

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 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.

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

35 Defining a food web seems simple; it is the representation of the interactions (edges) between species (nodes),
36 however the definition of ‘edges’ and ‘nodes’, as well as the scale at which they are aggregated can take
37 many forms (Poisot, Stouffer, et al., 2016). Networks can be constructed at the population (the links among
38 individuals), community (the links between species), or metacommunity (changes between locations) level.
39 Even if one were to limit their scope to thinking of interaction networks only in terms of food webs at the
40 community-level there are still many ways to define the various components of the network Panel A of 1,
41 one needs to understand the different intentions/assumptions that are made when a food web is constructed.
42 Although the main goal of constructing a food web is to capture and represent the feeding links between
43 species there are many ways to define the nodes (*e.g.*, species or taxonomic group), edges (*e.g.*, *potential* or
44 *realised* feeding links), the magnitude of the edges (*e.g.*, binary vs probabilistic), and even how the network
45 itself is delimited (does it represent an aggregation of interactions over time?).

46 [Figure 1 about here.]

47 1.0.1 How do we define a node?

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

58 1.0.2 What is meant by an edge?

59 At its core, links within food webs can be thought of as a representation of either feeding links between
60 species - be that realised (Pringle, 2020) or potential (Dunne, 2006), or representative of fluxes within
61 the community/system *e.g.*, energy transfer or material flow (Lindeman, 1942). How we specify links will
62 influence the resulting structure of the network - and the inferences we will make thereof. For example taking
63 a food web that consists of links representing all *potential* feeding links for a community (*i.e.*, a metaweb)

will be meaningless if one is interested in understanding the flow of energy through the network as the links 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 Putting the parts together

The ingredients one uses to construct networks generates a unique representation of the mechanisms (see Section 2) that allow inference and reasoning about the structure, aspects of dynamics (*e.g.*, stability), and potentially the function of communities (*e.g.*, flux). It is thus important to keep in mind that different networks are going to be representing different processes and that can only be used for inference of some but not all aspects of the community at large. Here it may be meaningful to contextualise the different ‘types’ of food webs within the larger research programmes (or even practical needs) that have been driving the construction of them.

Before thinking about the ways in which we can predict networks it is perhaps meaningful to take a step back and think about the different criteria that must be met in order for an interaction to be able to occur between two species, specifically thinking of this in terms of distinguishing between the feasibility versus realisation of an interaction and how these are determined (and defined by) different ‘rules’/mechanisms. If we look at this feasibility-reality continuum (Figure 2) it is clear how the different predictive approaches (methods) tend to fall within one of the broader categories identified (distinguished) in the triangle. This is not to say that this shortcoming should be viewed as a ‘bug’ but rather a ‘feature’ of the field as it allows one to engage with, as well as construct networks at different scales, which is particularly valuable if one takes into consideration the considerable ‘data cost’ of predicting well resolved, realised networks in comparison to constructing high-level metawebs. However, it is important that there is an awareness and acknowledgement of where within this feasibility-reality one is working at and how this will impact and limit the contexts in which the resulting network can be used and applied within.

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

94 processes that underpin accurate prediction. Our thesis centres on a four-tier conceptualization of networks:
95 evolutionary compatibility, co-occurrence, feasibility, abundance, predator choice, and non-trophic interac-
96 tions. In the following sections we review each of these and then provide a synthesis among them.

97 **2.1 Understanding the processes that determine species interactions**

98 Processes that are all-or-nothing (possibility) vs processes that are context dependent (likelihood). Processes
99 form the underlying logic of models (and arguably, no, for sure even empirical data) capture. This means
100 also the interplay of the two, *i.e.*, the use of models to ‘gap fill’ within existing empirical dataset (Biton et
101 al., 2024; Stock, 2021). Ultimately when we put this all together it will influence how we can (and should)
102 use the resulting network. Here we present Figure 2 some of the processes that have been shown to influence
103 either/or the feasibility (possibility) of an interaction occurring between two species or if a feasible interaction
104 is realised (likelihood of realisation) within the specific environmental/community context. Of course these
105 processes do not function in a vacuum and do interact with/influence one another but it is still beneficial
106 to present them as such as these are often the underlying processes that influence model development, the
107 criteria for data collection in the field, and the scale of organisation for which they are relevant (species,
108 population, community).

109 [Figure 2 about here.]

110 **Evolutionary compatibility**

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

123 **(Co)occurrence**

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

134 **Abundance**

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

141 **Predator choice (energetic cost)**

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

152 **Indirect interactions**

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

₁₅₅ ‘directly’ through *e.g.*, competition or ‘indirectly’ *e.g.*, mutualistic/facilitative interactions will alter the fine-
₁₅₆ scale distribution and abundance of some species (Kéfi et al., 2012, 2015).

₁₅₇ It should be self evident that the different processes discussed above are all ultimately going to influence the
₁₅₈ realisation of interactions as well as the structure of a network, however they are acting at different scales of
₁₅₉ organisation. Both the **co-occurrence** and the **evolutionary compatibility** are valid at the scale of the
₁₆₀ species pair of interest, that is the *possibility* of an interaction being present/absent is assessed at the pairwise
₁₆₁ level and one is left with a ‘list’ of interactions that are present/absent. Although it is possible to build a
₁₆₂ network (*i.e.*, metaweb) from this information it is important to be aware that the structure of this network
₁₆₃ is not constrained by real-world dynamics or conditions (*i.e.*, community context), just because species are
₁₆₄ able to interact does not mean that they will (Poisot et al., 2015). In order to construct a network who’s
₁₆₅ structure is a closer approximation of reality (localised interactions) one needs to take into consideration
₁₆₆ properties of the community as a whole and not just the two species of interest.

₁₆₇ **downsampling paragraph??**

₁₆₈ 3 Network prediction is nuanced

₁₆₉ The different models that are used to either predict or construct networks have an underlying philosophy
₁₇₀ that often only captures one or a few of the processes discussed in Section 2.1, has implications for how the
₁₇₁ resulting network is defined Section 1, which will ultimately delimit and define what inferences can be made
₁₇₂ from the resulting network. Selecting a model for the task of network prediction should come down to two
₁₇₃ things; what *aspect* of a food web one is interested in predicting, and what data are available, necessary,
₁₇₄ and sufficient, and what is the purpose of wanting to predict a network? It is important that a researcher
₁₇₅ is aware of this to ensure that the appropriate model is selected. Broadly researchers will be interested in
₁₇₆ predicting/constructing two different types of networks; *metawebs*, which is essentially a list of all interactions
₁₇₇ that are *possible* for a specific community (*i.e.*, at the scale of the species pairs), or being able to predict
₁₇₈ location specific, *realised*, networks for the community (*i.e.*, at the scale of the community). The nature
₁₇₉ of metawebs means that they are unable to capture the structural metrics of realised/‘real-world’ networks
₁₈₀ (Caron et al., 2024). The researcher is also constrained by the data needs of both the model as well as the
₁₈₁ network type; for example in order to predict a realised network one needs additional community/population
₁₈₂ level data (*e.g.*, abundance), making metawebs a more feasible choice in data-poor contexts (*e.g.*, Strydom et
₁₈₃ al. (2023) construct a metaweb using a species list and a phylogenetic tree). The final question is assessing
₁₈₄ the purpose of predicting a network - is it to create a series of simulated, species agnostic but still ecologically

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

188 3.1 Models that predict structure

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

199 3.2 How do we predict food webs?

200 There as many ways to predict networks as what there is to define them and along with taking into con-
201 sideration the points raised in the previous section it is also beneficial to think about the context in which
202 the different models were developed - and how this will influence the networks that they produce... Also it
203 is not feasibly possible to list every single approach that has been developed to predict networks and so we
204 will present what we believe to be the broad families that represent the different approaches to predicting
205 networks Table 1, particularly how these relate to the processes identified in Section 2.1, as well as models
206 that predict network structure (see Section 3.1). A more extensive overview of the different models that fall
207 with in the different model families can be found in SuppMat 1 and for a more detailed breakdown of the
208 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	

²⁰⁹ There is a bit of a ‘point of conflict’ between those calling for ‘pixel perfect’, regional scale data (Pringle,
²¹⁰ 2020; Pringle & Hutchinson, 2020) and for the means to generate networks that are ecologically plausible
²¹¹ *representations* (*sensu* structural networks). This represents two challenges; one is that models that repre-
²¹² sent generalisations of networks often lack the ability to retrieve any species/community specificity which
²¹³ limits their utility for real world, species-driven scenarios *e.g.*, species driven conservation efforts (Dunn et
²¹⁴ al., 2009), however networks that are constructed through either (most) empirical observations or through
²¹⁵ predictive means are fundamentally going to represent metawebs, *i.e.*, lack constrained links, a representation
²¹⁶ of structure, or energy flow...

²¹⁷ 4 Making Progress with Networks

²¹⁸ 4.1 Further development of models and tools

²¹⁹ As we show in Table 1 there has been a suite of models that have been developed to predict trophic links,
²²⁰ however we are lacking in tools that are explicitly taking into consideration estimating both the feasibility
²²¹ as well as realisation of links, *i.e.*, both interactions and structure simultaneously (Strydom et al., 2021).
²²² This could be addressed either through the development of tools that do both (predict both interactions and
²²³ structure), or it might be possible to do a ensemble modelling approach (Becker et al., 2022). Alternatively
²²⁴ the development of tools that will allow for the downsampling of metawebs into realised networks (*e.g.*,
²²⁵ Roopnarine, 2006), although deciding exactly what is driving differences between local networks and the
²²⁶ regional metaweb might not be that simple (Saravia et al., 2022). Probably also something that aligns with
²²⁷ trying to predict interaction strength - because that would be the gold standard. Probably also worth just

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

230 **4.2 At what scale should we be predicting/using networks?**

231 Look at Hutchinson et al. (2019)

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

246 **4.3 How should we use different networks?**

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

254 **4.4 Feasible, realised, or sustainable?**

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

²⁵⁷ However in the realised space there is also the question of the long term ‘energetic feasibility’ of an interaction
²⁵⁸ - just because an interaction is possible in the now is it able to sustain a population in the long term. And
²⁵⁹ what is the scale for that long term - are we thinking at the generational scale? Because ultimately when we
²⁶⁰ are constructing a network we are aggregating not only across space but also across time... This is probably
²⁶¹ again a Lokta-Volterra space question and something that the dynamic foodweb model (BEFW, Curtsdotter
²⁶² et al. (2019)) is addressing, but again it is integrating this with the feasible/realised axis.

²⁶³ 5 Concluding remarks

²⁶⁴ I think a big take home will (hopefully) be how different approaches do better in different situations and so
²⁶⁵ you as an end user need to take this into consideration and pick accordingly. I think Petchey et al. (2011)
²⁶⁶ might have (and share) some thoughts on this. I feel like I need to look at Berlow et al. (2008) but maybe
²⁶⁷ not exactly in this context but vaguely adjacent. This is sort of the crux of the argument presented in
²⁶⁸ Brimacombe et al. (2024) as well.

²⁶⁹ Do we expect there to be differences when thinking about unipartite vs bipartite networks? Is there underlying
²⁷⁰ ecology/theory that would assume that different mechanisms (and thus models) are relevant in these two
²⁷¹ ‘systems’.

- ²⁷² • The Terry & Lewis (2020) paper looks at some methods but is specifically looking at a bipartite world...

²⁷³ References

- ²⁷⁴ Allesina, S., & Pascual, M. (2009). Food web models: A plea for groups. *Ecology Letters*, 12(7), 652–662.
²⁷⁵ <https://doi.org/10.1111/j.1461-0248.2009.01321.x>
- ²⁷⁶ Banville, F., Strydom, T., Blyth, P., Brimacombe, C., Catchen, M. D., Dansereau, G., Higino, G., Malpas,
²⁷⁷ T., Mayall, H., Norman, K., Gravel, D., & Poisot, T. (2024). *Deciphering probabilistic species interaction*
²⁷⁸ *networks*. EcoEvoRxiv. <https://doi.org/10.32942/X28G8Z>
- ²⁷⁹ Becker, D. J., Albery, G. F., Sjodin, A. R., Poisot, T., Bergner, L. M., Chen, B., Cohen, L. E., Dallas, T.
²⁸⁰ A., Eskew, E. A., Fagre, A. C., Farrell, M. J., Guth, S., Han, B. A., Simmons, N. B., Stock, M., Teeling,
²⁸¹ E. C., & Carlson, C. J. (2022). Optimising predictive models to prioritise viral discovery in zoonotic
²⁸² 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)
- ²⁸³ Beckerman, A. P., Petchey, O. L., & Warren, P. H. (2006). Foraging biology predicts food web complexity.
²⁸⁴ *Proceedings of the National Academy of Sciences*, 103(37), 13745–13749. <https://doi.org/10.1073/pnas.0603039103>

- 286 Berlow, E. L., Brose, U., & Martinez, N. D. (2008). The “Goldilocks factor” in food webs. *Proceedings of*
287 *the National Academy of Sciences*, 105(11), 4079–4080. <https://doi.org/10.1073/pnas.0800967105>
- 288 Berlow, E. L., Neutel, A.-M., Cohen, J. E., de Ruiter, P. C., Ebenman, B., Emmerson, M., Fox, J. W., Jansen,
289 V. A. A., Iwan Jones, J., Kokkoris, G. D., Logofet, D. O., McKane, A. J., Montoya, J. M., & Petchey, O.
290 (2004). Interaction strengths in food webs: Issues and opportunities. *Journal of Animal Ecology*, 73(3),
291 585–598. <https://doi.org/10.1111/j.0021-8790.2004.00833.x>
- 292 Biton, B., Puzis, R., & Pilosof, S. (2024). *Inductive link prediction boosts data availability and enables*
293 *cross-community link prediction in ecological networks*.
- 294 Blanchet, F. G., Cazelles, K., & Gravel, D. (2020). Co-occurrence is not evidence of ecological interactions.
295 *Ecology Letters*, 23(7), 1050–1063. <https://doi.org/10.1111/ele.13525>
- 296 Brimacombe, C., Bodner, K., & Fortin, M.-J. (2024). *Applying a method before its proof-of-concept: A*
297 *cautionary tale using inferred food webs*. <https://doi.org/10.13140/RG.2.2.22076.65927>
- 298 Brimacombe, C., Bodner, K., Michalska-Smith, M., Poisot, T., & Fortin, M.-J. (2023). Shortcomings
299 of reusing species interaction networks created by different sets of researchers. *PLOS Biology*, 21(4),
300 e3002068. <https://doi.org/10.1371/journal.pbio.3002068>
- 301 Canard, E., Mouquet, N., Marescot, L., Gaston, K. J., Gravel, D., & Mouillot, D. (2012). Emergence of
302 Structural Patterns in Neutral Trophic Networks. *PLOS ONE*, 7(8), e38295. <https://doi.org/10.1371/journal.pone.0038295>
- 303 Caron, D., Brose, U., Lurgi, M., Blanchet, F. G., Gravel, D., & Pollock, L. J. (2024). Trait-matching models
304 predict pairwise interactions across regions, not food web properties. *Global Ecology and Biogeography*,
305 33(4), e13807. <https://doi.org/10.1111/geb.13807>
- 306 Cherif, M., Brose, U., Hirt, M. R., Ryser, R., Silve, V., Albert, G., Arnott, R., Berti, E., Cirtwill, A.,
307 Dyer, A., Gauzens, B., Gupta, A., Ho, H.-C., Portalier, S. M. J., Wain, D., & Wootton, K. (2024). The
308 environment to the rescue: Can physics help predict predator–prey interactions? *Biological Reviews*,
309 n/a(n/a). <https://doi.org/10.1111/brv.13105>
- 310 Clegg, T., Ali, M., & Beckerman, A. P. (2018). The impact of intraspecific variation on food web structure.
311 *Ecology*, 99(12), 2712–2720. <https://doi.org/10.1002/ecy.2523>
- 312 Curtsdotter, A., Banks, H. T., Banks, J. E., Jonsson, M., Jonsson, T., Laubmeier, A. N., Traugott, M., &
313 Bommarco, R. (2019). Ecosystem function in predator–prey food webs—confronting dynamic models with
314 empirical data. *Journal of Animal Ecology*, 88(2), 196–210. <https://doi.org/10.1111/1365-2656.12892>
- 315 Dalla Riva, G. V., & Stouffer, D. B. (2016). Exploring the evolutionary signature of food webs’ backbones
316 using functional traits. *Oikos*, 125(4), 446–456. <https://doi.org/10.1111/oik.02305>
- 317 Dansereau, G., Barros, C., & Poisot, T. (2023). *Spatially explicit predictions of food web structure from*

- 319 regional level data.
- 320 Delmas, E., Besson, M., Brice, M.-H., Burkle, L. A., Riva, G. V. D., Fortin, M.-J., Gravel, D., Guimarães,
321 P. R., Hembry, D. H., Newman, E. A., Olesen, J. M., Pires, M. M., Yeakel, J. D., & Poisot, T. (2019).
322 Analysing ecological networks of species interactions. *Biological Reviews*, 94(1), 16–36. <https://doi.org/10.1111/brv.12433>
- 323
- 324 Dunn, R. R., Harris, N. C., Colwell, R. K., Koh, L. P., & Sodhi, N. S. (2009). The sixth mass coextinction:
325 Are most endangered species parasites and mutualists? *Proceedings. Biological Sciences*, 276(1670),
326 3037–3045. <https://doi.org/10.1098/rspb.2009.0413>
- 327 Dunne, J. A. (2006). The Network Structure of Food Webs. In J. A. Dunne & M. Pascual (Eds.), *Ecological
328 networks: Linking structure and dynamics* (pp. 27–86). Oxford University Press.
- 329 Estay, S. A., Fortin, M.-J., & López, D. N. (2023). Editorial: Patterns and processes in ecological networks
330 over space. *Frontiers in Ecology and Evolution*, 11.
- 331 Fricke, E. C., Hsieh, C., Middleton, O., Gorczynski, D., Cappello, C. D., Sanisidro, O., Rowan, J., Svenning,
332 J.-C., & Beaudrot, L. (2022). Collapse of terrestrial mammal food webs since the Late Pleistocene.
333 *Science*, 377(6609), 1008–1011. <https://doi.org/10.1126/science.abn4012>
- 334 Golubski, A. J., & Abrams, P. A. (2011). Modifying modifiers: What happens when interspecific interactions
335 interact? *Journal of Animal Ecology*, 80(5), 1097–1108. <https://doi.org/10.1111/j.1365-2656.2011.01852.x>
- 336
- 337 Gómez, J. M., Verdú, M., & Perfectti, F. (2010). Ecological interactions are evolutionarily conserved across
338 the entire tree of life. *Nature*, 465(7300), 918–921. <https://doi.org/10.1038/nature09113>
- 339 Higino, G. T., Banville, F., Dansereau, G., Muñoz, N. R. F., Windsor, F., & Poisot, T. (2023). Mismatch
340 between IUCN range maps and species interactions data illustrated using the Serengeti food web. *PeerJ*,
341 11, e14620. <https://doi.org/10.7717/peerj.14620>
- 342 Hutchinson, M. C., Bramon Mora, B., Pilosof, S., Barner, A. K., Kéfi, S., Thébault, E., Jordano, P., &
343 Stouffer, D. B. (2019). Seeing the forest for the trees: Putting multilayer networks to work for community
344 ecology. *Functional Ecology*, 33(2), 206–217. <https://doi.org/10.1111/1365-2435.13237>
- 345 Jordano, P. (2016a). Chasing Ecological Interactions. *PLOS Biology*, 14(9), e1002559. <https://doi.org/10.1371/journal.pbio.1002559>
- 346
- 347 Jordano, P. (2016b). Sampling networks of ecological interactions. *Functional Ecology*. <https://doi.org/10.1111/1365-2435.12763>
- 348
- 349 Kéfi, S., Berlow, E. L., Wieters, E. A., Joppa, L. N., Wood, S. A., Brose, U., & Navarrete, S. A. (2015).
350 Network structure beyond food webs: Mapping non-trophic and trophic interactions on Chilean rocky
351 shores. *Ecology*, 96(1), 291–303. <https://doi.org/10.1890/13-1424.1>

- 352 Kéfi, S., Berlow, E. L., Wieters, E. A., Navarrete, S. A., Petchey, O. L., Wood, S. A., Boit, A., Joppa, L. N.,
353 Lafferty, K. D., Williams, R. J., Martinez, N. D., Menge, B. A., Blanchette, C. A., Iles, A. C., & Brose,
354 U. (2012). More than a meal... integrating non-feeding interactions into food webs: More than a meal
355 *Ecology Letters*, 15(4), 291–300. <https://doi.org/10.1111/j.1461-0248.2011.01732.x>
- 356 Krause, A. E., Frank, K. A., Mason, D. M., Ulanowicz, R. E., & Taylor, W. W. (2003). Compartments
357 revealed in food-web structure. *Nature*, 426(6964), 282–285. <https://doi.org/10.1038/nature02115>
- 358 Lindeman, R. L. (1942). The Trophic-Dynamic Aspect of Ecology. *Ecology*, 23(4), 399–417. <https://doi.org/10.2307/1930126>
- 360 Maiorano, L., Montemaggiore, A., Ficetola, G. F., O'Connor, L., & Thuiller, W. (2020). TETRA-EU 1.0: A
361 species-level trophic metaweb of European tetrapods. *Global Ecology and Biogeography*, 29(9), 1452–1457.
362 <https://doi.org/10.1111/geb.13138>
- 363 Momal, R., Robin, S., & Ambroise, C. (2020). Tree-based inference of species interaction networks from
364 abundance data. *Methods in Ecology and Evolution*, 11(5), 621–632. <https://doi.org/10.1111/2041-210X.13380>
- 366 Morales-Castilla, I., Matias, M. G., Gravel, D., & Araújo, M. B. (2015). Inferring biotic interactions from
367 proxies. *Trends in Ecology & Evolution*, 30(6), 347–356. <https://doi.org/10.1016/j.tree.2015.03.014>
- 368 Pawar, S., Dell, A. I., & Savage, V. M. (2012). Dimensionality of consumer search space drives trophic
369 interaction strengths. *Nature*, 486(7404), 485–489. <https://doi.org/10.1038/nature11131>
- 370 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2008). Size, foraging, and food web
371 structure. *Proceedings of the National Academy of Sciences*, 105(11), 4191–4196. <https://doi.org/10.1073/pnas.0710672105>
- 373 Petchey, O. L., Beckerman, A. P., Riede, J. O., & Warren, P. H. (2011). Fit, efficiency, and biology: Some
374 thoughts on judging food web models. *Journal of Theoretical Biology*, 279(1), 169–171. <https://doi.org/10.1016/j.jtbi.2011.03.019>
- 376 Pichler, M., Boreux, V., Klein, A.-M., Schleuning, M., & Hartig, F. (2020). Machine learning algorithms
377 to infer trait-matching and predict species interactions in ecological networks. *Methods in Ecology and
378 Evolution*, 11(2), 281–293. <https://doi.org/10.1111/2041-210X.13329>
- 379 Pilosof, S., Porter, M. A., Pascual, M., & Kéfi, S. (2017). The multilayer nature of ecological networks.
380 *Nature Ecology & Evolution*, 1(4), 101. <https://doi.org/10.1038/s41559-017-0101>
- 381 Poisot, T. (2023). Guidelines for the prediction of species interactions through binary classification. *Methods
382 in Ecology and Evolution*, 14(5), 1333–1345. <https://doi.org/10.1111/2041-210X.14071>
- 383 Poisot, T., Bergeron, G., Cazelles, K., Dallas, T., Gravel, D., MacDonald, A., Mercier, B., Violet, C., &
384 Vissault, S. (2021). Global knowledge gaps in species interaction networks data. *Journal of Biogeography*,

- 385 48(7), 1552–1563. <https://doi.org/10.1111/jbi.14127>
- 386 Poisot, T., Cirtwill, A., Cazelles, K., Gravel, D., Fortin, M.-J., & Stouffer, D. (2016). The structure of
387 probabilistic networks. *Methods in Ecology and Evolution*, 7(3), 303–312. <https://doi.org/10.1111/mec.12700>
- 388 Poisot, T., Gravel, D., Leroux, S., Wood, S. A., Fortin, M.-J., Baiser, B., Cirtwill, A. R., Araújo, M. B.,
389 & Stouffer, D. B. (2016). Synthetic datasets and community tools for the rapid testing of ecological
390 hypotheses. *Ecography*, 39(4), 402–408. <https://doi.org/10.1111/ecog.01941>
- 391 Poisot, T., Stouffer, D. B., & Gravel, D. (2015). Beyond species: Why ecological interaction networks vary
392 through space and time. *Oikos*, 124(3), 243–251. <https://doi.org/10.1111/oik.01719>
- 393 Poisot, T., Stouffer, D. B., & Kéfi, S. (2016). Describe, understand and predict: Why do we need networks
394 in ecology? *Functional Ecology*, 30(12), 1878–1882. <https://www.jstor.org/stable/48582345>
- 395 Pollock, L. J., Tingley, R., Morris, W. K., Golding, N., O’Hara, R. B., Parris, K. M., Vesk, P. A., &
396 McCarthy, M. A. (2014). Understanding co-occurrence by modelling species simultaneously with a Joint
397 Species Distribution Model (JSDM). *Methods in Ecology and Evolution*, 5(5), 397–406. <https://doi.org/10.1111/2041-210X.12180>
- 398 Pringle, R. M. (2020). Untangling Food Webs. In *Unsolved Problems in Ecology* (pp. 225–238). Princeton
399 University Press. <https://doi.org/10.1515/9780691195322-020>
- 400 Pringle, R. M., & Hutchinson, M. C. (2020). Resolving Food-Web Structure. *Annual Review of Ecology,
401 Evolution and Systematics*, 51(Volume 51, 2020), 55–80. <https://doi.org/10.1146/annurev-ecolsys-110218-024908>
- 402 Proulx, S. R., Promislow, D. E. L., & Phillips, P. C. (2005). Network thinking in ecology and evolution.
403 *Trends in Ecology & Evolution*, 20(6), 345–353. <https://doi.org/10.1016/j.tree.2005.04.004>
- 404 Rooney, N., McCann, K. S., & Moore, J. C. (2008). A landscape theory for food web architecture. *Ecology
405 Letters*, 11(8), 867–881. <https://doi.org/10.1111/j.1461-0248.2008.01193.x>
- 406 Roopnarine, P. D. (2006). Extinction Cascades and Catastrophe in Ancient Food Webs. *Paleobiology*, 32(1),
407 1–19. <https://www.jstor.org/stable/4096814>
- 408 Saravia, L. A., Marina, T. I., Kristensen, N. P., De Troch, M., & Momo, F. R. (2022). Ecological network
409 assembly: How the regional metaweb influences local food webs. *Journal of Animal Ecology*, 91(3),
410 630–642. <https://doi.org/10.1111/1365-2656.13652>
- 411 Segar, S. T., Fayle, T. M., Srivastava, D. S., Lewinson, T. M., Lewis, O. T., Novotny, V., Kitching, R. L.,
412 & Maunsell, S. C. (2020). The Role of Evolution in Shaping Ecological Networks. *Trends in Ecology &
413 Evolution*, 35(5), 454–466. <https://doi.org/10.1016/j.tree.2020.01.004>
- 414 Stock, M. (2021). Pairwise learning for predicting pollination interactions based on traits and phylogeny.
415 *Ecological Modelling*, 14.
- 416

- 418 Stouffer, D. B. (2019). All ecological models are wrong, but some are useful. *Journal of Animal Ecology*,
419 88(2), 192–195. <https://doi.org/10.1111/1365-2656.12949>
- 420 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Hemming, V.,
421 Mercier, B., Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2022). Food web reconstruction
422 through phylogenetic transfer of low-rank network representation. *Methods in Ecology and Evolution*,
423 13(12), 2838–2849. <https://doi.org/10.1111/2041-210X.13835>
- 424 Strydom, T., Bouskila, S., Banville, F., Barros, C., Caron, D., Farrell, M. J., Fortin, M.-J., Mercier, B.,
425 Pollock, L. J., Runghen, R., Dalla Riva, G. V., & Poisot, T. (2023). Graph embedding and transfer
426 learning can help predict potential species interaction networks despite data limitations. *Methods in
427 Ecology and Evolution*, 14(12), 2917–2930. <https://doi.org/10.1111/2041-210X.14228>
- 428 Strydom, T., Catchen, M. D., Banville, F., Caron, D., Dansereau, G., Desjardins-Proulx, P., Forero-Muñoz,
429 N. R., Higino, G., Mercier, B., Gonzalez, A., Gravel, D., Pollock, L., & Poisot, T. (2021). A roadmap
430 towards predicting species interaction networks (across space and time). *Philosophical Transactions of
431 the Royal Society B: Biological Sciences*, 376(1837), 20210063. <https://doi.org/10.1098/rstb.2021.0063>
- 432 Terry, J. C. D., & Lewis, O. T. (2020). Finding missing links in interaction networks. *Ecology*, 101(7), e03047.
433 <https://doi.org/10.1002/ecy.3047>
- 434 Williams, R. J., & Martinez, N. D. (2000). Simple rules yield complex food webs. *Nature*, 404(6774), 180–183.
435 <https://doi.org/10.1038/35004572>
- 436 Williams, R. J., & Martinez, N. D. (2008). Success and its limits among structural models of complex food
437 webs. *Journal of Animal Ecology*, 77(3), 512–519. <https://doi.org/10.1111/j.1365-2656.2008.01362.x>
- 438 Wootton, K. L., Curtsdotter, A., Roslin, T., Bommarco, R., & Jonsson, T. (2023). Towards a modular theory
439 of trophic interactions. *Functional Ecology*, 37(1), 26–43. <https://doi.org/10.1111/1365-2435.13954>
- 440 Xie, J.-R., Zhang, P., Zhang, H.-F., & Wang, B.-H. (2017). Completeness of Community Structure in
441 Networks. *Scientific Reports*, 7(1), 5269. <https://doi.org/10.1038/s41598-017-05585-6>
- 442 Yodzis, P. (1982). The Compartmentation of Real and Assembled Ecosystems. *The American Naturalist*,
443 120(5), 551–570. <https://doi.org/10.1086/284013>

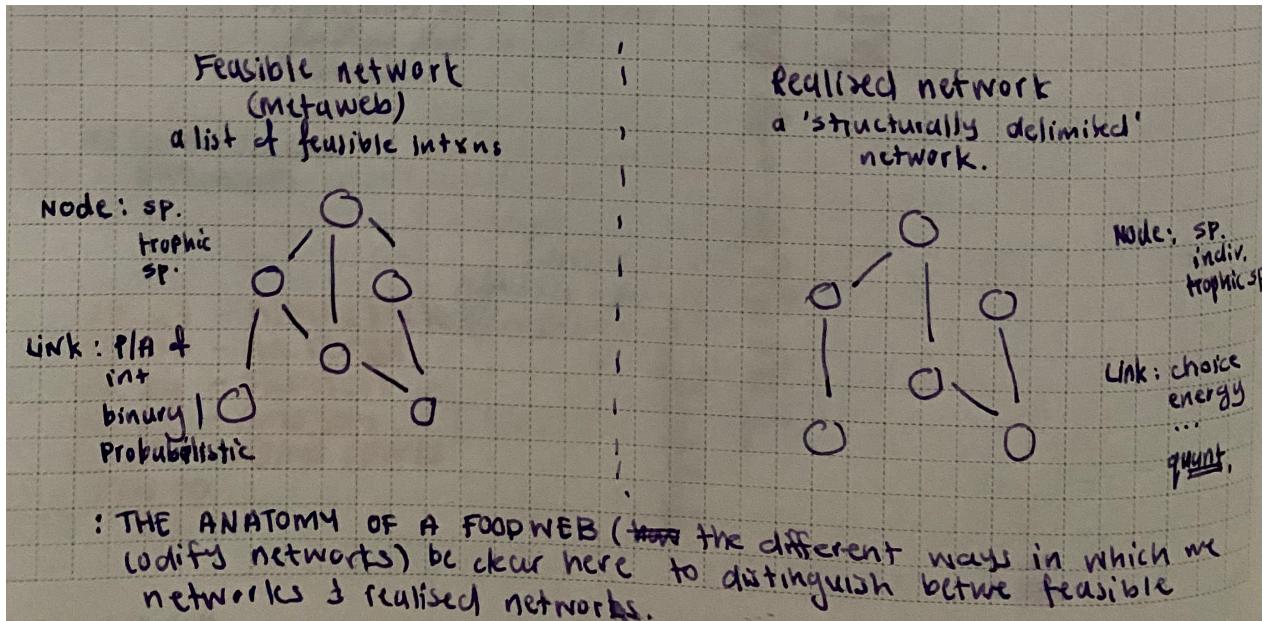


Figure 1: The many ways in which a food web can be defined and described at the node, edge, and even network level.

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.

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			(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 2: TODO.