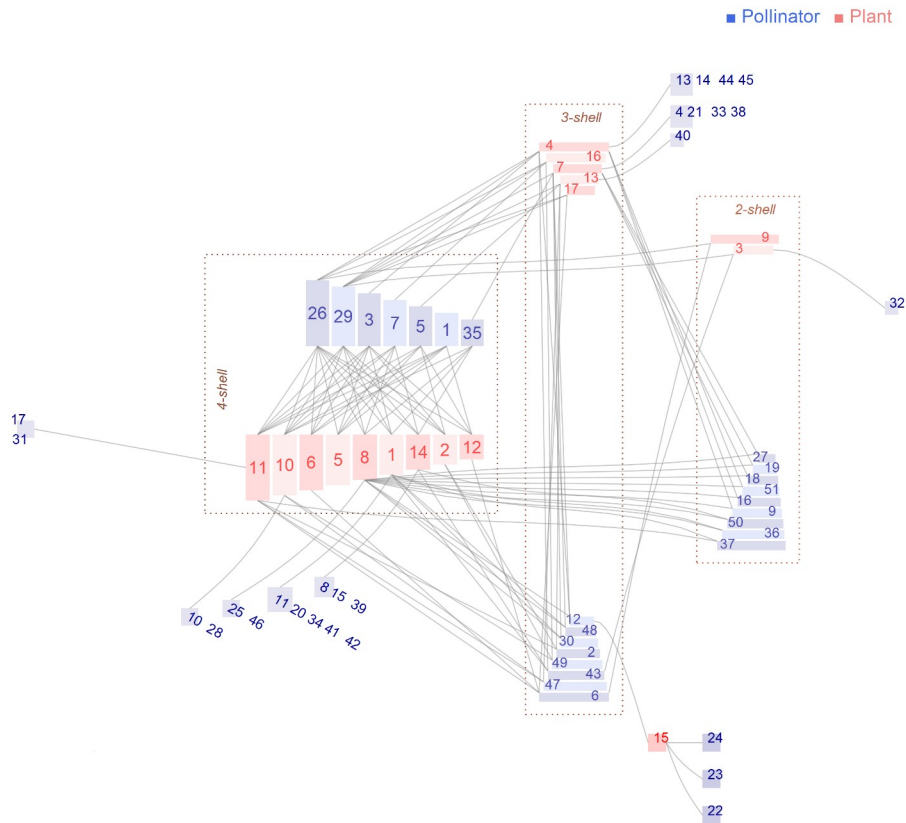


BipartGraph

Network: M_PL_039



User Guide

R2.0 April 2025

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Contents

1 Introduction.....	4
2 Installation.....	5
2.1 Fast-track, install and use BipartGraph with Docker.....	5
2.2 Requirements for native install.....	6
2.3 First step: download the software.....	6
2.4 Second step: install R.....	7
2.5 Third step: setting up the application.....	9
2.6 Installation on Linux.....	11
2.7 Running <i>BipartGraph</i>	12
3 Data management.....	13
4 The ziggurat plot.....	15
4.1 Explore the interactive ziggurat.....	18
4.2 Modifying the look and feel of the ziggurat plot.....	19
4.3 Printable ziggurat.....	26
5 The bipartite plot.....	29
6 The matrix plot.....	31
7 The polar plot.....	33
Figure 37: Polar graph of a plant – pollinator in Garajonay (Spain), including labels and histograms. Compare with fig. 26.....	34
Useful hacks.....	35
References.....	35

1 Introduction

BipartGraph is an interactive application to visualize bipartite ecological networks, using the *k*core decomposition method [1,2].

The most common visualization of this kind of network is the bipartite graph. It underlines the existence of two communities, but links among species are difficult to distinguish even with a reduced number of nodes. When the size of the network grows, the graph becomes a *hairball*, an expression common in visualization for messed plots (fig. 1).

It is an exercise of graphical intuition to identify the central core and almost impossible to guess the centrality of species. As a result, it is uncommon to find plots of networks with more than a dozen species per guild in the research literature, although typical mutualistic networks are larger. This problem is not due to a lack of skills of the user, it is a limitation of the graph itself.

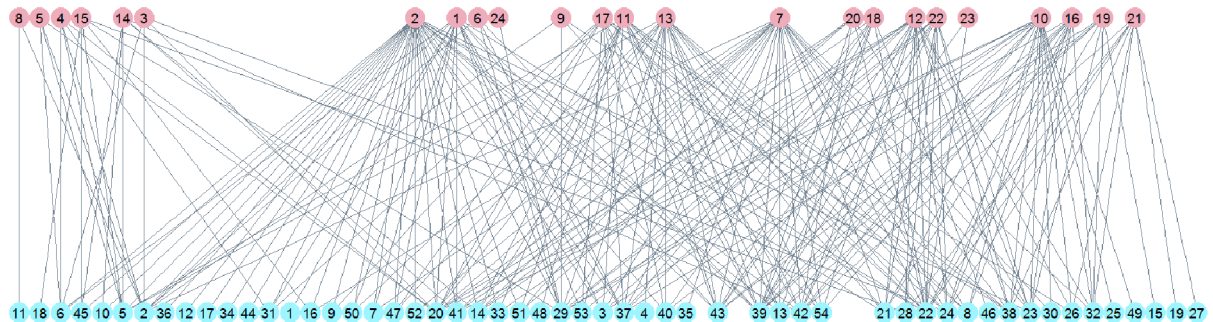


Figure 1: Bipartite graph of a mutualistic community with 78 species [3].

The *k*-core decomposition offers a natural way to group species with similar connectivity and so it enables a more powerful spatial distribution.

You do not need to be an expert in analysis of graphs to enjoy this program, just install it and start playing with the different options.

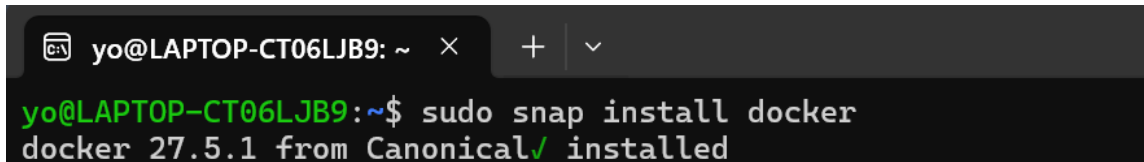
2 Install BipartGraph

BipartGraph is an interactive application developed in R language. Either if you are familiar with R, or if you have never worked with R or with any other programming language at all, this document guides you step by step through the installation procedure.

2.1 Fast-track, install and use BipartGraph with docker

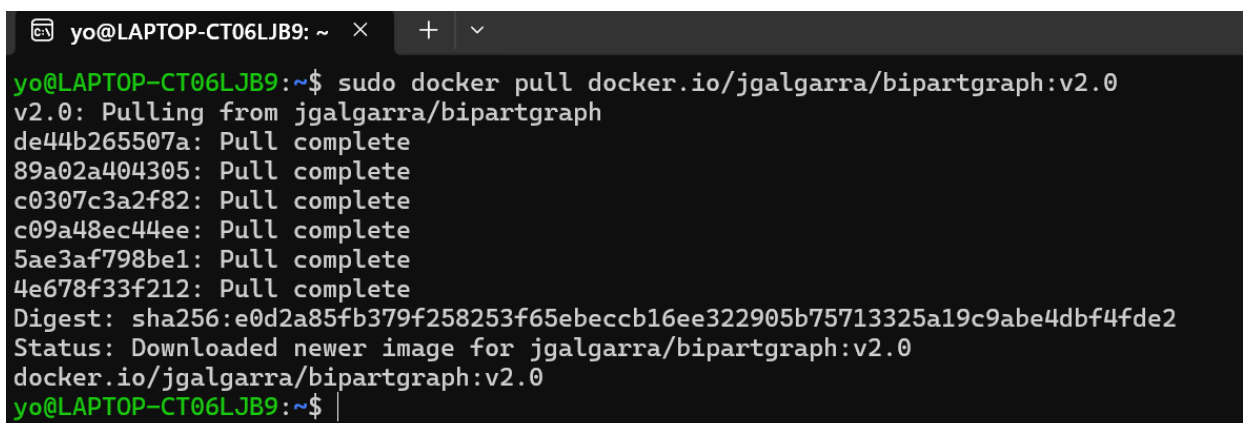
Installing a docker image of BipartGraph is the easiest way to run the application. First you need to install docker, the provider documentation is excellent <https://docs.docker.com/engine/install/ubuntu/> (or any other Linux distro). If you are using Windows, you can use the Windows Subsystem for Linux (WSL) following the instructions at <https://learn.microsoft.com/en-us/windows/wsl/install>.

From the command line install `docker` typing:



```
yo@LAPTOP-CT06LJB9: ~ × + v
yo@LAPTOP-CT06LJB9:~$ sudo snap install docker
docker 27.5.1 from Canonical✓ installed
```

Once you have installed `docker`, download the BipartGraph image.



```
yo@LAPTOP-CT06LJB9: ~ × + v
yo@LAPTOP-CT06LJB9:~$ sudo docker pull docker.io/jgalgarra/bipartgraph:v2.0
v2.0: Pulling from jgalgarra/bipartgraph
de44b265507a: Pull complete
89a02a404305: Pull complete
c0307c3a2f82: Pull complete
c09a48ec44ee: Pull complete
5ae3af798be1: Pull complete
4e678f33f212: Pull complete
Digest: sha256:e0d2a85fb379f258253f65ebecb16ee322905b75713325a19c9abe4dbf4fde2
Status: Downloaded newer image for jgalgarra/bipartgraph:v2.0
docker.io/jgalgarra/bipartgraph:v2.0
yo@LAPTOP-CT06LJB9:~$ |
```

BipartGraph is now ready to run. The following command launches the application:

```
yo@LAPTOP-CT06LJB9: ~ × + v
yo@LAPTOP-CT06LJB9:~$ sudo docker run -p 127.0.0.1:8080:8080 docker.io/jgalgarra/bipartgraph:v2.0 &
[1] 2999
yo@LAPTOP-CT06LJB9:~$ |
```

You can avoid typing it each time you launch the application saving it as a shell script file.

```
sudo docker run -p 127.0.0.1:8080:8080 docker.io/jgalgarra/bipartgraph:v2.0
# Uncomment to open your browser automatically
# firefox 127.0.0.1
```

If you are running docker on your WSL subsystem and want to connect from your Windows browser, or if you installed the docker image on a server machine and want to connect from a client, then open manually your browser and type <http://127.0.0.1:8080> to find BipartGraph up and running.

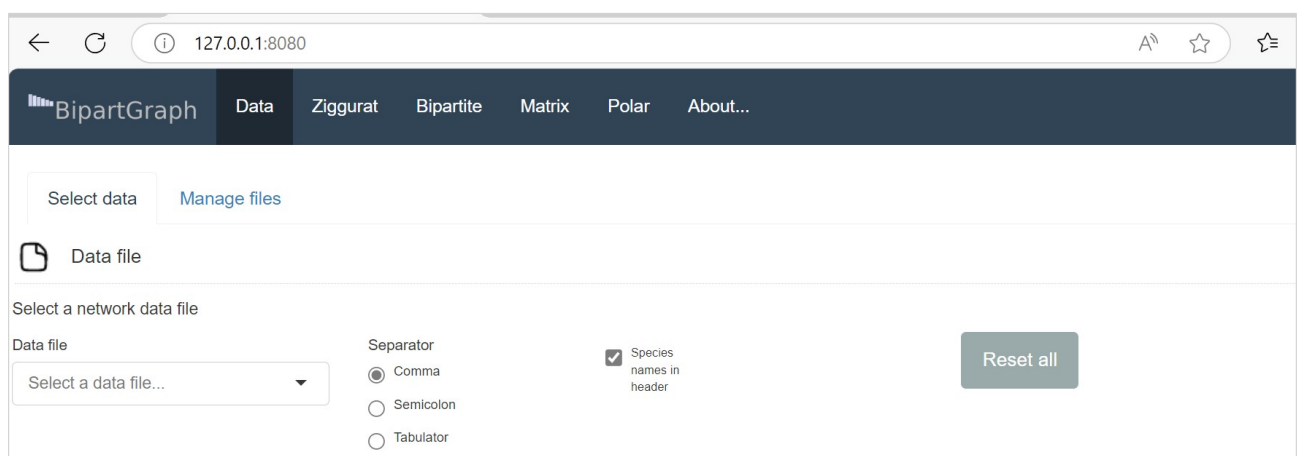


Figure 2: *BipartGraph* user interface

Skip the following sections and go straight to 2.7

2.2 Requirements for native installation

There are only two requirements to install *BipartGraph*, a working R environment and any web browser (*Firefox*, *Chrome* or *Safari* if possible). We recommend at least 8 GB of RAM in your machine. R is an open source project, you will find the download and installation instructions for different operating systems at <https://cran.r-project.org/>

2.3 First step: download the software

Bipartgraph is available as open source software under MIT license in github. Open your browser and type : <https://github.com/jgalgarra/bipartgraph>

Notice the green button **Clone or download** that provides two ways to get the software (Fig. 3).

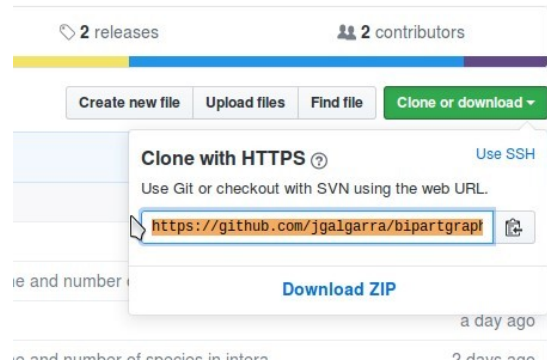


Figure 3: BipartGraph repository at github.com

First one is using git, the control version tool (<https://git-scm.com/>). If you know how git works just clone the jgalgarra/bipartgraph repository.

```
> git clone https://github.com/jgalgarra/bipartgraph
```

A new directory called bipartgraph appears. This is the recommended method, because at any time you may update your local software with the git pull command.

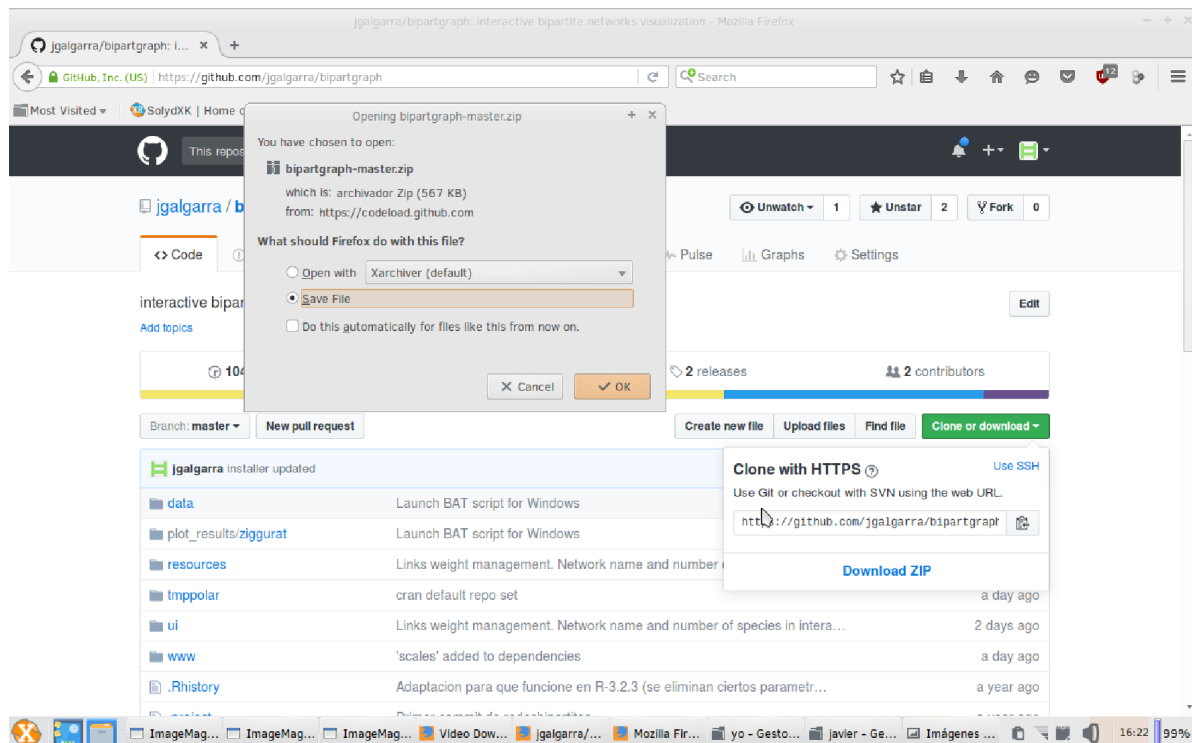


Figure 4: Downloading the BipartGraph ZIP file

What if you are not a software developer and do not want to install `git`? Download the ZIP file instead (fig. 4), uncompress it, and you will see a new directory called `bipartgraph-master` with the same contents as the original repository.

2.4 Second step: install R

You need the release `R 4.3.0` or later. If you have never installed R, pick the last available release from the download page, it will be fine for this purpose.

A) Windows

Figure 5 shows the installer program. *Your attention please!* The installation program will suggest a path. **Do not change it unless you are sure of what you are doing.** For instance, in Windows systems, volume `C:` is usually restricted to users with administrator privileges. Let the R installer to choose the best location for your user. Please, write the name of the installation folder somewhere (the notepad is a good choice), because you need it for the next step.

Once you install R, check that it is ready to run. What does this mean? If you type `R` in the command line the application starts. If you are a Windows user, it is rather probable that you get this disappointing message: `R is not a recognized command as an internal or external command.`

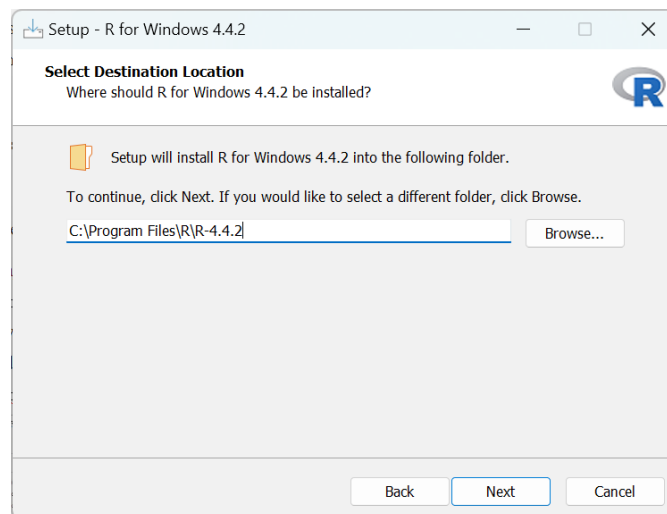


Figure 5: Installer program for Windows. The name of the installation folder is important to set the PATH variable in Windows.

There are two methods to overcome this problem in Windows:

1. **Simple and safe.** Go to the directory where you installed `bipartgraph`. Select the file called `global`, right click and select “Open with” and then “Choose another app” (the option name may be slightly different, this screen was captured in Windows 11). Navigate to the installation folder that you wrote in your notepad. Inside this folder click on the `bin` folder and then select `Rscript`.

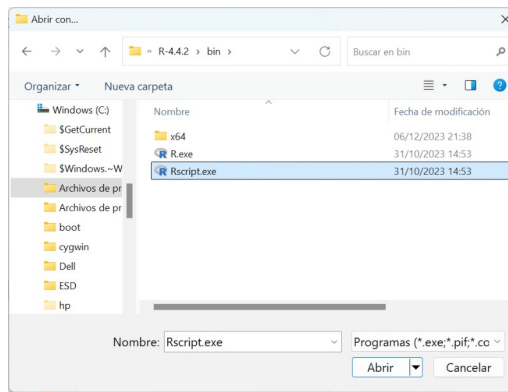


Figure 6: Choose Rscript.exe to run the .R files

After you perform this action the R icon is displayed by the name of the scripts.

2. Include the R bin folder in the path variable. In the example of figure 5, it is C:\Program Files\R\R-4.4.2\bin. You must add \bin to the name of the installation folder you copied in the notepad. To modify the value of the variable Path in Windows we suggest you this useful page, the procedure depends on the release <http://www.dowdandassociates.com/blog/content/howto-set-an-environmentvariable-in-windows-gui/>.

B) UX like systems (including Linux an MacOS)

For Debian-based distributions there is a detailed set of instructions if you find problems installing R 4.3 or later. Check section 2.6 and then come back.

Figure 7 is a screen capture of your terminal after launching R.

```
yo@LAPTOP-CT06LJB9: ~$ R

R version 4.3.3 (2024-02-29) -- "Angel Food Cake"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Figure 7: Launching R from the command shell. The release number (4.3.3 in this example) appears in the first row of information.

2.5 Third step: setting up the application

Once you have downloaded and uncompressed the ZIP file from `github.com` or performed a `git clone` of the `bipartgraph` repository, the software is ready for the final set up. Move to the `bipartgraph` directory (`bipartgraph-master` if you installed from the ZIP).

A) Windows

Double-click on `install_bipartgraph.R`. If you have set up R in your Path variable you may also install from the Windows command line or PowerShell typing:
`Rscript install_bipartgraph.R`

B) UX like

Type in the terminal:

```
Rscript install_bipartgraph.R
```

The installation procedure is very fast in Windows because all packages are precompiled. In Linux it may take several minutes because your machine will compile several packages. Please, be patient and do not close the terminal until the procedure finishes.

Workaround

Depending on your user privileges, `install_bipartgraph` may fail in Linux if the current user has no permission to write in the package directory. If so and only if so, type instead:

```
sudo Rscript install_bipartgraph.R
```

C) Final Check

Once the script finishes, the procedure is done. Check that everything was installed properly. Open a new terminal (or command line), go to the `bipartgraph` directory, or `bipartgraph-master` if you installed from the ZIP file. Double-click on the `plot_test.R` (Windows) icon or type in the command line (UX like): `Rscript plot_test.R`

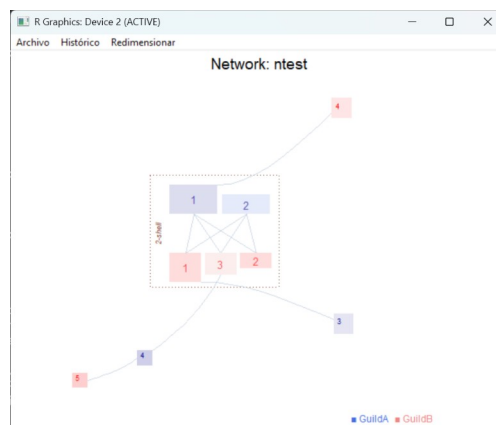


Figure 8: Result after running the script `plot_test.R`

Can you see a window with figure 8? If so, the installation ended successfully.

2.6 Hacks for installation on Linux

This section explains how to overcome common problems when installing Bipartgrah on a Debian based Linux. With minor modifications is valid for any other distro.

You need a gcc compiler in your machine. If you are a developer and you have got it, kcorebip will install smoothly. Otherwise, you will get a message telling that Rtools is not available. In that case follow the instructions of the following page to install Rtools:

<https://cran.r-project.org/bin/windows/Rtools/>

Run the script linux_dependencies

```
> sudo sh < linux_dependencies
```

This script downloads and installs the R runtime environment and the libraries to compile dependencies. Run this command to install the gcc compiler

```
> sudo apt install build-essential
```

DOWNLOAD ZIP from <https://github.com/jgalgarra/bipartgraph> (then UNZIP and let "bipartgraph-master" folder on any path of your user home; go to that folder) or `git clone` the repository and go to the "bipartgraph-master" folder.

```
> Rscript install_bipartgraph.R
```

If you get... "This is the end, my friend. Installation completed", everything went OK :-)

You can check that installation is fine with the following command:

```
> Rscript plot_test.R
```

2.7 Running *BipartGraph*

The application is now ready to run. If you are running *BipartGraph* with docker read section 2.1. Otherwise, launch the script double clicking on `bipartgraph.R` icon (Windows) or write in the command line (UX like):

```
Rscript bipartgraph.R
```

Your default web browser will open a new tab with a local URL. If everything went right you have reached the landing page.

Click on **Data** (main menu) and then click on the **Data** file box and select `M_PL_008.csv`. Click on the **Interactive Ziggurat** tab (main menu) and you will see the network plot of figure 9.

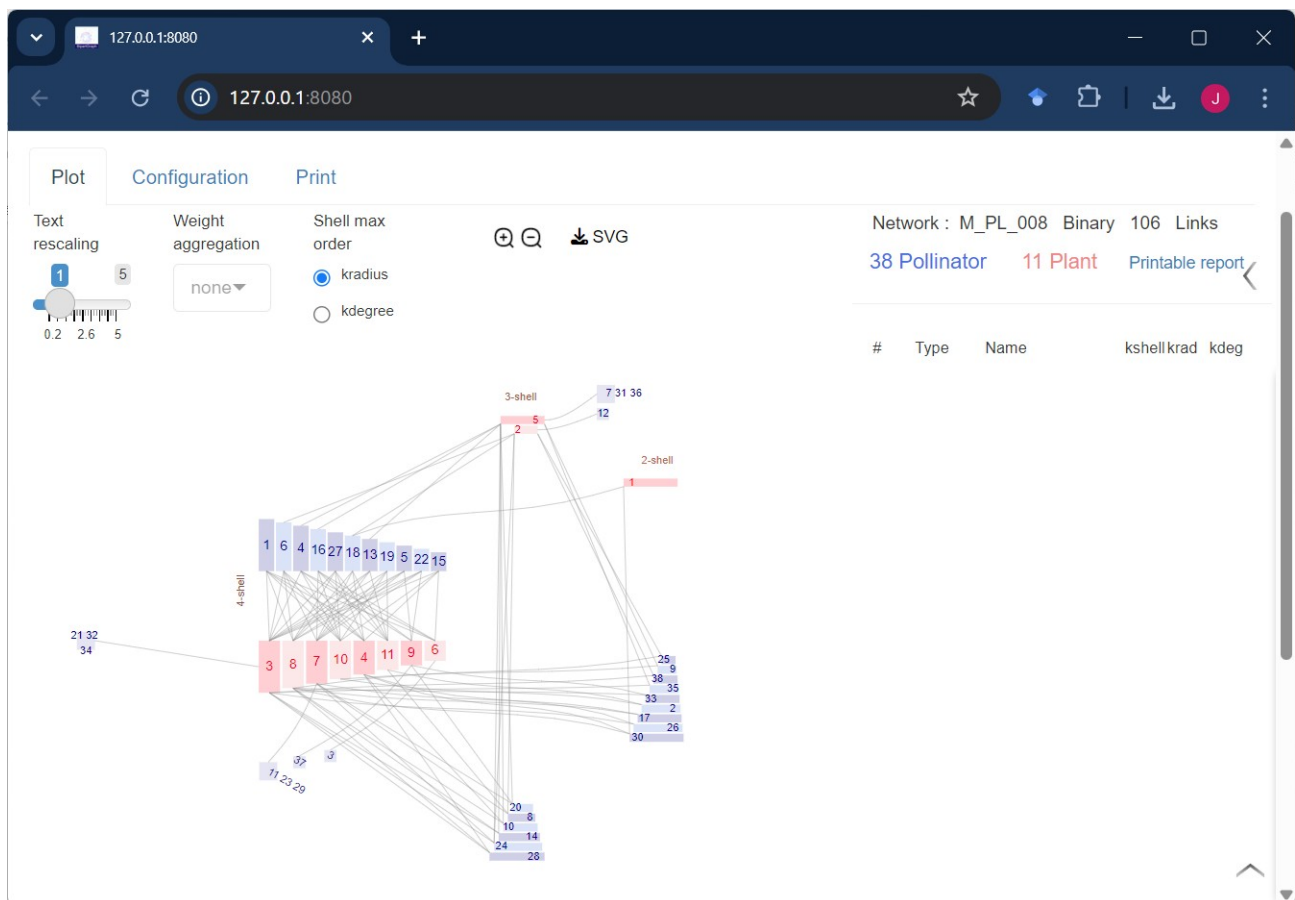


Figure 9: Ziggurat plot

3 Data management

BipartGraph is a tool to plot bipartite ecological communities, but you may use it with any kind of bipartite network. In this guide we use examples of mutualism and parasitism that are well documented in the [web of life_database](#) [4].

	A	B	C	D	E	F	G	H	I	J
1		Echium wildpreti	Pimpinella cubrae	Pterocarpus lasiospermus	Mentha longifolia	Erysimum scoparium	Spartocytisus supranubius	Tolpis webbia	Argyrenthemum teneriffae	Scrophularia
2	Anastoechus latifrons	1	0	0	1	0	1	1	0	0
3	Anthophora alluaudi	1	0	0	1	0	1	0	0	0
4	Apis mellifera	1	1	1	0	1	1	0	1	1
5	Eudynesus reflexus	0	1	0	1	0	1	1	0	0
6	Geron hesperidion	0	1	1	0	1	0	1	1	1
7	Enstalis tenax	1	1	1	1	0	0	1	0	0
8	Megachile canariensis	1	0	1	0	1	1	1	0	0
9	Anthrax anthrax	1	1	1	0	0	1	0	0	0
10	Eucera gracilipes	1	0	0	0	1	1	0	0	0
11	Hylaeus canariensis	1	1	0	0	0	1	1	0	0
12	Lasioglossum viride	1	1	1	0	0	0	0	0	0
13	Limnaemyia soror	1	1	0	1	0	0	0	0	1
14	Cephalodromia sp1 M_PL_008	0	1	0	0	0	0	1	1	1
15	Cyclirius webbiana	0	0	1	1	1	0	0	0	0
16	Estheria simonyi	1	0	1	1	0	0	0	0	0
17	Lasioglossum actifrons	0	1	0	1	0	0	0	0	0
18	Melecta curvispinosa	1	0	1	0	1	0	0	0	0
19	Osmia canariensis	0	0	1	0	1	0	0	0	0
20	Andrena velleitoni	0	0	0	0	0	1	1	0	0
21	Colletes dimidiatus	0	0	0	1	0	1	0	0	0
22	Gasteropterus sp1 M_PL_008	0	1	1	0	0	0	0	0	0
23	Lucilia sericata	0	0	1	0	0	0	0	0	1
24	Macroglossum stellatarum	1	0	0	0	1	0	0	0	0
25	Scaeva albomaculata	0	0	1	0	0	0	0	0	0
26	Stomothina lunata	1	0	0	1	0	0	0	0	0
27	Unidentified sp1 M_PL_008	0	0	0	0	0	0	0	0	1
28	Anthidium manicatum	0	0	0	0	0	0	0	0	0
29	Bibio elmoi	0	0	0	1	0	0	0	0	0
30	Dermasothus gracile	0	1	0	0	0	0	0	0	0
31	Drosophila sp1 M_PL_008	0	0	0	0	0	0	0	0	1
32	Lasioglossum chalcodes	1	0	0	0	0	0	0	0	0
33	Leptochilus eatoni	0	1	0	0	0	0	0	0	0
34	Nyctia lugubris	0	1	0	0	0	0	0	0	0
35	Peleteria ruficornis	0	0	0	1	0	0	0	0	0
36	Phylloscopus collybita	1	0	0	0	0	0	0	0	0
37	Serinus canarius	1	0	0	0	0	0	0	0	0

Figure 10: Interaction matrix of network M_PL_008 [5]

Data are stored as .csv files. Fields are separated by commas, semicolons or tabs. The first row stores the binomial names of guild A species and the first column those of guild B. When you upload your own data, remember that the application waits to find that information there. If you do not have it, or it does not make sense at all in your environment, just type the numerical values and uncheck the option Name species in header when you select to analyze your network. BipartGraph will label species following the order in the input file. If the interaction matrix is binary, the cell of *species A* m; *species B* n will be set to 1. If it is weighted, to a positive real; 0 means that there is no link. We provide examples with the default installation software. To upload your own data, click on the Data tab of the main menu and then on Manage Files.

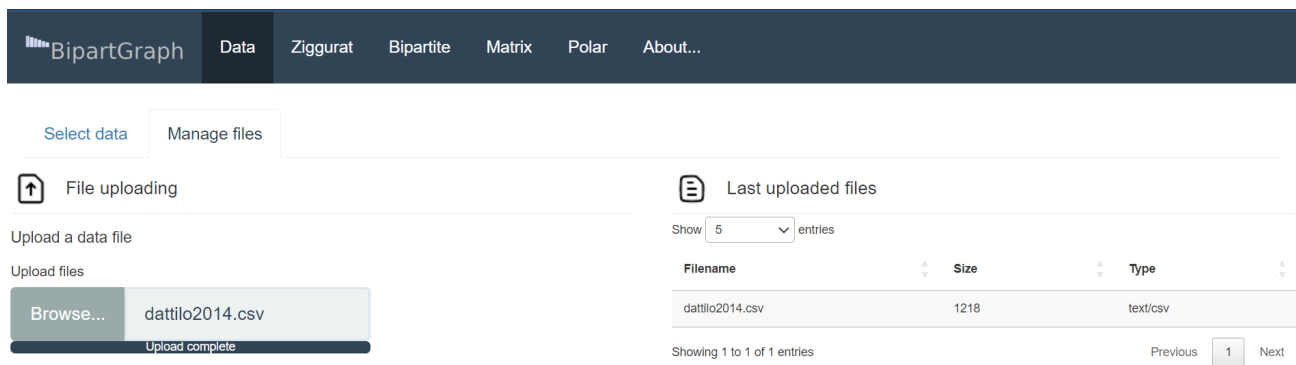


Figure 11: Uploading a file

Click again on **Select Data** and choose any file. The table shows the interaction matrix. You can change Guild A and Guild B labels, *BipartGraph* will remember the new ones next time you open the same file.

The **Network Anaylisis** button creates a .csv file with the individual *k-magnitudes* of all nodes. With **Reset all**, session restarts and all configuration parameters are set to their default values.

The **Species names** button downloads just the species names of a network, this list may be convenient for the caption of a LaTeX image, for instance.

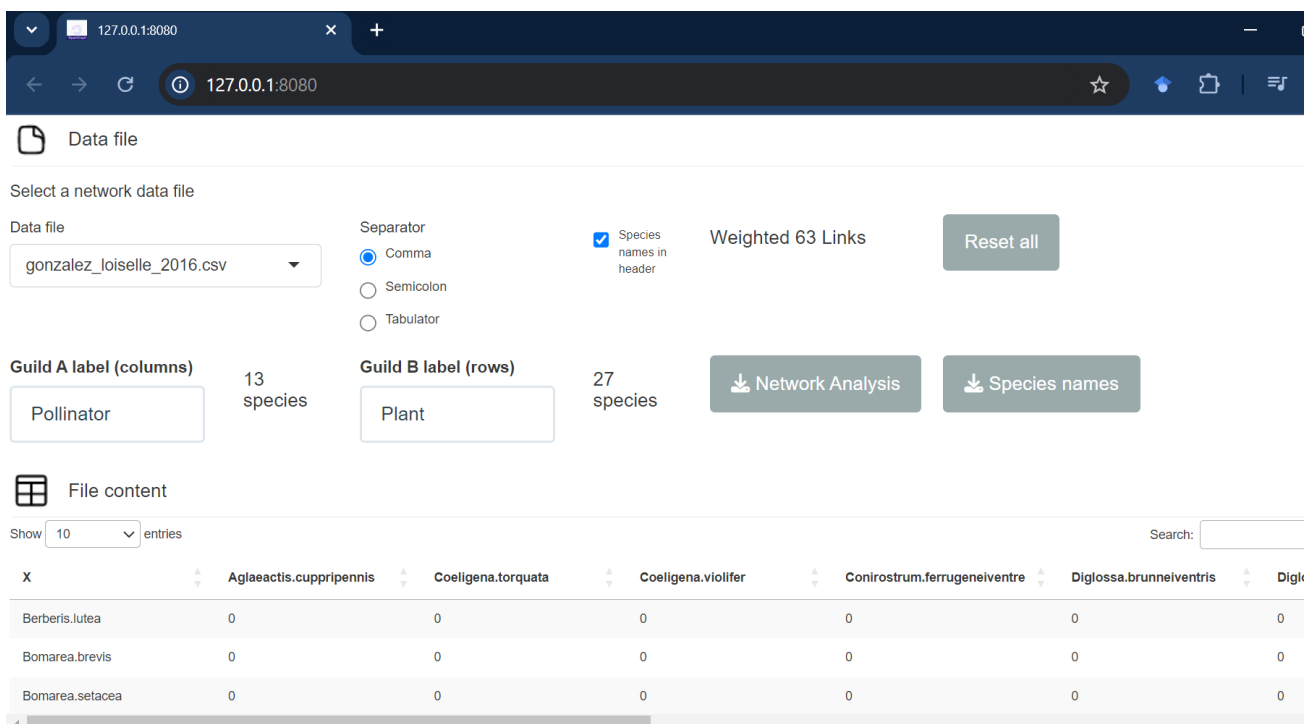


Figure 12: Network data

4 The ziggurat plot

The ziggurat graph is an original kind of visualization. The idea behind it, is splitting species in sets by their *k-shell* numbers [2]. If you are not interested in *k-magnitudes* at all, it is enough to know that the *k-shell* number is a measure of connectivity. Groups of nodes that share the same *k-shell* number are depicted as small ziggurats.

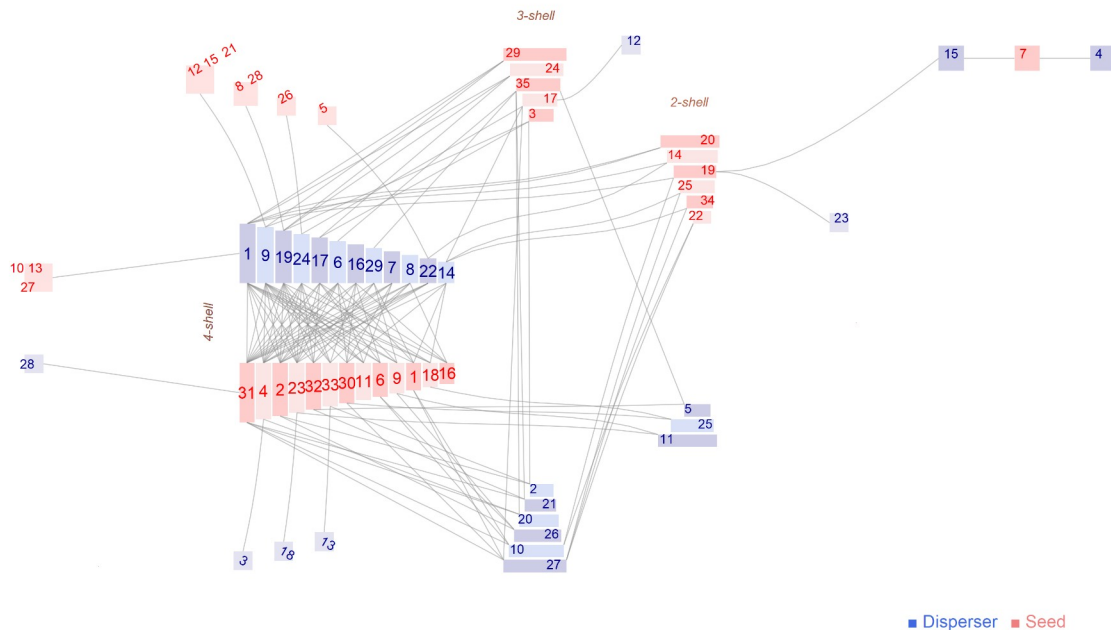


Figure 13: Ziggurat plot of an eating fruit birds network in Brazil, M_SD_012 [4]

Although networks are quite different in size and connectivity, they share building units that will help you to get a clean glimpse of the structure (fig. 14). The building blocks are **nodes** and **links**. Bipartite networks have two kinds of nodes that conventionally we call **guilds**. In this example there are frugivore species of birds, playing the role of seed *dispersers* (guild A), and plant species that yield those *seeds* (guild B). If two species interact, there is a link between them, for instance *bird 18* feeds on fruits of *plant 23*. The bird species, in turn, benefits the species plant by fostering its reproduction through seed dispersal. Links among nodes of the same guild are not possible in bipartite networks.

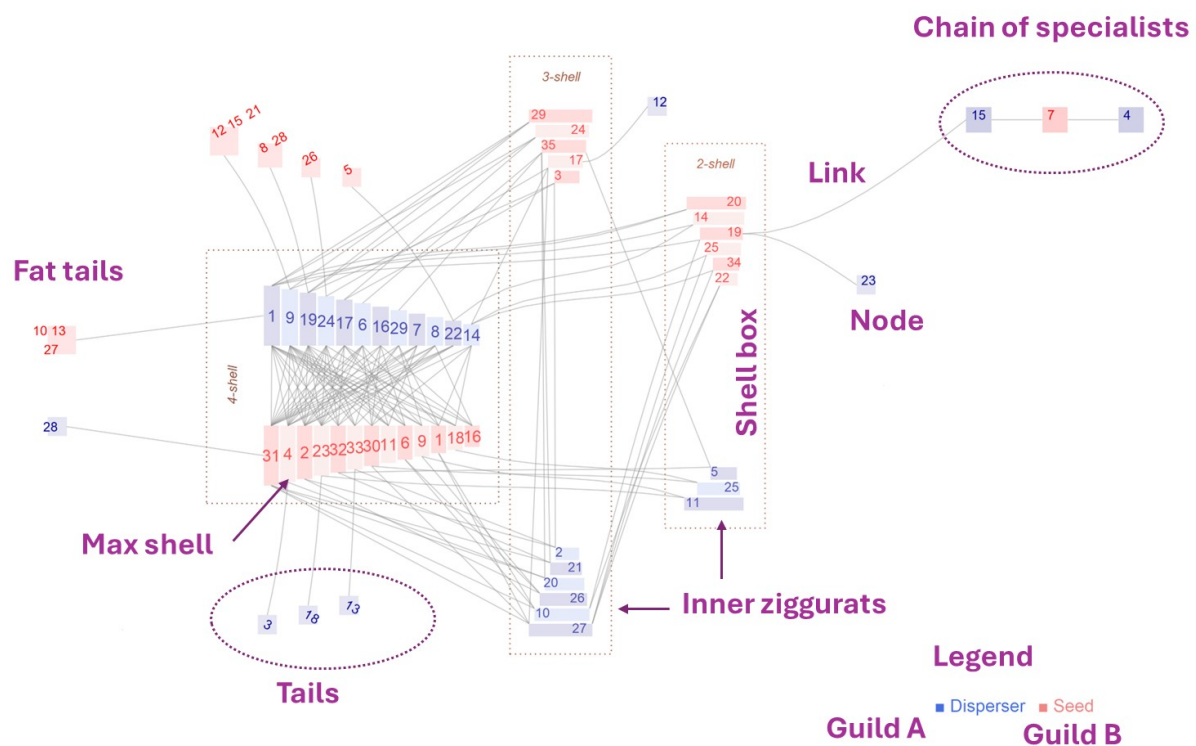


Figure 14: Elements of the ziggurat plot

Links have no label and share a common color. Nodes are filled with the color of their guild, with two slightly different tones to help visual perception, by default. Each species is numbered by its order within the input file. So, *plant 1* is the species recorded in column 1 and *bird 5* in row 5.

Node size does not convey any information in for ziggurat plot, shapes just make it more readable. Although species of a same guild and shell appear stacked in the ziggurat, they do not have share **any** other property. *Plants 2, 10, 20, 26* and *27* belong to the *3-shell*, this is the only fact relevant for this plot.

The **legend** informs about name each guild, the left element is always *guild A*. Ziggurats may optionally appear enclosed by dotted rectangles that we call **shell boxes** with a box label. The shell with the highest *k-index* (4 in the example) is the **max shell**. It is located at the center of the plot. Shells of lower indexes (3 and 2) are arranged following an almond-shape distribution. We call them **inner ziggurats**.

Nodes of *1-shell* are scattered around the plot. They may be part of two structures, ***tails*** and ***chains of specialists***. A tail is just one species of 1-shell linked to one species of a higher shell of the opposite guild, for instance, *bird 5* and *plant 3* are tails.

When multiple nodes of *1-shell* are tied to the same species of any of the ziggurats, they are clustered to reduce the number of lines. Species *Plant 12*, *15* and *21* are linked to the generalist *disperser 9*.

Chains of specialists are less common than tails. They are sets of species of *1-shell* linked to species of *1-shell* of the opposite guild. *Bird 15–plant 7–bird 4* is an example of a chain of specialists.

With this organization, we have a clear view of structure and interconnections. The central almond shape area leaves a wide space for the links, so they do not over-cross the boxes. Other structural details are easy to catch with this visualization. It is also clear why *bird species 4* and *plant 7* are in dangerous position. They depend on another specialist, *bird 15*, that has only one link with one *2-shell* species, so if this species gets extinct in that environment, the chain of specialists disconnects from the network giant component.

Sometimes, the field scientists record species not linked to the giant component. These ***outsider*** species are plotted as a subnetwork under the ziggurat plot (fig. 15).

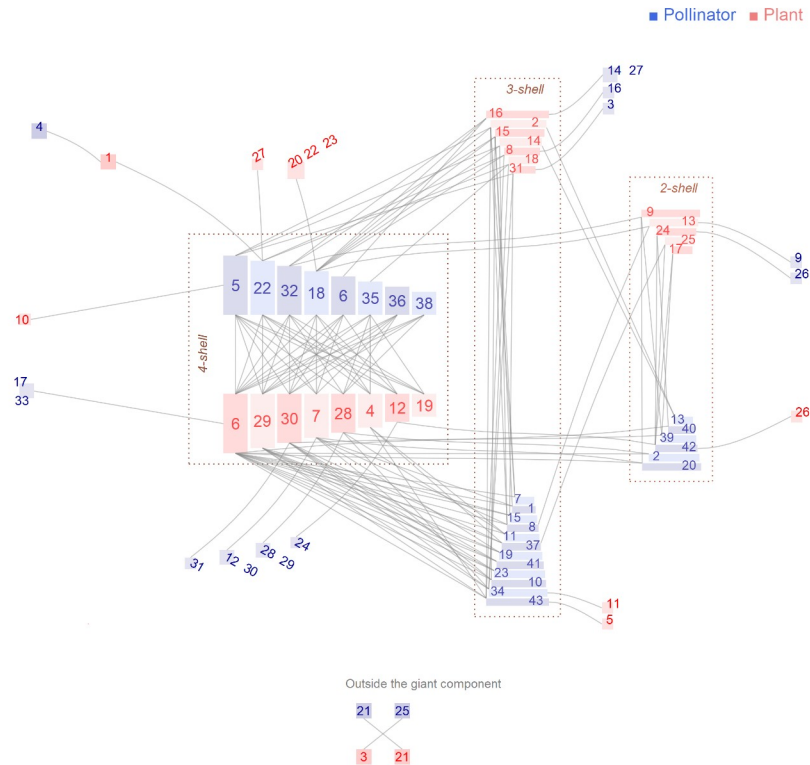


Figure 15: Plant – pollinator community M_PL_041 in Syndicate, Dominica Island [6]

4.1 Explore the interactive ziggurat

Go to **Data** and select the `M_PL_008.csv` and then click on **Interactive Ziggurat**. The plot is displayed on the left, inside the **Plot** panel.

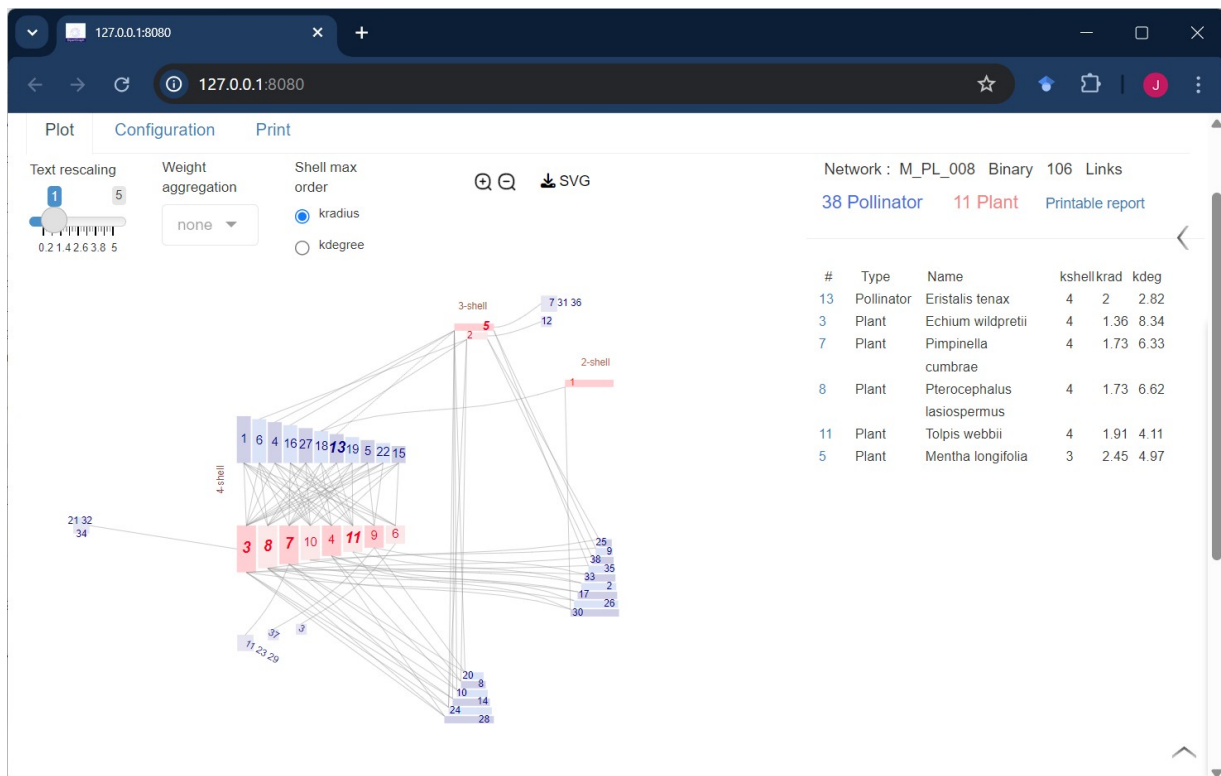


Figure 16: Interactive Ziggurat

When you pass the mouse over each species box, a tooltip shows its binomial name and *k* magnitudes.

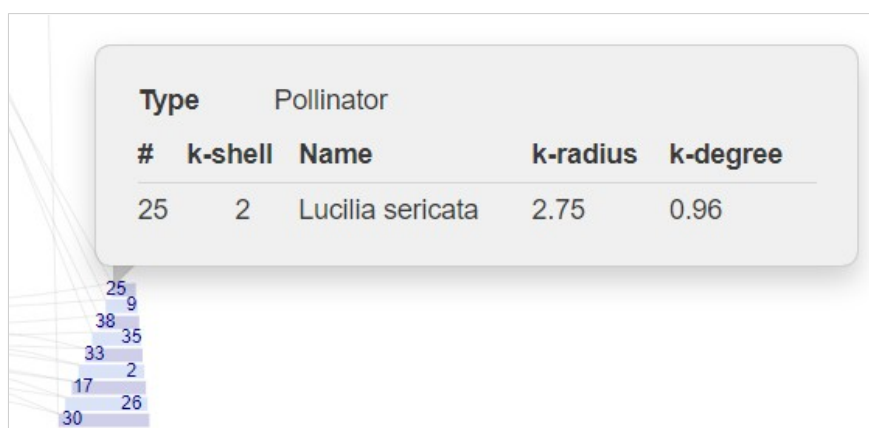


Figure 17: Species tooltip

If you click on one of these boxes, the links to other species are highlighted as dashed lines, and the labels of those neighbors look larger.

On the right panel, you may see the information table of the selected species (*disperser 13* and all its partners in fig. 16). Clicking on the species number in the table, the application

opens the Wikipedia information about that species. If the binomial name is not properly written in the data file you will get an error. Sometimes, Wikipedia may redirect you to some disambiguation page.

4.2 Modifying the look and feel of the ziggurat plot

The elements of a ziggurat are configurable for the sake of clarity and beauty. Let's start with the simple ones, *links*. Please, select the file RA_HP_001.csv, a host-parasite network, with 18 host species, 10 parasite species and 61 links. If it is the first time you load it, change the Guild A label to Host and Guild B label to Parasite in the Data panel. *BipartGraph* will remember this setting next time you load this network file. Click Interactive Ziggurat on the main menu, and you will get a fancy default visualization of this small network (fig. 18).

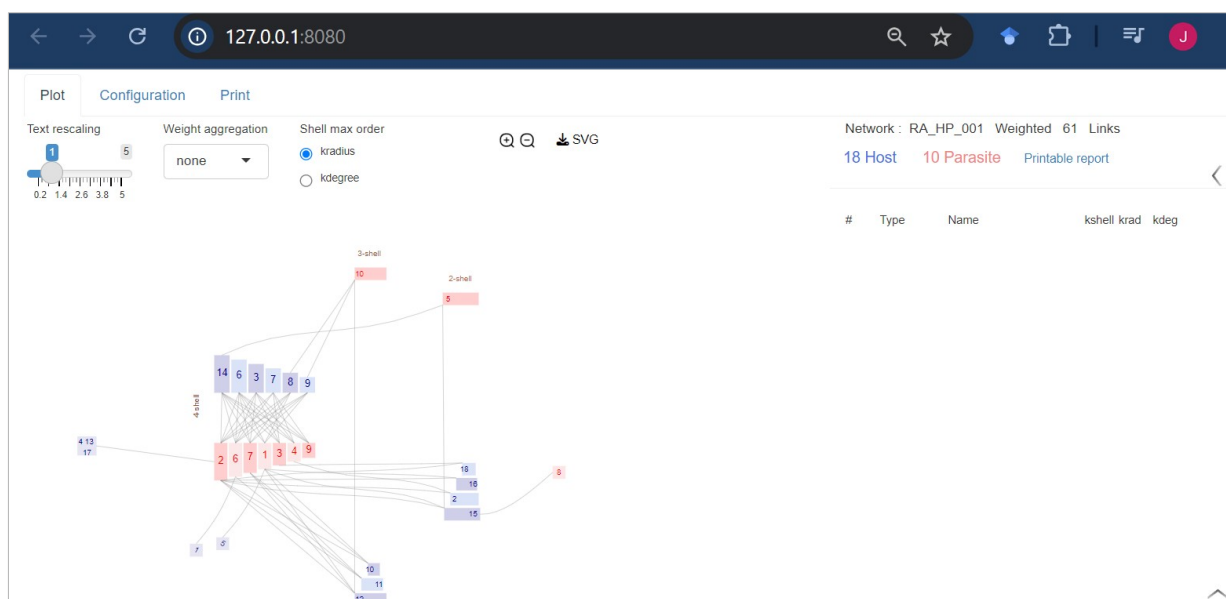


Figure 18: Host – parasite network in Azharia [7].

At any time, you may display all species names clicking on the upper right corner (or lower right) corner arrows to show/hide a vertical (horizontal) slider (fig. 19).

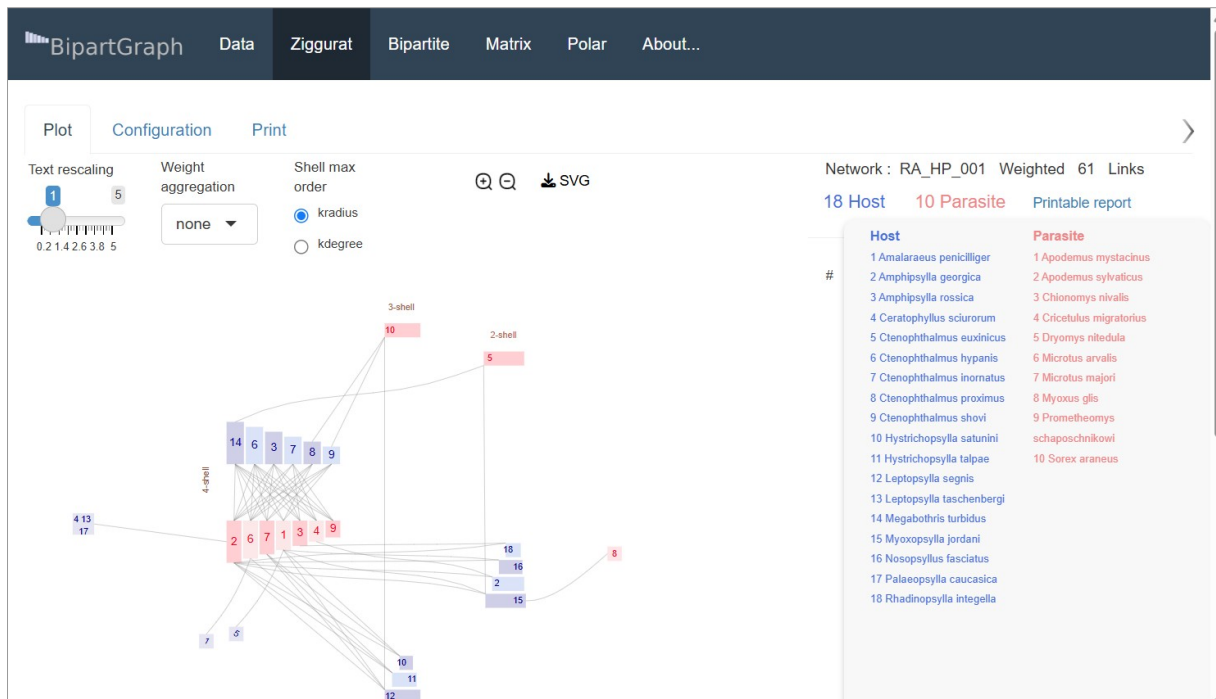


Figure 19: Vertical slider with species names.

Click on **Configuration** tab and the first thing you see are the link controls. There are 5 of them (fig. 20).

- **Show links.** This box is checked by default. If you uncheck it, links will hide. This may be useful when working with very big network, because link processing is the most time consuming task. You may decide hide them while you configure other elements.
- **Use spline.** Links come in two flavors, straight lines (*parasite 7 – host 6*) and splines, smoothly curved lines (*parasite – host 10*). If you uncheck this box, every link will be straight shaped and the plot will have a more *rude* look.
- **Spline points.** Number of points of each spline, the bigger the smoother and more time consumig. The default value is 50, do not increase it very much unless you are producing a very high quality plot for a journal.
- **Link width.** If the network is binary (there are only 1's and 0's in the in the interaction matrix) all links have the same width. If weighted, Weight aggregation lets you choose to make their width proportional to the interaction strength (ln or log10 of these values) or ignore weight (no) and plot them as if the network were binary.
- **Color and Transparency** define how the links are filled. The transparency ranges from 0.1 (almost invisible) to 1 (opaque color).

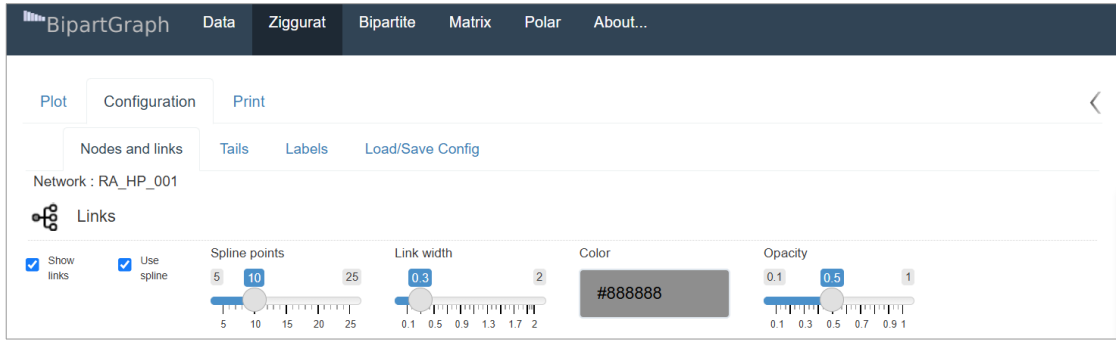


Figure 20: Link configuration control.

Let's go back to figure 18 to make some adjustments. First, uncheck the **Use spline** box (the Spline points control has no meaning if you use straight line links). You can make the width proportional to the interaction strength. Select **ln** in **Weight aggregation**, the width of each link will be proportional to the natural logarithm of its strength (the value recorded in the interaction matrix). Click again on **Interactive Ziggurat / Configuration**.

To test the effect of other configuration parameter, increase the **Link width** slider up to 0.5, move the **Transparency** control to 0.2 and pick a green tone color **#087007** (you can write it inside the **Color** box).

That's all, now it's time to see how the ziggurat changes. Click on the **Plot** tab and the software will plot again the network (fig. 21). Perhaps it will not win a plot beauty contest, colors pop up your eyes and straight links make it less pleasant than the default fig. 18. On the other hand, you can detect that *host 7* is much prone to have parasites of *species 6* than of *species 10*.

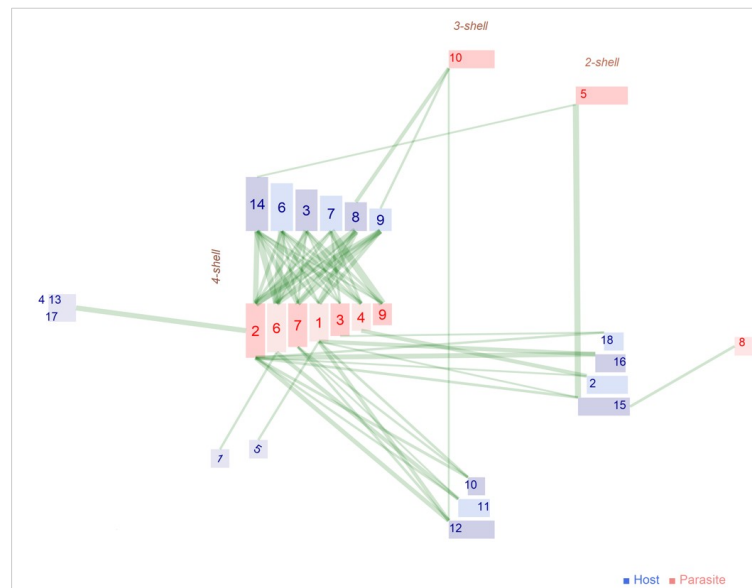


Figure 21: Host - parasite network in Azharia [7], with modified link properties.

Now that we have learned how to modify **links**, let's move on to more exciting elements of the graph. The network of figure 15 is larger. There are some details that need improvement, for instance the height of the nodes of the **inner ziggurats**, they look

smashed. Go to **Configuration**, move the **Nodes height** slider to 1.5 and click on **Plot** again.

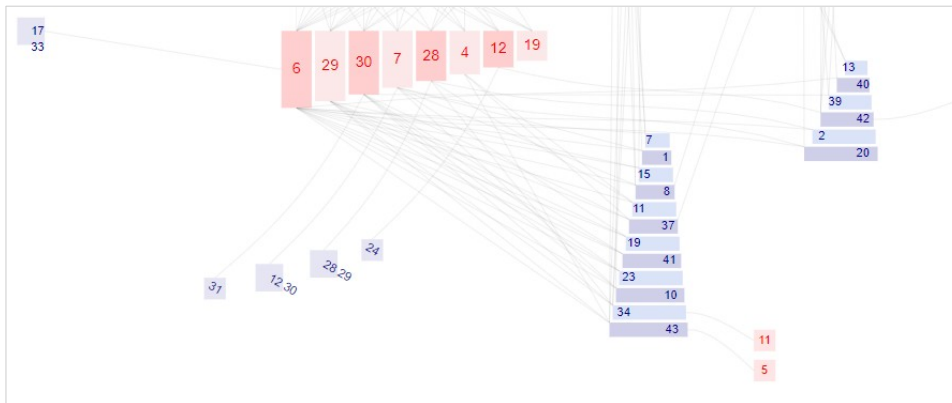


Figure 22: Detail of plant – pollinator community M_PL_041 in Syndicate, Dominica Island [6]

Boxes are fancier now, but links from *2-shell* towards *4-shell* overcross the ziggurat of pollinators of *3-shell*. We can move it upwards or downwards with the **Inner ziggurats vertical displacement** control. The ziggurat that is troubling you is the *3-shell* of guild A (if you do not know which guild you are dealing with, the color of the legend will tell you).

Please, move the 3-shell A slider to -0.1 (roughly move it down a 10% of the original position). The *chain of specialists* in the upper left end of figure 15 is a bit long. Click the **Tails** tab and reduce the distance.

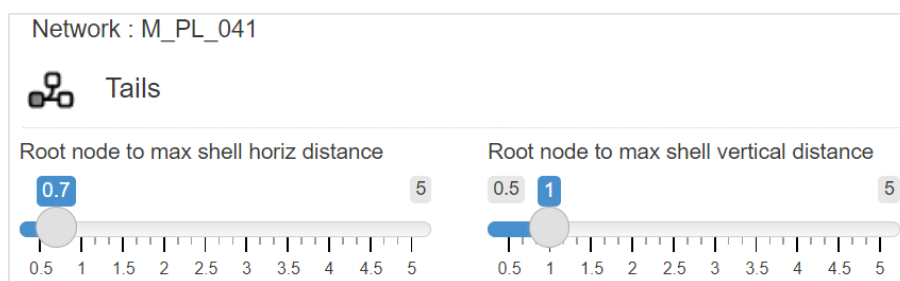


Figure 23: Tail display control sliders

Finally, move the *outsiders*, clicking on the **Nodes and links** tab:

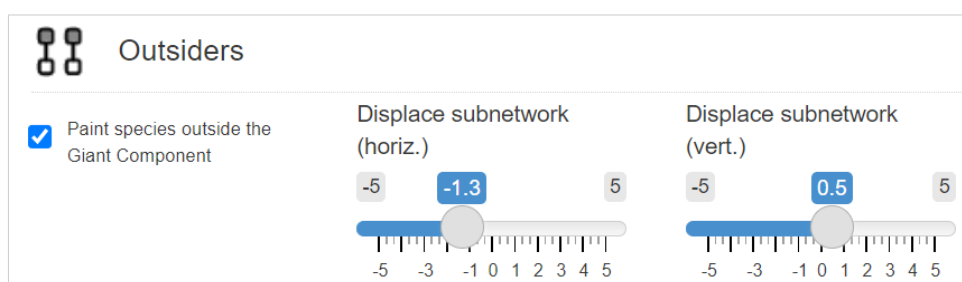


Figure 24: Outsider species display control sliders

After you apply all these changes, the ziggurat plot you get is the figure 25. Of course, you could keep on tuning parameters.

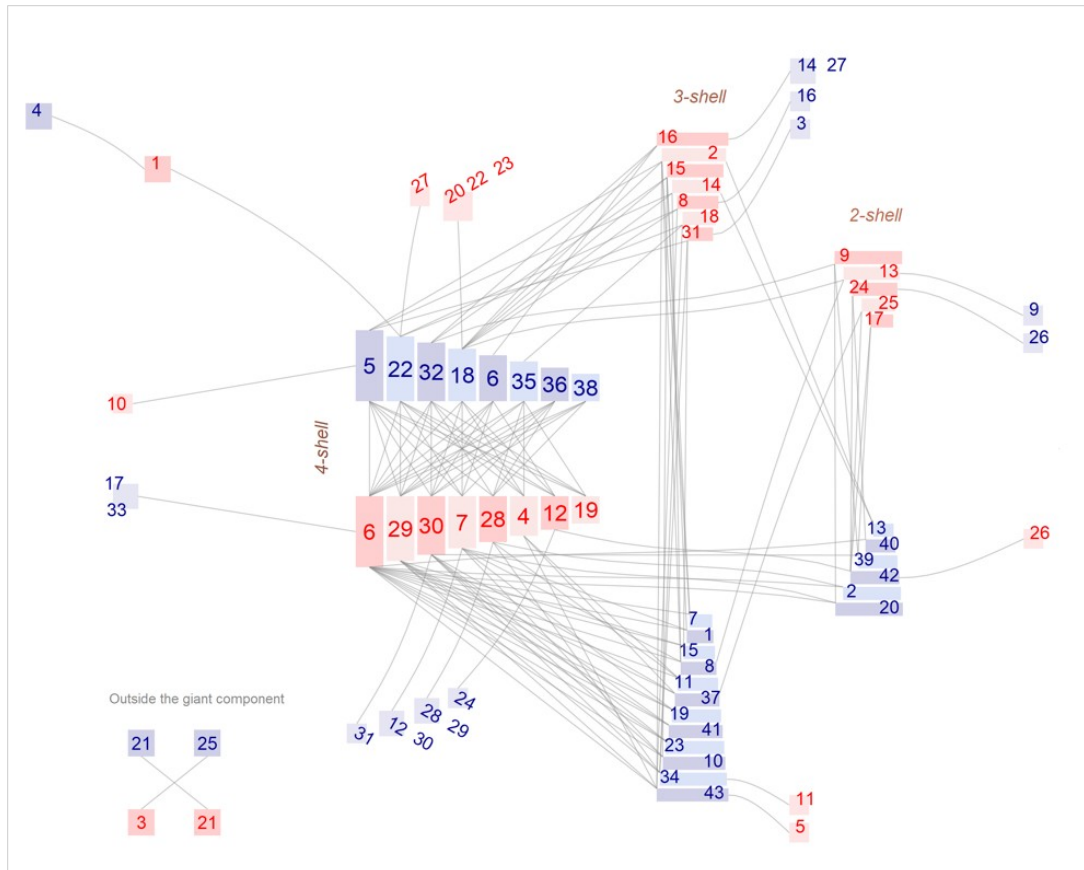


Figure 25: Ziggurat graph of a plant – pollinator community in Syndicate, Dominica Island [5] after visual adjustments.

For instance, outsiders may be a bit disturbing, and you may hide them or reduce their area. This network is weighted, try to change link properties as we did in the previous example and see how the plot tells a different story.

A new example will show how to deal with other elements of the ziggurat. Go to **Data** and before selecting a new file push the **Reset all** button. This action restores the default values of all the controls. Now, select the `M_PL_012.csv` file and display the interactive ziggurat.

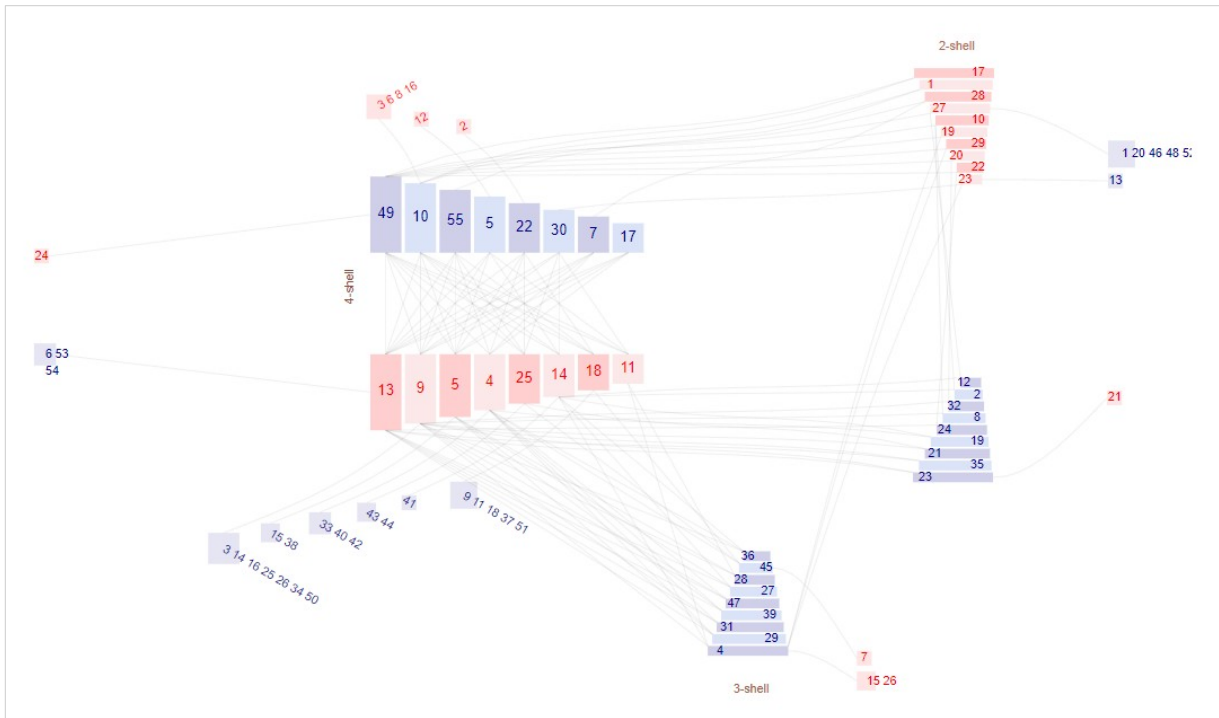
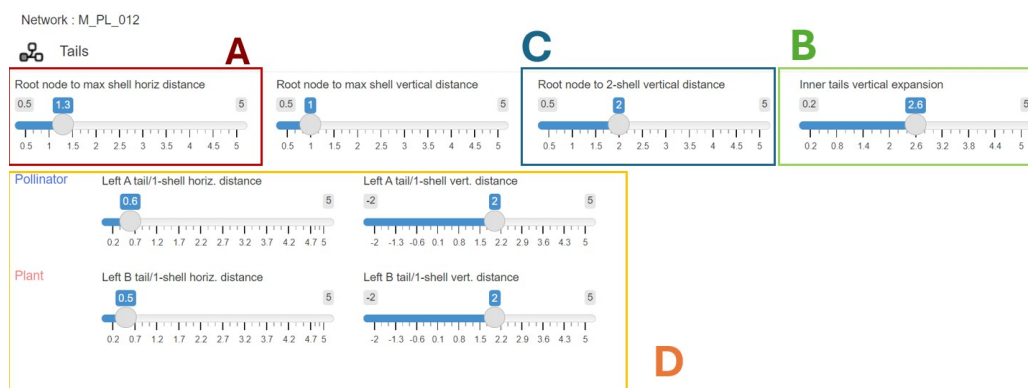


Figure 26: Ziggurat graph of a plant – pollinator in Garajonay (Spain), recorded by Jens Olesen. Unpublished.

This community has a high number of species in *1-shell*, grouped in *tails*. Pay attention to the tails that are above and below the *max shell*. The graph is overcrowded and it would be nice making additional room for them, expanding their horizontal distance (**A**). Then, we increase the vertical distance among tails connected to inner ziggurats (**B**), like plants 7, 15 and 26. The third step is widening the gap of the two tails connected to plants *2-shell* (**C**). The last modification pulls up/down and right the left tails, those connected to the leftmost species of the *max shell* (**D**).



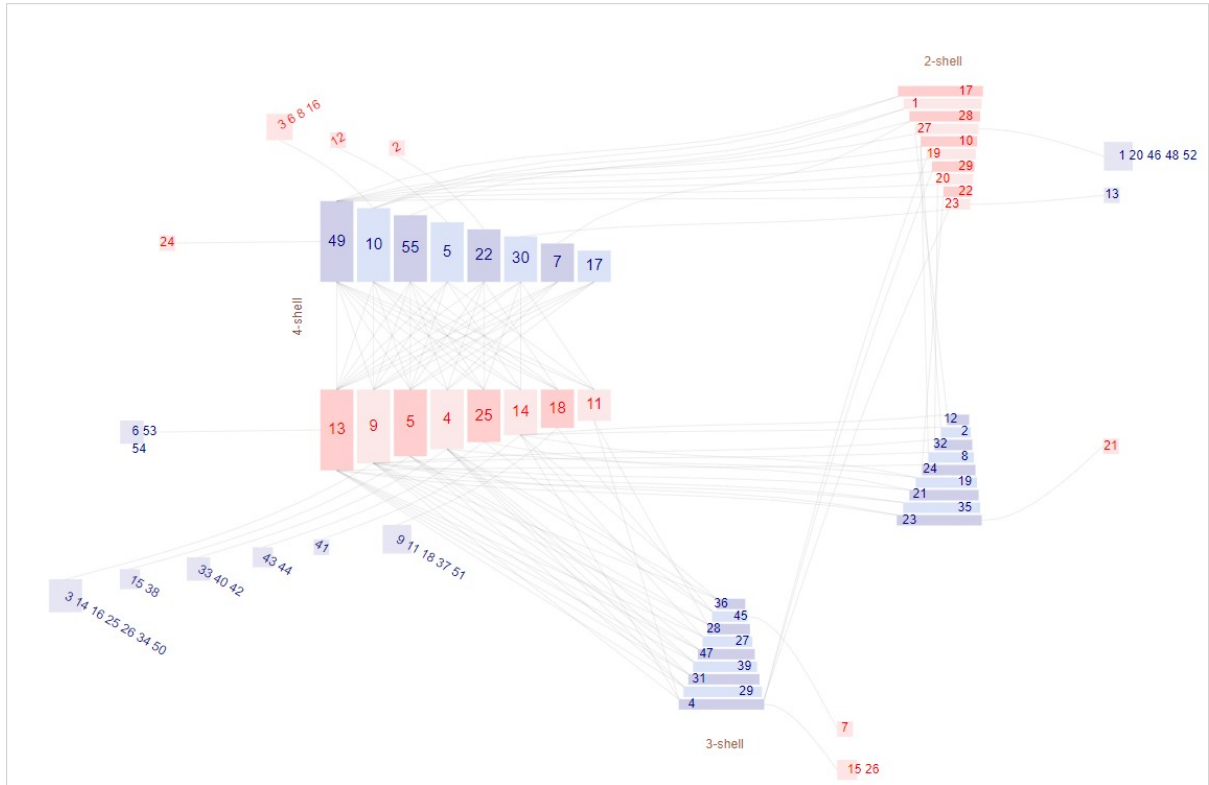
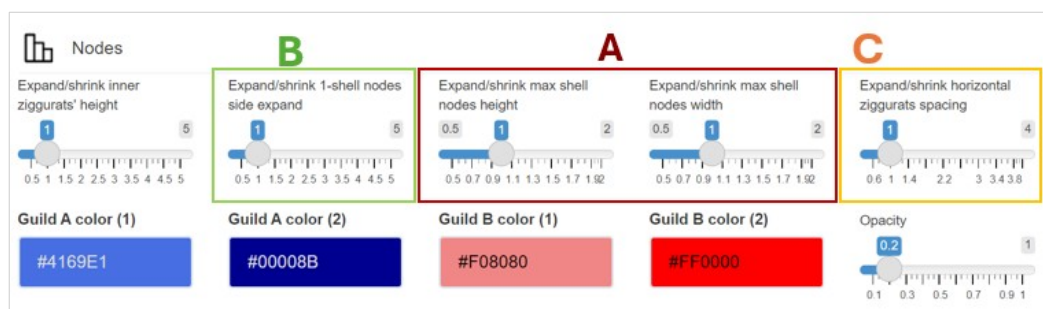


Figure 27: Ziggurat graph of a plant – pollinator in Garajonay (Spain), after visual adjustments.

The dimensions of the *max shell* triangle are controlled with two sliders Max shell height expand and Max shell width expand (A). The area of all boxes of *1-shell* may be increased by the factor 1-shell nodes expand (B). There are four color pickers for guild nodes, please use it with care. *BipartGraph* will remember your choice next time you load the same network. Transparency works as explained above when talking about *links*. The horizontal inner shells separation widens the horizontal gap between ziggurats (C).



Let's take a small portion of network M_PL_031 to show the behavior of *specialists* controls (fig. 21). They expand or contract these chains. The distance of the root node is modified by First node horiz/vert distance to network if tied to nodes in any ziggurat except *2-shell*, that has their own controls.

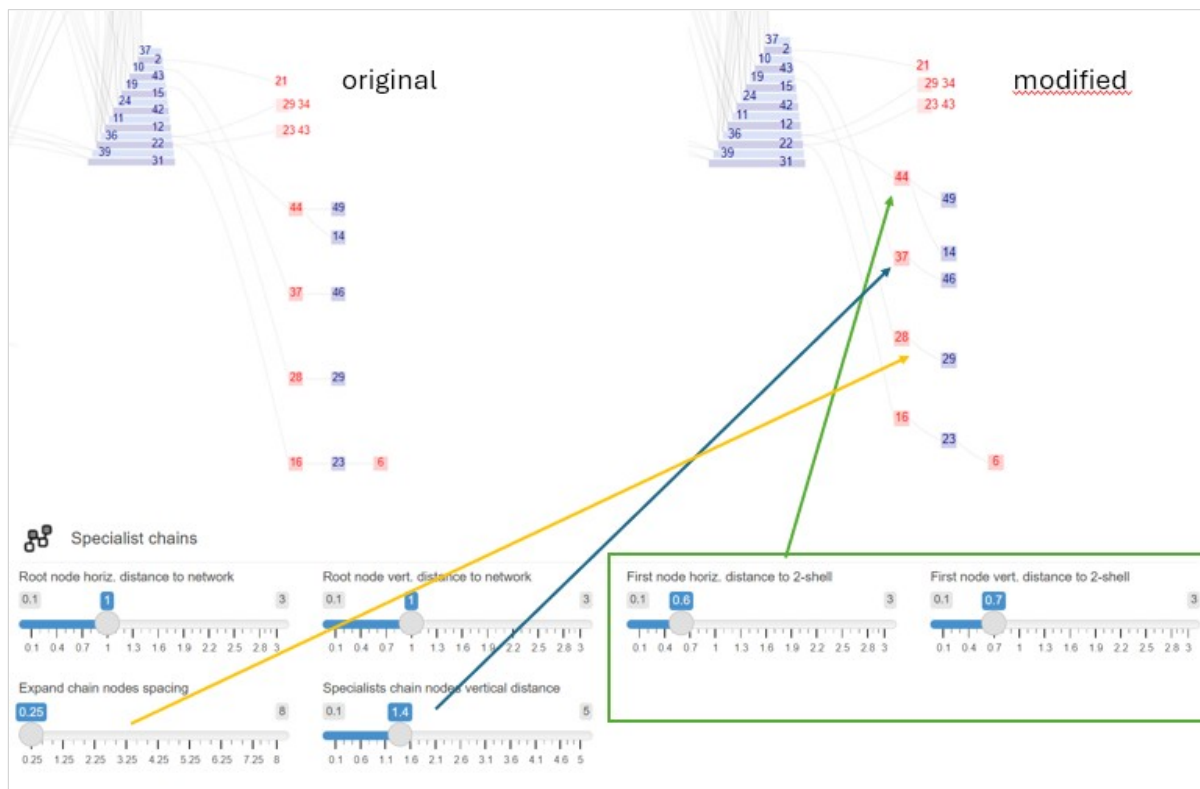


Figure 28: Changing the configuration of the chains of specialists.

Expand chain boxes separation controls the horizontal distance among nodes of any chain and Specialists chain nodes vertical distance the vertical gap.

By default, each guild is filled with two different tones of color, but you can pick just one checking the One color per guild box.

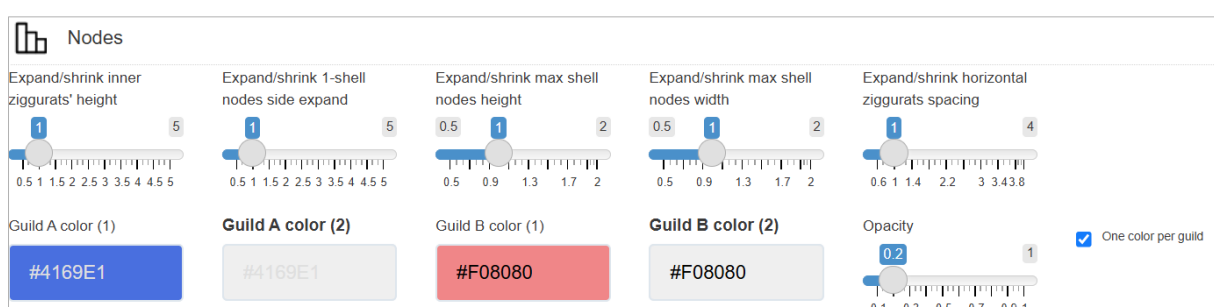


Figure 29: Choosing one color per guild.

4.3 Printable ziggurat

Once you have got a clean ziggurat it is quite possible that you need to produce a high quality plot for your research. That is what the **Print** tab of the main menu will do for you.

Select again the network `M_PL_012.csv` and visualize the default **Interactive Ziggurat**. Now, go to **Print** and click the button **Plot Download**. Your browser will download a file called `M_PL_012-ziggurat.png` (fig. 30). Compare it with the interactive plot (fig. 26). It is

almost identical, but there are minor visual differences. In the printed plot the name of the network and legend can be displayed, and perhaps the sizes of labels and legend are slightly different.

The interactive and printed plots are built with two different technologies, the first one is an SVG object, the second a ggplot2 object. These details are not important for you as an end user of the application, but depending on the resolution of your screen and the installed fonts, sizes may differ. In the Plot view you have a control to rescale at once all labels. The default value or rescaling is 1, if you increase it, the size of labels plot will grow compared to the printed ones. It may be useful for final adjustments.

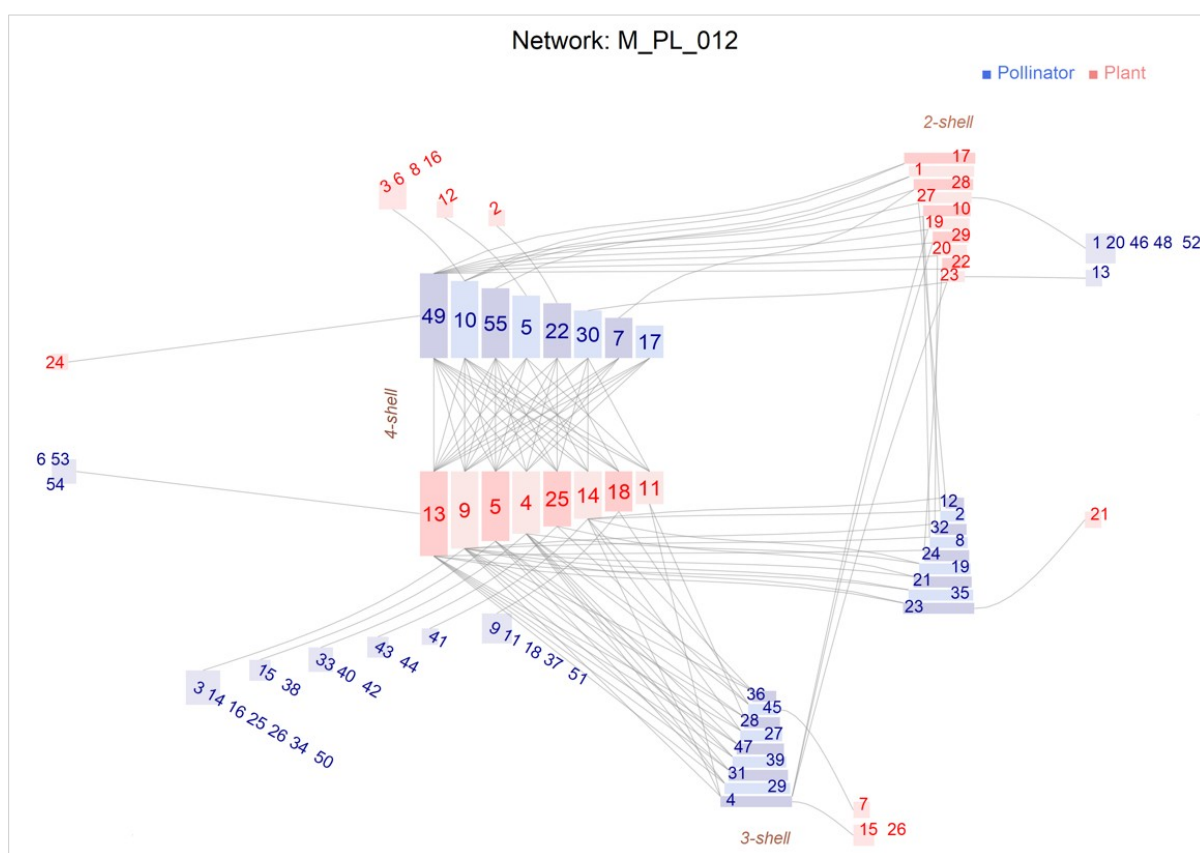


Figure 30: Printed Ziggurat graph of a plant - pollinator in Garajonay (Spain).

Go back to the Print pane. Options are quite straightforward, you may change the orientation (Landscape), resolution and title and legend options. The Aspect Ratio is a special control that only affects the printed version. If it is bigger than 1 the graph is stretched in the vertical direction, the opposite if it is smaller. You can choose four file formats for the printed plot: png, jpg, eps, tiff, svg and pdf.

When you get a nice printed ziggurat you may want to save the display parameters configuration for reproducibility. This is what the **Download generating code** button does. Click on it and you will see the full invocation of the R `ziggurat_graph()` function. The meaning of each invocation parameter is explained in the `kcorebip` user manual. This

package was installed in your computer during the process and the guide explains how to run the code:

https://github.com/jgalgarra/kcorebip/blob/master/inst/doc/kcorebip_man.pdf

If you are not a programmer but want to get the printed ziggurat again using the code, follow these steps, please. Create a directory called `MyRCode` where you want, and copy there the file `M_PL_012-ziggurat-code.txt` that the application generated. Create a folder called `data` inside that directory and copy there the input data files, for instance the `M_PL_012.csv` that you used as an example and lives in `biparthgraph/data`.

Create inside `MyRCode` the folder `plot_results`, and inside `plot_results` the folder `ziggurat`.

Copy and paste this code and save it in a file called `genziggurat.R` in the `MyRCode` directory.

```
library(kcorebip)
source("M_PL_012-ziggurat-code.txt")
```

Your new directory should look like that, with the file `M_PL_012.csv` in the `data` folder and an empty `ziggurat` folder inside `plot_results`.

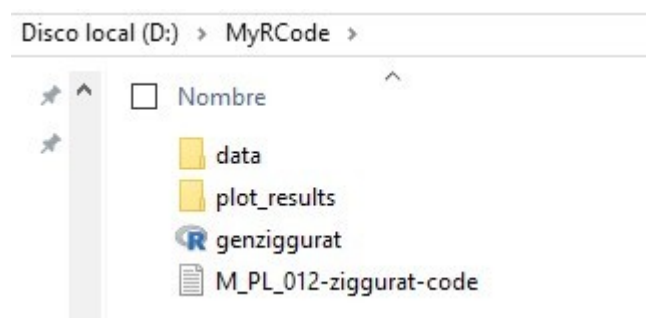


Figure 31: Downloading a ziggurat generating code.

Go to the command line and run

```
> Rscript genziggurat.R
```

When the script finishes the `M_PL_012_ziggurat.png` file is available inside `plot_results/ziggurat`.

If you are not a developer but you want to save the tuned parameters for the future, then go to the **Config/Load Save Config** pane. Use the **Save plot configuration** to save the values in a text file. You can read it later with the **Browse** dialogue, to choose any configuration file. Checking **Show contents** will show the values of each parameter that has been stored in that particular file.

5 The bipartite plot

The bipartite plot is the conventional way to depict a bipartite network. Nodes of both guilds are aligned in two parallel lines (horizontal or vertical is a matter of convenience), ordered by degree. A straight line between two nodes of different guilds means that there is a link and its width may be proportional to the strength of the interaction. The bipartite plot becomes a *hair ball* as the number nodes and links increases. There are some minor mitigation strategies to overcome this problem. This package offers the *legacy* style for bipartite plot, following the traditional layout, but distributing evenly the nodes of the smallest guild. This solution makes the diagram more readable.

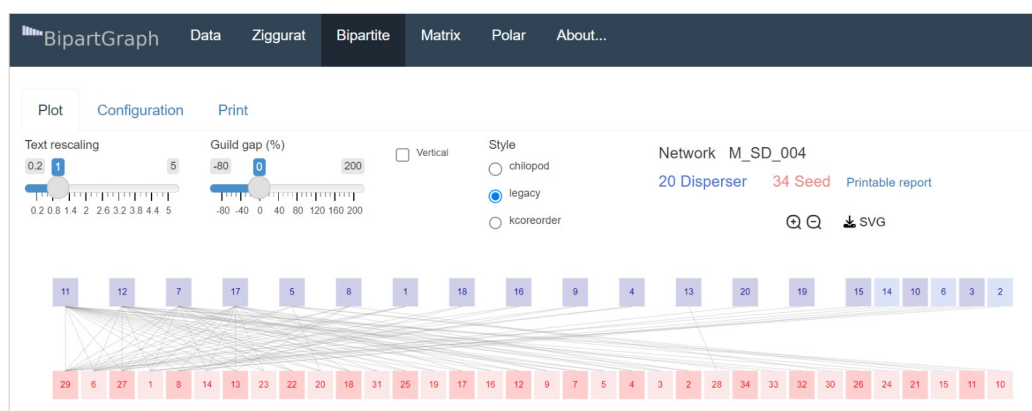


Figure 32: Legacy bipartite plot of disperser network M_SD_004

There are some details that you can deduce at a glance. The more generalist species are those that lay on the left side of the plot and the pair *disperser 13/plant 28* is disconnected of the giant component of the network. We can get further visual information tuning input parameters.

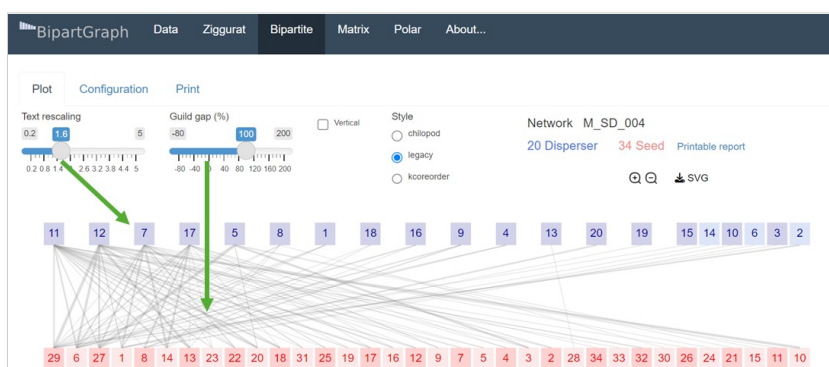


Figure 33: Legacy bipartite plot

The *kcorder* style reorders nodes according to their *k-shell* numbers (fig. 34). It is easy to spot the different *k-shells*, with species of 4-shell being the most interconnected. On their left, we find 1-shell, on their right, 3-shell, 2-shell and finally, species disconnected of the giant component. The only difference between *legacy* and *kcorder* styles is the order of the species, but information is still concentrated in the two lines of nodes.

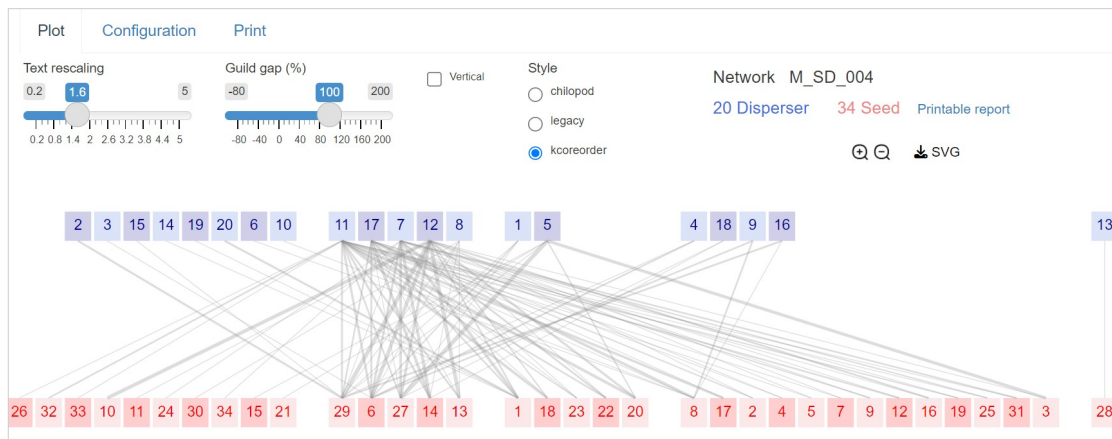


Figure 34: *kcorder* bipartite plot of disperser network M_SD_004

What if we could keep the whole idea of bipartite plot but spreading part of the visual information in two dimensions? That is the idea behind the third style, the *chilopod plot*. The name refers to the resemblance of this plot with a centipede. Nodes of 1-shell that we call tails in the ziggurat plot are moved away from the guild lines, and appear as short appendices. We apply the same grouping idea that in ziggurat's fat tails: nodes that have just one link and are tied to the same species of a higher shell, are plotted together (fig. 35).

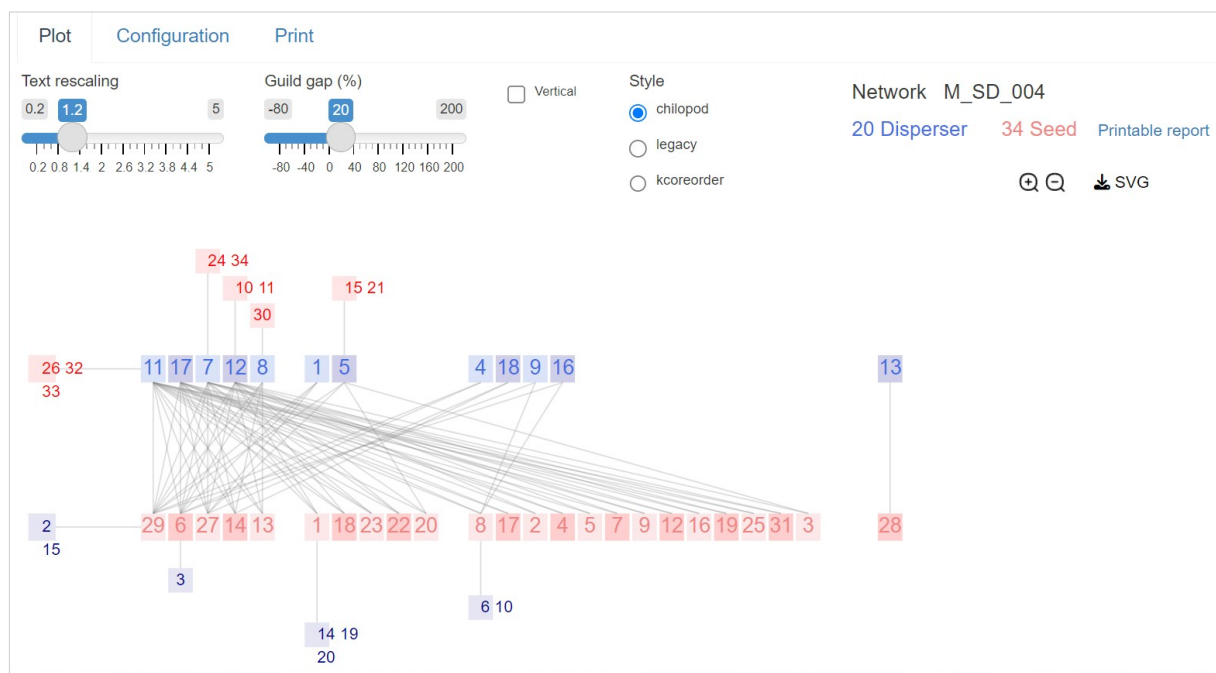


Figure 35: *chilopod* bipartite plot of disperser network M_SD_004

The bipartite plot offers the same options of customization and code generation than the ziggurat plot.

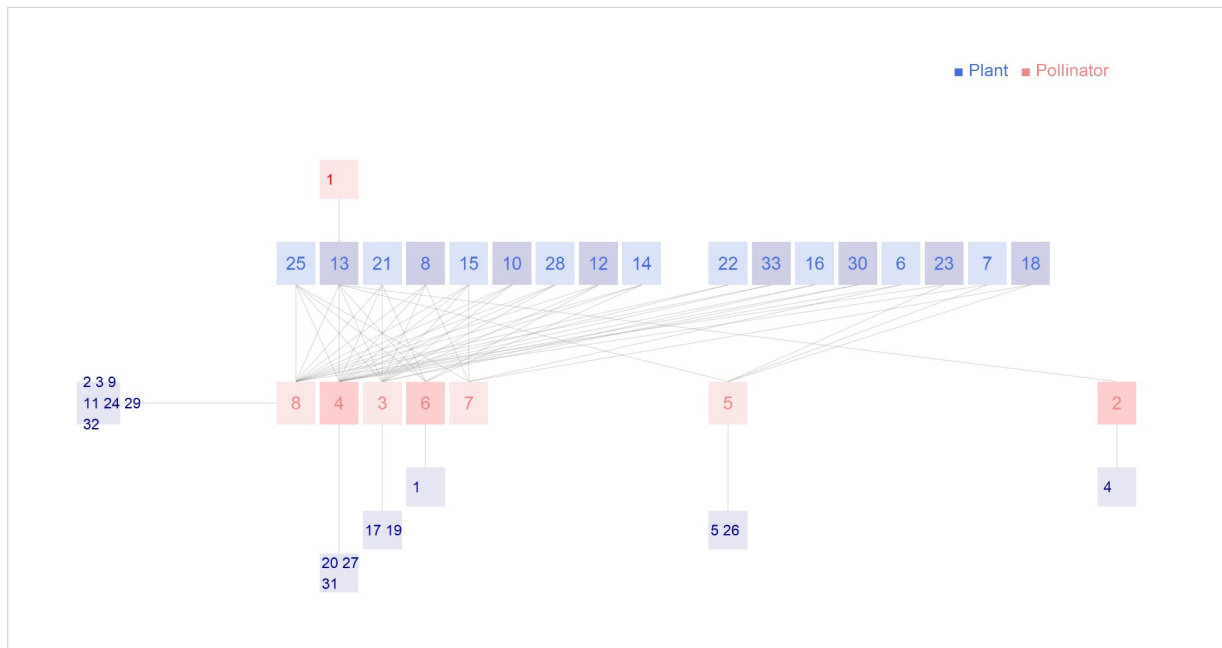


Figure 36: *chilopod* bipartite plot of a mutualistic network in Sicily [9]

6 The matrix plot

The Matrix Plot is another traditional way of plotting bipartite networks. It is just the depiction of the interaction matrix, with species of guild A as columns and species of guild B as rows. For binary matrices, the cell i, j is filled with solid color if there is a link between species i of guild A and species j of guild B. For weighted networks, the interaction strength is usually encoded as a color gradient. Nodes are sorted by their degree in descending order. This kind of plot is simple, and is useful to spot spatial properties as nestedness, but it is pretty hard to discover chains of specialists.

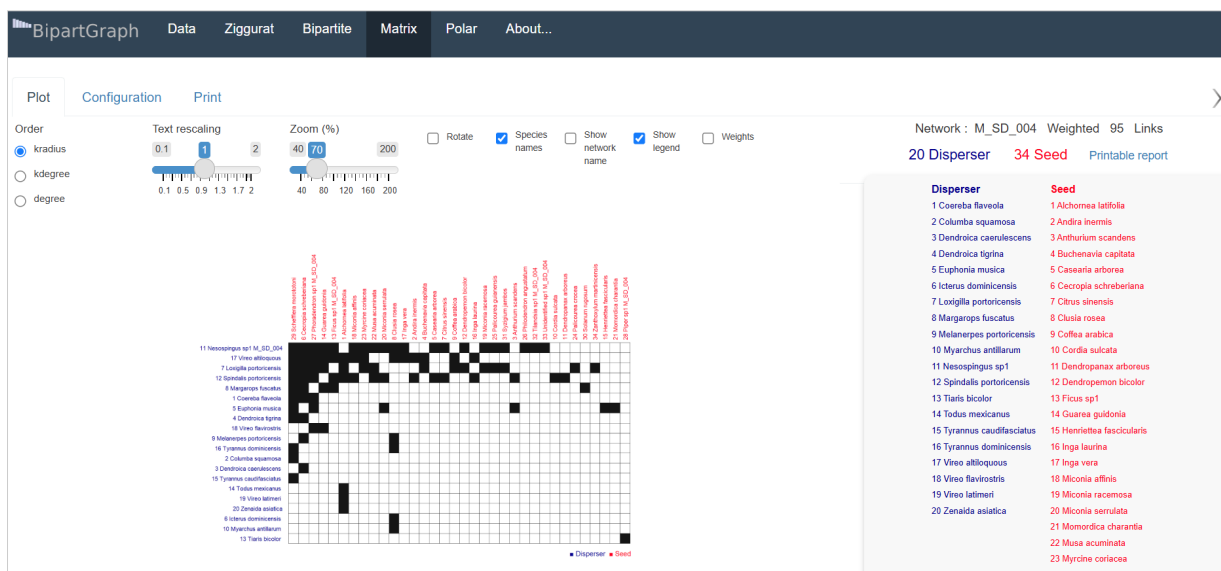


Figure 37: Matrix plot of disperser network M_SD_004

The function allows to flip the matrix to show it in landscape layout for convenience, as in this example. Besides the traditional order by degree, BipartGraph offers order by *kradius* and *kdegree*.

Species names may be removed, and this feature is of special interest when the network is large.

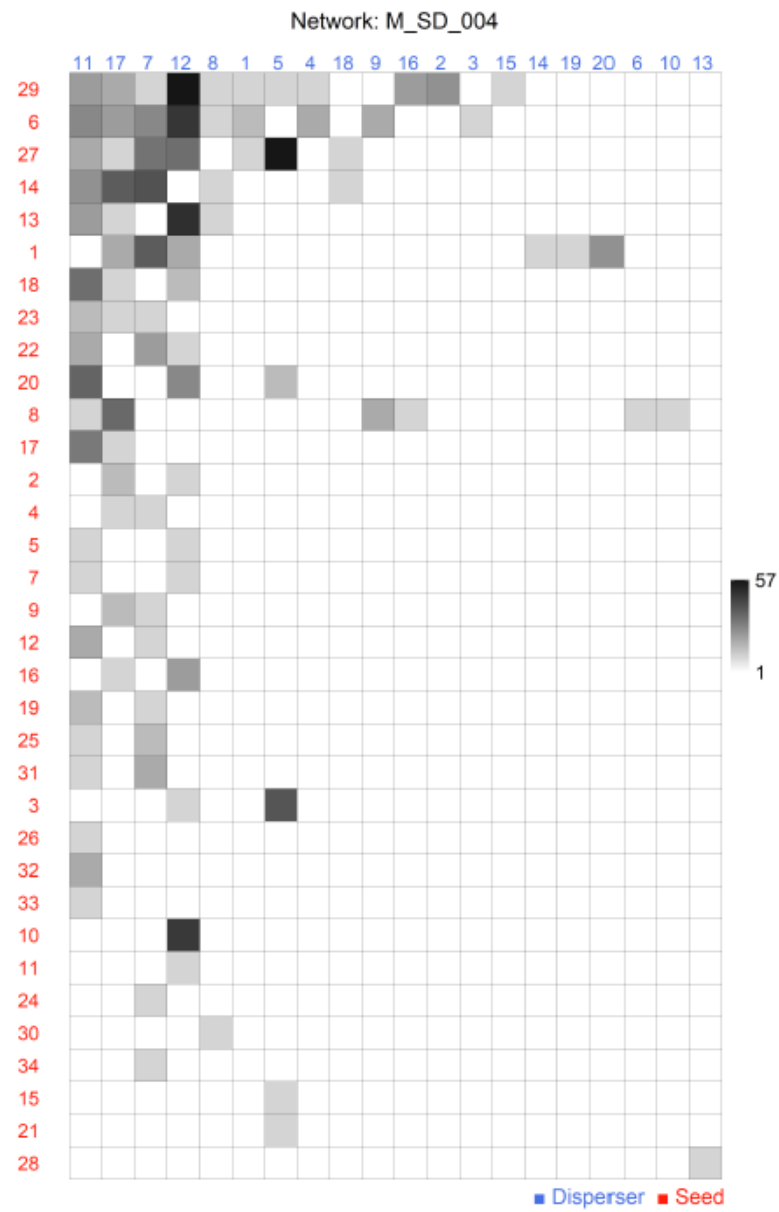


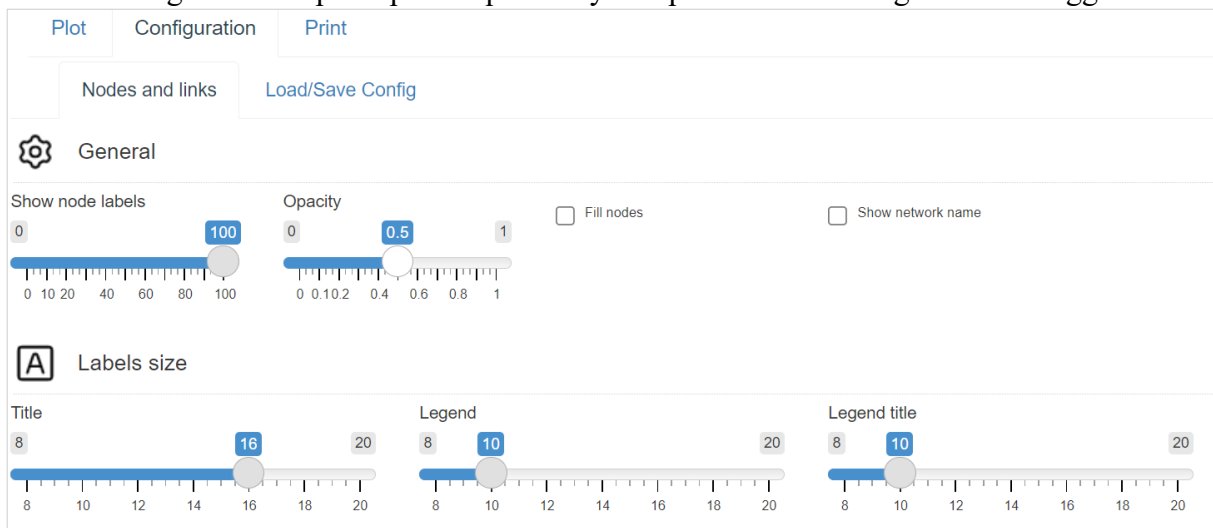
Figure 38: Rotated matrix plot of disperser network M_SD_004

7 The polar plot

The goal of the polar graph is showing species centrality and network compactness. It provides a quick overview of network distribution. It was inspired by the fingerprint-like graph, developed by Alvarez-Hamelin et al. [8] to plot very large k -decomposed networks.

Species are plotted at k -radius from the center. Angles are assigned by the visualization algorithm to reduce overlapping, with the condition that each guild lies inside one of the half planes. The area of each node is proportional to its k -degree and color represents the k -shell. This visualization does not include links. The user may choose adding the histograms of k -magnitudes, a handy option because they convey a wealth of structural information. Polar graphs are specially useful when comparing different networks side by side, even if they are of very different sizes.

The configuration of polar plot is quite easy compared to the configuration of ziggurat.



The screenshot shows a web-based configuration interface for a polar plot. At the top, there are three tabs: 'Plot' (selected), 'Configuration', and 'Print'. Below these, there are two sub-tabs: 'Nodes and links' and 'Load/Save Config'. The main configuration area is titled 'General' and contains several controls:

- Show node labels:** A slider ranging from 0 to 100, with a blue marker at 100.
- Opacity:** A slider ranging from 0 to 1, with a blue marker at 0.5.
- Fill nodes:** An unchecked checkbox.
- Show network name:** An unchecked checkbox.
- Labels size:** A section with three sliders:
 - Title:** A slider ranging from 8 to 20, with a blue marker at 16.
 - Legend:** A slider ranging from 8 to 20, with a blue marker at 10.
 - Legend title:** A slider ranging from 8 to 20, with a blue marker at 10.

The color is set by the algorithm, you may choose the level of transparency and if you want to fill them. The pixels box controls the size of the image in screen and may be useful to adapt it to your equipment.

If you want to add the node number, use Show node labels. It tells the application how many node labels to show, from highest degree to lowest. If the network is big the labels may spoil the plot. You can choose to fill the nodes and the level of opacity.

The Labels size control plays the same role than for the ziggurat plot.

Once the plot is displayed you may download it or its generating code, just the same that happens with the ziggurat plot. An important difference is that the polar plot shown in the browser and the printed version are the same object, so screen resolution does not matter.



Figure 39: Polar graph of a plant – pollinator in Garajonay (Spain), including labels and histograms. Compare with fig. 26

Useful hacks

In your `bipartgraph` directory there is a file called `CONFIG.txt` with the following contents:

```
LANGUAGE;PORT;LabelA;LabelB;ColorGuildA1;ColorGuildA2;ColorGuildB1;ColorGuildB2;Wiki  
pediaSubdomain
```

```
"en";8080;"Plant";"Pollinator";"#4169E1";"#00008B";"#F08080";"#FF0000";"en"
```

You may change the default language, application TCP port, labels of guilds and colors. It would be nice if you make a copy before editing it. In case you delete by accident this file, the application starts with these default values but you cannot modify them.

References

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