

Food web visualisation: heatmap, interactive graph, animated flow network

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Abstract

1. Food webs are the physical foundations of ecosystems. Visualisations help to find and present structural patterns of these weighted networks and are essential in research, conservation practice, and education. There has been no open-source library drawing weighted food webs with fractional trophic levels clearly. The existing approaches are scattered across separate libraries and programming languages.
2. We provide an ensemble of mutually complementary visualisation methods that enable a general overview of the system, as well as a clear presentation of its details: <https://github.com/ibs-pan/foodwebviz>. We use colours, sizes,

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positions, zoom, and movement for precise identification of flows, their magnitudes, and connectivity patterns. Vertical positions of nodes highlight the fractional trophic level as the most significant structural variable in a food web. The visualisations are in the form of modular and extensible Python functions. Jupyter notebooks display them interactively in HTML.

3. A heatmap of food web flows or diet proportions shows their general pattern at a glance while retaining their precise identification. An interactive graph allows tracing the flow of matter over subsequent links. The user can select nodes, zoom, adjust layout parameters and manually drag-and-drop nodes. An intuitive animation of particles moving between nodes uses colours and time dimension to trace connections better. It shows the multivariate food web aspects in one graph, together with a structural indicator, the trophic level. A bar plot and a heatmap summarise exchanges of matter between trophic levels.
4. We bring several complementary and customisable methods together to facilitate accompanying every food web publication and analysis with its visualisation. Users can tinker with the interactive output and method parameters to reach the desired effect. Aesthetically appealing images presenting empirical data help to communicate the importance of species interconnectedness and ecosystem complexity to the broader public. Visualisation tools facilitate incorporating real-world examples in education.

Keywords— food web, network visualisation, ecological network, animated flow network, interactive graph, trophic level, flow matrix heatmap

1 Introduction

Food webs describe how much matter flows between functional groups of species and how much matter these groups exchange with the environment. Food webs thus define the physical backbone of ecosystems depicting flows of energy and crucial elements.

One of the goals of food web modelling is to improve our perception of their structure. Here, a visual representation is beneficial for overall understanding and deeper analysis. However, visualisations greatly simplify the underlying object. They can assist a quantitative analysis, but can not deliver insights of the same strength. Their reception is subjective.

The inherent complexity of food webs makes them difficult to visualize. The earliest published examples were simple and easy to draw [Petersen, 1915, Egerton, 2007]. This is no longer the case, as many contributions cover eighty or more nodes. With a growing number of species and flows, such networks become less transparent and harder to grasp.

A successful visualization reconciles two basic needs. First, it provides a suitable overview of the system, offering a quick and clear understanding of general patterns. Second, it allows getting into necessary details and peculiarities.

In most cases, unfortunately, food webs illustrated as traditional graphs fail to deliver either of these features. The restriction to two-dimensional screens and papers means that in more complex graphs the intersecting links introduce additional ambiguity. A large and dense food web loses intelligibility even for unweighted networks where links signify only the existence of interaction, neglecting its strength. In dense networks of 50 nodes and more, people have difficulties even with relatively basic tasks. Physiological observations [Yoghourdjian et al., 2021] established that for finding the shortest path between nodes. Systematic studies of network layout clarity have begun with [Noack, 2007], and [Venturini et al., 2021]. In the future, they might offer guidance in optimising network layouts. Various graph visualisation types and their

applications were described in [Pocock et al., 2016].

Weighted food webs strongly differ from their unweighted simplifications [Scotti et al., 2007].

The flow values in real-world networks can span up to ten orders of magnitude [Okey et al., 2006].

This large hierarchy is an opportunity to see the most important nodes and relations. It makes presenting the information graphically even more difficult though. Successful visualizations of small networks illustrate this scaling well [Banašek-Richter, 2004]. The same principle that succeeded there, fails to offer any clarity in food webs with greatly varying levels of aggregation of species [Hinke et al., 2004].

Several existing visualisation packages plot food webs. The Food Web Designer [Sint and Traugott, 2015] uses colour, link width, and vertical arrangement of nodes into trophic layers. However, its limitation to three layers does not suffice for real-world food webs. Trophic levels are easily higher than four and modern visualisations should be able to deal with fractional trophic levels, too.

Network3D/Webs on the Web [Yoon et al., 2005] employed the third dimension and hierarchy dictated by trophic level to disentangle structural properties of dense food webs. However, it dealt only with unweighted networks and is not publicly available anymore. Moreover, it struggled with the clarity of food webs of just 40 nodes [Mendonça et al., 2018].

The Cheddar ecological community analysis package [Hudson et al., 2013] provided only generic network visualisation and did not aim at its clarity. Most importantly, its figures focused on showing patterns rather than making individual nodes identifiable.

The Python programming language is convenient for scientific applications. Our interactive visualisations rely on IPython [Perez and Granger, 2007] and Jupyter [Kluyver et al., 2016]. Other Python libraries make embedding them in comprehensive scientific analyses possible. Numpy [Oliphant, 2015] facilitates numerical computations, scikit-learn [Pedregosa et al., 2011] offers an array of statistical and machine-learning tools. As a multi-purpose language with an

intuitive syntax Python stands out from alternatives, such as Java, C++, and R, by greatly reducing programming time.

In what follows we will introduce and explore five well-structured methods of weighted food web visualization, combined as a Python package. This not only facilitates manipulation and visualization of such networks but offers the benefits of modularity and ease of customization. The first method represents a food web as a heatmap, inspired by the 'matrix' method of [Pocock et al., 2016]. It is suitable to present all flows of matter at once while retaining their precise identification. Flows can be normalised, to present e.g. diet fractions.

The second method provides an interactive graph visualization. We highlight the trophic level hierarchy by vertical node positions and optimise their horizontal coordinates for clarity. We thus combine two approaches known in general network analysis, called "weighted parallel coordinates" and "force-directed" in [Pocock et al., 2016].

The third function creates a particle flow animation. The particle densities reflect the differences between the flow magnitudes, while their movement helps the eye to identify the nodes they connect. Particle colours represent the source node trophic level. The sizes of nodes map the biomass stocks of the groups of organisms they represent.

The last two methods show a simple overview of the network. A stacked bar plot displays a percentage distribution of flows from one trophic level to another. A heatmap uses colours to visualize the sum of all flows between trophic levels.

The understanding of the strong interdependence of organisms in ecosystems through better knowledge of food webs will also benefit the broader public. In education, the concept of trophic chains could be replaced by a more realistic treatment of actual food webs. Proper visualisations of empirical food webs could greatly help in creating lasting mental images. The simplistic picture of linear predator-prey chains leads to an implicit misconception about their isolation. The path of an individual carbon atom through the ecosystem is very complex. Each of the

involved actors indirectly influences all others. We feel that proper visualizations of real-world food webs are urgently needed in popular science and education.

The rest of the paper is organized as follows. Section 2 defines food webs in quantitative terms. In Section 3 we propose methods of food webs visualization and explain how they solve the most common problems. We conclude the article with a discussion of limitations and future outlook (Section 4).

2 Materials and methods

A food web represents an ecosystem as a collection of species or functional groups of species (nodes) connected by feeding relationships. Flows of biomass are most commonly expressed in the units of the total wet or dry weight, or mass of carbon. Phosphorus and nitrogen are other important flow currencies.

Mathematically, a food web is a weighted and directed network (graph) of n nodes, characterized by their biomass stocks $b_i : i = 1, \dots, n$. The nodes are subdivided into living and non-living (detrital). Flow (link) F_{ij} from node i to node j represents consumption (predation), as well as egestion and mortality going to detritus. Nodes also exchange matter with the environment. The associated flows are represented as imports, exports, and respirations.

The trophic level [Odum and Heald, 1975] of a node i is defined as:

$$\tau_i = \begin{cases} 1 & \text{for non-living (detrital) nodes, or if } \sum_{k=1}^n F_{ki} = 0 \\ 1 + \sum_{j=1}^n \frac{F_{ji}}{\sum_{k=1}^n F_{ki}} \tau_j & \text{for other nodes.} \end{cases} \quad (1)$$

The open-source *foodwebviz* Python code is available at: <https://github.com/ibs-pan/foodwebviz> and [Pawluczuk and Iskrzyński, 2022]. It is implemented in an object-oriented manner which supports modularity and ease of customization. The food web class is wrapped around networkx [Hagberg et al., 2008] library. The visualisation methods rely on plotly [Plotly,

2019] and pyvis [Perrone, 2015] libraries. The package reads food webs from text files in SCOR format [Ulanowicz and Kay, 1991, Borrett and Lau, 2014], as well as from CSV or XLS files.

Our methods return figure objects which can be further adjusted to users' needs.

We include a few published empirical weighted food webs: Prince William Sound, Alaska [Dalsgaard et al., 1997], carbon, nitrogen and phosphorus networks of the continental shelf north of Richards Bay, South Africa [Scharler et al., 2016], the cypress wetland ecosystem, Florida [Ulanowicz et al., 1997], and the Chesapeake Bay mesohaline carbon network [Baird and Ulanowicz, 1989]. Further examples might be added and appropriately referenced in the future development of the package.

3 The five visualisation methods of *foodwebviz*

Here, we introduce five visualization methods optimized for weighted food webs. These methods are designed to show different perspectives with varying levels of detail.

3.1 Heatmap of network flows

The heatmap method allows a general overview of the whole network. It enables also a detailed inspection of individual flows through an interactive interface.

Fig. 1 shows a sample visualization created using this method. The heatmap representation of a food web has the network's nodes on its axes, sorted according to their trophic level. The colour intensity represents the biomass flow from the node in the row to the node in the column. Additionally, trophic levels related to the nodes are shown as the background colour. Tooltips visible in an interactive notebook contain information about the exact flow values. The user can also zoom to the area of interest.

Parameters of this method allow for several customizations. First of all, the user can decide

whether to include boundary flows, which are external imports, exports, and nodes' respiration values. Second, the heatmap biomass flows can be normalised e.g. to the total inflows (to show diet proportions) of the target node, or to the biomass of the source node (as in a donor-control model), or to the sum of all flows in the network (total system throughflow, TST). The available normalization options are presented in Table 1. Third, there is a possibility to interchange the axes. Lastly, nodes' trophic levels can be hidden.

Normalisation	Description
log	logarithm of the original weight
diet	each weight is divided by the node's sum of input weights
donor_control	each weight is divided by the biomass of the source node
predator_control	each weight is divided by the biomass of the target node
mixed_control	each weight is divided by the product of the biomasses of the source and target nodes
linear	each weight is shown unmodified
TST	each weight is divided by the sum of all weights in a network

Table 1: Normalization methods available for interactive heatmaps in *foodwebviz* package.

3.2 Network as a graph

A natural way of representing graphs (networks) is just to draw the nodes connected by links. To improve clarity, we present them in an interactive, adjustable form. To highlight the structure of food webs, we represent the node's trophic level through its vertical position and label colour.

A static result is shown in Fig. 2.

When drawing graphs, clarity demands adjusting node positions to minimize clutter and

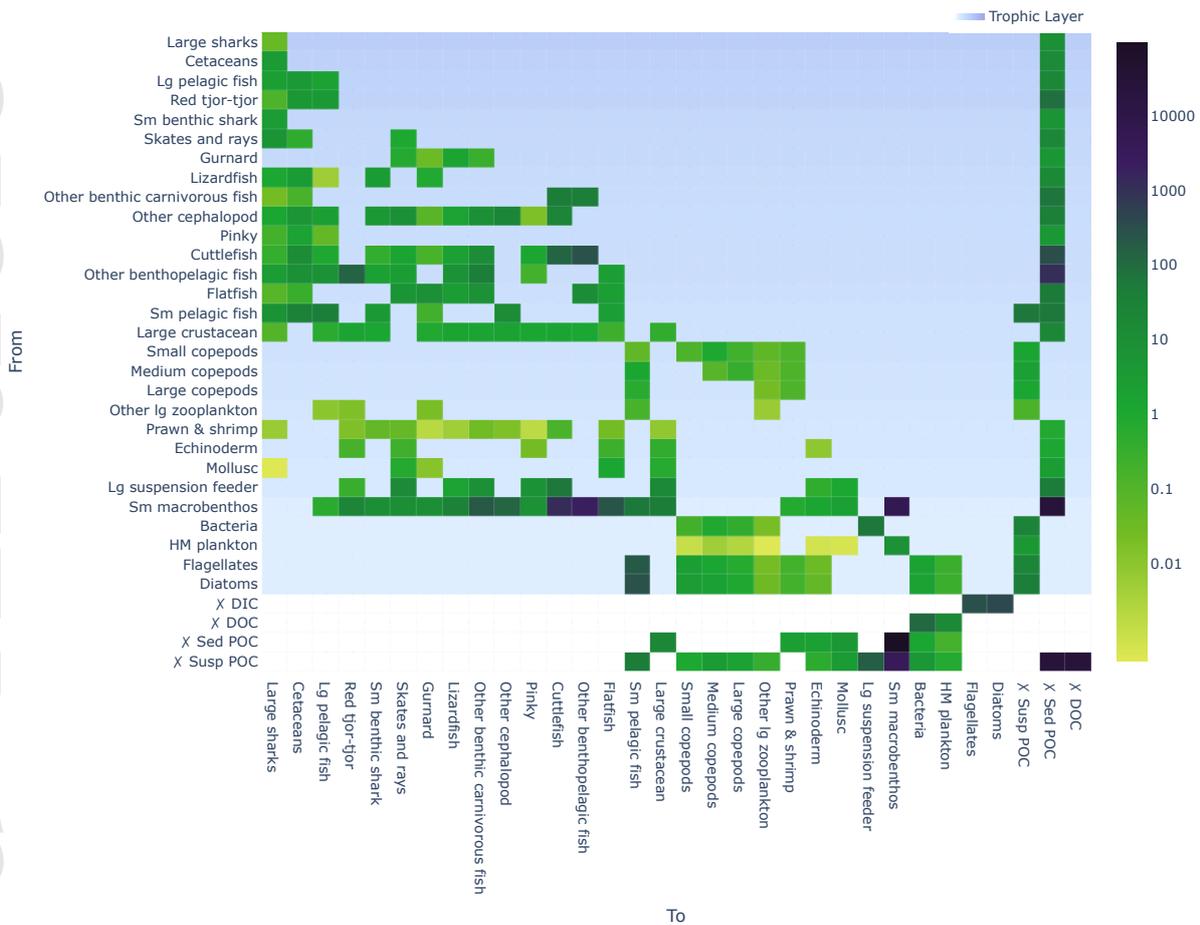


Figure 1: Carbon flows in Richards Bay [Scharler et al., 2016], South Africa, represented as a heatmap. Colour intensity represents the biomass flow from the node in the row to the node in the column. Species are ordered according to their trophic level, indicated by the background colour.

overlap of nodes and links. A hierarchical repulsion algorithm uses an analogy with a physical system: nodes repel each other and links act as springs. This algorithm is used to optimize the horizontal positions of nodes and the user can adjust its parameters. The user can zoom, and manually move nodes, e.g. to move between positions that are stable under the automatic

algorithm.

As graph visualization is not feasible for large and dense food webs, we argue that this method is suitable for exposing smaller parts of the network. Therefore, the method's parameters allow selecting nodes that should be included in the visualisation. This way one can track chains of subsequent flows, as well as view neighbourhoods of particular nodes. This complements the heatmap, suitable to expose all flows in the network.

3.3 Animated flow network

An animated graph intuitively presents matter moving in a trophic network. Fig. 3 shows a snapshot of the animated Richards Bay food web [Scharler et al., 2016], containing 33 nodes. The movement of particles helps to visually identify their source and target, granting an advantage over the conventional static representations.

The density of particles moving between nodes encodes the food web flows, and node sizes map the biomass stocks. The exact map used to squeeze many orders of magnitude of flows to smaller, more practical intervals can be specified by the user as an optional argument. The default map is based on the square root function. We found this transformation exposes the many orders of magnitude differences among flows better than e.g. the logarithm. For clarity, we chose to plot only the flows ending at living nodes. Every living node respire and has a mortality/egestion flow going to detritus. Drawing all these flows typically does not add much structural information compared to the space they occupy.

Nodes are coloured according to their trophic level. Flow particles carry the colour of their source node, which enhances clarity. The user can adjust the range of node sizes, numbers of particles, the length of the animation, decide whether to draw imports and exports.

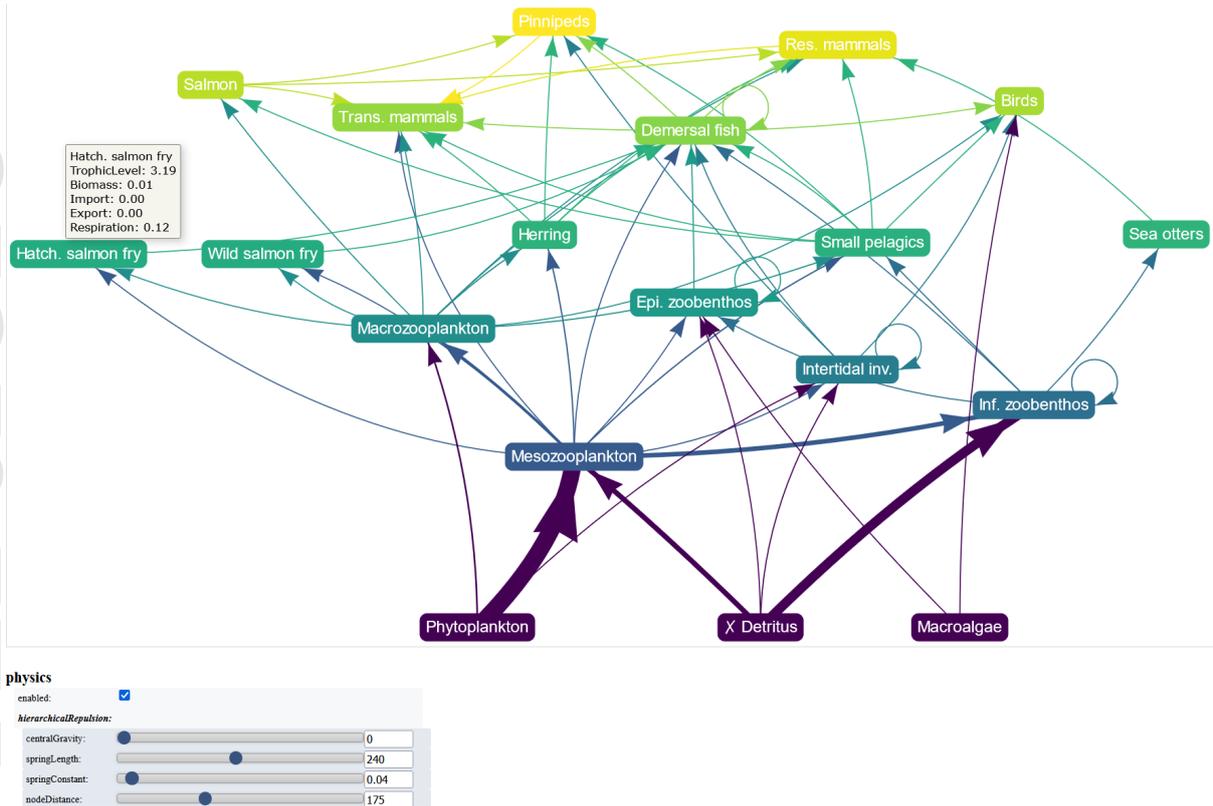


Figure 2: A screenshot of the interactive graph of the whole food web of the Prince William Sound, Alaska [Dalsgaard et al., 1997]. Hovering over one of the 19 nodes displays additional information about them. Nodes are coloured according to their trophic level. The arrow width is proportional to the logarithm of the flow. A control panel allows for adjustment of the parameters for the horizontal node placement algorithm. Nodes can also be moved manually.

3.4 Distribution of trophic level flows

One can aggregate nodes into integer trophic levels to summarize certain aspects of a food web. A stacked bar plot shows percentages of system flows from one such trophic layer to another, as presented in Fig. 4. colour bars and numbers indicate the flow distribution around each trophic level, marked on the Y-axis.

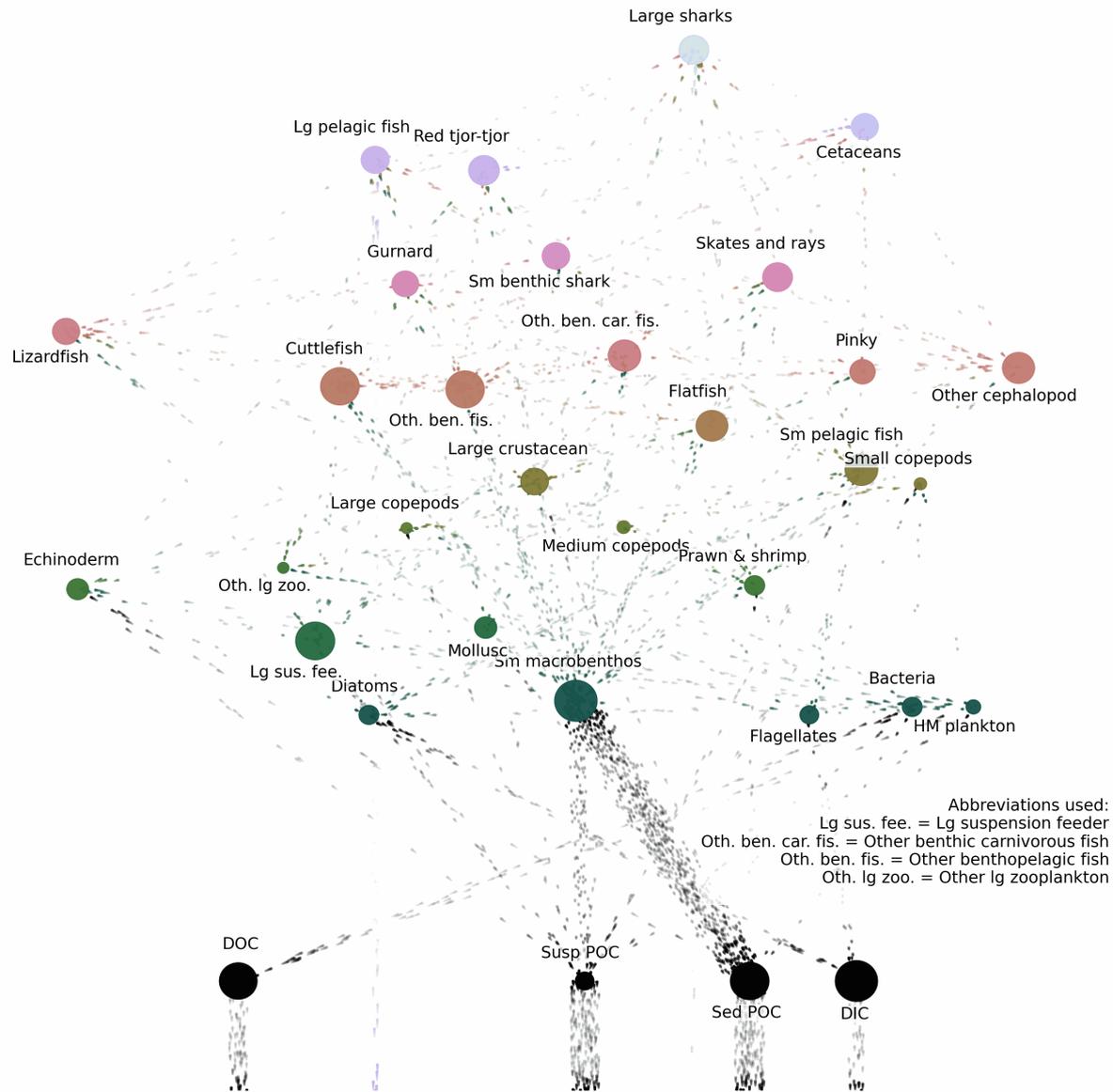


Figure 3: A frame from the animated food web of Richards Bay, South Africa [Scharler et al., 2016]. The density of moving particles maps flow magnitudes and node sizes encode the biomass stocks. Only flows to living nodes are shown. Imports from the environment enter from the figure bottom. Colour and vertical position represent the trophic level of a node. Particles carry the colour of their source node.

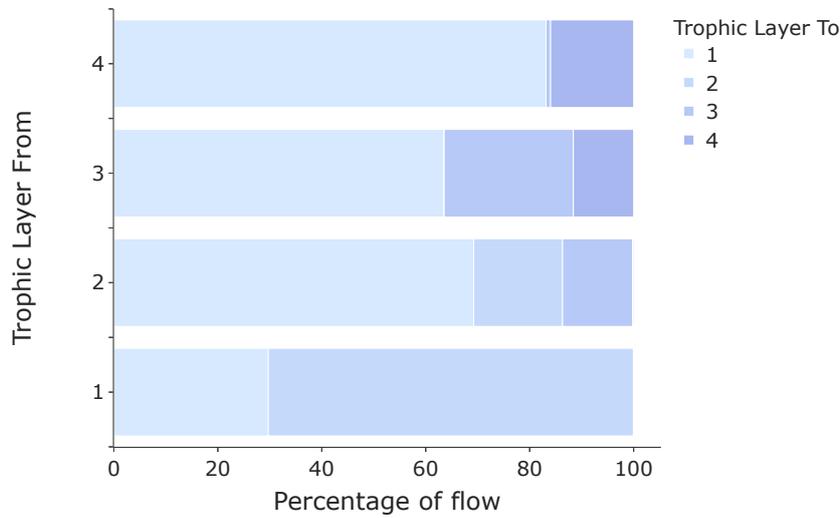


Figure 4: The percentage distribution of flows exchanged between the trophic levels of the Richards Bay [Scharler et al., 2016] food web. Each bar shows flows leaving a trophic layer. Colour marks the target trophic layer.

3.5 Heatmap of trophic level flows

Similarly, a heatmap visualization of flows between trophic layers gives a summary of the network at a glance (Fig. 5). The colour of cells maps the sum of all flows between integer trophic levels placed on the axes. A logarithmic scale is available. This method complements the bar plot.

4 Discussion

Two-dimensional screens and paper limit the clarity of all visualisations of dense networks, such as food webs. Adding another dimension can partly alleviate this problem. Three-dimensional

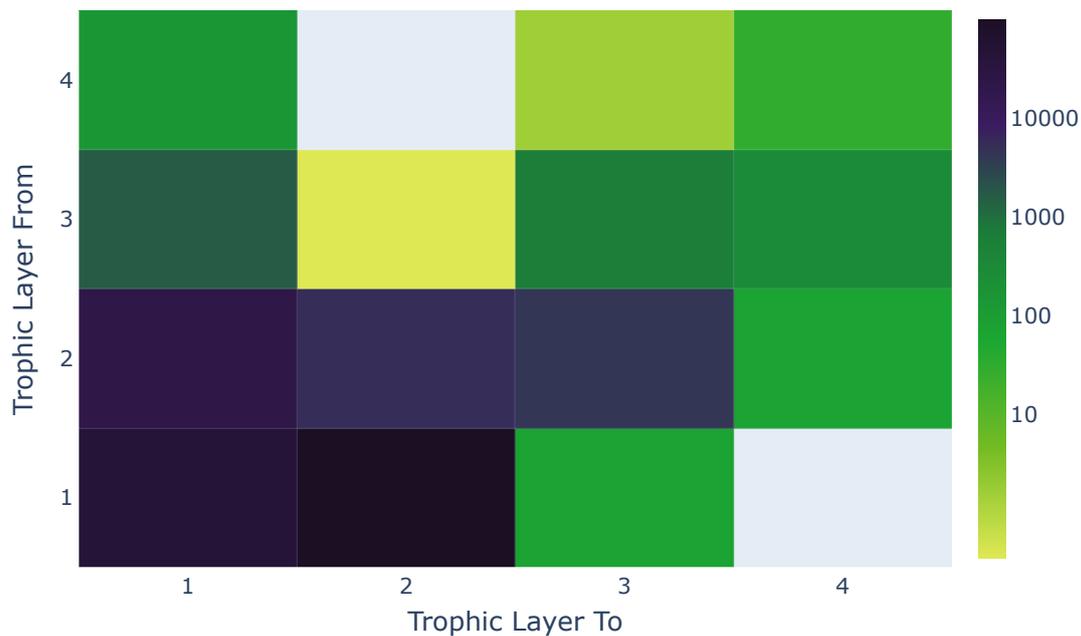


Figure 5: Flows between Richards Bay [Scharler et al., 2016] food web trophic levels represented as a heatmap.

representations of networks [Yoon et al., 2005] added depth. We take advantage of time, combining images in animations and allowing users to tinker with interactive graphs, zooming, selecting, and moving their parts. However, these solutions only shift the issue of clarity towards higher densities and numbers of nodes. If a network is too large, a graph visualisation is suitable for exposing smaller parts of the network rather than its entirety.

We expect the range of tools provided in the package will fit various modeller’s needs. The flow heatmap is useful at all research stages, from the first food web overview to double-checking the links of specific nodes. The interactive graph is a natural tool for exposing a subnetwork of interest. Animated food webs may prove especially valuable in engaging the general public and in education thanks to their aesthetic appeal.

The particle flow animation can be further modified to illustrate mass conservation and cycling in ecosystems. The challenge lies in the big hierarchy between flow magnitudes, which makes it impossible to retain a linear relationship between the flow and the number of particles. Thus, mass conservation within e.g. an order of magnitude could be presented for a simplified subnetwork. In the most general case, mortality and egestion further obscure the whole picture.

Programmatical visualisations do not optimally draw all networks, even if they are acceptable in a typical case. This guided us in developing *foodwebviz* as a versatile and customisable tool the user can tinker with to reach the desired effect.

5 Author contributions

LP wrote the heatmap, interactive graph and barplot methods; was responsible for the code integrity and contributed to writing the manuscript. MI designed the methodology, wrote the animation and took the lead in writing the manuscript.

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7 Conflict of interest

The authors declare no conflicts of interest.

8 Data availability

The source code together with a tutorial and examples of visualisations is freely available at <https://doi.org/10.5281/zenodo.6201935> [Pawluczuk and Iskrzyński, 2022] under the BSD 3-Clause license. For a more detailed software description, see Section 2.

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