’. The fundamental difference between these two different types of networks 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 an idea of the *complete* diet of a species (Strydom et al., 2023). Although metawebs are typically ‘constrained’ to a collection of species that also co-occur, there is no reason that a metaweb cannot include species that do not co-occur (although this would require some degree of prediction/assumptions to identify those possible interactions). In contrast realised networks are highly localised and 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 km<sup>2</sup> 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. 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 Scales, Context, and Processes

The interplay between network representation and network 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 realisation of

91 interactions, namely: evolutionary compatibility, co-occurrence, feasibility, abundance, predator choice, and  
92 non-trophic interactions; while simultaneously contextualising them within, and linking them to the different  
93 network representations Figure 1. We can think of the different network representations to be conceptually  
94 analogous to the fundamental and realised niche, whereby the metaweb represents the ‘fundamental diet  
95 niche’ of a species and a realised network represents the ‘realised diet’ of a species and are thus determined  
96 by different processes. Of course these processes do not function in a vacuum and do interact with/influence  
97 one another, but it is still beneficial to present them in a categorical manner as these different processes are  
98 often the underpinning logic in the development of prediction/network models, the criteria for data collection  
99 in the field, and the scale of organisation for which they are relevant (species, population, or community),  
100 which is all ultimately captured and encapsulated by the different network representations.

101 [Figure 1 about here.]

## 102 2.1 The processes that determine species interactions

### 103 Evolutionary compatibility

104 There is compelling evidence that the possibility of an interaction occurring between two species is the result  
105 of their shared (co)evolutionary history (Dalla Riva & Stouffer, 2016; Gómez et al., 2010; Segar et al., 2020).  
106 In the more proximal sense this is manifested as the ‘trait complementarity’ between two species, whereby  
107 one species (the predator) has the ‘correct’ set of traits that allow it to chase, capture, kill, and consume  
108 the other species (the prey). For species pairs where this condition is not met the link is deemed to be  
109 forbidden (Jordano, 2016b); *i.e.*, not physically possible and will always be absent within the network. In the  
110 context of trying to determine the feasibility (*i.e.*, the *possibility*) of an interaction, phylogeny is an excellent  
111 predictor (Fricke et al., 2022; Strydom et al., 2022) and allows one to construct what can be considered to  
112 be a metaweb. In terms of thinking about the anatomy of an ‘feasibility network’ one should be aware that  
113 it is possible to represent interactions as either binary (feasible/forbidden; *i.e.*, the traditional definition of a  
114 metaweb Dunne (2006)) or as a probability (Banville et al., 2024), where the probability represents how likely  
115 that the interaction between two species is feasible (what is the possibility of this interaction occurring?).

### 116 (Co)occurrence

117 Although the outright assumption that because two species are co-occurring it must mean that they are  
118 interacting is inherently flawed (Blanchet et al., 2020), it is of course impossible for two species to interact (at  
119 least in terms of feeding links) if they are not co-occurring in time and space. Thus co-occurrence data alone is  
120 insufficient to build an accurate and ecologically meaningful representation of a food web having information

on the co-occurrence of species can further aid us in refining metawebs by allowing us to downsample the network based on the species found in a specific location, or even add additional uncertainty based in how likely species are to co-occur (Dansereau et al., 2024). Additionally the interplay between the interaction between a species pair and their co-occurrence is meaningful when one is operating in the space of trying to determine the distribution of a species (Higino et al., 2023), and forms a key component of some of the next generation species distribution models *e.g.*, joint SDMs (Pollock et al., 2014).

## 127 **Abundance**

128 The abundance of the different species within the community can influence the likelihood of an interaction  
129 occurring in a myriad of ways *e.g.*, the likelihood of two species meeting, or the long term availability of  
130 prey. There is the argument that structure of networks (and the interactions that they are composed of)  
131 are driven by only the abundance of the different species and not their characteristics (traits), *sensu* neutral  
132 processes (Canard et al., 2012; Momal et al., 2020). Alternatively the abundance of species in a community  
133 can influence which interactions are ultimately realised (Banville et al., 2024; Poisot et al., 2015).

## 134 **Predator choice (energetic cost)**

135 Ultimately, predator choice is underpinned by the energetic cost-benefit of trying to catch, kill, and consume  
136 prey, and is well described within both optimal foraging theory [ref] and metabolic theory [ref], which rests  
137 on the idea that the prey a predator chooses to target is one that will have the greatest return on energy  
138 with the lowest energetic cost. With a body of evidence that suggests that body size might be the underlying  
139 driver, and thus suitable proxy for understanding these processes (Yodzis & Innes, 1992) There are additional  
140 bodies of work that attempt to include the cost of movement that the environment imposes on an individual  
141 (Cherif et al., 2024) as well as 2D/3D search space (Pawar et al., 2012).

## 142 **Indirect/higher order interactions**

143 The realisation (presence/absence) or strength of trophic interactions themselves can also be modified by  
144 other, indirect (non-trophic), interactions (Golubski & Abrams, 2011; Pilosof et al., 2017), this can be either  
145 ‘directly’ through *e.g.*, competition or ‘indirectly’ *e.g.*, mutualistic/facilitative interactions will alter the fine-  
146 scale distribution and abundance of some species (Kéfi et al., 2012, 2015) as well as persistence (Buche et al.,  
147 2024).

## 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 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 (*i.e.*, community context), 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 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.

*something about ‘physical’/landscape scale as well as time scale??*

### 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 [ref] and challenging to execute in a way that captures the different 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 its structure (Strydom, Catchen, 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, 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, which ultimately delimits and defines what inferences can be made from the resulting network. Here we will introduce the three different types of network representations (metawebs, realised networks, and structural networks), how they link back to 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**

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 across time/through 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 diet shifts, these details would be lost at the scale of the metaweb 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

#### **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 [Rooney]

#### **2: A seasonal metaweb**

Knowledge at the finer scale is also valuable to understand/identify that there are in fact differences between the seasons

#### **3: A seasonal realised network**

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.

#### **4: A structural network**

#### **Data trade off**

Above we highlight the practical uses of the different network configurations but we also need to take into consideration the barriers to construction/associated data needs/cost and acknowledge them. Basically in the ideal world we would have all this information at hand but in reality we might be sitting with

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 based on the trait compatibility between predator  
 185 and prey (*i.e.* their evolutionary compatibility) to determine ‘feeding rules’ (Morales-Castilla et al., 2015).  
 186 These feeding rules are broadly elucidated in two different ways; mechanistic feeding rules can be explicitly  
 187 defined and applied to a community (Dunne et al., 2008; *e.g.*, Shaw et al., 2024) or they are inferred from  
 188 a community for which there is interaction data and the ‘rules’ are then applied to a different community  
 189 (Caron et al., 2022; Cirtwill et al., 2019; Desjardins-Proulx et al., 2017; Eklöf et al., 2013; Llewelyn et  
 190 al., 2023; Pichler et al., 2020; Strydom et al., 2022; *e.g.*, Strydom et al., 2023). The fundamental difference  
 191 between these two model groups is that ‘mechanistic models’ rely on expert knowledge and make assumptions  
 192 on trait-feeding relationships, whereas the ‘pattern finding’ models are dependent on existing datasets from  
 193 which to elucidate feeding rules. These models are useful for determining all feasible interactions for a specific  
 194 community, and owing to the availability of empirical interaction datasets (Gray et al., 2015; *e.g.*, Poelen  
 195 et al., 2014; Poisot, Baiser, et al., 2016), as well as the development of model testing/benchmarking tools  
 196 (Poisot, 2023), means that these models can be validated and (with relative confidence) be used to construct  
 197 first draft networks for communities for which we have no data (Strydom et al., 2022), and are valuable  
 198 for constructing networks where we lack any interaction data *e.g.*, prehistoric networks (Fricke et al., 2022;  
 199 Yeakel et al., 2014) or even to predict interactions for contemporary species that do not currently co-occur  
 200 and thus we have no way of empirically evaluating if the interaction is feasible or not.

201 **3.2 Models that predict realised networks (realised interactions)**

202 In order to construct realised networks models need to incorporate *both* the feasibility of interactions (*i.e.*,  
 203 determine the entire diet breadth of a species) as well as then determine which interactions are realised (*i.e.*,  
 204 incorporate the ‘cost’ of interactions). As far as we are aware there is no model that explicitly accounts for  
 205 both of these ‘rules’ and rather *only* account for processes that determine the realisation of an interaction  
 206 (*i.e.*, abundance, predator choice, or non-trophic interactions). Although the use of allometry *i.e.*, body size  
 207 (Beckerman et al., 2006; *e.g.*, Valdovinos et al., 2023) may represent a first step in capturing ‘evolutionary  
 208 compatibility’ alongside more energy (predator choice) driven processes accounting for additional traits is still  
 209 needed (*e.g.*, Van De Walle et al., 2023 show how incorporating prey defensive properties alongside body size  
 210 improves predictions). In terms of models that do formalise these processes, diet models (Beckerman et al.,

211 2006; Petchey et al., 2008) have been used construct networks based on both predator choice (as determined  
212 by the handling time, energy content, and predator attack rate) as well as abundance (prey density). Wootton  
213 et al. (2023) developed a model that moves the energy of the system into different modules related to the  
214 process of the predator acquiring energy from the prey *i.e.*, compartmentation in food webs (Krause et al.,  
215 2003).

### 216 **3.3 Models that predict structure (interaction agnostic)**

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

## 231 **4 Making Progress with Networks**

### 232 **4.1 Further development of models and tools**

233 There has been a suite of models that have been developed to predict trophic links, however we are lacking in  
234 tools that are explicitly taking into consideration estimating both the feasibility as well as realisation of links,  
235 *i.e.*, both interactions and structure simultaneously (Strydom, Catchen, et al., 2021). This could be addressed  
236 either through the development of tools that do both (predict both interactions and structure), or to develop  
237 an ensemble modelling approach (Becker et al., 2022). Alternatively the development of tools that will allow  
238 for the downsampling of metawebs into realised networks (*e.g.*, Roopnarine, 2006), although deciding exactly  
239 what is driving differences between local networks and the regional metaweb might not be that simple (Saravia

et al., 2022). Probably also something that aligns with trying to predict interaction strength - because that would be the gold standard (*e.g.*, Wells & O'Hara, 2013). Probably also worth just plainly stating that feasibility of developing a model that is both broadly generalisable, but also has local specificity is probably not attainable (Stouffer, 2019), and more specifically the potential use of models to untangle/identify the different processes that shape interaction networks (Song & Levine, 2024), *e.g.*, Curtsdotter et al. (2019) showcase the use of models to disentangle the drivers of community function and Strydom, Dalla Riva, et al. (2021) who identified that networks are less complex than they could be, suggesting that there are constraints on network assembly. In addition to the more intentional development of models we also need to consider the validation of these models, there have been developments and discussions for assessing how well a model recovers pairwise interactions (Poisot, 2023; Strydom, Catchen, et al., 2021), although the rate of false-negatives that may be present in the testing data still present a challenge (Catchen et al., 2023), and we still lack clear strategies for benchmarking the ability of models to recover structure (Allesina et al., 2008).

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

Look at Hutchinson et al. (2019)

We lack a clear agenda (and conceptualisation) as to what the appropriate level of aggregation is for a 'network'. Realistically most empirical networks are more aligned with metawebs as opposed to realised networks as they are often the result of some sort of aggregation of observations across time, this creates a two-fold problem. Firstly, we need to think about how this affects any sort of development of theory that sits closer to the 'realised network' side of the spectrum - how often are we trying to ask and answer questions about realised networks using feasible networks? The second is that this lack of 'direction' as to how we should define a network is (actually) probably one of the biggest barriers that is affecting the use of networks in applied settings... By define I mean both delimiting the time and geographic scale at which a network is aggregated at (Estay et al., 2023). We know that space plays a role influence both network properties (Galiana et al., 2018), as well as dynamics (Fortin et al., 2021; Rooney et al., 2008). And so does time *e.g.*, seasonal rewiring (Brimacombe et al., 2021; Laender et al., 2010). There is also a bit of an interplay with time and data and the different scales that they may be integrated at - co-occurrence may span decades and just because two species have been recorded in the same space does not mean it was at the same timescale (Brimacombe et al., 2024).

268 **4.3 Feasible, realised, or sustainable?**

269 When do we determine a link to be ‘real’... In the context of metawebs this is perhaps clearer - if all things  
270 were equal (*i.e.*, community context is irrelevant) would the predator be able to consume the prey. However  
271 in the realised space there is also the question of the long term ‘energetic feasibility’ of an interaction - just  
272 because an interaction is possible in the now is it able to sustain a population in the long term. And what  
273 is the scale for that long term - are we thinking at the generational scale? Because ultimately when we  
274 are constructing a network we are aggregating not only across space but also across time... This is probably  
275 again a Lokta-Volterra space question and something that the dynamic foodweb models (Curtsdotter et al.,  
276 2019; Delmas et al., 2017; Lajaaiti et al., 2024) are addressing, but again it is integrating this with the  
277 feasible/realised axis. And of course the Petchey dilemma of even what networks should we be feeding into  
278 these dynamic models.

279 **5 The future value of networks**

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

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

292 The Terry & Lewis (2020) paper looks at some methods but is specifically looking at a bipartite  
293 world...

294 **References**

- 295 Allesina, S., Alonso, D., & Pascual, M. (2008). A General Model for Food Web Structure. *Science*, 320(5876),  
296 658–661. <https://doi.org/10.1126/science.1156269>
- 297 Allesina, S., & Pascual, M. (2009). Food web models: A plea for groups. *Ecology Letters*, 12(7), 652–662.  
298 <https://doi.org/10.1111/j.1461-0248.2009.01321.x>
- 299 Banville, F., Strydom, T., Blyth, P., Brimacombe, C., Catchen, M. D., Dansereau, G., Higino, G., Malpas,  
300 T., Mayall, H., Norman, K., Gravel, D., & Poisot, T. (2024). *Deciphering probabilistic species interaction*  
301 *networks*. EcoEvoRxiv. <https://doi.org/10.32942/X28G8Z>
- 302 Becker, D. J., Albery, G. F., Sjodin, A. R., Poisot, T., Bergner, L. M., Chen, B., Cohen, L. E., Dallas, T.  
303 A., Eskew, E. A., Fagre, A. C., Farrell, M. J., Guth, S., Han, B. A., Simmons, N. B., Stock, M., Teeling,  
304 E. C., & Carlson, C. J. (2022). Optimising predictive models to prioritise viral discovery in zoonotic  
305 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)
- 306 Beckerman, A. P., Petchey, O. L., & Warren, P. H. (2006). Foraging biology predicts food web complexity.  
307 *Proceedings of the National Academy of Sciences*, 103(37), 13745–13749. <https://doi.org/10.1073/pnas.0603039103>
- 308
- 309 Berlow, E. L., Brose, U., & Martinez, N. D. (2008). The “Goldilocks factor” in food webs. *Proceedings of  
310 the National Academy of Sciences*, 105(11), 4079–4080. <https://doi.org/10.1073/pnas.0800967105>
- 311 Berlow, E. L., Neutel, A.-M., Cohen, J. E., de Ruiter, P. C., Ebenman, B., Emmerson, M., Fox, J. W., Jansen,  
312 V. A. A., Iwan Jones, J., Kokkoris, G. D., Logofet, D. O., McKane, A. J., Montoya, J. M., & Petchey, O.  
313 (2004). Interaction strengths in food webs: Issues and opportunities. *Journal of Animal Ecology*, 73(3),  
314 585–598. <https://doi.org/10.1111/j.0021-8790.2004.00833.x>
- 315 Biton, B., Puzis, R., & Pilosof, S. (2024). *Inductive link prediction boosts data availability and enables  
316 cross-community link prediction in ecological networks*.
- 317 Blanchet, F. G., Cazelles, K., & Gravel, D. (2020). Co-occurrence is not evidence of ecological interactions.  
318 *Ecology Letters*, 23(7), 1050–1063. <https://doi.org/10.1111/ele.13525>
- 319 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2021). Inferred seasonal interaction rewiring of a freshwater  
320 stream fish network. *Ecography*, 44(2), 219–230. <https://doi.org/10.1111/ecog.05452>
- 321 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2024). *Applying a method before its proof-of-concept: A  
322 cautionary tale using inferred food webs*. <https://doi.org/10.13140/RG.2.2.22076.65927>
- 323 Brimacombe, C., Bodner, K., Michalska-Smith, M., Poisot, T., & Fortin, M.-J. (2023). Shortcomings  
324 of reusing species interaction networks created by different sets of researchers. *PLOS Biology*, 21(4),  
325 e3002068. <https://doi.org/10.1371/journal.pbio.3002068>

- 326 Buche, L., Bartomeus, I., & Godoy, O. (2024). Multitrophic Higher-Order Interactions Modulate Species  
327 Persistence. *The American Naturalist*, 203(4), 458–472. <https://doi.org/10.1086/729222>
- 328 Canard, E., Mouquet, N., Marescot, L., Gaston, K. J., Gravel, D., & Mouillot, D. (2012). Emergence of  
329 Structural Patterns in Neutral Trophic Networks. *PLOS ONE*, 7(8), e38295. <https://doi.org/10.1371/journal.pone.0038295>
- 330 Caron, D., Brose, U., Lurgi, M., Blanchet, F. G., Gravel, D., & Pollock, L. J. (2024). Trait-matching models  
331 predict pairwise interactions across regions, not food web properties. *Global Ecology and Biogeography*,  
332 33(4), e13807. <https://doi.org/10.1111/geb.13807>
- 333 Caron, D., Maiorano, L., Thuiller, W., & Pollock, L. J. (2022). Addressing the Eltonian shortfall with  
334 trait-based interaction models. *Ecology Letters*, 25(4), 889–899. <https://doi.org/10.1111/ele.13966>
- 335 Catchen, M. D., Poisot, T., Pollock, L. J., & Gonzalez, A. (2023). *The missing link: Discerning true from  
336 false negatives when sampling species interaction networks.*
- 337 Cherif, M., Brose, U., Hirt, M. R., Ryser, R., Silve, V., Albert, G., Arnott, R., Berti, E., Cirtwill, A.,  
338 Dyer, A., Gauzens, B., Gupta, A., Ho, H.-C., Portalier, S. M. J., Wain, D., & Wootton, K. (2024). The  
339 environment to the rescue: Can physics help predict predator–prey interactions? *Biological Reviews*,  
340 n/a(n/a). <https://doi.org/10.1111/brv.13105>
- 341 Cirtwill, A. R., Ekkl, A., Roslin, T., Wootton, K., & Gravel, D. (2019). A quantitative framework for  
342 investigating the reliability of empirical network construction. *Methods in Ecology and Evolution*, 10(6),  
343 902–911. <https://doi.org/10.1111/2041-210X.13180>
- 344 Clegg, T., Ali, M., & Beckerman, A. P. (2018). The impact of intraspecific variation on food web structure.  
345 *Ecology*, 99(12), 2712–2720. <https://doi.org/10.1002/ecy.2523>
- 346 Curtsdotter, A., Banks, H. T., Banks, J. E., Jonsson, M., Jonsson, T., Laubmeier, A. N., Traugott, M., &  
347 Bommarco, R. (2019). Ecosystem function in predator–prey food webs—confronting dynamic models with  
348 empirical data. *Journal of Animal Ecology*, 88(2), 196–210. <https://doi.org/10.1111/1365-2656.12892>
- 349 Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs' backbones  
350 using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>
- 351 Dallas, T., Park, A. W., & Drake, J. M. (2017). Predicting cryptic links in host-parasite networks. *PLOS  
352 Computational Biology*, 13(5), e1005557. <https://doi.org/10.1371/journal.pcbi.1005557>
- 353 Dansereau, G., Barros, C., & Poisot, T. (2024). Spatially explicit predictions of food web structure from  
354 regional-level data. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 379(1909).  
355 <https://doi.org/10.1098/rstb.2023.0166>
- 356 Delmas, E., Besson, M., Brice, M.-H., Burkle, L. A., Riva, G. V. D., Fortin, M.-J., Gravel, D., Guimarães,  
357 P. R., Hembry, D. H., Newman, E. A., Olesen, J. M., Pires, M. M., Yeakel, J. D., & Poisot, T. (2019).  
358

- 359 Analysing ecological networks of species interactions. *Biological Reviews*, 94(1), 16–36. <https://doi.org/10.1111/brv.12433>
- 360
- 361 Delmas, E., Brose, U., Gravel, D., Stouffer, D. B., & Poisot, T. (2017). Simulations of biomass dynamics in  
362 community food webs. *Methods in Ecology and Evolution*, 8(7), 881–886. <https://doi.org/10.1111/2041-210X.12713>
- 363
- 364 Desjardins-Proulx, P., Laigle, I., Poisot, T., & Gravel, D. (2017). Ecological interactions and the Netflix  
365 problem. *PeerJ*, 5, e3644. <https://doi.org/10.7717/peerj.3644>
- 366 Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological  
367 networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.
- 368 Dunne, J. A., Williams, R. J., Martinez, N. D., Wood, R. A., & Erwin, D. H. (2008). Compilation and  
369 Network Analyses of Cambrian Food Webs. *PLOS Biology*, 6(4), e102. <https://doi.org/10.1371/journal.pbio.0060102>
- 370
- 371 Eklöf, A., Tang, S., & Allesina, S. (2013). Secondary extinctions in food webs: A Bayesian network approach.  
372 *Methods in Ecology and Evolution*, 4(8), 760–770. <https://doi.org/10.1111/2041-210X.12062>
- 373 Estay, S. A., Fortin, M.-J., & López, D. N. (2023). Editorial: Patterns and processes in ecological networks  
374 over space. *Frontiers in Ecology and Evolution*, 11.
- 375 Fortin, M.-J., Dale, M. R. T., & Brimacombe, C. (2021). Network ecology in dynamic landscapes. *Proceedings  
376 of the Royal Society B: Biological Sciences*, 288(1949), rspb.2020.1889, 20201889. <https://doi.org/10.1098/rspb.2020.1889>
- 377
- 378 Fricke, E. C., Hsieh, C., Middleton, O., Gorczynski, D., Cappello, C. D., Sanisidro, O., Rowan, J., Svenning,  
379 J.-C., & Beaudrot, L. (2022). Collapse of terrestrial mammal food webs since the Late Pleistocene.  
380 *Science*, 377(6609), 1008–1011. <https://doi.org/10.1126/science.abn4012>
- 381 Galiana, N., Lurgi, M., Claramunt-López, B., Fortin, M.-J., Leroux, S., Cazelles, K., Gravel, D., & Montoya,  
382 J. M. (2018). The spatial scaling of species interaction networks. *Nature Ecology & Evolution*, 2(5),  
383 782–790. <https://doi.org/10.1038/s41559-018-0517-3>
- 384 García-Callejas, D., Godoy, O., Buche, L., Hurtado, M., Lanuza, J. B., Allen-Perkins, A., & Bartomeus, I.  
385 (2023). Non-random interactions within and across guilds shape the potential to coexist in multi-trophic  
386 ecological communities. *Ecology Letters*, 26(6), 831–842. <https://doi.org/10.1111/ele.14206>
- 387 Golubski, A. J., & Abrams, P. A. (2011). Modifying modifiers: What happens when interspecific interactions  
388 interact? *Journal of Animal Ecology*, 80(5), 1097–1108. <https://doi.org/10.1111/j.1365-2656.2011.01852.x>
- 389
- 390 Gómez, J. M., Verdú, M., & Perfectti, F. (2010). Ecological interactions are evolutionarily conserved across  
391 the entire tree of life. *Nature*, 465(7300), 918–921. <https://doi.org/10.1038/nature09113>

- 392 Gray, C., Figueroa, D. H., Hudson, L. N., Ma, A., Perkins, D., & Woodward, G. (2015). Joining the dots:  
393 An automated method for constructing food webs from compendia of published interactions. *Food Webs*,  
394 5, 11–20. <https://doi.org/10.1016/j.fooweb.2015.09.001>
- 395 Higino, G. T., Banville, F., Dansereau, G., Muñoz, N. R. F., Windsor, F., & Poisot, T. (2023). Mismatch  
396 between IUCN range maps and species interactions data illustrated using the Serengeti food web. *PeerJ*,  
397 11, e14620. <https://doi.org/10.7717/peerj.14620>
- 398 Hui, C., & Richardson, D. M. (2019). How to Invade an Ecological Network. *Trends in Ecology & Evolution*,  
399 34(2), 121–131. <https://doi.org/10.1016/j.tree.2018.11.003>
- 400 Hutchinson, M. C., Bramon Mora, B., Pilosof, S., Barner, A. K., Kéfi, S., Thébault, E., Jordano, P., &  
401 Stouffer, D. B. (2019). Seeing the forest for the trees: Putting multilayer networks to work for community  
402 ecology. *Functional Ecology*, 33(2), 206–217. <https://doi.org/10.1111/1365-2435.13237>
- 403 Jordano, P. (2016a). Chasing Ecological Interactions. *PLOS Biology*, 14(9), e1002559. <https://doi.org/10.1371/journal.pbio.1002559>
- 404 Jordano, P. (2016b). Sampling networks of ecological interactions. *Functional Ecology*. <https://doi.org/10.1111/1365-2435.12763>
- 405 Kéfi, S., Berlow, E. L., Wieters, E. A., Joppa, L. N., Wood, S. A., Brose, U., & Navarrete, S. A. (2015).  
406 Network structure beyond food webs: Mapping non-trophic and trophic interactions on Chilean rocky  
407 shores. *Ecology*, 96(1), 291–303. <https://doi.org/10.1890/13-1424.1>
- 408 Kéfi, S., Berlow, E. L., Wieters, E. A., Navarrete, S. A., Petchey, O. L., Wood, S. A., Boit, A., Joppa, L. N.,  
409 Lafferty, K. D., Williams, R. J., Martinez, N. D., Menge, B. A., Blanchette, C. A., Iles, A. C., & Brose,  
410 U. (2012). More than a meal... integrating non-feeding interactions into food webs: More than a meal ....  
411 *Ecology Letters*, 15(4), 291–300. <https://doi.org/10.1111/j.1461-0248.2011.01732.x>
- 412 Krause, A. E., Frank, K. A., Mason, D. M., Ulanowicz, R. E., & Taylor, W. W. (2003). Compartments  
413 revealed in food-web structure. *Nature*, 426(6964), 282–285. <https://doi.org/10.1038/nature02115>
- 414 Laender, F. D., Oevelen, D. V., Soetaert, K., & Middelburg, J. J. (2010). Carbon transfer in a herbivore-  
415 and microbial loop-dominated pelagic food webs in the southern Barents Sea during spring and summer.  
416 *Marine Ecology Progress Series*, 398, 93–107. <https://doi.org/10.3354/meps08335>
- 417 Lajaaiti, I., Bonnici, I., Kéfi, S., Mayall, H., Danet, A., Beckerman, A. P., Malpas, T., & Delmas, E. (2024).  
418 *EcologicalNetworksDynamics.jl* A Julia package to simulate the temporal dynamics of complex ecological  
419 networks (p. 2024.03.20.585899). bioRxiv. <https://doi.org/10.1101/2024.03.20.585899>
- 420 Lindeman, R. L. (1942). The Trophic-Dynamic Aspect of Ecology. *Ecology*, 23(4), 399–417. <https://doi.org/10.2307/1930126>
- 421 Llewelyn, J., Strona, G., Dickman, C. R., Greenville, A. C., Wardle, G. M., Lee, M. S. Y., Doherty, S.,

- 425 Shabani, F., Saltré, F., & Bradshaw, C. J. A. (2023). Predicting predator–prey interactions in terrestrial  
426 endotherms using random forest. *Ecography*, 2023(9), e06619. <https://doi.org/10.1111/ecog.06619>
- 427 Maiorano, L., Montemaggiori, A., Ficetola, G. F., O'Connor, L., & Thuiller, W. (2020). TETRA-EU 1.0: A  
428 species-level trophic metaweb of European tetrapods. *Global Ecology and Biogeography*, 29(9), 1452–1457.  
429 <https://doi.org/10.1111/geb.13138>
- 430 Momal, R., Robin, S., & Ambroise, C. (2020). Tree-based inference of species interaction networks from  
431 abundance data. *Methods in Ecology and Evolution*, 11(5), 621–632. <https://doi.org/10.1111/2041-210X.13380>
- 432 Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from  
433 proxies. *Trends in Ecology & Evolution*, 30(6), 347–356. <https://doi.org/10.1016/j.tree.2015.03.014>
- 434 Pawar, S., Dell, A. I., & Savage, V. M. (2012). Dimensionality of consumer search space drives trophic  
435 interaction strengths. *Nature*, 486(7404), 485–489. <https://doi.org/10.1038/nature11131>
- 436 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2008). Size, foraging, and food web  
437 structure. *Proceedings of the National Academy of Sciences*, 105(11), 4191–4196. <https://doi.org/10.1073/pnas.0710672105>
- 438 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2011). Fit, efficiency, and biology: Some  
439 thoughts on judging food web models. *Journal of Theoretical Biology*, 279(1), 169–171. <https://doi.org/10.1016/j.jtbi.2011.03.019>
- 440 Pichler, M., Boreux, V., Klein, A.-M., Schleuning, M., & Hartig, F. (2020). Machine learning algorithms  
441 to infer trait-matching and predict species interactions in ecological networks. *Methods in Ecology and  
442 Evolution*, 11(2), 281–293. <https://doi.org/10.1111/2041-210X.13329>
- 443 Pilosof, S., Porter, M. A., Pascual, M., & Kéfi, S. (2017). The multilayer nature of ecological networks.  
444 *Nature Ecology & Evolution*, 1(4), 101. <https://doi.org/10.1038/s41559-017-0101>
- 445 Poelen, J. H., Simons, J. D., & Mungall, C. J. (2014). Global biotic interactions: An open infrastructure to  
446 share and analyze species-interaction datasets. *Ecological Informatics*, 24, 148–159. <https://doi.org/10.1016/j.ecoinf.2014.08.005>
- 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., Bergeron, G., Cazelles, K., Dallas, T., Gravel, D., MacDonald, A., Mercier, B., Violet, C., &  
453 Vissault, S. (2021). Global knowledge gaps in species interaction networks data. *Journal of Biogeography*,

- 458 48(7), 1552–1563. <https://doi.org/10.1111/jbi.14127>
- 459 Poisot, T., Cirtwill, A., Cazelles, K., Gravel, D., Fortin, M.-J., & Stouffer, D. (2016). The structure of  
460 probabilistic networks. *Methods in Ecology and Evolution*, 7(3), 303–312. <https://doi.org/10.1111/mee.12520>
- 461 Poisot, T., Stouffer, D. B., & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary  
462 through space and time. *Oikos*, 124(3), 243–251. <https://doi.org/10.1111/oik.01719>
- 463 Poisot, T., Stouffer, D. B., & Kéfi, S. (2016). Describe, understand and predict: Why do we need networks  
464 in ecology? *Functional Ecology*, 30(12), 1878–1882. <https://www.jstor.org/stable/48582345>
- 465 Pollock, L. J., Tingley, R., Morris, W. K., Golding, N., O'Hara, R. B., Parris, K. M., Vesk, P. A., &  
466 McCarthy, M. A. (2014). Understanding co-occurrence by modelling species simultaneously with a Joint  
467 Species Distribution Model (JSDM). *Methods in Ecology and Evolution*, 5(5), 397–406. <https://doi.org/10.1111/2041-210X.12180>
- 468 Pringle, R. M. (2020). Untangling Food Webs. In *Unsolved Problems in Ecology* (pp. 225–238). Princeton  
469 University Press. <https://doi.org/10.1515/9780691195322-020>
- 470 Proulx, S. R., Promislow, D. E. L., & Phillips, P. C. (2005). Network thinking in ecology and evolution.  
471 *Trends in Ecology & Evolution*, 20(6), 345–353. <https://doi.org/10.1016/j.tree.2005.04.004>
- 472 Rooney, N., McCann, K. S., & Moore, J. C. (2008). A landscape theory for food web architecture. *Ecology  
473 Letters*, 11(8), 867–881. <https://doi.org/10.1111/j.1461-0248.2008.01193.x>
- 474 Roopnarine, P. D. (2006). Extinction Cascades and Catastrophe in Ancient Food Webs. *Paleobiology*, 32(1),  
475 1–19. <https://www.jstor.org/stable/4096814>
- 476 Saravia, L. A., Marina, T. I., Kristensen, N. P., De Troch, M., & Momo, F. R. (2022). Ecological network  
477 assembly: How the regional metaweb influences local food webs. *Journal of Animal Ecology*, 91(3),  
478 630–642. <https://doi.org/10.1111/1365-2656.13652>
- 479 Segar, S. T., Fayle, T. M., Srivastava, D. S., Lewinsohn, T. M., Lewis, O. T., Novotny, V., Kitching, R. L.,  
480 & Maunsell, S. C. (2020). The Role of Evolution in Shaping Ecological Networks. *Trends in Ecology &  
481 Evolution*, 35(5), 454–466. <https://doi.org/10.1016/j.tree.2020.01.004>
- 482 Shaw, J. O., Dunhill, A. M., Beckerman, A. P., Dunne, J. A., & Hull, P. M. (2024). *A framework for  
483 reconstructing ancient food webs using functional trait data* (p. 2024.01.30.578036). bioRxiv. <https://doi.org/10.1101/2024.01.30.578036>
- 484 Song, C., & Levine, J. M. (2024). *Rigorous (in)validation of ecological models* (p. 2024.09.19.613075). bioRxiv.  
485 <https://doi.org/10.1101/2024.09.19.613075>
- 486 Stock, M. (2021). Pairwise learning for predicting pollination interactions based on traits and phylogeny.  
487 *Ecological Modelling*, 14.
- 488 Stouffer, D. B. (2019). All ecological models are wrong, but some are useful. *Journal of Animal Ecology*,  
489 118, 22–32.

- 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 Strydom, T., Dalla Riva, G. V., & Poisot, T. (2021). SVD Entropy Reveals the High Complexity of Ecological  
505 Networks. *Frontiers in Ecology and Evolution*, 9. <https://doi.org/10.3389/fevo.2021.623141>
- 506 Terry, J. C. D., & Lewis, O. T. (2020). Finding missing links in interaction networks. *Ecology*, 101(7), e03047.  
507 <https://doi.org/10.1002/ecy.3047>
- 508 Valdovinos, F. S., Hale, K. R. S., Dritz, S., Glaum, P. R., McCann, K. S., Simon, S. M., Thébault, E., Wetzel,  
509 W. C., Wootton, K. L., & Yeakel, J. D. (2023). A bioenergetic framework for aboveground terrestrial  
510 food webs. *Trends in Ecology & Evolution*, 38(3), 301–312. <https://doi.org/10.1016/j.tree.2022.11.004>
- 511 Van De Walle, R., Logghe, G., Haas, N., Massol, F., Vandegehuchte, M. L., & Bonte, D. (2023). Arthro-  
512 pod food webs predicted from body size ratios are improved by incorporating prey defensive properties.  
513 *Journal of Animal Ecology*, 92(4), 913–924. <https://doi.org/10.1111/1365-2656.13905>
- 514 Wells, K., & O'Hara, R. B. (2013). Species interactions: Estimating per-individual interaction strength and  
515 covariates before simplifying data into per-species ecological networks. *Methods in Ecology and Evolution*,  
516 4(1), 1–8. <https://doi.org/10.1111/j.2041-210x.2012.00249.x>
- 517 Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404(6774), 180–183.  
518 <https://doi.org/10.1038/35004572>
- 519 Williams, R. J., & Martinez, N. D. (2008). Success and its limits among structural models of complex food  
520 webs. *Journal of Animal Ecology*, 77(3), 512–519. <https://doi.org/10.1111/j.1365-2656.2008.01362.x>
- 521 Wootton, K. L., Curtsdotter, A., Roslin, T., Bommarco, R., & Jonsson, T. (2023). Towards a modular theory  
522 of trophic interactions. *Functional Ecology*, 37(1), 26–43. <https://doi.org/10.1111/1365-2435.13954>
- 523 Xie, J.-R., Zhang, P., Zhang, H.-F., & Wang, B.-H. (2017). Completeness of Community Structure in

- 524 Networks. *Scientific Reports*, 7(1), 5269. <https://doi.org/10.1038/s41598-017-05585-6>
- 525 Yeakel, J. D., Pires, M. M., Rudolf, L., Dominy, N. J., Koch, P. L., Guimarães, P. R., & Gross, T. (2014).
- 526 Collapse of an ecological network in Ancient Egypt. *PNAS*, 111(40), 14472–14477. <https://doi.org/10.1073/pnas.1408471111>
- 528 Yodzis, P. (1982). The Compartmentation of Real and Assembled Ecosystems. *The American Naturalist*,
- 529 120(5), 551–570. <https://doi.org/10.1086/284013>
- 530 Yodzis, P., & Innes, S. (1992). Body Size and Consumer-Resource Dynamics. *The American Naturalist*,
- 531 139(6), 1151–1175. <https://doi.org/10.1086/285380>

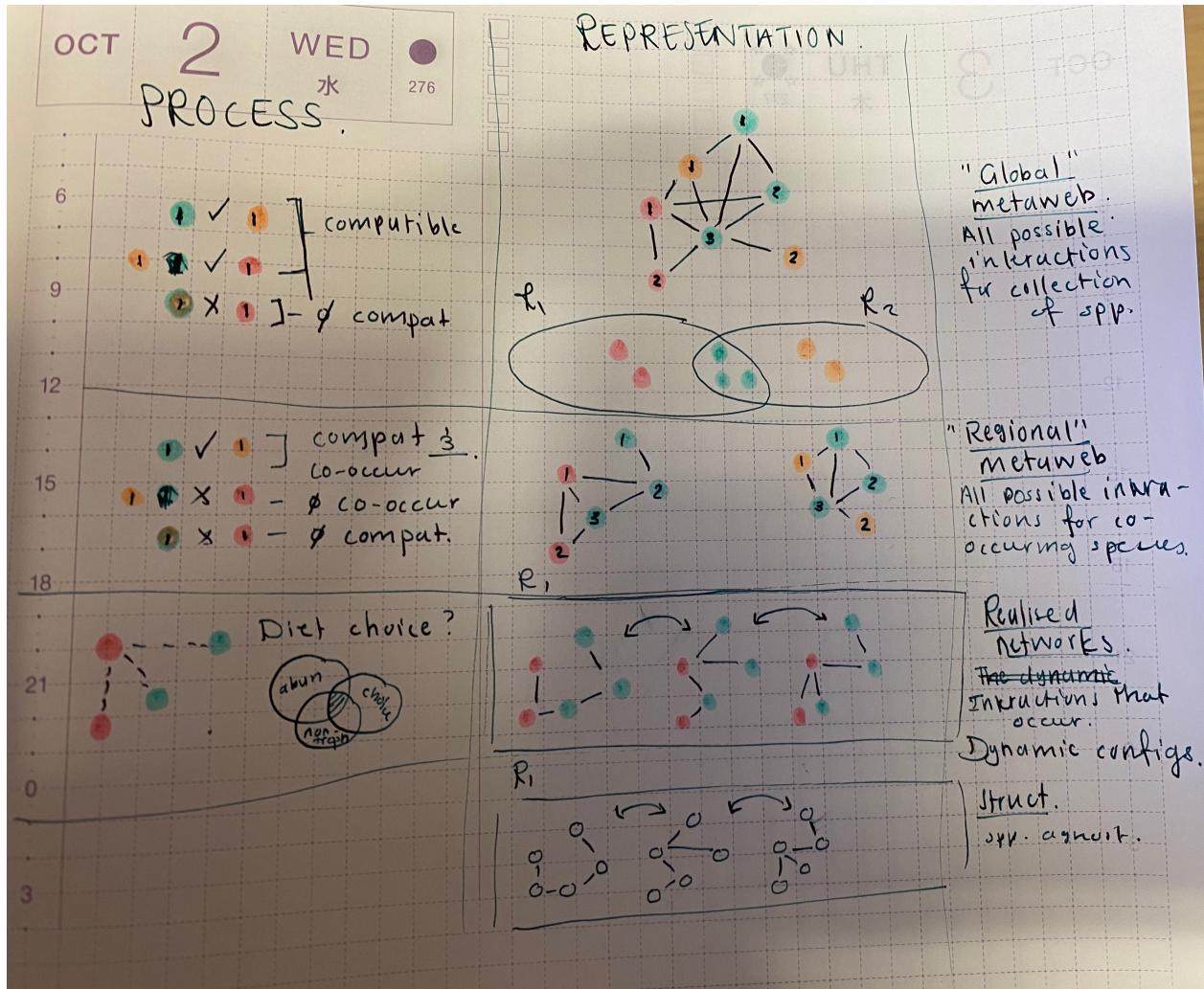


Figure 1: Aligning the various processes that determine interactions with the different network representations. First we start with a 'global metaweb' this network which captures all possible interactions for an arbitrary collection of species, we can further refine this network by taking in to consideration 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.