

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

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

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

Keywords: food web, network construction, scientific ignorance

1 At the heart of modern biodiversity science are a set of concepts and theories about biodiversity, stability
2 and function. These relate to the abundance, distribution and services that biodiversity provides, and how
3 biodiversity – as an interconnected set of species – responds to multiple stressors. The interaction between
4 species (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 km² scale based on fine-scale species co-occurrence) but represents a shift towards capturing the higher level processes that determine the *realisation* of an interaction. 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; specifically if the processes captures an all-or-nothing (possibility) vs
94 context dependent (likelihood) determination of interactions between species. Of course these processes do
95 not function in a vacuum and do interact with/influence one another, but it is still beneficial to present them
96 in a categorical manner as these different processes are often the underpinning logic in the development of
97 prediction/network models, the criteria for data collection in the field, and the scale of organisation for which
98 they are relevant (species, population, or community).

99 [Figure 1 about here.]

100 2.1 The processes that determine species interactions

101 Evolutionary compatibility

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

114 (Co)occurrence

115 Although the outright assumption that because two species are co-occurring it must mean that they are
116 interacting is inherently flawed (Blanchet et al., 2020), it is of course impossible for two species to interact (at
117 least in terms of feeding links) if they are not co-occurring in time and space. Thus co-occurrence data alone is
118 insufficient to build an accurate and ecologically meaningful representation of a food web having information
119 on the co-occurrence of species can further aid us in refining metawebs by allowing us to downsample the
120 network based on the species found in a specific location, or even add additional uncertainty based in how

121 likely species are to co-occur (Dansereau et al., 2024). Additionally the interplay between the interaction
122 between a species pair and their co-occurrence is meaningful when one is operating in the space of trying to
123 determine the distribution of a species (Higino et al., 2023), and forms a key component of some of the next
124 generation species distribution models *e.g.*, joint SDMs (Pollock et al., 2014).

125 **Abundance**

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

132 **Predator choice (energetic cost)**

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

140 **Indirect/higher order interactions**

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

146 **2.2 Contextualising the processes that determine species interactions**

147 It should be self evident that the different processes discussed above are all ultimately going to influence the
148 realisation of interactions as well as the structure of a network, however they are acting at different scales
149 of organisation. Both the **co-occurrence** and the **evolutionary compatibility** are valid at the scale of
150 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 whose 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 (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 existing empirical dataset (Biton et al., 2024; 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 — it can be argued that even the collection of empirical data is in and of itself a ‘model’ as it is still only a *representation* of the system. Different models have different underlying philosophies that often only capture one or a few of the processes discussed in Section 2, has implications for how the resulting network is defined Section 1, which will ultimately delimit and define what inferences can be made from the resulting network. Here we will introduce the three different types of network representations, 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 representation 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 seasonal metawebs...

178 **3.1 How do we predict food webs?**

179 There as many ways to predict networks as what there is to define them and along with taking into consid-
180 eration the points raised in the previous section it is also beneficial to think about the context in which the
181 different models were developed - and how this will influence the networks that they produce...

182 There is a bit of a ‘point of conflict’ between those calling for ‘pixel perfect’, regional scale data (Pringle,
183 2020; Pringle & Hutchinson, 2020) and for the means to generate networks that are ecologically plausible
184 *representations* (*sensu* structural networks). This represents two challenges; one is that models that repre-
185 sent generalisations of networks often lack the ability to retrieve any species/community specificity which
186 limits their utility for real world, species-driven scenarios *e.g.*, species driven conservation efforts (Dunn et
187 al., 2009), however networks that are constructed through either (most) empirical observations or through
188 predictive means are fundamentally going to represent metawebs, *i.e.*, lack constrained links, a representation
189 of structure, or energy flow...

190 **3.1.1 Models that predict metawebs (feasible interactions)**

191 This is perhaps the most developed group of models; with a variety of approaches having been developed that
192 typically determine the feasibility of an interaction based on the trait compatibility between predator and
193 prey (*i.e.* their evolutionary compatibility) to determine ‘feeding rules’ (Morales-Castilla et al., 2015). These
194 feeding rules are broadly elucidated in two different ways; mechanistic feeding rules can be explicitly defined
195 and applied to a community (Dunne et al., 2008; *e.g.*, Shaw et al., 2024) or they are inferred from a community
196 for which there is interaction data and the ‘rules’ are then applied to a different community (Caron et al.,
197 2022; Cirtwill et al., 2019; Desjardins-Proulx et al., 2017; Eklöf et al., 2013; Llewelyn et al., 2023; Pichler et
198 al., 2020; Strydom et al., 2022; *e.g.*, Strydom et al., 2023). The fundamental difference between these two
199 model groups is that ‘mechanistic models’ rely on expert knowledge and make assumptions on trait-feeding
200 relationships, whereas the ‘pattern finding’ models are dependent on existing datasets from which to elucidate
201 feeding rules. These models are useful for determining all feasible interactions for a specific community, and
202 owing to the availability of datasets (Gray et al., 2015; *e.g.*, Poelen et al., 2014; Poisot, Baiser, et al., 2016),
203 as well as the development of model testing/benchmarking tools (Poisot, 2023), means that these models
204 can be validated and (with relative confidence) be used to construct first draft networks for communities for
205 which we have no data (Strydom et al., 2022), and are valuable for constructing networks where we lack any
206 interaction data *e.g.*, prehistoric networks (Fricke et al., 2022; Yeakel et al., 2014).

207 **3.1.2 Models that predict realised networks (realised interactions)**

208 In order to construct realised networks models need to incorporate *both* the feasibility of interactions (*i.e.*,
209 determine the entire diet breadth of a species) as well as then determine which interactions are realised (*i.e.*,
210 incorporate the ‘cost’ of interactions). As far as we are aware there is no model that explicitly accounts for
211 both of these ‘rules’ and rather *only* account for processes that determine the realisation of an interaction
212 (*i.e.*, abundance, predator choice, or non-trophic interactions). Although the use of allometry *i.e.*, body size
213 (Beckerman et al., 2006; *e.g.*, Valdovinos et al., 2023) may represent a first step in capturing ‘evolutionary
214 compatibility’ alongside more energy (predator choice) driven processes accounting for additional traits is still
215 needed (*e.g.*, Van De Walle et al., 2023 show how incorporating prey defensive properties alongside body size
216 improves predictions). In terms of models that do formalise these processes, diet models (Beckerman et al.,
217 2006; Petchey et al., 2008) have been used construct networks based on both predator choice (as determined
218 by the handling time, energy content, and predator attack rate) as well as abundance (prey density). Woottton
219 et al. (2023) developed a model that moves the energy of the system into different modules related to the
220 process of the predator acquiring energy from the prey *i.e.*, compartmentation in food webs (Krause et al.,
221 2003).

222 **3.1.3 Models that predict structure (interaction agnostic)**

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

237 **4 Making Progress with Networks**

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

239 There has been a suite of models that have been developed to predict trophic links, however we are lacking in
240 tools that are explicitly taking into consideration estimating both the feasibility as well as realisation of links,
241 *i.e.*, both interactions and structure simultaneously (Strydom, Catchen, et al., 2021). This could be addressed
242 either through the development of tools that do both (predict both interactions and structure), or to develop
243 an ensemble modelling approach (Becker et al., 2022). Alternatively the development of tools that will allow
244 for the downsampling of metawebs into realised networks (*e.g.*, Roopnarine, 2006), although deciding exactly
245 what is driving differences between local networks and the regional metaweb might not be that simple (Saravia
246 et al., 2022). Probably also something that aligns with trying to predict interaction strength - because that
247 would be the gold standard (*e.g.*, Wells & O'Hara, 2013). Probably also worth just plainly stating that
248 feasibility of developing a model that is both broadly generalisable, but also has local specificity is probably
249 not attainable (Stouffer, 2019), and more specifically the potential use of models to untangle/identify the
250 different processes that shape interaction networks (Song & Levine, 2024), *e.g.*, Curtsdotter et al. (2019)
251 showcase the use of models to disentangle the drivers of community function and Strydom, Dalla Riva, et
252 al. (2021) who identified that networks are less complex than they could be, suggesting that there are
253 constraints on network assembly. In addition to the more intentional development of models we also need to
254 consider the validation of these models, there have been developments and discussions for assessing how well
255 a model recovers pairwise interactions (Poisot, 2023; Strydom, Catchen, et al., 2021), although the rate of
256 false-negatives that may be present in the testing data still present a challenge (Catchen et al., 2023), and we
257 still lack clear strategies for benchmarking the ability of models to recover structure (Allesina et al., 2008).

258 **4.2 At what scale should we be predicting and using networks?**

259 Look at Hutchinson et al. (2019)

260 We lack a clear agenda (and conceptualisation) as to what the appropriate level of aggregation is for a
261 'network'. Realistically most empirical networks are more aligned with metawebs as opposed to realised
262 networks as they are often the result of some sort of aggregation of observations across time, this creates a
263 two-fold problem. Firstly, we need to think about how this affects any sort of development of theory that sits
264 closer to the 'realised network' side of the spectrum - how often are we trying to ask and answer questions
265 about realised networks using feasible networks? The second is that this lack of 'direction' as to how we
266 should define a network is (actually) probably one of the biggest barriers that is affecting the use of networks

267 in applied settings... By define I mean both delimiting the time and geographic scale at which a network is
268 aggregated at (Estay et al., 2023). We know that space plays a role - the motility of different species will
269 influence both the dynamics of networks but also serve to link smaller ‘subnetworks’/community (Fortin et
270 al., 2021; Rooney et al., 2008). And so does time *e.g.*, seasonal rewiring (Brimacombe et al., 2021; Laender
271 et al., 2010). There is also a bit of an interplay with time and data and the different scales that they may
272 be integrated at - co-occurrence may span decades and just because two species have been recorded in the
273 same space does not mean it was at the same timescale (Brimacombe et al., 2024).

274 4.3 Feasible, realised, or sustainable?

275 When do we determine a link to be ‘real’... In the context of metawebs this is perhaps clearer - if all things
276 were equal (*i.e.*, community context is irrelevant) would the predator be able to consume the prey. However
277 in the realised space there is also the question of the long term ‘energetic feasibility’ of an interaction - just
278 because an interaction is possible in the now is it able to sustain a population in the long term. And what
279 is the scale for that long term - are we thinking at the generational scale? Because ultimately when we
280 are constructing a network we are aggregating not only across space but also across time... This is probably
281 again a Lokta-Volterra space question and something that the dynamic foodweb models (Curtsdotter et al.,
282 2019; Delmas et al., 2017; Lajaaiti et al., 2024) are addressing, but again it is integrating this with the
283 feasible/realised axis. And of course the Petchey dilemma of even what networks should we be feeding into
284 these dynamic models.

285 5 The future value of networks

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

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

²⁹⁶ to evaluate this we need to think of the ‘ability’ a specific network representation has to capture the process
²⁹⁷ of interest as well as the ‘suitability’ of using that representation to answer the question, as is highlighted in
²⁹⁸ Box 1.

²⁹⁹ The Terry & Lewis (2020) paper looks at some methods but is specifically looking at a bipartite
³⁰⁰ world...

³⁰¹ References

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

- 327 stream fish network. *Ecography*, 44(2), 219–230. <https://doi.org/10.1111/ecog.05452>
- 328 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2024). *Applying a method before its proof-of-concept: A*
329 *cautionary tale using inferred food webs.* <https://doi.org/10.13140/RG.2.2.22076.65927>
- 330 Brimacombe, C., Bodner, K., Michalska-Smith, M., Poisot, T., & Fortin, M.-J. (2023). Shortcomings
331 of reusing species interaction networks created by different sets of researchers. *PLOS Biology*, 21(4),
332 e3002068. <https://doi.org/10.1371/journal.pbio.3002068>
- 333 Buche, L., Bartomeus, I., & Godoy, O. (2024). Multitrophic Higher-Order Interactions Modulate Species
334 Persistence. *The American Naturalist*, 203(4), 458–472. <https://doi.org/10.1086/729222>
- 335 Canard, E., Mouquet, N., Marescot, L., Gaston, K. J., Gravel, D., & Mouillot, D. (2012). Emergence of
336 Structural Patterns in Neutral Trophic Networks. *PLOS ONE*, 7(8), e38295. <https://doi.org/10.1371/journal.pone.0038295>
- 337
- 338 Caron, D., Brose, U., Lurgi, M., Blanchet, F. G., Gravel, D., & Pollock, L. J. (2024). Trait-matching models
339 predict pairwise interactions across regions, not food web properties. *Global Ecology and Biogeography*,
340 33(4), e13807. <https://doi.org/10.1111/geb.13807>
- 341 Caron, D., Maiorano, L., Thuiller, W., & Pollock, L. J. (2022). Addressing the Eltonian shortfall with
342 trait-based interaction models. *Ecology Letters*, 25(4), 889–899. <https://doi.org/10.1111/ele.13966>
- 343 Catchen, M. D., Poisot, T., Pollock, L. J., & Gonzalez, A. (2023). *The missing link: Discerning true from*
344 *false negatives when sampling species interaction networks.*
- 345 Cherif, M., Brose, U., Hirt, M. R., Ryser, R., Silve, V., Albert, G., Arnott, R., Berti, E., Cirtwill, A.,
346 Dyer, A., Gauzens, B., Gupta, A., Ho, H.-C., Portalier, S. M. J., Wain, D., & Wootton, K. (2024). The
347 environment to the rescue: Can physics help predict predator–prey interactions? *Biological Reviews*,
348 n/a(n/a). <https://doi.org/10.1111/brv.13105>
- 349 Cirtwill, A. R., Ekklf, A., Roslin, T., Wootton, K., & Gravel, D. (2019). A quantitative framework for
350 investigating the reliability of empirical network construction. *Methods in Ecology and Evolution*, 10(6),
351 902–911. <https://doi.org/10.1111/2041-210X.13180>
- 352 Clegg, T., Ali, M., & Beckerman, A. P. (2018). The impact of intraspecific variation on food web structure.
353 *Ecology*, 99(12), 2712–2720. <https://doi.org/10.1002/ecy.2523>
- 354 Curtsdotter, A., Banks, H. T., Banks, J. E., Jonsson, M., Jonsson, T., Laubmeier, A. N., Traugott, M., &
355 Bommarco, R. (2019). Ecosystem function in predator–prey food webs—confronting dynamic models with
356 empirical data. *Journal of Animal Ecology*, 88(2), 196–210. <https://doi.org/10.1111/1365-2656.12892>
- 357 Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs’ backbones
358 using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>
- 359 Dansereau, G., Barros, C., & Poisot, T. (2024). Spatially explicit predictions of food web structure from

- 360 regional-level data. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 379(1909).
- 361 <https://doi.org/10.1098/rstb.2023.0166>
- 362 Delmas, E., Besson, M., Brice, M.-H., Burkle, L. A., Riva, G. V. D., Fortin, M.-J., Gravel, D., Guimarães,
363 P. R., Hembry, D. H., Newman, E. A., Olesen, J. M., Pires, M. M., Yeakel, J. D., & Poisot, T. (2019).
364 Analysing ecological networks of species interactions. *Biological Reviews*, 94(1), 16–36. <https://doi.org/10.1111/brv.12433>
- 365
- 366 Delmas, E., Brose, U., Gravel, D., Stouffer, D. B., & Poisot, T. (2017). Simulations of biomass dynamics in
367 community food webs. *Methods in Ecology and Evolution*, 8(7), 881–886. <https://doi.org/10.1111/2041-210X.12713>
- 368
- 369 Desjardins-Proulx, P., Laigle, I., Poisot, T., & Gravel, D. (2017). Ecological interactions and the Netflix
370 problem. *PeerJ*, 5, e3644. <https://doi.org/10.7717/peerj.3644>
- 371 Dunn, R. R., Harris, N. C., Colwell, R. K., Koh, L. P., & Sodhi, N. S. (2009). The sixth mass coextinction:
372 Are most endangered species parasites and mutualists? *Proceedings. Biological Sciences*, 276(1670),
373 3037–3045. <https://doi.org/10.1098/rspb.2009.0413>
- 374 Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological
375 networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.
- 376 Dunne, J. A., Williams, R. J., Martinez, N. D., Wood, R. A., & Erwin, D. H. (2008). Compilation and
377 Network Analyses of Cambrian Food Webs. *PLOS Biology*, 6(4), e102. <https://doi.org/10.1371/journal.pbio.0060102>
- 378
- 379 Eklöf, A., Tang, S., & Allesina, S. (2013). Secondary extinctions in food webs: A Bayesian network approach.
380 *Methods in Ecology and Evolution*, 4(8), 760–770. <https://doi.org/10.1111/2041-210X.12062>
- 381 Estay, S. A., Fortin, M.-J., & López, D. N. (2023). Editorial: Patterns and processes in ecological networks
382 over space. *Frontiers in Ecology and Evolution*, 11.
- 383 Fortin, M.-J., Dale, M. R. T., & Brimacombe, C. (2021). Network ecology in dynamic landscapes. *Proceedings
384 of the Royal Society B: Biological Sciences*, 288(1949), rspb.2020.1889, 20201889. <https://doi.org/10.1098/rspb.2020.1889>
- 385
- 386 Fricke, E. C., Hsieh, C., Middleton, O., Gorczynski, D., Cappello, C. D., Sanisidro, O., Rowan, J., Svenning,
387 J.-C., & Beaudrot, L. (2022). Collapse of terrestrial mammal food webs since the Late Pleistocene.
388 *Science*, 377(6609), 1008–1011. <https://doi.org/10.1126/science.abn4012>
- 389 García-Callejas, D., Godoy, O., Buche, L., Hurtado, M., Lanuza, J. B., Allen-Perkins, A., & Bartomeus, I.
390 (2023). Non-random interactions within and across guilds shape the potential to coexist in multi-trophic
391 ecological communities. *Ecology Letters*, 26(6), 831–842. <https://doi.org/10.1111/ele.14206>
- 392 Golubski, A. J., & Abrams, P. A. (2011). Modifying modifiers: What happens when interspecific interactions

- 393 interact? *Journal of Animal Ecology*, 80(5), 1097–1108. <https://doi.org/10.1111/j.1365-2656.2011.01852>.
- 394 **x**
- 395 Gómez, J. M., Verdú, M., & Perfectti, F. (2010). Ecological interactions are evolutionarily conserved across
396 the entire tree of life. *Nature*, 465(7300), 918–921. <https://doi.org/10.1038/nature09113>
- 397 Gray, C., Figueroa, D. H., Hudson, L. N., Ma, A., Perkins, D., & Woodward, G. (2015). Joining the dots:
398 An automated method for constructing food webs from compendia of published interactions. *Food Webs*,
399 5, 11–20. <https://doi.org/10.1016/j.fooweb.2015.09.001>
- 400 Higino, G. T., Banville, F., Dansereau, G., Muñoz, N. R. F., Windsor, F., & Poisot, T. (2023). Mismatch
401 between IUCN range maps and species interactions data illustrated using the Serengeti food web. *PeerJ*,
402 11, e14620. <https://doi.org/10.7717/peerj.14620>
- 403 Hui, C., & Richardson, D. M. (2019). How to Invade an Ecological Network. *Trends in Ecology & Evolution*,
404 34(2), 121–131. <https://doi.org/10.1016/j.tree.2018.11.003>
- 405 Hutchinson, M. C., Bramon Mora, B., Pilosof, S., Barner, A. K., Kéfi, S., Thébault, E., Jordano, P., &
406 Stouffer, D. B. (2019). Seeing the forest for the trees: Putting multilayer networks to work for community
407 ecology. *Functional Ecology*, 33(2), 206–217. <https://doi.org/10.1111/1365-2435.13237>
- 408 Jordano, P. (2016a). Chasing Ecological Interactions. *PLOS Biology*, 14(9), e1002559. <https://doi.org/10.1371/journal.pbio.1002559>
- 409 Jordano, P. (2016b). Sampling networks of ecological interactions. *Functional Ecology*. <https://doi.org/10.1111/1365-2435.12763>
- 410 Kéfi, S., Berlow, E. L., Wieters, E. A., Joppa, L. N., Wood, S. A., Brose, U., & Navarrete, S. A. (2015).
411 Network structure beyond food webs: Mapping non-trophic and trophic interactions on Chilean rocky
412 shores. *Ecology*, 96(1), 291–303. <https://doi.org/10.1890/13-1424.1>
- 413 Kéfi, S., Berlow, E. L., Wieters, E. A., Navarrete, S. A., Petchey, O. L., Wood, S. A., Boit, A., Joppa, L. N.,
414 Lafferty, K. D., Williams, R. J., Martinez, N. D., Menge, B. A., Blanchette, C. A., Iles, A. C., & Brose,
415 U. (2012). More than a meal... integrating non-feeding interactions into food webs: More than a meal
416 *Ecology Letters*, 15(4), 291–300. <https://doi.org/10.1111/j.1461-0248.2011.01732.x>
- 417 Krause, A. E., Frank, K. A., Mason, D. M., Ulanowicz, R. E., & Taylor, W. W. (2003). Compartments
418 revealed in food-web structure. *Nature*, 426(6964), 282–285. <https://doi.org/10.1038/nature02115>
- 419 Laender, F. D., Oevelen, D. V., Soetaert, K., & Middelburg, J. J. (2010). Carbon transfer in a herbivore-
420 and microbial loop-dominated pelagic food webs in the southern Barents Sea during spring and summer.
421 *Marine Ecology Progress Series*, 398, 93–107. <https://doi.org/10.3354/meps08335>
- 422 Lajaaiti, I., Bonnici, I., Kéfi, S., Mayall, H., Danet, A., Beckerman, A. P., Malpas, T., & Delmas, E. (2024).
423 *EcologicalNetworksDynamics.jl* A Julia package to simulate the temporal dynamics of complex ecological
424

- 426 networks (p. 2024.03.20.585899). bioRxiv. <https://doi.org/10.1101/2024.03.20.585899>
- 427 Lindeman, R. L. (1942). The Trophic-Dynamic Aspect of Ecology. *Ecology*, 23(4), 399–417. <https://doi.org/10.2307/1930126>
- 428 Llewelyn, J., Strona, G., Dickman, C. R., Greenville, A. C., Wardle, G. M., Lee, M. S. Y., Doherty, S.,
429 Shabani, F., Saltré, F., & Bradshaw, C. J. A. (2023). Predicting predator-prey interactions in terrestrial
430 endotherms using random forest. *Ecography*, 2023(9), e06619. <https://doi.org/10.1111/ecog.06619>
- 431 Maiorano, L., Montemaggiore, A., Ficetola, G. F., O'Connor, L., & Thuiller, W. (2020). TETRA-EU 1.0: A
432 species-level trophic metaweb of European tetrapods. *Global Ecology and Biogeography*, 29(9), 1452–1457.
433 <https://doi.org/10.1111/geb.13138>
- 434 Momal, R., Robin, S., & Ambroise, C. (2020). Tree-based inference of species interaction networks from
435 abundance data. *Methods in Ecology and Evolution*, 11(5), 621–632. <https://doi.org/10.1111/2041-210X.13380>
- 436 Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from
437 proxies. *Trends in Ecology & Evolution*, 30(6), 347–356. <https://doi.org/10.1016/j.tree.2015.03.014>
- 438 Pawar, S., Dell, A. I., & Savage, V. M. (2012). Dimensionality of consumer search space drives trophic
439 interaction strengths. *Nature*, 486(7404), 485–489. <https://doi.org/10.1038/nature11131>
- 440 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2008). Size, foraging, and food web
441 structure. *Proceedings of the National Academy of Sciences*, 105(11), 4191–4196. <https://doi.org/10.1073/pnas.0710672105>
- 442 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2011). Fit, efficiency, and biology: Some
443 thoughts on judging food web models. *Journal of Theoretical Biology*, 279(1), 169–171. <https://doi.org/10.1016/j.jtbi.2011.03.019>
- 444 Pichler, M., Boreux, V., Klein, A.-M., Schleuning, M., & Hartig, F. (2020). Machine learning algorithms
445 to infer trait-matching and predict species interactions in ecological networks. *Methods in Ecology and
446 Evolution*, 11(2), 281–293. <https://doi.org/10.1111/2041-210X.13329>
- 447 Pilosof, S., Porter, M. A., Pascual, M., & Kéfi, S. (2017). The multilayer nature of ecological networks.
448 *Nature Ecology & Evolution*, 1(4), 101. <https://doi.org/10.1038/s41559-017-0101>
- 449 Poelen, J. H., Simons, J. D., & Mungall, C. J. (2014). Global biotic interactions: An open infrastructure to
450 share and analyze species-interaction datasets. *Ecological Informatics*, 24, 148–159. <https://doi.org/10.1016/j.ecoinf.2014.08.005>
- 451 Poisot, T. (2023). Guidelines for the prediction of species interactions through binary classification. *Methods
452 in Ecology and Evolution*, 14(5), 1333–1345. <https://doi.org/10.1111/2041-210X.14071>
- 453 Poisot, T., Baiser, B., Dunne, J., Kéfi, S., Massol, F., Mouquet, N., Romanuk, T. N., Stouffer, D. B., Wood, S.

- 459 A., & Gravel, D. (2016). Mangal – making ecological network analysis simple. *Ecography*, 39(4), 384–390.
- 460 <https://doi.org/10.1111/ecog.00976>
- 461 Poisot, T., Bergeron, G., Cazelles, K., Dallas, T., Gravel, D., MacDonald, A., Mercier, B., Violet, C., &
- 462 Vissault, S. (2021). Global knowledge gaps in species interaction networks data. *Journal of Biogeography*,
- 463 48(7), 1552–1563. <https://doi.org/10.1111/jbi.14127>
- 464 Poisot, T., Cirtwill, A., Cazelles, K., Gravel, D., Fortin, M.-J., & Stouffer, D. (2016). The structure of
- 465 probabilistic networks. *Methods in Ecology and Evolution*, 7(3), 303–312. <https://doi.org/10.1111/mec.12800>
- 466 Poisot, T., Stouffer, D. B., & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary
- 467 through space and time. *Oikos*, 124(3), 243–251. <https://doi.org/10.1111/oik.01719>
- 468 Poisot, T., Stouffer, D. B., & Kéfi, S. (2016). Describe, understand and predict: Why do we need networks
- 469 in ecology? *Functional Ecology*, 30(12), 1878–1882. <https://www.jstor.org/stable/48582345>
- 470 Pollock, L. J., Tingley, R., Morris, W. K., Golding, N., O'Hara, R. B., Parris, K. M., Vesk, P. A., &
- 471 McCarthy, M. A. (2014). Understanding co-occurrence by modelling species simultaneously with a Joint
- 472 Species Distribution Model (JSDM). *Methods in Ecology and Evolution*, 5(5), 397–406. <https://doi.org/10.1111/2041-210X.12180>
- 473
- 474 Pringle, R. M. (2020). Untangling Food Webs. In *Unsolved Problems in Ecology* (pp. 225–238). Princeton
- 475 University Press. <https://doi.org/10.1515/9780691195322-020>
- 476 Pringle, R. M., & Hutchinson, M. C. (2020). Resolving Food-Web Structure. *Annual Review of Ecology,*
- 477 *Evolution and Systematics*, 51(Volume 51, 2020), 55–80. <https://doi.org/10.1146/annurev-ecolsys-110218-024908>
- 478
- 479 Proulx, S. R., Promislow, D. E. L., & Phillips, P. C. (2005). Network thinking in ecology and evolution.
- 480 *Trends in Ecology & Evolution*, 20(6), 345–353. <https://doi.org/10.1016/j.tree.2005.04.004>
- 481 Rooney, N., McCann, K. S., & Moore, J. C. (2008). A landscape theory for food web architecture. *Ecology*
- 482 *Letters*, 11(8), 867–881. <https://doi.org/10.1111/j.1461-0248.2008.01193.x>
- 483 Roopnarine, P. D. (2006). Extinction Cascades and Catastrophe in Ancient Food Webs. *Paleobiology*, 32(1),
- 484 1–19. <https://www.jstor.org/stable/4096814>
- 485 Saravia, L. A., Marina, T. I., Kristensen, N. P., De Troch, M., & Momo, F. R. (2022). Ecological network
- 486 assembly: How the regional metaweb influences local food webs. *Journal of Animal Ecology*, 91(3),
- 487 630–642. <https://doi.org/10.1111/1365-2656.13652>
- 488 Segar, S. T., Fayle, T. M., Srivastava, D. S., Lewinson, T. M., Lewis, O. T., Novotny, V., Kitching, R. L.,
- 489 & Maunsell, S. C. (2020). The Role of Evolution in Shaping Ecological Networks. *Trends in Ecology &*
- 490 *Evolution*, 35(5), 454–466. <https://doi.org/10.1016/j.tree.2020.01.004>
- 491 Shaw, J. O., Dunhill, A. M., Beckerman, A. P., Dunne, J. A., & Hull, P. M. (2024). *A framework for*

- 492 reconstructing ancient food webs using functional trait data (p. 2024.01.30.578036). bioRxiv. <https://doi.org/10.1101/2024.01.30.578036>
- 493
- 494 Song, C., & Levine, J. M. (2024). *Rigorous (in)validation of ecological models* (p. 2024.09.19.613075). bioRxiv.
- 495 <https://doi.org/10.1101/2024.09.19.613075>
- 496 Stock, M. (2021). Pairwise learning for predicting pollination interactions based on traits and phylogeny.
- 497 *Ecological Modelling*, 14.
- 498 Stouffer, D. B. (2019). All ecological models are wrong, but some are useful. *Journal of Animal Ecology*,
- 499 88(2), 192–195. <https://doi.org/10.1111/1365-2656.12949>
- 500 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Hemming, V.,
- 501 Mercier, B., Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2022). Food web reconstruction
- 502 through phylogenetic transfer of low-rank network representation. *Methods in Ecology and Evolution*,
- 503 13(12), 2838–2849. <https://doi.org/10.1111/2041-210X.13835>
- 504 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Mercier, B.,
- 505 Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2023). Graph embedding and transfer
- 506 learning can help predict potential species interaction networks despite data limitations. *Methods in*
- 507 *Ecology and Evolution*, 14(12), 2917–2930. <https://doi.org/10.1111/2041-210X.14228>
- 508 Strydom, T., Catchen, M. D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., Forero-Muñoz,
- 509 N. R., Higino, G., Mercier, B., Gonzalez, A., Gravel, D., Pollock, L., & Poisot, T. (2021). A roadmap
- 510 towards predicting species interaction networks (across space and time). *Philosophical Transactions of*
- 511 *the Royal Society B: Biological Sciences*, 376(1837), 20210063. <https://doi.org/10.1098/rstb.2021.0063>
- 512 Strydom, T., Dalla Riva, G. V., & Poisot, T. (2021). SVD Entropy Reveals the High Complexity of Ecological
- 513 Networks. *Frontiers in Ecology and Evolution*, 9. <https://doi.org/10.3389/fevo.2021.623141>
- 514 Terry, J. C. D., & Lewis, O. T. (2020). Finding missing links in interaction networks. *Ecology*, 101(7), e03047.
- 515 <https://doi.org/10.1002/ecy.3047>
- 516 Valdovinos, F. S., Hale, K. R. S., Dritz, S., Glaum, P. R., McCann, K. S., Simon, S. M., Thébault, E., Wetzel,
- 517 W. C., Wootton, K. L., & Yeakel, J. D. (2023). A bioenergetic framework for aboveground terrestrial
- 518 food webs. *Trends in Ecology & Evolution*, 38(3), 301–312. <https://doi.org/10.1016/j.tree.2022.11.004>
- 519 Van De Walle, R., Logghe, G., Haas, N., Massol, F., Vandegehuchte, M. L., & Bonte, D. (2023). Arthro-
- 520 pod food webs predicted from body size ratios are improved by incorporating prey defensive properties.
- 521 *Journal of Animal Ecology*, 92(4), 913–924. <https://doi.org/10.1111/1365-2656.13905>
- 522 Wells, K., & O’Hara, R. B. (2013). Species interactions: Estimating per-individual interaction strength and
- 523 covariates before simplifying data into per-species ecological networks. *Methods in Ecology and Evolution*,
- 524 4(1), 1–8. <https://doi.org/10.1111/j.2041-210x.2012.00249.x>

- 525 Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404(6774), 180–183.
- 526 <https://doi.org/10.1038/35004572>
- 527 Williams, R. J., & Martinez, N. D. (2008). Success and its limits among structural models of complex food
528 webs. *Journal of Animal Ecology*, 77(3), 512–519. <https://doi.org/10.1111/j.1365-2656.2008.01362.x>
- 529 Wootton, K. L., Curtsdotter, A., Roslin, T., Bommarco, R., & Jonsson, T. (2023). Towards a modular theory
530 of trophic interactions. *Functional Ecology*, 37(1), 26–43. <https://doi.org/10.1111/1365-2435.13954>
- 531 Xie, J.-R., Zhang, P., Zhang, H.-F., & Wang, B.-H. (2017). Completeness of Community Structure in
532 Networks. *Scientific Reports*, 7(1), 5269. <https://doi.org/10.1038/s41598-017-05585-6>
- 533 Yeakel, J. D., Pires, M. M., Rudolf, L., Dominy, N. J., Koch, P. L., Guimarães, P. R., & Gross, T. (2014).
534 Collapse of an ecological network in Ancient Egypt. *PNAS*, 111(40), 14472–14477. <https://doi.org/10.1073/pnas.1408471111>
- 535
- 536 Yodzis, P. (1982). The Compartmentation of Real and Assembled Ecosystems. *The American Naturalist*,
537 120(5), 551–570. <https://doi.org/10.1086/284013>
- 538 Yodzis, P., & Innes, S. (1992). Body Size and Consumer-Resource Dynamics. *The American Naturalist*,
539 139(6), 1151–1175. <https://doi.org/10.1086/285380>

the "driver" of the interaction
≠ the underlying theory (1:1) & the
'way' we get to the answer is diff
e.g. co-occurrence is about sharing
space/time but we use niche theory/
env. filtering as the means to determine
co-occurrence.

JUN	27	THU	木	179
			(mechanism)	
			what determines	
			interaction	
6		Body of theory		
15	Species	fund. niches env. filter	co- occurrence	
21		buck bones (mora)	"capacity"	
0	pop.	truit-match		
3	indiv.	neutral. funct. resp.	pop size / dynamics	
15		"physicw" 2D 3D prey choice	energy	
0				?? allometric scaling ??
3				: THEORY OF WHAT DETERMINES FEEDING LINKS (INTERACTIONS) BETWEEN SPECIES

Figure 1: TODO.