

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

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

Keywords: food web, network construction, scientific ignorance

1 At the heart of modern biodiversity science are a set of concepts and theories about biodiversity, stability
2 and function. These relate to the abundance, distribution and services that biodiversity provides, and how
3 biodiversity – as an interconnected set of species – responds to multiple stressors. The interaction between
4 species (or individuals) is one of the fundamental building blocks of ecological communities provide a powerful
5 abstraction that can help quantify, conceptualise, and understand biodiversity dynamics, and ultimately,
6 one hopes, make prediction, mitigate change and manage services [ref]. Such network representations of
7 biodiversity (including within species diversity) are increasingly argued to be an asset to predictive ecology,
8 climate change mitigation and resource management. Here, it is argued that characterising biodiversity in
9 a network will allow deeper capacity to understand and predict the abundance, distribution, dynamics and
10 services provided by multiple species facing multiple stressors.

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

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

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

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

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

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

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 an 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.

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...

34

35 1 Setting the Scene: The Not So Basics of Nodes and Edges

36 Defining a food web seems simple; it is the representation of the interactions (edges) between species (nodes),
37 however the definition of ‘edges’ and ‘nodes’, as well as the scale at which they are aggregated can take many
38 forms (Poisot, Stouffer, et al., 2016). An awareness of variance in the way a food web can be defined is critical
39 as it represents the ‘object’ that is used to make inferences either about the interactions between species, or
40 how the structure influences ecosystem level processes. One thus needs to be aware of both the criteria that
41 is used to define nodes and edges, and what processes or mechanisms the aggregation of the two represents,
42 as this will ultimately determine and delimit the way in which a network should be used.

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’ or segregation of species by life stages. Representing nodes as non-taxonomic species can be
47 useful in certain contexts (Williams & Martinez, 2000; Yodzis, 1982) and in cases where the adult and larval
48 stages of a species have different diets it may make ecological sense (Clegg et al., 2018) meaning that it is
49 not uncommon that networks often have nodes that have different definitions of a ‘species’ *e.g.* consisting
50 of both taxonomic and trophic species. Practical implications of how we are aggregating the nodes is that
51 the resolution may not always be ‘pixel perfect’ *i.e.*, we may be unable to assess the co-extinction risk of a
52 species pair, however there is value in having nodes that represent an aggregation of species, as these convey
53 a much more general overview of how the links are distributed within the community.

54 1.0.2 What is meant by an edge?

55 At its core, links within food webs can be thought of as a representation of either feeding links between
56 species - be that realised (Pringle, 2020) or potential (Dunne, 2006), or representative of fluxes within
57 the community/system *e.g.*, energy transfer or material flow (Lindeman, 1942). How we specify links will
58 influence the resulting structure of the network - and the inferences we will make thereof. For example taking
59 a food web that consists of links representing all *potential* feeding links for a community (*i.e.*, a metaweb)
60 will be meaningless if one is interested in understanding the flow of energy through the network as the links
61 within a metaweb do not represent environmental/energetic constraints. 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 can include species that do not co-occur (although this would require some degree of prediction/assumption 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, metawebs and realised networks are representing different mechanisms that are determining and constraining both the interactions between species as well as the resulting network structure, specifically providing context as to either the *potential* of an interaction occurring between two species (metawebs) or the subset of potential interactions that are *realised* in the field (realised networks).

2 From Nodes and Edges to Scales, Context, and Processes

Armed with these basics, it is now possible to review the scales and assumptions that are made by a wide range of tools to assist in constructing networks against poor data with the hope of capturing important processes

92 that underpin accurate prediction. Our thesis centres on a five-tier conceptualization of networks: evolution-
93 ary compatibility, co-occurrence, feasibility, abundance, predator choice, and non-trophic interactions. In
94 the following sections we review each of these and then provide a synthesis among them.

95 **2.1 Understanding the processes that determine species interactions**

96 Processes that are all-or-nothing (possibility) vs processes that are context dependent (likelihood). Processes
97 form the underlying logic of models (and arguably, no, for sure even empirical data). This means also the
98 interplay of the two, *i.e.*, the use of models to ‘gap fill’ within existing empirical dataset (Biton et al., 2024;
99 Stock, 2021). Ultimately when we put this all together it will influence how we can (and should) use the
100 resulting network. Here we present Figure 1 some of the processes that have been shown to influence either/or
101 the feasibility (possibility) of an interaction occurring between two species or if a feasible interaction is realised
102 (likelihood of realisation) within the specific environmental/community context. Of course these processes
103 do not function in a vacuum and do interact with/influence one another but it is still beneficial to present
104 them as such as these are often the underlying processes that influence model development, the criteria for
105 data collection in the field, and the scale of organisation for which they are relevant (species, population,
106 community).

107 [Figure 1 about here.]

108 **Evolutionary compatibility**

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

121 **(Co)occurrence**

122 Although the outright assumption that because two species are co-occurring it must mean that they are
123 interacting is inherently flawed (Blanchet et al., 2020), it is of course impossible for two species to interact (at
124 least in terms of feeding links) if they are not co-occurring in time and space. Thus co-occurrence data alone is
125 insufficient to build an accurate and ecologically meaningful representation of a food web having information
126 on the co-occurrence of species can further aid us in refining metawebs by allowing us to downsample the
127 network based on the species found in a specific location, or even add additional uncertainty based in how
128 likely species are to co-occur (Dansereau et al., 2023). Additionally the interplay between the interaction
129 between a species pair and their co-occurrence is meaningful when one is operating in the space of trying to
130 determine the distribution of a species (Higino et al., 2023), and forms a key component of some of the next
131 generation species distribution models *e.g.*, joint SDMs (Pollock et al., 2014).

132 **Abundance**

133 The abundance of the different species within the community can influence the likelihood of an interaction
134 occurring in a myriad of ways. There is the argument that networks (and the interactions that make them up)
135 are driven by only the abundance of the different species and not the characteristics (traits), *sensu* neutral
136 processes and have been formalised with the neutral model (Canard et al., 2012), as well as statistical tools
137 (Momal et al., 2020). Alternatively the abundance of species in a community can influence which interactions
138 are ultimately realised (Banville et al., 2024; Poisot et al., 2015).

139 **Predator choice (energetic cost)**

140 Ultimately, predator choice is underpinned by the energetic cost-benefit of trying to catch, kill, and consume
141 prey, and is well described within optimal foraging theory [ref] and rests on the idea that the prey a predator
142 chooses to target is one that will have the greatest return on energy with the lowest energetic cost. There are
143 additional bodies of work that attempt to include the cost of movement that the environment imposes on an
144 individual (Cherif et al., 2024) as well as 2D/3D search space (Pawar et al., 2012). In terms of formalising
145 these processes in the context of predicting networks using diet models (Beckerman et al., 2006; Petchey et al.,
146 2008) that have predator choice determined by the handling time, energy content, prey density, and predator
147 attack rate. Wootton et al. (2023) developed a model that moves the energy of the system into different
148 modules related to the process of the predator acquiring energy from the prey *i.e.*, compartmentation in food
149 webs (Krause et al., 2003).

150 **Indirect interactions**

151 The realisation (presence/absence) or strength of trophic interactions themselves can also be modified by
152 other, indirect (non-trophic), interactions (Golubski & Abrams, 2011; Pilosof et al., 2017), this can be either

₁₅₃ ‘directly’ through *e.g.*, competition or ‘indirectly’ *e.g.*, mutualistic/facilitative interactions will alter the fine-
₁₅₄ scale distribution and abundance of some species (Kéfi et al., 2012, 2015).

₁₅₅ It should be self evident that the different processes discussed above are all ultimately going to influence the
₁₅₆ realisation of interactions as well as the structure of a network, however they are acting at different scales of
₁₅₇ organisation. Both the **co-occurrence** and the **evolutionary compatibility** are valid at the scale of the
₁₅₈ species pair of interest, that is the *possibility* of an interaction being present/absent is assessed at the pairwise
₁₅₉ level and one is left with a ‘list’ of interactions that are present/absent. Although it is possible to build a
₁₆₀ network (*i.e.*, metaweb) from this information it is important to be aware that the structure of this network
₁₆₁ is not constrained by real-world dynamics or conditions (*i.e.*, community context), just because species are
₁₆₂ able to interact does not mean that they will (Poisot et al., 2015). In order to construct a network who’s
₁₆₃ structure is a closer approximation of reality (localised interactions) one needs to take into consideration
₁₆₄ properties of the community as a whole and not just the two species of interest.

₁₆₅ **downsampling paragraph??**

₁₆₆ 3 Network prediction is nuanced

₁₆₇ The different models that are used to either predict or construct networks have an underlying philosophy
₁₆₈ that often only captures one or a few of the processes discussed in Section 2.1, has implications for how the
₁₆₉ resulting network is defined Section 1, which will ultimately delimit and define what inferences can be made
₁₇₀ from the resulting network. Selecting a model for the task of network prediction should come down to two
₁₇₁ things; what *aspect* of a food web one is interested in predicting, and what data are available, necessary,
₁₇₂ and sufficient, and what is the purpose of wanting to predict a network? It is important that a researcher
₁₇₃ is aware of this to ensure that the appropriate model is selected. Broadly researchers will be interested in
₁₇₄ predicting/constructing two different types of networks; *metawebs*, which is essentially a list of all interactions
₁₇₅ that are *possible* for a specific community (*i.e.*, at the scale of the species pairs), or being able to predict
₁₇₆ location specific, *realised*, networks for the community (*i.e.*, at the scale of the community). The nature
₁₇₇ of metawebs means that they are unable to capture the structural metrics of realised/‘real-world’ networks
₁₇₈ (Caron et al., 2024). The researcher is also constrained by the data needs of both the model as well as the
₁₇₉ network type; for example in order to predict a realised network one needs additional community/population
₁₈₀ level data (*e.g.*, abundance), making metawebs a more feasible choice in data-poor contexts (*e.g.*, Strydom et
₁₈₁ al. (2023) construct a metaweb using a species list and a phylogenetic tree). The final question is assessing
₁₈₂ the purpose of predicting a network - is it to create a series of simulated, species agnostic but still ecologically

183 plausible, networks [*e.g.*,] or to predict a network for a specific community at a specific location. It is these
184 three points that will ultimately dictate which model is going to best allow one to predict the appropriate
185 network.

186 3.1 Models that predict structure

187 Although we identify mechanisms that determine species interactions in Section 2.1 not all models that are
188 used to predict networks operate at this ‘mechanistic’ level (at least in absolute terms), but rather represent
189 the *structure* of a network based on a series of *a priori* assumptions of network connectance (*e.g.*, the niche
190 model Williams & Martinez (2000); although see Allesina & Pascual (2009) for a parameter-free model) or
191 other structural features of a *realised* network (*e.g.*, stochastic block model, Xie et al. (2017)). Importantly
192 these structural models do not make species specific predictions (they are usually species agnostic and treat
193 nodes as trophic species) and so cannot be used to determine if an interaction is either possible *or* realised
194 between two species (*i.e.*, one cannot use these models to determine if species *a* eats species *b*). Although this
195 means this suite of models are unsuitable as tools for predicting interactions, they have been shown to be
196 sufficient tools to predict the structure of networks (Williams & Martinez, 2008).

197 3.2 How do we predict food webs?

198 There as many ways to predict networks as what there is to define them and along with taking into con-
199 sideration the points raised in the previous section it is also beneficial to think about the context in which
200 the different models were developed - and how this will influence the networks that they produce... Also it
201 is not feasibly possible to list every single approach that has been developed to predict networks and so we
202 will present what we believe to be the broad families that represent the different approaches to predicting
203 networks Table 1, particularly how these relate to the processes identified in Section 2.1, as well as models
204 that predict network structure (see Section 3.1). A more extensive overview of the different models that fall
205 with in the different model families can be found in SuppMat 1 and for a more detailed breakdown of the
206 different ‘traits’ of the model families refer to SuppMat 2.

Table 1: A summary of the different families of tools that can be used to generate food webs.

Model family	Assumptions	Data/process	'Limitation'	Network type	Key reference
null	Links are randomly distributed within a network		parameter assumptions, species agnostic	structural network	
neutral	Network structure is random, but species abundance determines links between nodes	abundance	parameter assumptions	structural network	Canard et al. (2012)
resource	Networks are interval, species can be ordered on a 'niche axis'		parameter assumptions, species agnostic	structural network	Williams & Martinez (2008)
generative	Networks are determined by their structural features		need real world networks	structural network	
energetic	Interactions are determined by energetic costs	abundance + energy	does not account for forbidden links in terms of evolutionary compatibility	'energy' network	
graph embedding	Interactions can be predicted from the latent traits of networks	evolutionary compatibility	need real world networks	metaweb	Strydom et al. (2023)

Model family	Assumptions	Data/process	'Limitation'	Network type	Key reference
trait matching	Interactions can be inferred by a mechanistic frame-work/relationships	evolutionary compatibility	well studied species/communities	metaweb	Morales-Castilla et al. (2015)
binary classifiers	Interactions can be predicted by learning the relationship between interactions and ecologically relevant predictors	evolutionary compatibility	need real world networks	metaweb	Pichler et al. (2020)
expert knowledge	'Boots on the ground'	evolutionary compatibility	well studied species/communities	metaweb	
data scavenging	Webscraping to create networks from online databases		need real world networks	metaweb	Poisot, Gravel, et al. (2016) (if you squint?)

Model family	Assumptions	Data/process	'Limitation'	Network type	Key reference
co-occurrence	co-occurrence patterns arise from interactions so we can use these patterns to reverse engineer the interactions	co-occurrence	does not account for forbidden links in terms of evolutionary compatibility or account for energy constraints	co-occurrence network	

²⁰⁷ There is a bit of a ‘point of conflict’ between those calling for ‘pixel perfect’, regional scale data (Pringle,
²⁰⁸ 2020; Pringle & Hutchinson, 2020) and for the means to generate networks that are ecologically plausible
²⁰⁹ *representations* (*sensu* structural networks). This represents two challenges; one is that models that repre-
²¹⁰ sent generalisations of networks often lack the ability to retrieve any species/community specificity which
²¹¹ limits their utility for real world, species-driven scenarios *e.g.*, species driven conservation efforts (Dunn et
²¹² al., 2009), however networks that are constructed through either (most) empirical observations or through
²¹³ predictive means are fundamentally going to represent metawebs, *i.e.*, lack constrained links, a representation
²¹⁴ of structure, or energy flow...

²¹⁵ 4 Making Progress with Networks

²¹⁶ 4.1 Further development of models and tools

²¹⁷ As we show in Table 1 there has been a suite of models that have been developed to predict trophic links,
²¹⁸ however we are lacking in tools that are explicitly taking into consideration estimating both the feasibility
²¹⁹ as well as realisation of links, *i.e.*, both interactions and structure simultaneously (Strydom et al., 2021).
²²⁰ This could be addressed either through the development of tools that do both (predict both interactions and
²²¹ structure), or it might be possible to do a ensemble modelling approach (Becker et al., 2022). Alternatively
²²² the development of tools that will allow for the downsampling of metawebs into realised networks (*e.g.*,
²²³ Roopnarine, 2006), although deciding exactly what is driving differences between local networks and the
²²⁴ regional metaweb might not be that simple (Saravia et al., 2022). Probably also something that aligns with
²²⁵ trying to predict interaction strength - because that would be the gold standard. Probably also worth just

226 plainly stating that feasibility of developing a model that is both broadly generalisable, but also has local
227 specificity is probably not attainable (Stouffer, 2019)

228 **4.2 At what scale should we be predicting/using networks?**

229 Look at Hutchinson et al. (2019)

230 We lack a clear agenda (and conceptualisation) as to what the appropriate level of aggregation is for a
231 ‘network’. Realistically most empirical networks are more aligned with metawebs as opposed to realised
232 networks as they are often the result of some sort of aggregation of observations across time, this creates a
233 two-fold problem. Firstly, we need to think about how this affects any sort of development of theory that sits
234 closer to the ‘realised network’ side of the spectrum - how often are we trying to ask and answer questions
235 about realised networks using feasible networks? The second is that this lack of ‘direction’ as to how we
236 should define a network is (actually) probably one of the biggest barriers that is affecting the use of networks
237 in applied settings... By define I mean both delimiting the time and geographic scale at which a network is
238 aggregated at (Estay et al., 2023). This is important because it can influence the inferences made, *e.g.*, the
239 large body of work (landscape theory for food web architecture) that showcases how different species use the
240 landscape will influence network dynamics (Rooney et al., 2008). There is also a bit of an interplay with
241 time and data and the different scales that they may be integrated at - co-occurrence may span decades and
242 just because two species have been recorded in the same space does not mean it was at the same timescale
243 (Brimacombe et al., 2024)

244 **4.3 How should we use different networks?**

245 What for and how we can use networks is perhaps one of the biggest ‘gaps’ we have in network ecology
246 (Tim’s EBV ms), and there is a serious need to start drawing clear, ecological links between network form
247 and function (although see Delmas et al., 2019). That being said one of the most important things we can
248 do is to be aware of the parameter space that is possible given a specific definition of a network and operate
249 within those parameters. And we should use this in how we also evaluate/benchmark the performance of the
250 different models as well; Poisot (2023) presents a set of guidelines for assessing how well a model recovers
251 pairwise interactions but we lack any clear strategies for benchmarking structure.

252 **4.4 Feasible, realised, or sustainable?**

253 When do we determine a link to be ‘real’... In the context of feasible networks this is perhaps clearer - if
254 all things were equal (*i.e.*, community context is irrelevant) would the predator be able to consume the

255 prey. However in the realised space there is also the question of the long term ‘energetic feasibility’ of an
256 interaction - just because an interaction is possible in the now is it able to sustain a population in the long
257 term. And what is the scale for that long term - are we thinking at the generational scale? Because ultimately
258 when we are constructing a network we are aggregating not only across space but also across time... This is
259 probably again a Lokta-Volterra space question and something that the dynamic foodweb model (Curtsdotter
260 et al., 2019; Delmas et al., 2017; Lajaaiti et al., 2024) is addressing, but again it is integrating this with the
261 feasible/realised axis.

262 5 Concluding remarks

263 I think a big take home will (hopefully) be how different approaches do better in different situations and so
264 you as an end user need to take this into consideration and pick accordingly. I think Petchey et al. (2011)
265 might have (and share) some thoughts on this. I feel like I need to look at Berlow et al. (2008) but maybe
266 not exactly in this context but vaguely adjacent. This is sort of the crux of the argument presented in
267 Brimacombe et al. (2024) as well.

268 Do we expect there to be differences when thinking about unipartite vs bipartite networks? Is there underlying
269 ecology/theory that would assume that different mechanisms (and thus models) are relevant in these two
270 ‘systems’.

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

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level of obj.		(mechanisms) what determines direct interaction		the "driver" of the interaction ≠ the underlying theory (l: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.
6	Species	fund. niches (inv. filter)	co- occurrence	
15		buckbones (mora) truit-match	"capacity"	
21	Pop.	neutral. funct. resp.	pop size/ dynamics	
0	indiv.	"physics" 2D 3D prey choice	energy	
3		?? allometric scaling??		
		: THEORY OF WHAT DETERMINES FEEDING LINKS (INTERACTIONS) BETWEEN SPECIES		

Figure 1: TODO.