

BipartGraph User Guide

BipartGraph User guide R1.0

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<https://github.com/jgalgarra/bipartgraph>

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1 Introduction

BipartGraph is an interactive application to visualize bipartite ecological networks, using the *k*-core decomposition method [1]. You will find the technical details of this type of analysis at <https://peerj.com/articles/3321>

The most common visualization of this kind of networks 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 grows, the graph becomes a *hairball*, an expression common in visualiation 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 finding graphs of networks with more than ten species per guild in the research literature, although typical mutualistic networks are bigger. This problem is not due to a lack of skills of the user, it is a limitation of the graph itself.

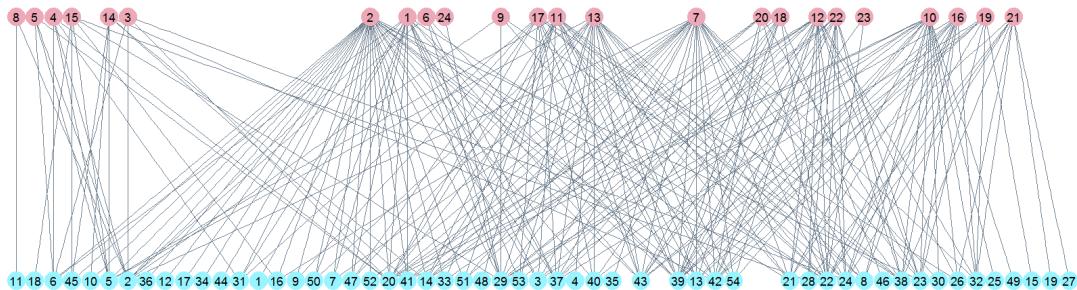


Figure 1: Bipartite graph of a mutualistic community with 78 species.

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 to play!

2 Installation

BipartGraph is an interactive application developed in R language . If you are familiar with R, congratulations, this guide will seem pretty easy to you. If you have not worked with R or with any other programming language at all, this document guides you step by step through the installation procedure.

2.1 Requirements

There are only two requirements to install *BipartGraph*, a working R environment and any web browser. R is an open source project, you will find the download and installation instructions for different operating systems at <https://cran.r-project.org/>.

You need the release R 3.2.0 or later. If you have never installed R, pick the last available release from the download page, it will be fine for this purpose.

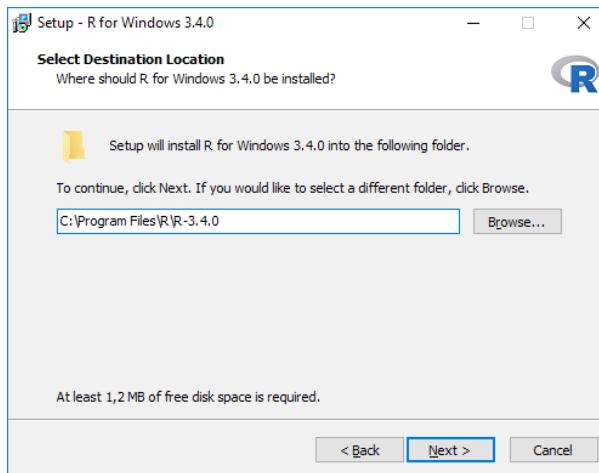


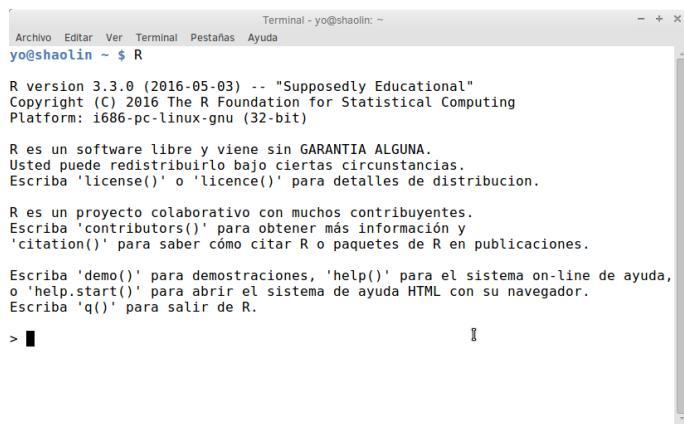
Figure 2: Installer program for Windows. The name of the installation folder is important to set the PATH variable in Windows.

Your attention please! The installation program will suggest you a default path. Do not change it unless you are sure that you have write permissions. For instance, in Windows systems, the volume C: uses to be restricted to users with Administrator privileges. Do not copy the path of figure 2, instead let the R installer to choose the best location for your user.

Once you install R, check that it is ready to run in the default path of your environment. 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. Please, include the R bin folder in the path variable. In the example of figure 2, it is C:\Program Files\R\R-3.4.0\bin

To set the variable we suggest you to read this useful page, the procedure depends on the Windows release <https://www.computerhope.com/issues/ch000549.htm>.

Figure 3 is an screen capture of how your terminal looks after you invoke R if you work in Linux. The appearance in Windows is quite the same.



```
Terminal - yo@shaolin: ~
Archivo Editar Ver Terminal Pestañas Ayuda
yo@shaolin ~ $ R
R version 3.3.0 (2016-05-03) -- "Supposedly Educational"
Copyright (C) 2016 The R Foundation for Statistical Computing
Platform: i686-pc-linux-gnu (32-bit)

R es un software libre y viene sin GARANTIA ALGUNA.
Usted puede redistribuirlo bajo ciertas circunstancias.
Escriba 'license()' o 'licence()' para detalles de distribucion.

R es un proyecto colaborativo con muchos contribuyentes.
Escriba 'contributors()' para obtener más información y
'citation()' para saber cómo citar R o paquetes de R en publicaciones.

Escriba 'demo()' para demostraciones, 'help()' para el sistema on-line de ayuda,
o 'help.start()' para abrir el sistema de ayuda HTML con su navegador.
Escriba 'q()' para salir de R.

> 
```

Figure 3: Launching R from the command shell. The release number (3.3.0 in this example) appears in the first row of information.

2.2 Download the software

Bipartgraph is available as open source software under MIT license in github. Open your browser and go to <https://github.com/jgalgarra/bipartgraph>. Notice the green button **Clone or download** that provides two ways to get the software (Fig. 4).

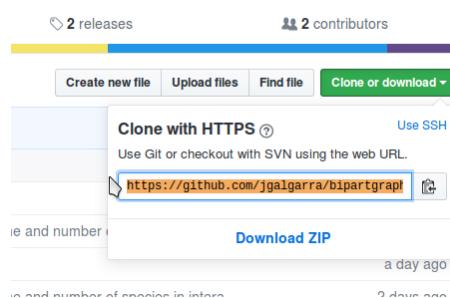


Figure 4: BipartGraph repository at github.com

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.

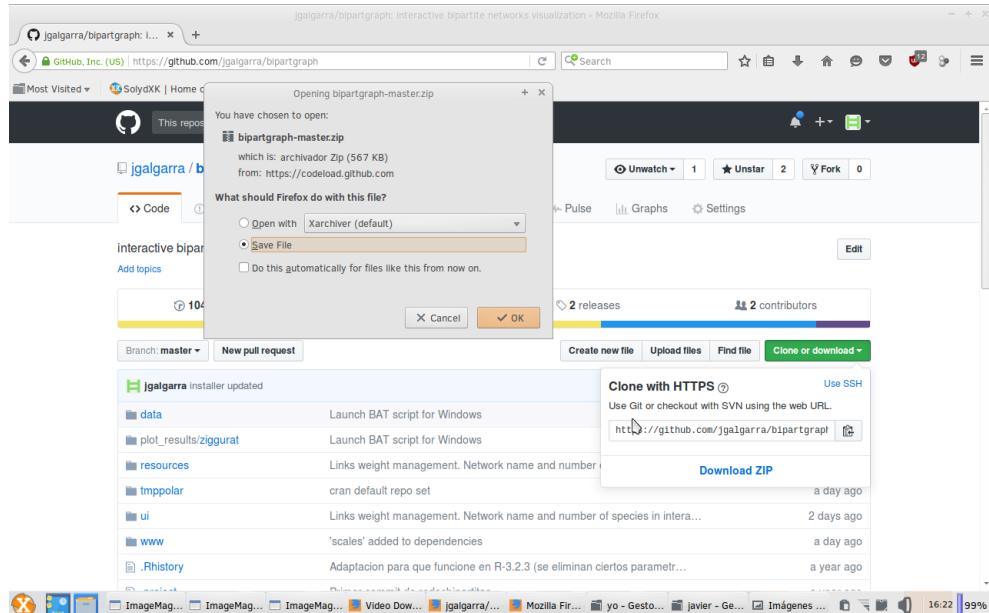


Figure 5: Downloading the *BipartGraph* ZIP file.

OK, but what happens if you are not a software developer and do not want to install `git`? Download the `ZIP` file (fig. 5), uncompress it, and you will have a new directory called `bipartgraph-master` with the same contents than the original repository. The only difference is the directory name.

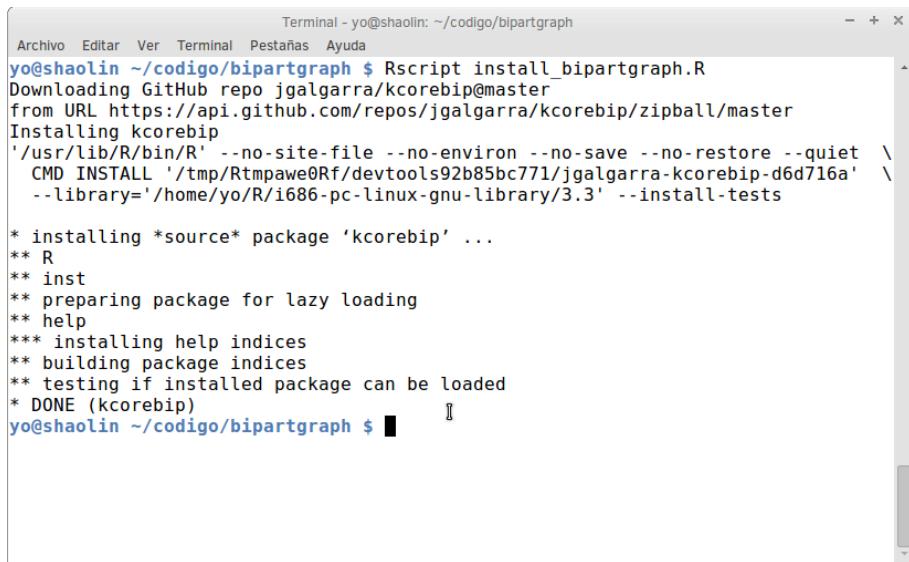
2.3 Setting up the application

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`). There is one script called `bipartgraph_install.R` that will do everything for you. If you are using a computer with `Windows` you may run it double-clicking on the `install_bipartgraph` icon.

It is also possible to launch the installation from the command line, this method is valid for any operating system. Type in the `Linux` terminal:

```
> Rscript install_bipartgraph.R
```



```

Terminal - yo@shaolin: ~/codigo/bipartgraph
Archivo Editar Ver Terminal Pestañas Ayuda
yo@shaolin ~/codigo/bipartgraph $ Rscript install_bipartgraph.R
Downloading GitHub repo jgalgarra/kcorebip@master
from URL https://api.github.com/repos/jgalgarra/kcorebip/zipball/master
Installing kcorebip
'/usr/lib/R/bin/R' --no-site-file --no-environ --no-save --no-restore --quiet \
CMD INSTALL '/tmp/RtmpawE0Rf/devtools92b85bc771/jgalgarra-kcorebip-d6d716a' \
--library='/home/yo/R/i686-pc-linux-gnu-library/3.3' --install-tests

* installing *source* package 'kcorebip' ...
** R
** inst
** preparing package for lazy loading
** help
*** installing help indices
** building package indices
** testing if installed package can be loaded
* DONE (kcorebip)
yo@shaolin ~/codigo/bipartgraph $ █

```

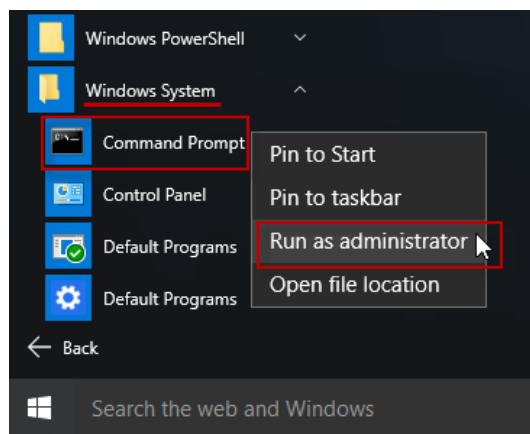
Figure 6: Running the installation script.

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

Depending on your user privileges, this command may fail in Linux if the current user has no permissions to write in the packages directory. To overcome that problem type instead:

```
> sudo Rscript install_bipartgraph.R
```

In Windows you may find troubles if you are not running the command line as Administrator. You get a message telling that the R library directory is not writable. Try opening the command line like this:



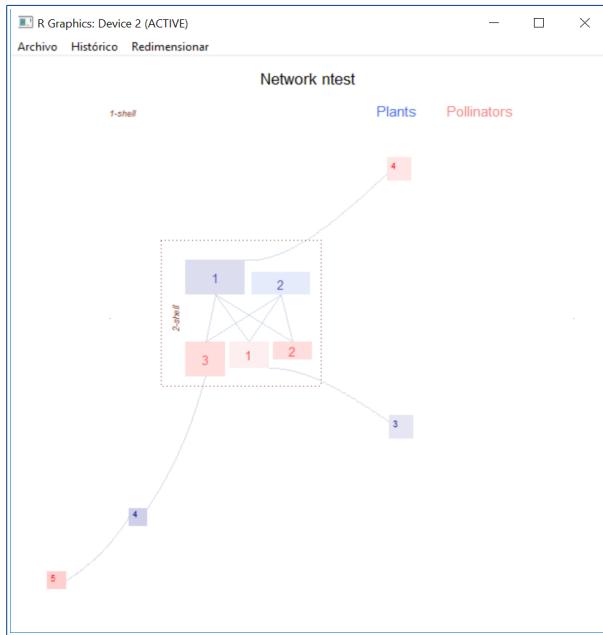
Once the script finishes, the installation procedure is complete.

Note for R smarties, the script installs the `kcorebip` package from the `github` repository `jgalgarra/kcorebip`, all the dependencies, and a full Shiny environment.

Check that everything was installed properly. Open a new terminal (or command line), go to to the `bipartgraph` directory, or `bipartgraph-master` if you installed from the ZIP file and type:

```
> Rscript plot_test.R
```

Can you see a window with this plot?. If so, the installation was OK.



The application is ready. Windows: double click on the `bipartgraph_win_launcher` icon. Your default browser will display the landing page.

Linux, launch this script:

```
> ./bipartgraph_linux_launcher
```

It may happen that for security reasons your computer does not allow opening a web browser from another application and you would get an error message. In that case, there is a different procedure to launch the command line:

```
> Rscript bipartgraph.R
```

Open your web broser and type in the navigation bar <http://localhost:8080>. If everything went right you have reached the landing page. Click on the Data file box and select `M_PL_008.csv`. Click on the Interactive Ziggurat tab (upper menu) and you will see the network plot (fig. 7).

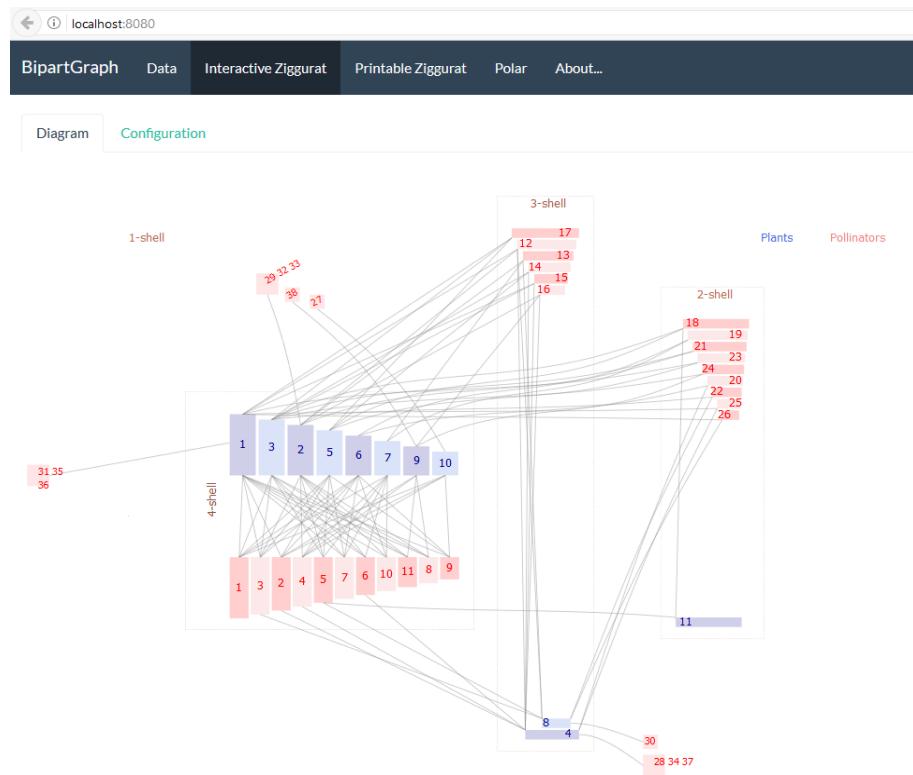


Figure 7: Ziggurat plot

3 Data management

BipartGraph is a tool to plot ecological communities, but you may use it with any bipartite network. In this guide we use examples of mutualism and parasitism well documented in the [web of life](#) database [2].

	A	B	C	D	E	F	G	H	I	J
1.		Echium wildpretii	Pimpinella cumbrae	Pterocephalus lasiospermus	Mentha longifolia	Erysimum scorpiarium	Spartocytisus supranubius	Tolpis webbi	Argyranthemum teneriffae	Scrophularia
2.	Anastoechus latifrons	1	0	0	1	1	1	1	1	0
3.	Anthophora alluaudi	1	0	0	1	1	1	1	0	0
4.	Apis mellifera	1	1	1	0	1	1	1	0	1
5.	Eudynnerus reflexus	0	1	0	1	0	1	1	1	0
6.	Geran hesperidon	0	1	1	0	1	0	0	1	1
7.	Eristalis tenax	1	1	1	1	0	0	0	1	0
8.	Megachile canariensis	1	0	1	1	1	1	1	1	0
9.	Anthrax anthrax	1	1	1	0	0	0	0	0	0
10.	Eucera gracilipes	1	0	0	0	1	1	1	0	0
11.	Hyleaon canariensis	1	1	0	0	0	1	1	1	0
12.	LasioGLOSSUM viride	1	1	1	0	0	0	0	0	0
13.	Linnaemyia soror	1	1	0	1	0	0	0	0	1
14.	Cephalodromia sp1 M_PL_008	0	1	0	0	0	0	0	1	1
15.	Cyclinus webbianus	0	0	1	1	1	0	0	0	0
16.	Estheria simonyi	1	0	1	1	0	0	0	0	0
17.	LasioGLOSSUM acutirostris	0	1	0	1	0	0	0	0	0
18.	Melecta curvispina	1	0	1	0	1	0	0	0	0
19.	Osmia canariensis	0	0	1	0	1	0	0	0	0
20.	Andrena wollestoni	0	0	0	0	0	1	1	1	0
21.	Colletes dimidiatus	0	0	0	0	1	0	1	0	0
22.	Gasteruption 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.	Stomorhinia lunata	1	0	0	1	0	0	0	0	0
27.	Unidentified sp1 M_PL_008	1	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	0	1	0	0	0	0
30.	Dermatoches 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.	Sennaria canariensis	1	0	0	0	0	0	0	0	0

Figure 8: Interaction matrix of network M_PL_008 [3]

Data are stored as `.csv` files. Fields are separated by commas, first row stores the binomial names of guild A species and first column those of guild B. When you upload your own data, remember that the application waits to found there that information. If you do not have it, or it does not make sense at all in your environment, leave the first row and the first column filled with void strings. *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 real number different of 0. 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.

The screenshot shows the BipartGraph interface with a dark header bar containing links for BipartGraph, Data, Interactive Ziggurat, Printable Ziggurat, Polar, and About... A secondary navigation bar below it has Select data and Manage files. On the left, there's a file upload section with a 'File uploading' button and a 'Last uploaded files' table showing one entry: 'burkle.csv'. Below this is a 'Upload files' section with a 'Browse...' button and a 'burkle.csv' preview.

Figure 9: 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 it next time you work with the same file.

The **Network Analysis** 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 screenshot shows the BipartGraph interface with a dark header bar containing links for BipartGraph, Data, Interactive Ziggurat, Printable Ziggurat, Polar, and About... A secondary navigation bar below it has Select data and Manage files. On the left, there's a 'Data file' section with a dropdown menu showing 'burkle.csv'. Below this are 'Guild A label' and 'Guild B label' sections, each with a dropdown menu showing 'Plant' and 'Pollinator' respectively. To the right is a 'Network Analysis' button. Further down is a 'File content' section with a table showing the interaction matrix for 24 species in Guild A and 54 species in Guild B. The table includes columns for X, Andrena_arabis, Andrena_carlini, Andrena_cressonii, Andrena_distans, Andrena_ergegeniae, Andrena_erythronii, Andrena_forbesii, Andrena_geranii, and Andrena_laciniata. At the bottom, there's a search bar and a page navigation section showing pages 1, 2, 3, and Next.

Figure 10: Ziggurat plot of an eating fruit birds network in Brazil [3]

4 The ziggurat graph

The ziggurat graph is an original kind of visualization. The idea behind it is splitting species in sets by their *k-shell* numbers. Each of these groups are represented as small ziggurats.

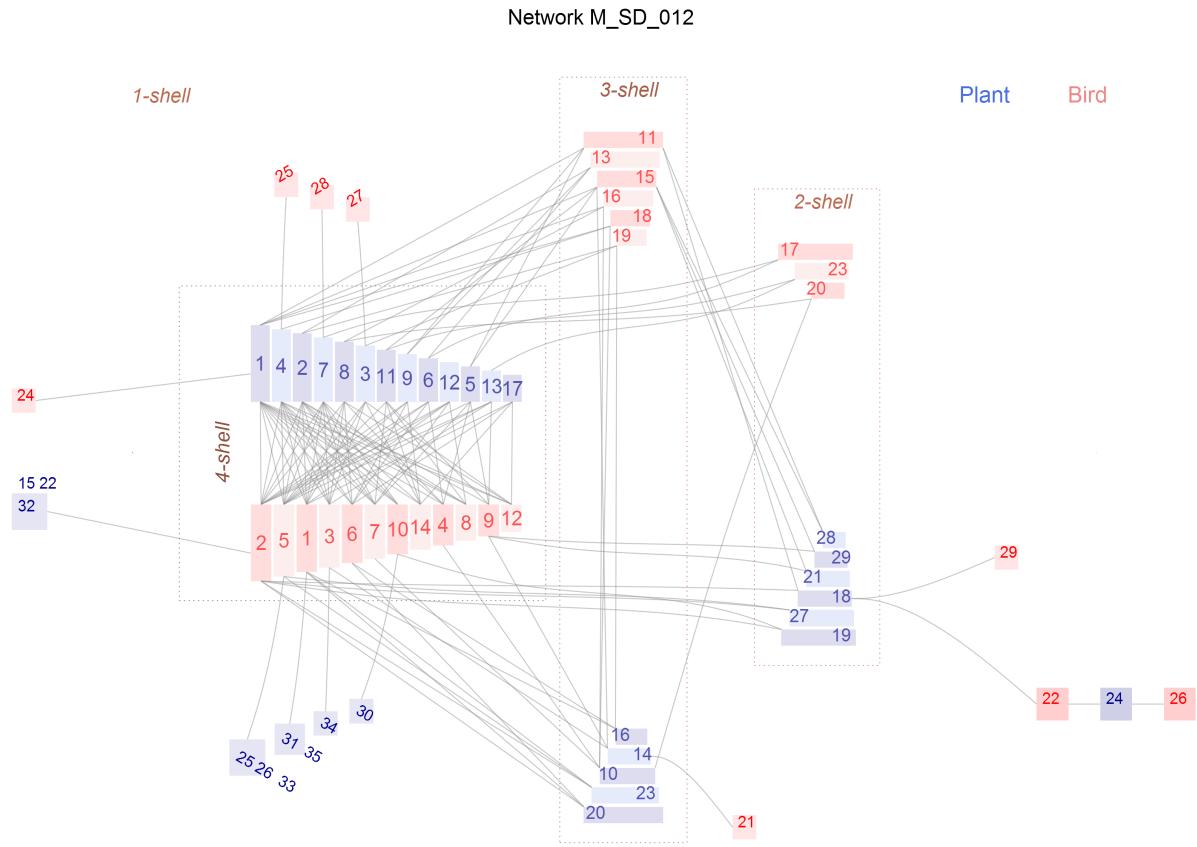


Figure 11: Ziggurat plot of an eating fruit birds network in Brazil [3]

Networks are very different in size and connectivity but they all share building units that will help you to get a clean view of the structure (fig. 12). The building blocks are **nodes** and **links**. Bipartite networks have two kind of nodes that conventionally we call **guilds**. In this example there are *plants* (guild A) and frugivore *birds* (guild B). If two species interact, there is a link between them, for instance *bird 19* eats fruits of *plant 18*. The bird feeds on the plant and foster its reproduction by seed dispersal. Links among species of the same guild do not exist in bipartite networks.

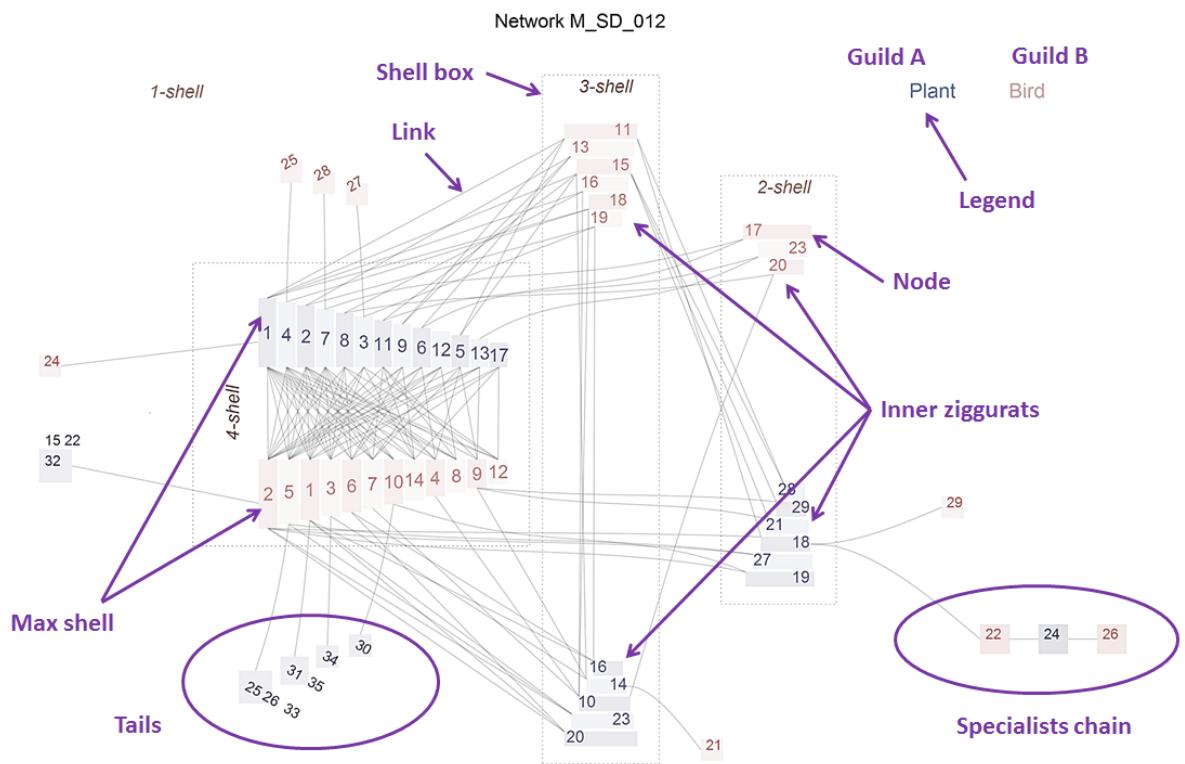


Figure 12: Elements of the ziggurat plot

All links have the same color and no label. Nodes are filled with the color of their guild, with two slightly different tones to help visual perception. Each species is labeled with its order in the input file. So, *plant 1* is the species recorded in column 1 and *bird 5* in row 5. This is the only meaning of this number.

Node size does not convey any information in the ziggurat graph, 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 16, 14, 10, 23 and 20* belong to the *3-shell*, this is the only fact relevant for this plot.

The **legend** tells us how we choose to name each guild, the left element is always *guild A*. Ziggurats 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**. This shell is located at the centre of the plot, with the species of both guilds in two mirrored triangles. Shells of lower indexes (3 and 2) are arranged following an almond distribution. We call them **inner ziggurats**.

Nodes of *1-shell* are scattered around the plot. They may be part of two structures, **tails** and **specialists chains**. A tail is just one species of *1-shell* linked to one species of an higher shell of the opposite guild, for instance, *bird 27* and *plant 30* are tails.

When multiple species of *1-shell* are connected to the same node of any of the ziggurats, they

are clustered to reduce the number of lines. *Plants* 15, 22 and 32 are linked to the generalist *bird* 2.

Specialists chains are much less common than tails. They are set of species of *1-shell* linked to species of *1-shell* of the other guild. *Bird* 26 – *plant* 24 – *plant* 18 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 overcross the boxes. Other structural details are easy to catch with this visualization. It is also clear why *bird species* 26 and *plant* 24 are in a dangerous position. They depend on another specialist, *pollinator* 22, that has only one link with *2-shell*.

Sometimes, the field observers record species not linked to the giant component. These **outsider** species are plotted as a subnetwork under the ziggurat plot (fig. 13).

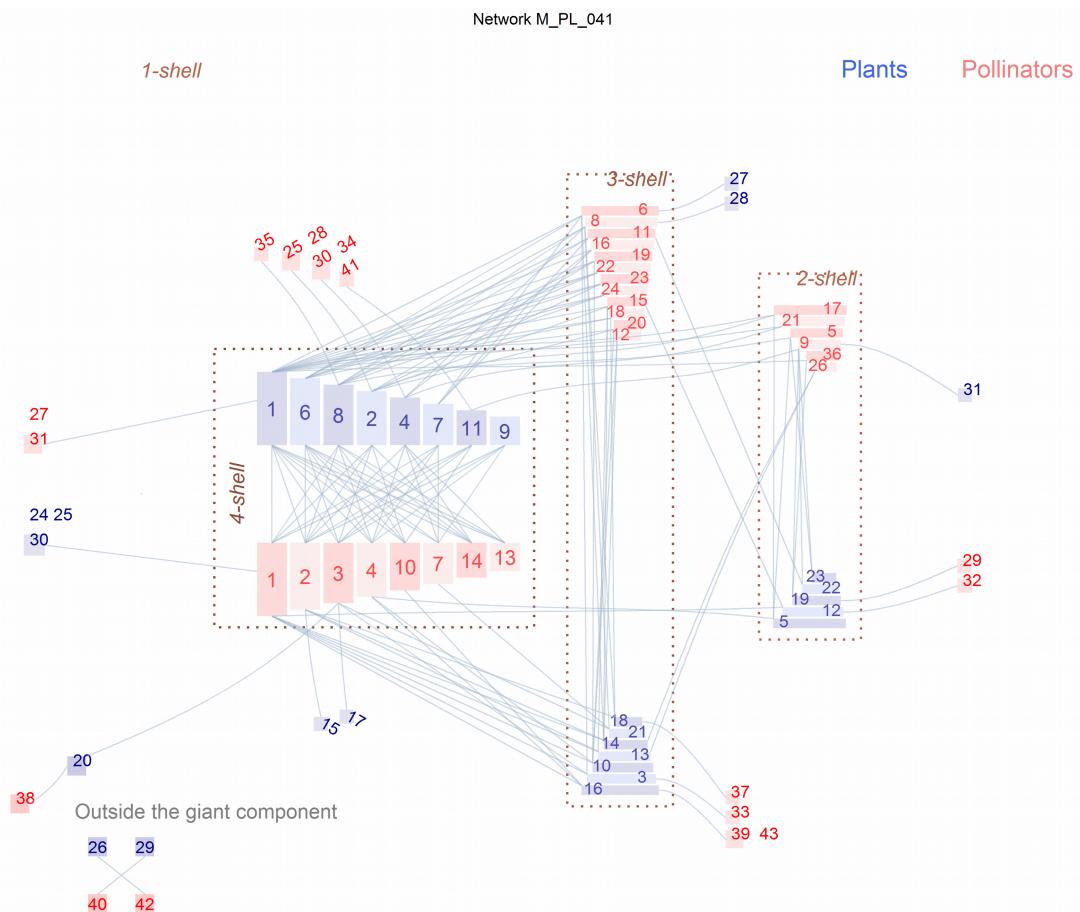


Figure 13: Plant – pollinator community in Syndicate, Dominica Island [4].

4.1 Explore the interactive ziggurat

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

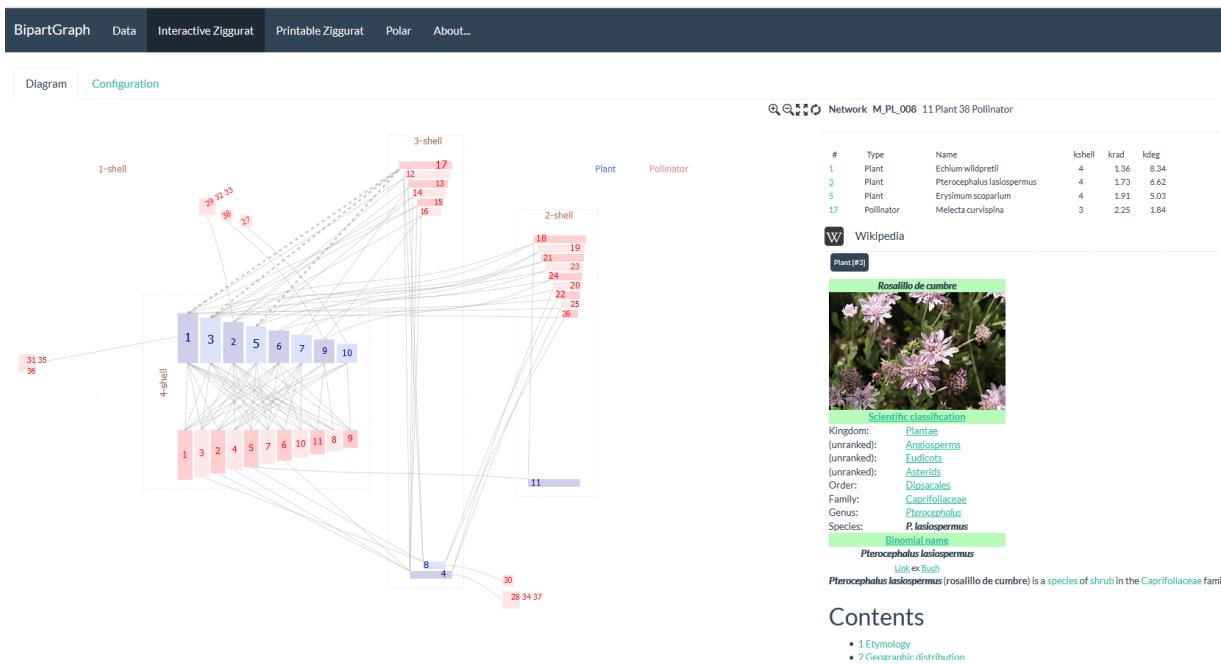
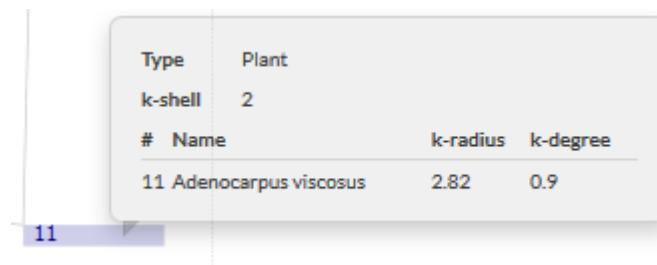


Figure 14: Interactive Ziggurat

When you pass the mouse over one species box, a tooltip shows its binomial name and k -parameters.



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 bigger.

On the right panel, you may see the information table of the selected species (*Pterocephalus lasiospermus* in fig. 14). 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 parasite species, 10 host species and 61 links. If it is the first time you load it, change the **Guild A** label to Parasite and **Guild B** label to Host in the **Data** panel. **BipartGraph** will remember this setting next time you load these data. Click **Interactive Ziggurat** on the main menu, and you will get a fancy default visualization of this small network (fig. 16).

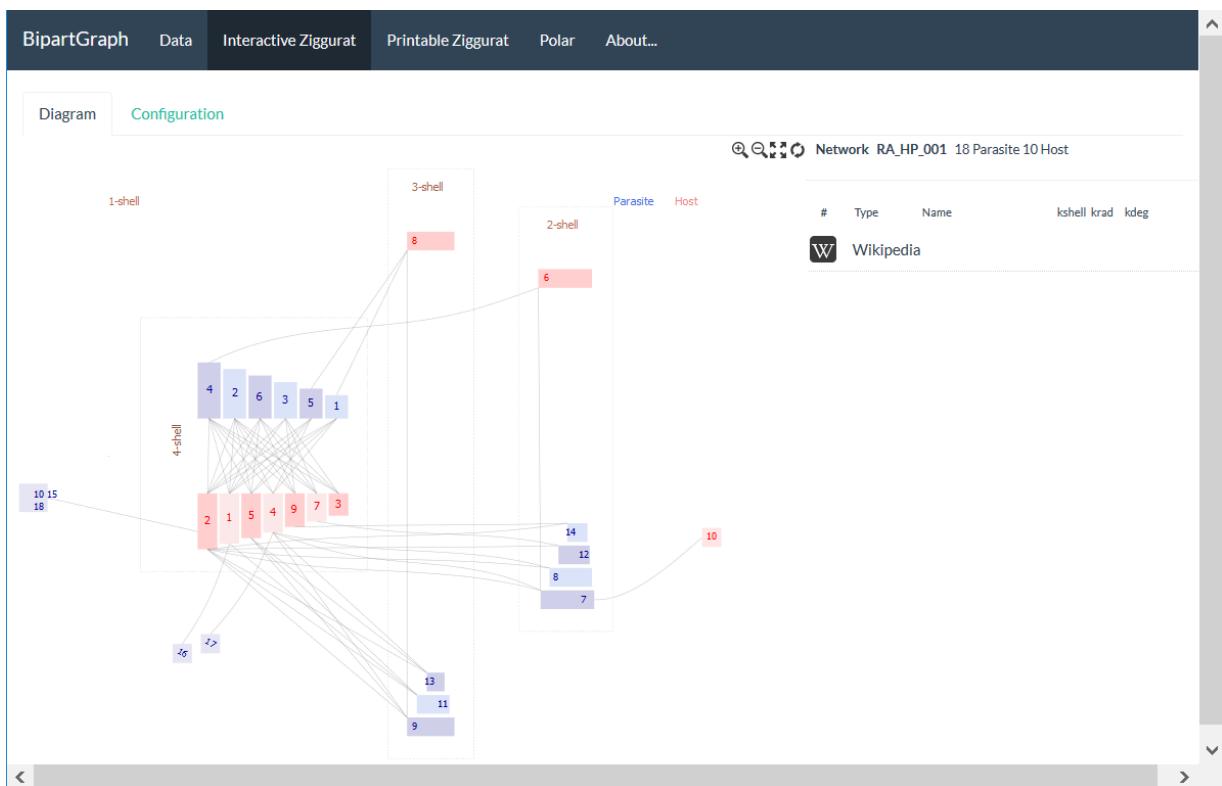


Figure 15: Host – parasite network in Azharia [5].

Click on **Configuration** tab and the first thing you see are the link controls. There are 5 of them (fig. 16).

- **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, all links 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 interaction matrix) all links have the same width. If weighted, **Weight aggregation** lets you choose to make their width proportional to the interaction strength (**In** or \log_{10} 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).

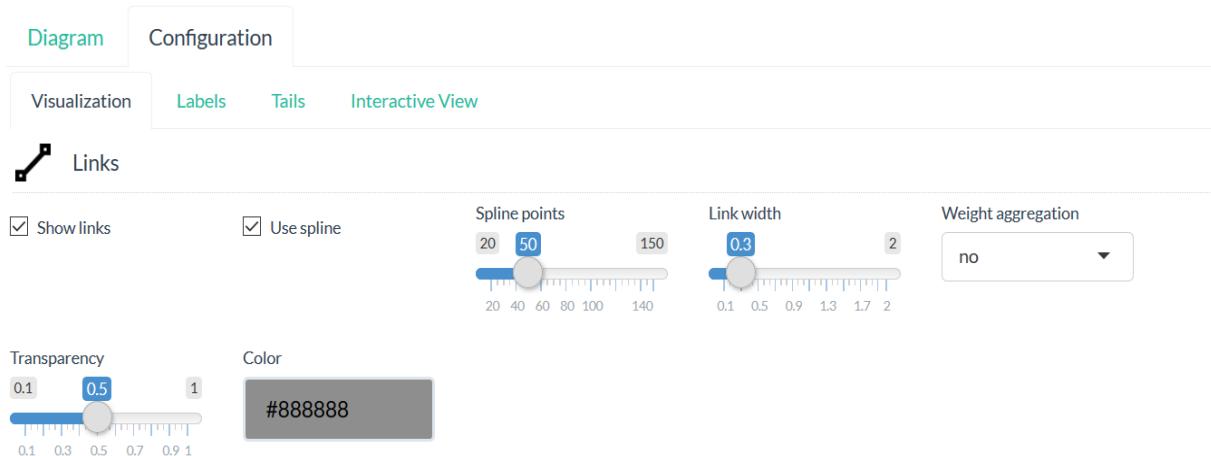


Figure 16: Link configuration control.

Let's go back to figure 15 to make some adjustments. First, uncheck the **Use spline** box (the **Spline points** control has no meaning if you use straight line links). We want to make the width proportional to the interaction strength but just in this moment we do not remember if the network is weighted or not. Click **Data** on the main menu and observe the **File Content**. The interaction matrix is not binary.

Click again on **Interactive Ziggurat / Configuration**. We select **In**, that means that the width of each link will be proportional to the natural logarithm of its strength (the value recorded in the interaction matrix).

To test the effect of other configuration parameter, increase the **Link width** slider up to 0.5, move the **Transparency** control to 0.3 and pick a green tone color **#087007** (you can write it in the **Color** box).

That's all, now it's time to see how the ziggurat changes. Click on the **Diagram** tab and the software will plot again the network (fig. 17). 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. 15. On the other hand, you can detect that *host 6* is much prone to have parasites of *species 7* than of *species 4*. We have learned how to modify **links**, now we move on to more exciting elements of the graph.

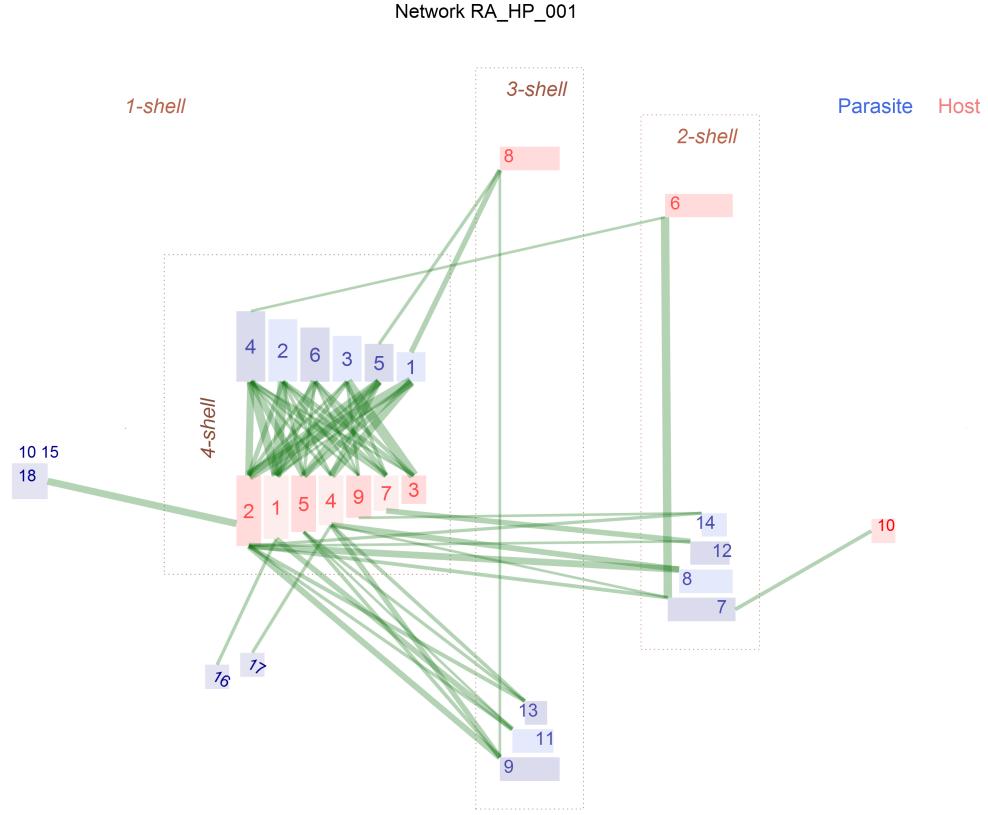
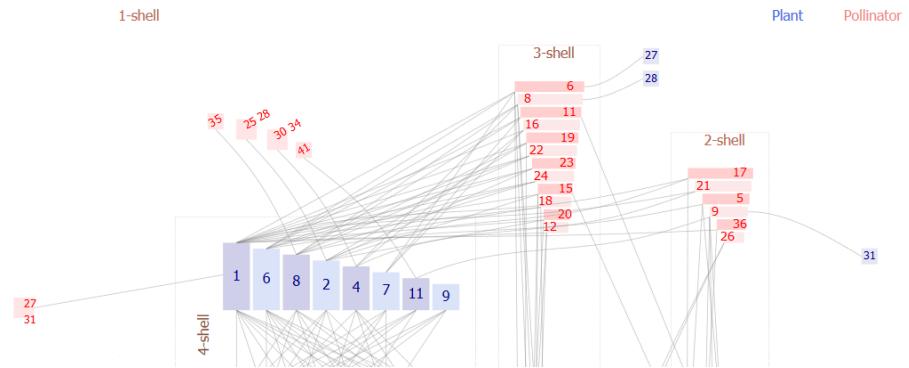


Figure 17: Host – parasite network in Azharia [5], with modified link properties.

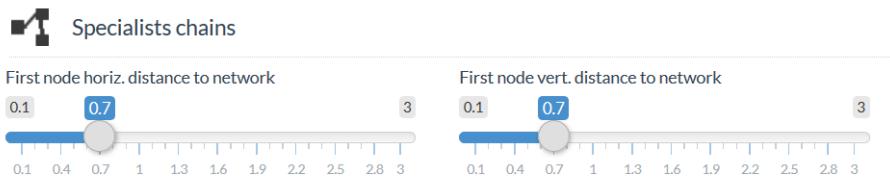
The network of figure 13 is bigger. There are some details that need improvement, for instance the height of the nodes of the **inner ziggurats**, they look smashed. Go to Configuration, move the Nodes height slider to 1.25 and click on Diagram again.



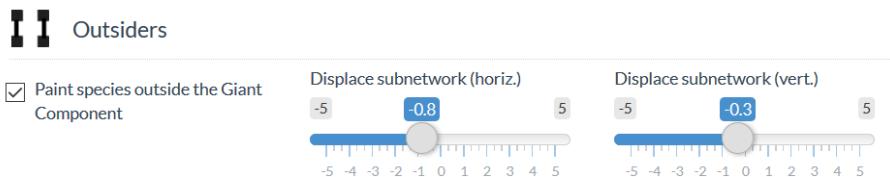
Boxes are fancier now, but links from *2-shell* towards *4-shell* now cross the ziggurat of pollinators of *3-shell*. We can move it upwards or downwards with the **Inner ziggurats vertical displacement control**. The ziggurat that is troubling you is the *3-shell* of guild B (if you do not know which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

Please, move the **3-shell B** slider to 0.2 (roughly move it up a 20% of the original position). The **chain of specialists** in the lower left end of figure 13 is a bit too long. Click the **Tails tab**

and reduce the distance.



Finally, move the **outsiders**, clicking on the Visualization tab:



After all this changes, the ziggurat plot that you get is the figure 18. Of course, you could keep on modifying parameters.

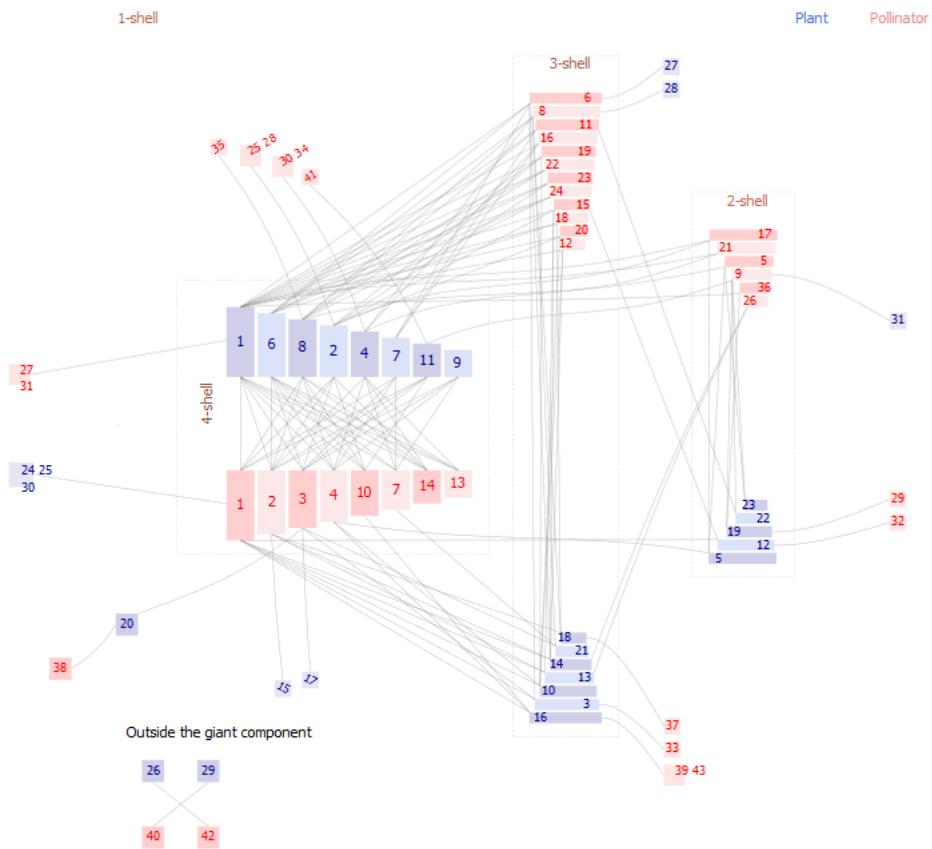


Figure 18: Ziggurat graph of a plant – pollinator community in Syndicate, Dominica Island [4] after visual adjustments.

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.

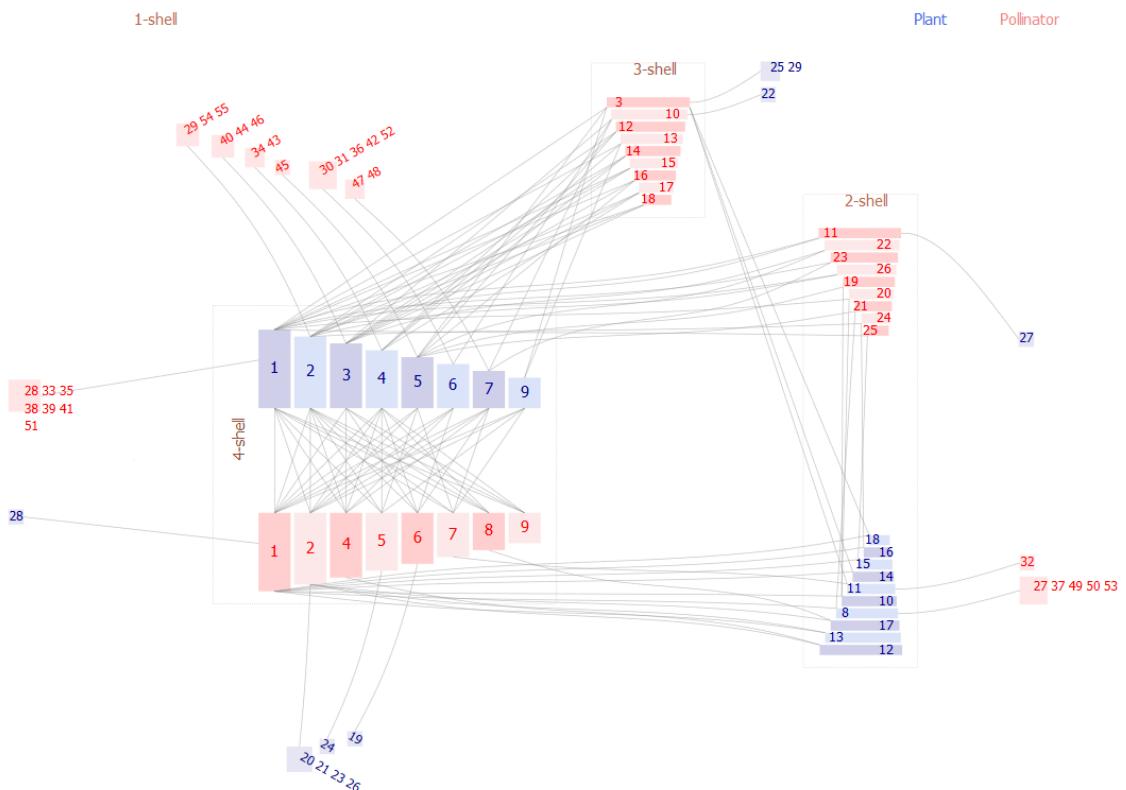
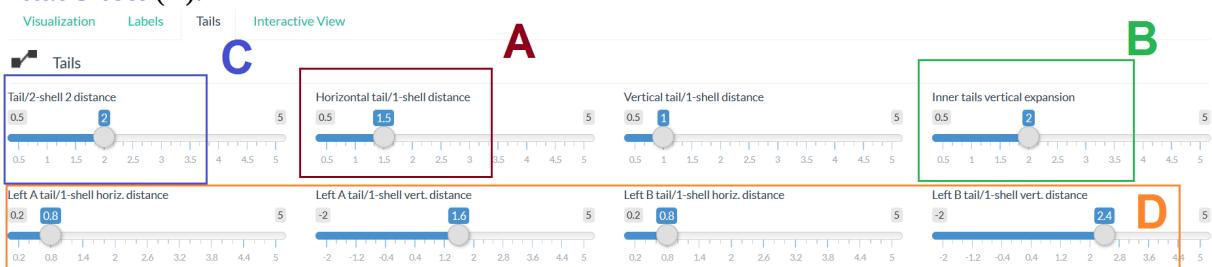


Figure 19: Ziggurat graph of a plant – pollinator in Garajonay (Spain), recorded by Jens Olesen. Unpublished.

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 22, 25 and 29. 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**).



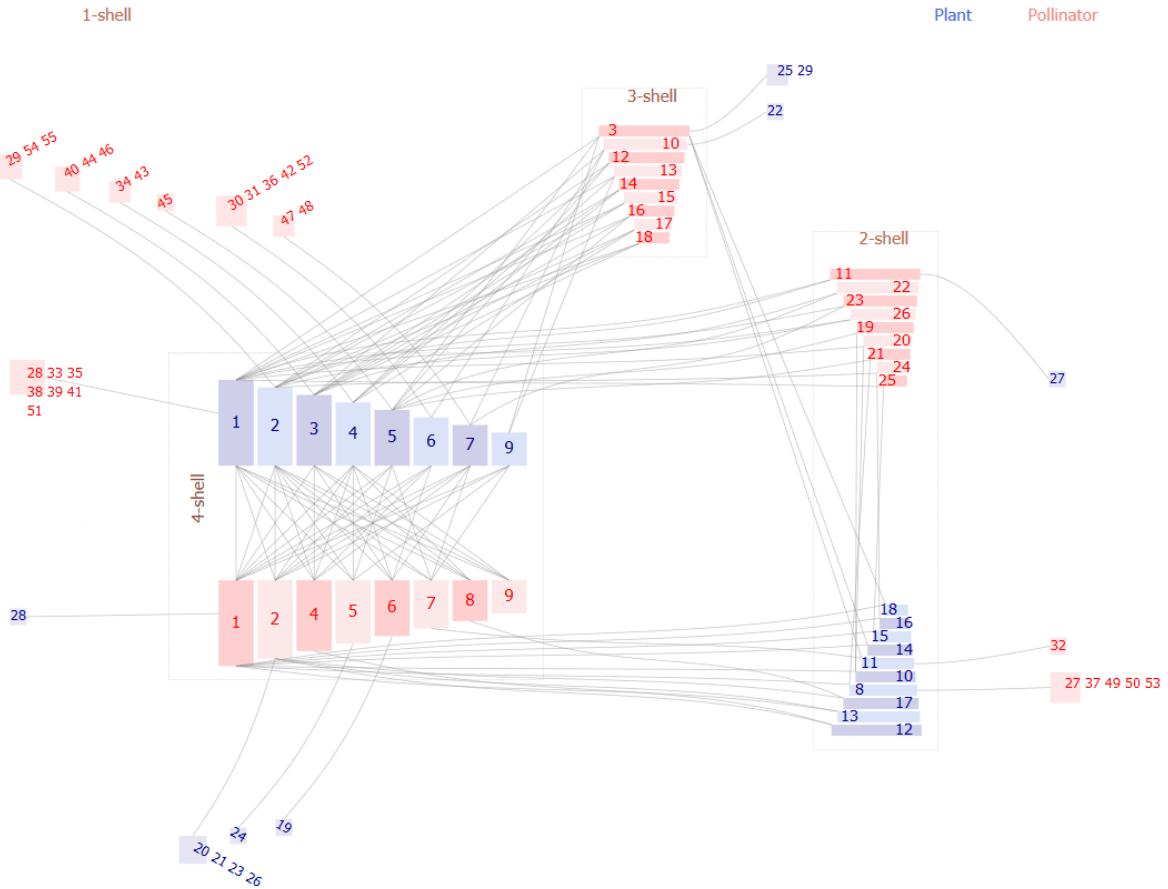
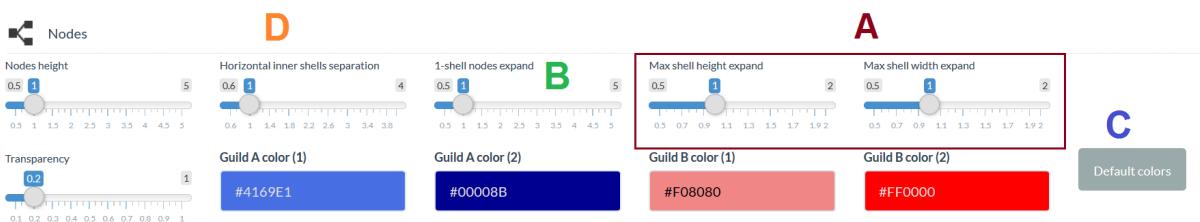


Figure 20: Ziggurat graph of a plant – pollinator in Garajonay (Spain), after visual adjustments.

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. In case you want to return to the default values, just press the panic button (**C**). Transparency works as explained above when talking about **links**. The horizontal inner shells separation widens the horizontal gap between ziggurats (**D**).



Let's take a small portion of network `M_PL_012` 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.

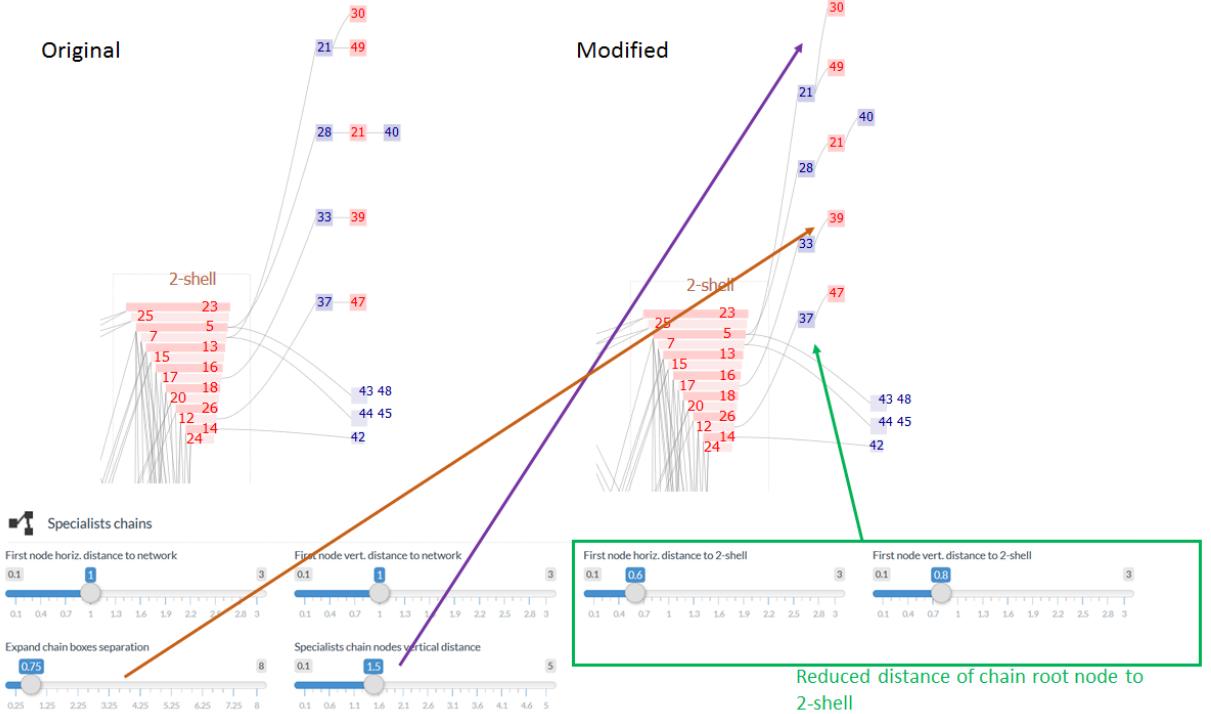


Figure 21: Changing the configuration of the chains of specialists.

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

4.3 Printable ziggurat

Once you have got a clean and nice ziggurat it is quite possible that you want to produce a high quality plot for your research. That is what the **Printable Ziggurat** 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 **Printable Ziggurat** and click the button **Plot Download**. Your broser will download a file called `M_PL_012-ziggurat.png` (fig. 22). Compare it with the interactive plot (fig. 19). It is almost identical, but there are minor visual differences. In the printed plot the name of the network is displayed on top, and perhaps the sizes of labels and legend are slightly different.

The interactive and printed plots are built with two different techonologies, 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 be different. In **Interactive Ziggurat > Interactive View** there is a control called **Text and links rescaling**. The default value is 1, if you increase it, the size of labels and width of the links of the interactive plot will grow compared to the printed ones. It may be useful to adjust it once if dimensions are rather different.

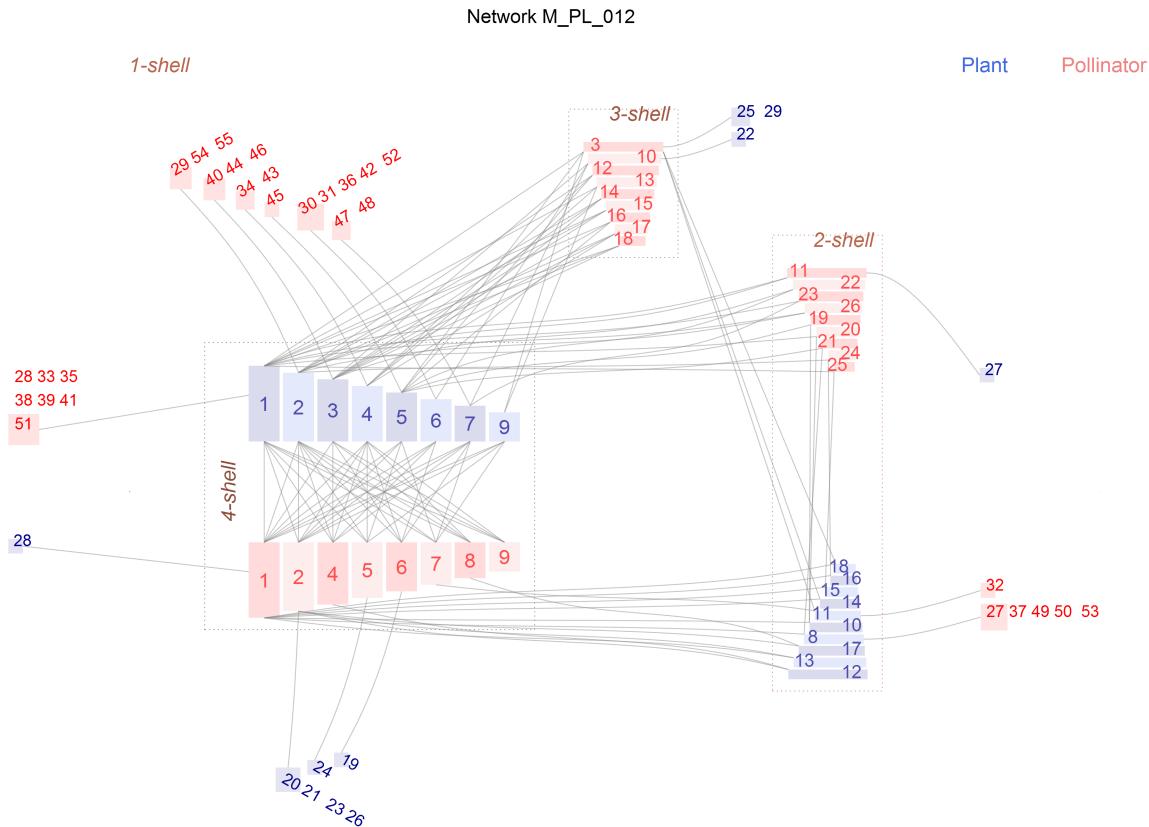


Figure 22: Printed Ziggurat graph of a plant – pollinator in Garajonay (Spain).

The other control, **Top crop (%)**, allows to cut the upper portion of the interactive ziggurat if there is too much white space. This may happen with very small networks.

Go back to the **Printable Ziggurat** pane. Options are quite straightforward, you may change the **Paper size**, orientation (**Landscape**), resolution and **Background Color** (do not do it unless you are very sure of what you want). 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.

When you get a very nice printed ziggurat you will want to save the 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, this is what you have to do. 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`

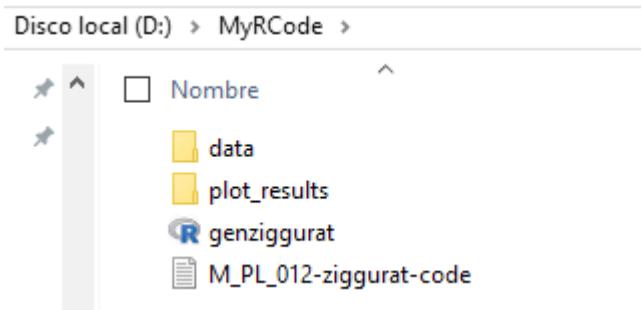
inside that directory and copy there the input data files, for instance the `M_PL_012.csv` that you used as an example and lives in `bipartigraph/data`.

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")
```

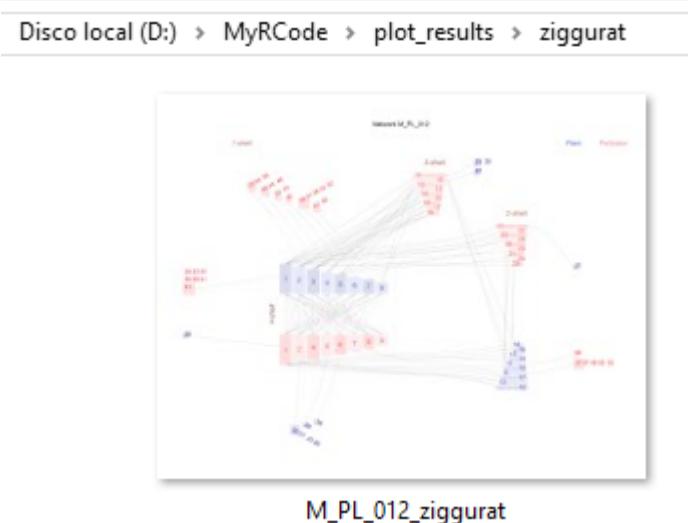
Your new directory should look like that, with the file `M_PL_012.csv` in the `data` folder and an empty `ziggurat` folder inside `plot_results`.



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`.

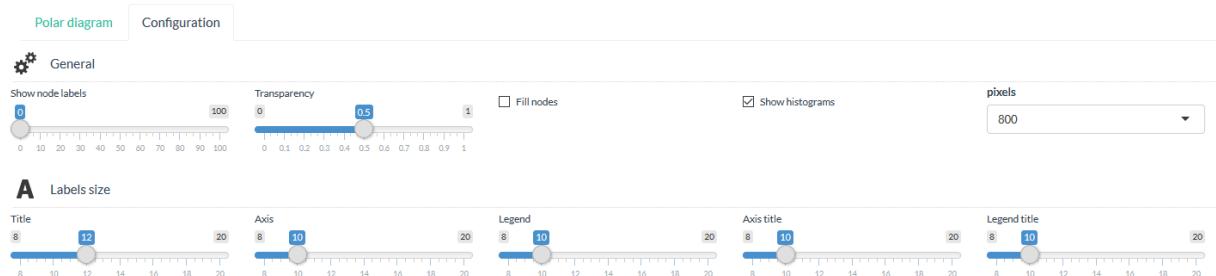


5 The polar graph

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. [6] 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 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.

The **Show histograms** checkbox shows or hides the *k-magnitude* histograms under the polar plot. The **Labels size** control plays the same role than in the ziggurat.

Once the plot is displayed you may download it or download 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 you do not need to worry about your screen resolution.

Network M_PL_041 NODF: 25.30 Modularity: 0.3502

Avg k-radius: 2.51 Avg k-degree: 2.11

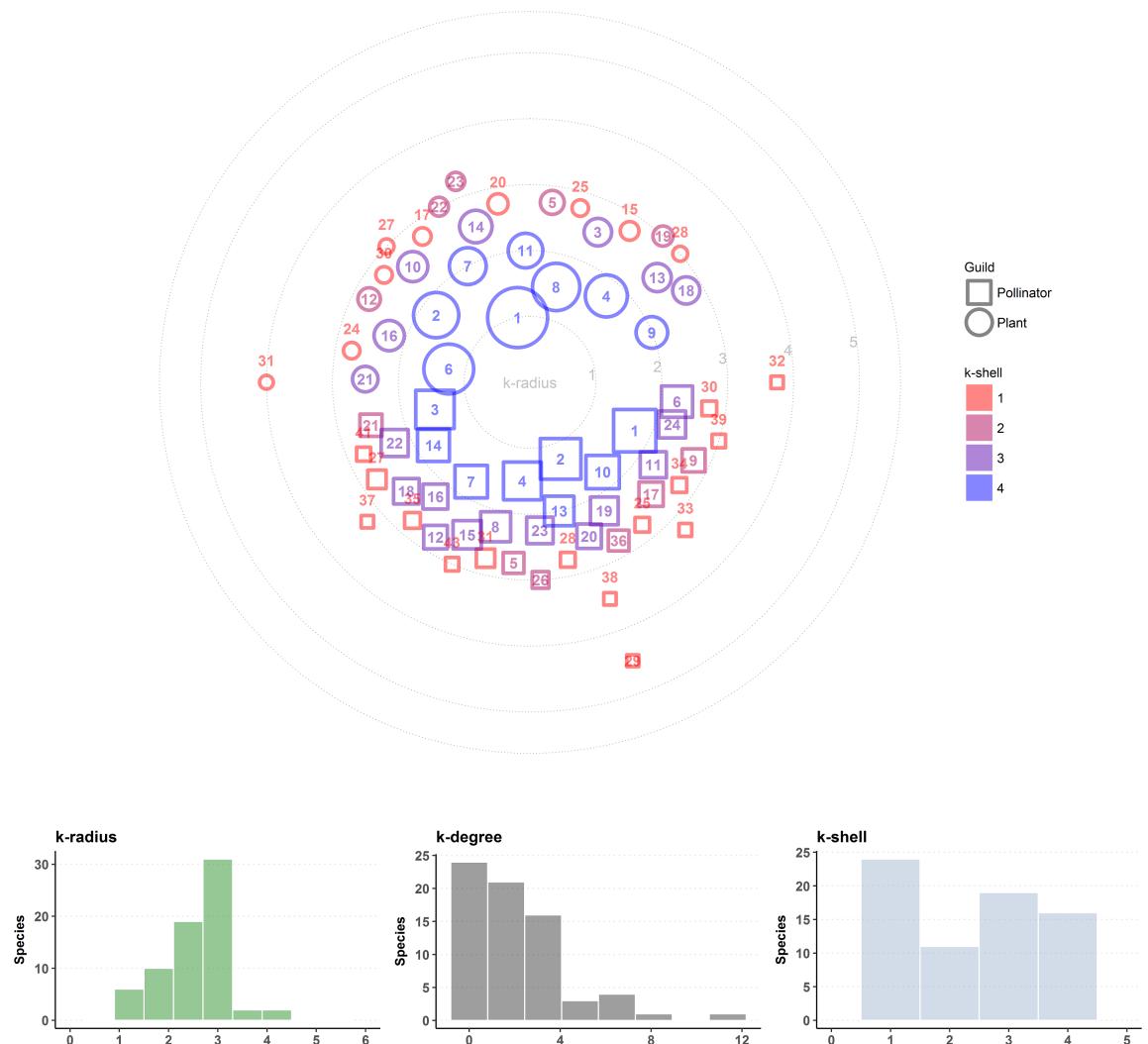


Figure 23: Polar graph of a plant - pollinator in Garajonay (Spain), including labels and histograms. Compare with fig. 19

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

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 can't change them.

References

- [1] GARCÍA-ALGARRA J, PASTOR JM, IRIONDO JM, GALEANO J., 2017. Ranking of critical species to preserve the functionality of mutualistic networks using the *k*-core decomposition. *PeerJ* 5:e3321 <https://doi.org/10.7717/peerj.3321>
- [2] BASCOMPTE, Jordi. Disentangling the web of life. *Science*, 2009, vol. 325, no 5939, p. 416–419.
- [3] GALETTI, M. and PIZO, MA., 1996. Fruit eating birds in a forest fragment in southeastern Brazil. *Ararajuba*, vol. 4, no. 2, p. 71–79.
- [4] INGVERSEN, T. T., 2006. *Plant-pollinator interactions on Jamaica and Dominica: The centrality, asymmetry and modularity of networks*. Master's thesis, Univeristy of Aarhus, Denmark.
- [5] HADFIELD, Jarrod D., et al. A tale of two phylogenies: comparative analyses of ecological interactions. *The American Naturalist*, 2013, vol. 183, no 2, p. 174–187
- [6] ALVAREZ-HAMELIN, J. Ignacio, et al. Large scale networks fingerprinting and visualization using the *k*-core decomposition. *Advances in neural information processing systems*, 2006, vol. 18, p. 41.