

# **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 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, *i.e.*, the definition of an edges shifts from being determined by interaction feasibility to that of energetic choices/consequences. Thus, different network representations are determined and constrained by different sets of assumptions as to what the processes are that determine the presence/absence of an interaction between two species as well as the resulting network structure.

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

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

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

97 [Figure 1 about here.]

## 98 2.1 The processes that determine species interactions

### 99 Evolutionary compatibility

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

### 111 (Co)occurrence

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

120 **Abundance**

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

129 **Predator choice (energetic cost)**

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

138 **Non-trophic interactions**

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

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

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

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

### 3 Network construction is nuanced

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

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

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.

#### **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

seasonal metawebs...

### 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’ and rather *only* account for processes that determine the realisation of an interaction  
 209 (*i.e.*, abundance, predator choice, or non-trophic interactions). Although the use of allometry *i.e.*, body size  
 210 (Beckerman et al., 2006; *e.g.*, Valdovinos et al., 2023) may represent a first step in capturing ‘evolutionary  
 211 compatibility’ alongside more energy (predator choice) driven processes we still need to account for other

traits that determine feeding compatibility (*e.g.*, Van De Walle et al., 2023 show how incorporating prey defensive properties alongside body size improves predictions). In terms of constructing realised networks, diet models (Beckerman et al., 2006; Petchey et al., 2008) have been used construct networks based on both predator choice (as determined by the handling time, energy content, and predator attack rate) as well as abundance (prey density) and progress has also been made in understanding the compartmentation of energy in networks and how this influences energy acquisition (Krause et al., 2003; Wootton et al., 2023). As realised networks are build on the concept of dynamic processes (the abundance of species will always be in flux) these networks are valuable for understanding the behaviour of networks over time or their response to change (Curtsdotter et al., 2019; Delmas et al., 2017; Lajaaiti et al., 2024). However, the are ‘costly’ to construct (requiring data about the entire community as it is the behaviour of the system that determines the behaviour of the part) and also lack the larger context afforded by metawebs.

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

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

238 **4 Making Progress with Networks**

239 **4.1 Further development of models and tools**

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

253 **4.2 At what scale should we be predicting and using networks?**

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

265 **5 The future value of networks**

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

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

278 [Figure 2 about here.]

Table 1: An informative table

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

Question (broad)	Question (specific)	Network representation
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??

## 279 References

- 280 Allesina, S., Alonso, D., & Pascual, M. (2008). A General Model for Food Web Structure. *Science*, 320(5876),  
 281 658–661. <https://doi.org/10.1126/science.1156269>
- 282 Allesina, S., & Pascual, M. (2009). Food web models: A plea for groups. *Ecology Letters*, 12(7), 652–662.  
 283 <https://doi.org/10.1111/j.1461-0248.2009.01321.x>
- 284 Banville, F., Strydom, T., Blyth, P., Brimacombe, C., Catchen, M. D., Dansereau, G., Higino, G., Malpas,  
 285 T., Mayall, H., Norman, K., Gravel, D., & Poisot, T. (2024). *Deciphering probabilistic species interaction*  
 286 *networks*. EcoEvoRxiv. <https://doi.org/10.32942/X28G8Z>
- 287 Becker, D. J., Albery, G. F., Sjodin, A. R., Poisot, T., Bergner, L. M., Chen, B., Cohen, L. E., Dallas, T.  
 288 A., Eskew, E. A., Fagre, A. C., Farrell, M. J., Guth, S., Han, B. A., Simmons, N. B., Stock, M., Teeling,  
 289 E. C., & Carlson, C. J. (2022). Optimising predictive models to prioritise viral discovery in zoonotic  
 290 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)
- 291 Beckerman, A. P., Petchey, O. L., & Warren, P. H. (2006). Foraging biology predicts food web complexity.  
 292 *Proceedings of the National Academy of Sciences*, 103(37), 13745–13749. <https://doi.org/10.1073/pnas.0603039103>
- 294 Berlow, E. L., Brose, U., & Martinez, N. D. (2008). The "Goldilocks factor" in food webs. *Proceedings of  
 295 the National Academy of Sciences*, 105(11), 4079–4080. <https://doi.org/10.1073/pnas.0800967105>
- 296 Berlow, E. L., Neutel, A.-M., Cohen, J. E., de Ruiter, P. C., Ebenman, B., Emmerson, M., Fox, J. W., Jansen,  
 297 V. A. A., Iwan Jones, J., Kokkoris, G. D., Logofet, D. O., McKane, A. J., Montoya, J. M., & Petchey, O.  
 298 (2004). Interaction strengths in food webs: Issues and opportunities. *Journal of Animal Ecology*, 73(3),  
 299 585–598. <https://doi.org/10.1111/j.0021-8790.2004.00833.x>
- 300 Biton, B., Puzis, R., & Pilosof, S. (2024). *Inductive link prediction boosts data availability and enables  
 301 cross-community link prediction in ecological networks*.

- 302 Blanchet, F. G., Cazelles, K., & Gravel, D. (2020). Co-occurrence is not evidence of ecological interactions.  
303 *Ecology Letters*, 23(7), 1050–1063. <https://doi.org/10.1111/ele.13525>
- 304 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2021). Inferred seasonal interaction rewiring of a freshwater  
305 stream fish network. *Ecography*, 44(2), 219–230. <https://doi.org/10.1111/ecog.05452>
- 306 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2024). *Applying a method before its proof-of-concept: A  
307 cautionary tale using inferred food webs.* <https://doi.org/10.13140/RG.2.2.22076.65927>
- 308 Brimacombe, C., Bodner, K., Michalska-Smith, M., Poisot, T., & Fortin, M.-J. (2023). Shortcomings  
309 of reusing species interaction networks created by different sets of researchers. *PLOS Biology*, 21(4),  
310 e3002068. <https://doi.org/10.1371/journal.pbio.3002068>
- 311 Brown, J. H., Gillooly, J. F., Allen, A. P., Savage, V. M., & West, G. B. (2004). Toward a Metabolic Theory  
312 of Ecology. *Ecology*, 85(7), 1771–1789. <https://doi.org/10.1890/03-9000>
- 313 Buche, L., Bartomeus, I., & Godoy, O. (2024). Multitrophic Higher-Order Interactions Modulate Species  
314 Persistence. *The American Naturalist*, 203(4), 458–472. <https://doi.org/10.1086/729222>
- 315 Canard, E., Mouquet, N., Marescot, L., Gaston, K. J., Gravel, D., & Mouillot, D. (2012). Emergence of  
316 Structural Patterns in Neutral Trophic Networks. *PLOS ONE*, 7(8), e38295. <https://doi.org/10.1371/journal.pone.0038295>
- 317 Caron, D., Brose, U., Lurgi, M., Blanchet, F. G., Gravel, D., & Pollock, L. J. (2024). Trait-matching models  
318 predict pairwise interactions across regions, not food web properties. *Global Ecology and Biogeography*,  
319 33(4), e13807. <https://doi.org/10.1111/geb.13807>
- 320 Caron, D., Maiorano, L., Thuiller, W., & Pollock, L. J. (2022). Addressing the Eltonian shortfall with  
321 trait-based interaction models. *Ecology Letters*, 25(4), 889–899. <https://doi.org/10.1111/ele.13966>
- 322 Catchen, M. D., Poisot, T., Pollock, L. J., & Gonzalez, A. (2023). *The missing link: Discerning true from  
323 false negatives when sampling species interaction networks.*
- 324 Cherif, M., Brose, U., Hirt, M. R., Ryser, R., Silve, V., Albert, G., Arnott, R., Berti, E., Cirtwill, A.,  
325 Dyer, A., Gauzens, B., Gupta, A., Ho, H.-C., Portalier, S. M. J., Wain, D., & Wootton, K. (2024). The  
326 environment to the rescue: Can physics help predict predator-prey interactions? *Biological Reviews*,  
327 n/a(n/a). <https://doi.org/10.1111/brv.13105>
- 328 Cirtwill, A. R., Ekkl, A., Roslin, T., Wootton, K., & Gravel, D. (2019). A quantitative framework for  
329 investigating the reliability of empirical network construction. *Methods in Ecology and Evolution*, 10(6),  
330 902–911. <https://doi.org/10.1111/2041-210X.13180>
- 331 Clegg, T., Ali, M., & Beckerman, A. P. (2018). The impact of intraspecific variation on food web structure.  
332 *Ecology*, 99(12), 2712–2720. <https://doi.org/10.1002/ecy.2523>
- 333 Curtsdotter, A., Banks, H. T., Banks, J. E., Jonsson, M., Jonsson, T., Laubmeier, A. N., Traugott, M., &

- 335 Bommarco, R. (2019). Ecosystem function in predator–prey food webs—confronting dynamic models with  
336 empirical data. *Journal of Animal Ecology*, 88(2), 196–210. <https://doi.org/10.1111/1365-2656.12892>
- 337 Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs' backbones  
338 using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>
- 339 Dallas, T., Park, A. W., & Drake, J. M. (2017). Predicting cryptic links in host-parasite networks. *PLOS  
340 Computational Biology*, 13(5), e1005557. <https://doi.org/10.1371/journal.pcbi.1005557>
- 341 Dansereau, G., Barros, C., & Poisot, T. (2024). Spatially explicit predictions of food web structure from  
342 regional-level data. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 379(1909).  
343 <https://doi.org/10.1098/rstb.2023.0166>
- 344 Delmas, E., Besson, M., Brice, M.-H., Burkle, L. A., Riva, G. V. D., Fortin, M.-J., Gravel, D., Guimarães,  
345 P. R., Hembry, D. H., Newman, E. A., Olesen, J. M., Pires, M. M., Yeakel, J. D., & Poisot, T. (2019).  
346 Analysing ecological networks of species interactions. *Biological Reviews*, 94(1), 16–36. <https://doi.org/10.1111/brv.12433>
- 347 Delmas, E., Brose, U., Gravel, D., Stouffer, D. B., & Poisot, T. (2017). Simulations of biomass dynamics in  
348 community food webs. *Methods in Ecology and Evolution*, 8(7), 881–886. [https://doi.org/10.1111/2041-210X.12713](https://doi.org/10.1111/2041-<br/>349 210X.12713)
- 350 Desjardins-Proulx, P., Laigle, I., Poisot, T., & Gravel, D. (2017). Ecological interactions and the Netflix  
351 problem. *PeerJ*, 5, e3644. <https://doi.org/10.7717/peerj.3644>
- 352 Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological  
353 networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.
- 354 Dunne, J. A., Williams, R. J., Martinez, N. D., Wood, R. A., & Erwin, D. H. (2008). Compilation and  
355 Network Analyses of Cambrian Food Webs. *PLOS Biology*, 6(4), e102. [https://doi.org/10.1371/journal.pbio.0060102](https://doi.org/10.1371/journal.<br/>356 pbio.0060102)
- 357 Eklöf, A., Tang, S., & Allesina, S. (2013). Secondary extinctions in food webs: A Bayesian network approach.  
358 *Methods in Ecology and Evolution*, 4(8), 760–770. <https://doi.org/10.1111/2041-210X.12062>
- 359 Estay, S. A., Fortin, M.-J., & López, D. N. (2023). Editorial: Patterns and processes in ecological networks  
360 over space. *Frontiers in Ecology and Evolution*, 11.
- 361 Fortin, M.-J., Dale, M. R. T., & Brimacombe, C. (2021). Network ecology in dynamic landscapes. *Proceedings  
362 of the Royal Society B: Biological Sciences*, 288(1949), rspb.2020.1889, 20201889. [https://doi.org/10.1098/rspb.2020.1889](https://doi.org/10.1098/<br/>363 rspb.2020.1889)
- 364 Fricke, E. C., Hsieh, C., Middleton, O., Gorczynski, D., Cappello, C. D., Sanisidro, O., Rowan, J., Svenning,  
365 J.-C., & Beaudrot, L. (2022). Collapse of terrestrial mammal food webs since the Late Pleistocene.  
366 *Science*, 377(6609), 1008–1011. <https://doi.org/10.1126/science.abn4012>
- 367

- 368 Galiana, N., Lurgi, M., Claramunt-López, B., Fortin, M.-J., Leroux, S., Cazelles, K., Gravel, D., & Montoya,  
369 J. M. (2018). The spatial scaling of species interaction networks. *Nature Ecology & Evolution*, 2(5),  
370 782–790. <https://doi.org/10.1038/s41559-018-0517-3>
- 371 García-Callejas, D., Godoy, O., Buche, L., Hurtado, M., Lanuza, J. B., Allen-Perkins, A., & Bartomeus, I.  
372 (2023). Non-random interactions within and across guilds shape the potential to coexist in multi-trophic  
373 ecological communities. *Ecology Letters*, 26(6), 831–842. <https://doi.org/10.1111/ele.14206>
- 374 Golubski, A. J., & Abrams, P. A. (2011). Modifying modifiers: What happens when interspecific interactions  
375 interact? *Journal of Animal Ecology*, 80(5), 1097–1108. <https://doi.org/10.1111/j.1365-2656.2011.01852.x>
- 376 x
- 377 Gómez, J. M., Verdú, M., & Perfectti, F. (2010). Ecological interactions are evolutionarily conserved across  
378 the entire tree of life. *Nature*, 465(7300), 918–921. <https://doi.org/10.1038/nature09113>
- 379 Gray, C., Figueroa, D. H., Hudson, L. N., Ma, A., Perkins, D., & Woodward, G. (2015). Joining the dots:  
380 An automated method for constructing food webs from compendia of published interactions. *Food Webs*,  
381 5, 11–20. <https://doi.org/10.1016/j.fooweb.2015.09.001>
- 382 Higino, G. T., Banville, F., Dansereau, G., Muñoz, N. R. F., Windsor, F., & Poisot, T. (2023). Mismatch  
383 between IUCN range maps and species interactions data illustrated using the Serengeti food web. *PeerJ*,  
384 11, e14620. <https://doi.org/10.7717/peerj.14620>
- 385 Hui, C., & Richardson, D. M. (2019). How to Invade an Ecological Network. *Trends in Ecology & Evolution*,  
386 34(2), 121–131. <https://doi.org/10.1016/j.tree.2018.11.003>
- 387 Hutchinson, M. C., Bramon Mora, B., Pilosof, S., Barner, A. K., Kéfi, S., Thébault, E., Jordano, P., &  
388 Stouffer, D. B. (2019). Seeing the forest for the trees: Putting multilayer networks to work for community  
389 ecology. *Functional Ecology*, 33(2), 206–217. <https://doi.org/10.1111/1365-2435.13237>
- 390 Jordano, P. (2016a). Chasing Ecological Interactions. *PLOS Biology*, 14(9), e1002559. <https://doi.org/10.1371/journal.pbio.1002559>
- 391 Jordano, P. (2016b). Sampling networks of ecological interactions. *Functional Ecology*. <https://doi.org/10.1111/1365-2435.12763>
- 392 Kéfi, S., Berlow, E. L., Wieters, E. A., Joppa, L. N., Wood, S. A., Brose, U., & Navarrete, S. A. (2015).  
393 Network structure beyond food webs: Mapping non-trophic and trophic interactions on Chilean rocky  
394 shores. *Ecology*, 96(1), 291–303. <https://doi.org/10.1890/13-1424.1>
- 395 Kéfi, S., Berlow, E. L., Wieters, E. A., Navarrete, S. A., Petchey, O. L., Wood, S. A., Boit, A., Joppa, L. N.,  
396 Lafferty, K. D., Williams, R. J., Martinez, N. D., Menge, B. A., Blanchette, C. A., Iles, A. C., & Brose,  
397 U. (2012). More than a meal... integrating non-feeding interactions into food webs: More than a meal ....  
398 *Ecology Letters*, 15(4), 291–300. <https://doi.org/10.1111/j.1461-0248.2011.01732.x>

- 401 Krause, A. E., Frank, K. A., Mason, D. M., Ulanowicz, R. E., & Taylor, W. W. (2003). Compartments  
402 revealed in food-web structure. *Nature*, 426(6964), 282–285. <https://doi.org/10.1038/nature02115>
- 403 Laender, F. D., Oevelen, D. V., Soetaert, K., & Middelburg, J. J. (2010). Carbon transfer in a herbivore-  
404 and microbial loop-dominated pelagic food webs in the southern Barents Sea during spring and summer.  
405 *Marine Ecology Progress Series*, 398, 93–107. <https://doi.org/10.3354/meps08335>
- 406 Lajaaiti, I., Bonnici, I., Kéfi, S., Mayall, H., Danet, A., Beckerman, A. P., Malpas, T., & Delmas, E. (2024).  
407 *EcologicalNetworksDynamics.jl* A Julia package to simulate the temporal dynamics of complex ecological  
408 networks (p. 2024.03.20.585899). bioRxiv. <https://doi.org/10.1101/2024.03.20.585899>
- 409 Lindeman, R. L. (1942). The Trophic-Dynamic Aspect of Ecology. *Ecology*, 23(4), 399–417. <https://doi.org/10.2307/1930126>
- 410 Llewelyn, J., Strona, G., Dickman, C. R., Greenville, A. C., Wardle, G. M., Lee, M. S. Y., Doherty, S.,  
411 Shabani, F., Saltré, F., & Bradshaw, C. J. A. (2023). Predicting predator–prey interactions in terrestrial  
412 endotherms using random forest. *Ecography*, 2023(9), e06619. <https://doi.org/10.1111/ecog.06619>
- 413 Momal, R., Robin, S., & Ambroise, C. (2020). Tree-based inference of species interaction networks from  
414 abundance data. *Methods in Ecology and Evolution*, 11(5), 621–632. <https://doi.org/10.1111/2041-210X.13380>
- 415 Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from  
416 proxies. *Trends in Ecology & Evolution*, 30(6), 347–356. <https://doi.org/10.1016/j.tree.2015.03.014>
- 417 Pawar, S., Dell, A. I., & Savage, V. M. (2012). Dimensionality of consumer search space drives trophic  
418 interaction strengths. *Nature*, 486(7404), 485–489. <https://doi.org/10.1038/nature11131>
- 419 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2008). Size, foraging, and food web  
420 structure. *Proceedings of the National Academy of Sciences*, 105(11), 4191–4196. <https://doi.org/10.1073/pnas.0710672105>
- 421 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2011). Fit, efficiency, and biology: Some  
422 thoughts on judging food web models. *Journal of Theoretical Biology*, 279(1), 169–171. <https://doi.org/10.1016/j.jtbi.2011.03.019>
- 423 Pichler, M., Boreux, V., Klein, A.-M., Schleuning, M., & Hartig, F. (2020). Machine learning algorithms  
424 to infer trait-matching and predict species interactions in ecological networks. *Methods in Ecology and  
425 Evolution*, 11(2), 281–293. <https://doi.org/10.1111/2041-210X.13329>
- 426 Pilosof, S., Porter, M. A., Pascual, M., & Kéfi, S. (2017). The multilayer nature of ecological networks.  
427 *Nature Ecology & Evolution*, 1(4), 101. <https://doi.org/10.1038/s41559-017-0101>
- 428 Poelen, J. H., Simons, J. D., & Mungall, C. J. (2014). Global biotic interactions: An open infrastructure to  
429 share and analyze species-interaction datasets. *Ecological Informatics*, 24, 148–159. <https://doi.org/10.432>

- 434 1016/j.ecoinf.2014.08.005
- 435 Poisot, T. (2023). Guidelines for the prediction of species interactions through binary classification. *Methods*  
436 in *Ecology and Evolution*, 14(5), 1333–1345. <https://doi.org/10.1111/2041-210X.14071>
- 437 Poisot, T., Baiser, B., Dunne, J., Kéfi, S., Massol, F., Mouquet, N., Romanuk, T. N., Stouffer, D. B., Wood, S.  
438 A., & Gravel, D. (2016). Mangal – making ecological network analysis simple. *Ecography*, 39(4), 384–390.  
439 <https://doi.org/10.1111/ecog.00976>
- 440 Poisot, T., Cirtwill, A., Cazelles, K., Gravel, D., Fortin, M.-J., & Stouffer, D. (2016). The structure of  
441 probabilistic networks. *Methods in Ecology and Evolution*, 7(3), 303–312. <https://doi.org/10.1111/2041-210X.12180>
- 442 Poisot, T., Stouffer, D. B., & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary  
443 through space and time. *Oikos*, 124(3), 243–251. <https://doi.org/10.1111/oik.01719>
- 444 Poisot, T., Stouffer, D. B., & Kéfi, S. (2016). Describe, understand and predict: Why do we need networks  
445 in ecology? *Functional Ecology*, 30(12), 1878–1882. <https://www.jstor.org/stable/48582345>
- 446 Pollock, L. J., Tingley, R., Morris, W. K., Golding, N., O’Hara, R. B., Parris, K. M., Vesk, P. A., &  
447 McCarthy, M. A. (2014). Understanding co-occurrence by modelling species simultaneously with a Joint  
448 Species Distribution Model (JSDM). *Methods in Ecology and Evolution*, 5(5), 397–406. <https://doi.org/10.1111/2041-210X.12180>
- 450 Pringle, R. M. (2020). Untangling Food Webs. In *Unsolved Problems in Ecology* (pp. 225–238). Princeton  
451 University Press. <https://doi.org/10.1515/9780691195322-020>
- 452 Proulx, S. R., Promislow, D. E. L., & Phillips, P. C. (2005). Network thinking in ecology and evolution.  
453 *Trends in Ecology & Evolution*, 20(6), 345–353. <https://doi.org/10.1016/j.tree.2005.04.004>
- 454 Pyke, G. (1984). Optimal Foraging Theory: A Critical Review. *Annual Review of Ecology, Evolution and  
455 Systematic*, 15, 523–575. <https://doi.org/10.1146/annurev.ecolsys.15.1.523>
- 456 Rooney, N., McCann, K. S., & Moore, J. C. (2008). A landscape theory for food web architecture. *Ecology  
457 Letters*, 11(8), 867–881. <https://doi.org/10.1111/j.1461-0248.2008.01193.x>
- 458 Roopnarine, P. D. (2006). Extinction Cascades and Catastrophe in Ancient Food Webs. *Paleobiology*, 32(1),  
459 1–19. <https://www.jstor.org/stable/4096814>
- 460 Saravia, L. A., Marina, T. I., Kristensen, N. P., De Troch, M., & Momo, F. R. (2022). Ecological network  
461 assembly: How the regional metaweb influences local food webs. *Journal of Animal Ecology*, 91(3),  
462 630–642. <https://doi.org/10.1111/1365-2656.13652>
- 463 Segar, S. T., Fayle, T. M., Srivastava, D. S., Lewinson, T. M., Lewis, O. T., Novotny, V., Kitching, R. L.,  
464 & Maunsell, S. C. (2020). The Role of Evolution in Shaping Ecological Networks. *Trends in Ecology &  
465 Evolution*, 35(5), 454–466. <https://doi.org/10.1016/j.tree.2020.01.004>
- 466 Shaw, J. O., Dunhill, A. M., Beckerman, A. P., Dunne, J. A., & Hull, P. M. (2024). *A framework for*

- 467 reconstructing ancient food webs using functional trait data (p. 2024.01.30.578036). bioRxiv. <https://doi.org/10.1101/2024.01.30.578036>
- 468
- 469 Soberón, J. (2007). Grinnellian and Eltonian niches and geographic distributions of species. *Ecology Letters*,  
470 10(12), 1115–1123. <https://doi.org/10.1111/j.1461-0248.2007.01107.x>
- 471 Song, C., & Levine, J. M. (2024). Rigorous (in)validation of ecological models (p. 2024.09.19.613075). bioRxiv.  
472 <https://doi.org/10.1101/2024.09.19.613075>
- 473 Staniczenko, P. P. A., Lewis, O. T., Jones, N. S., & Reed-Tsochas, F. (2010). Structural dynamics and  
474 robustness of food webs. *Ecology Letters*, 13(7), 891–899. <https://doi.org/10.1111/j.1461-0248.2010.01485.x>
- 475
- 476 Stock, M. (2021). Pairwise learning for predicting pollination interactions based on traits and phylogeny.  
477 *Ecological Modelling*, 14.
- 478 Stouffer, D. B. (2019). All ecological models are wrong, but some are useful. *Journal of Animal Ecology*,  
479 88(2), 192–195. <https://doi.org/10.1111/1365-2656.12949>
- 480 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Hemming, V.,  
481 Mercier, B., Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2022). Food web reconstruction  
482 through phylogenetic transfer of low-rank network representation. *Methods in Ecology and Evolution*,  
483 13(12), 2838–2849. <https://doi.org/10.1111/2041-210X.13835>
- 484 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Mercier, B.,  
485 Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2023). Graph embedding and transfer  
486 learning can help predict potential species interaction networks despite data limitations. *Methods in  
487 Ecology and Evolution*, 14(12), 2917–2930. <https://doi.org/10.1111/2041-210X.14228>
- 488 Strydom, T., Catchen, M. D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., Forero-Muñoz,  
489 N. R., Higino, G., Mercier, B., Gonzalez, A., Gravel, D., Pollock, L., & Poisot, T. (2021). A roadmap  
490 towards predicting species interaction networks (across space and time). *Philosophical Transactions of  
491 the Royal Society B: Biological Sciences*, 376(1837), 20210063. <https://doi.org/10.1098/rstb.2021.0063>
- 492 Terry, J. C. D., & Lewis, O. T. (2020). Finding missing links in interaction networks. *Ecology*, 101(7), e03047.  
493 <https://doi.org/10.1002/ecy.3047>
- 494 Valdovinos, F. S., Hale, K. R. S., Dritz, S., Glaum, P. R., McCann, K. S., Simon, S. M., Thébault, E., Wetzel,  
495 W. C., Wootton, K. L., & Yeakel, J. D. (2023). A bioenergetic framework for aboveground terrestrial  
496 food webs. *Trends in Ecology & Evolution*, 38(3), 301–312. <https://doi.org/10.1016/j.tree.2022.11.004>
- 497 Van De Walle, R., Logghe, G., Haas, N., Massol, F., Vandegheuchte, M. L., & Bonte, D. (2023). Arthro-  
498 pod food webs predicted from body size ratios are improved by incorporating prey defensive properties.  
499 *Journal of Animal Ecology*, 92(4), 913–924. <https://doi.org/10.1111/1365-2656.13905>

- 500 Wells, K., & O'Hara, R. B. (2013). Species interactions: Estimating per-individual interaction strength and  
501 covariates before simplifying data into per-species ecological networks. *Methods in Ecology and Evolution*,  
502 4(1), 1–8. <https://doi.org/10.1111/j.2041-210x.2012.00249.x>
- 503 Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404(6774), 180–183.  
504 <https://doi.org/10.1038/35004572>
- 505 Williams, R. J., & Martinez, N. D. (2008). Success and its limits among structural models of complex food  
506 webs. *Journal of Animal Ecology*, 77(3), 512–519. <https://doi.org/10.1111/j.1365-2656.2008.01362.x>
- 507 Wootton, K. L., Curtsdotter, A., Roslin, T., Bommarco, R., & Jonsson, T. (2023). Towards a modular theory  
508 of trophic interactions. *Functional Ecology*, 37(1), 26–43. <https://doi.org/10.1111/1365-2435.13954>
- 509 Xie, J.-R., Zhang, P., Zhang, H.-F., & Wang, B.-H. (2017). Completeness of Community Structure in  
510 Networks. *Scientific Reports*, 7(1), 5269. <https://doi.org/10.1038/s41598-017-05585-6>
- 511 Yeakel, J. D., Pires, M. M., Rudolf, L., Dominy, N. J., Koch, P. L., Guimarães, P. R., & Gross, T. (2014).  
512 Collapse of an ecological network in Ancient Egypt. *PNAS*, 111(40), 14472–14477. <https://doi.org/10.1073/pnas.1408471111>
- 513
- 514 Yodzis, P. (1982). The Compartmentation of Real and Assembled Ecosystems. *The American Naturalist*,  
515 120(5), 551–570. <https://doi.org/10.1086/284013>
- 516 Yodzis, P., & Innes, S. (1992). Body Size and Consumer-Resource Dynamics. *The American Naturalist*,  
517 139(6), 1151–1175. <https://doi.org/10.1086/285380>

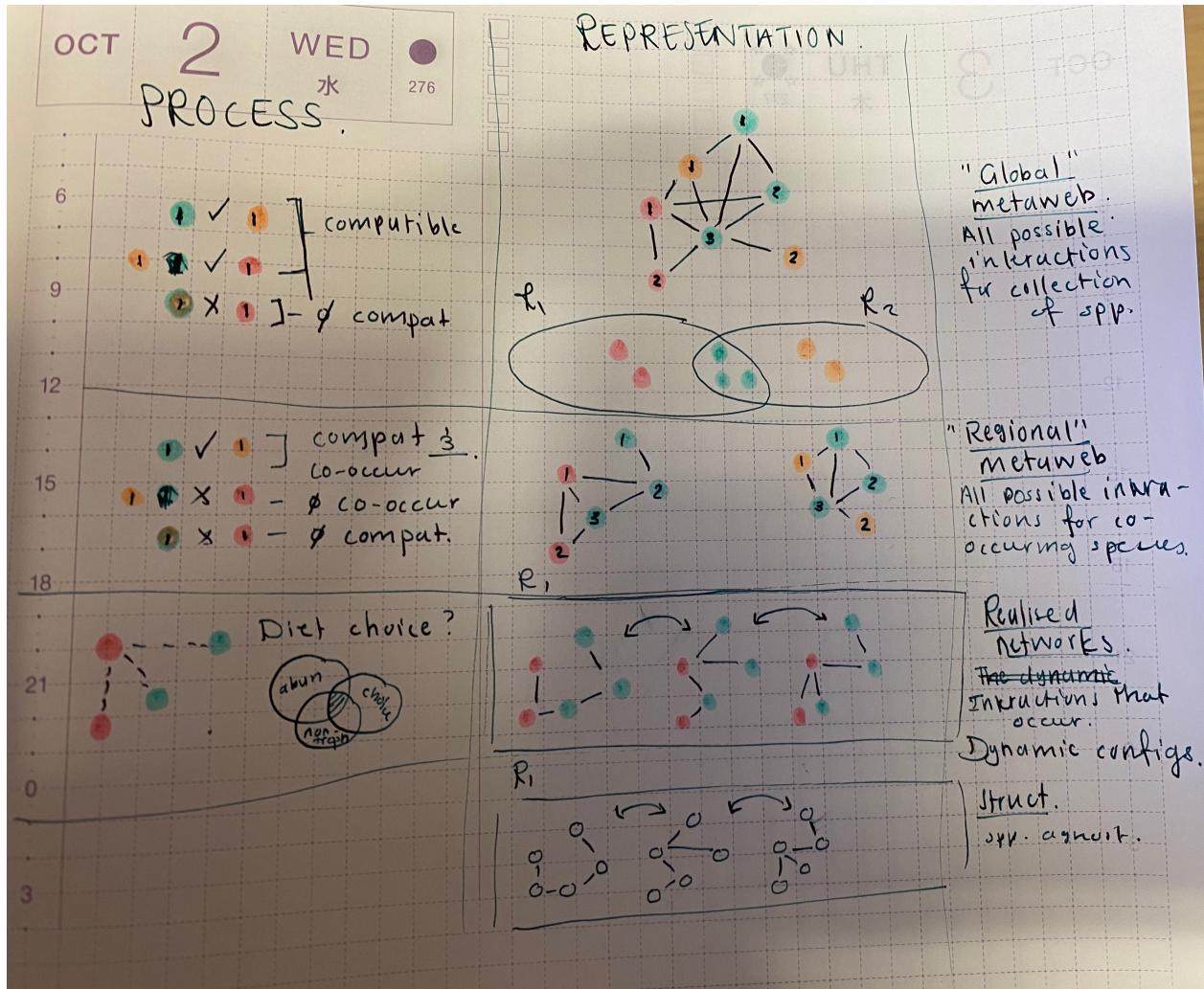


Figure 1: Aligning the various processes that determine interactions with the different network representations. First we start with a ‘global metaweb’ this network which captures all possible interactions for an arbitrary collection of species, we can further refine this network by taking in to consideration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

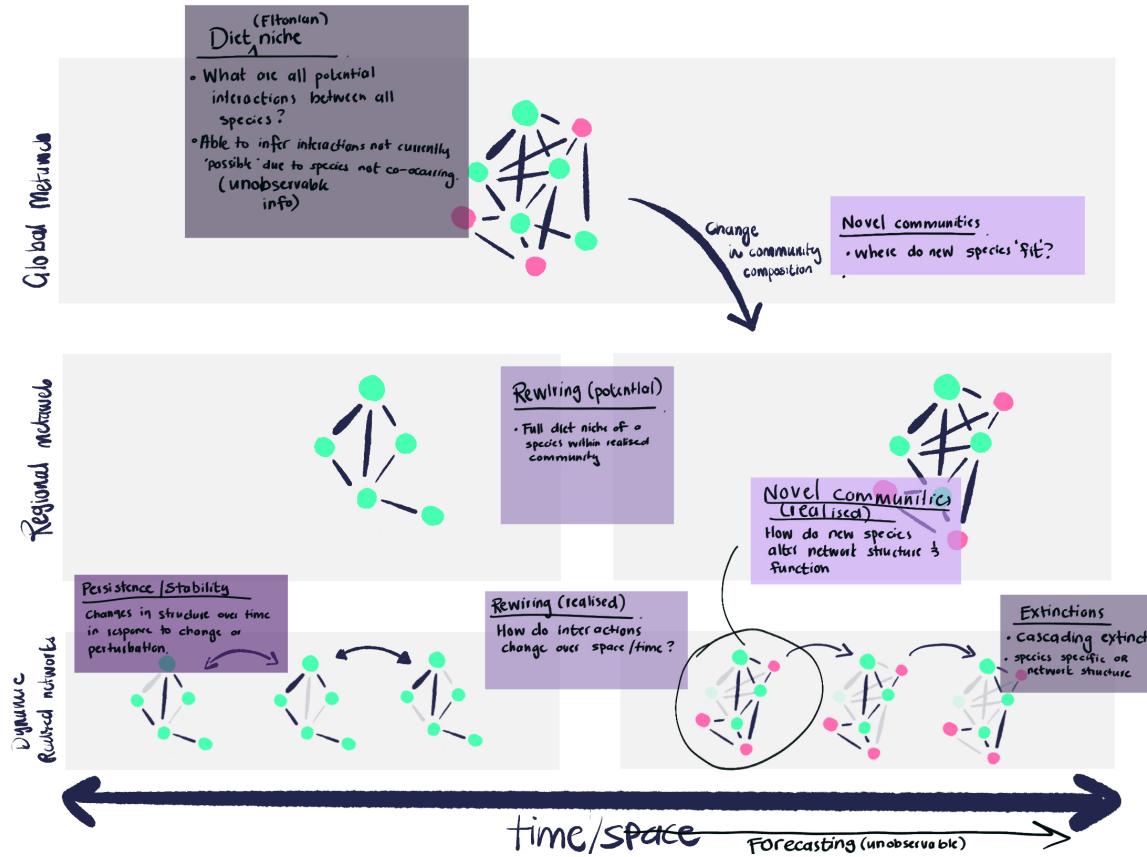


Figure 2: An attempt to try and visualise a way to map the different scales of network representations to the way in which we can interrogate/ask questions about them?