# Using the kcorebip package
Version 1.0

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December 27, 2024

## Introduction

This package performs the *k-core decomposition* analysis of a bipartite graph and provides two classical ways to plot it (*bipartite* and *matrix*), and three original ways: *ziggurat*, *polar* and *chilopod* . It works for any kind of bipartite network, but as it was developed to study ecological mutualistic communities you will find terminology and examples of that research field throughout this text[GA+18; GA+17].

## Install kcorebip

To install `kcorebip` the package `devtools` should be available in your computer. Load it with

```
library("devtools")
```
and then issue the following command:

```
install_github("jgalgarra/kcorebip")
```
**Warning**. A `gcc` compiler is required to install the packge. If you are a developer and you know you do have 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/

## Decomposition and definition of k-magnitudes

The *k-decomposition* is an iterative algorithm that prunes links of nodes with degree equal or less than $k$ [Sei83]. The process starts pruning nodes with degree 1 until all the remaining nodes have two or more links. Then it

with $k = 2$, and so on. After performing the *k-decomposition*, each species belongs to one of the *k-shells*. The highest value of $k$, i.e $ks_{max}$, corresponds to the innermost *core* $ks_{max} \equiv C^{A,B}$. For each *k-shell* there are two subsets, one per guild ($A$ and $B$), that we call $K_j^A, K_j^B$ where $j$ is the *k-shell* index.

In order to quantify the distance from a node to the innermost shell of the partner guild, we compute the average of the shortest paths to each node within that set. We define the $k_{radius}$ of node $m$ of class $A$ as the average distance to the species of $C^B$:

$$k_{radius}^A(m) = \frac{1}{\mid C^B \mid} \sum_{j \in C^B} dist_{mj} \qquad m \in A \qquad (1)$$

where $dist_{mj}$ is the shortest path from species $m$ to each of the $j$ species that belong to $C^B$. The same definition is valid for species of guild $B$ computing the average distance to $C^A$ instead. The minimum possible radius value is 1 for a node of the maximum shell that is directly linked to each node of the maximum shell set of the opposite guild.
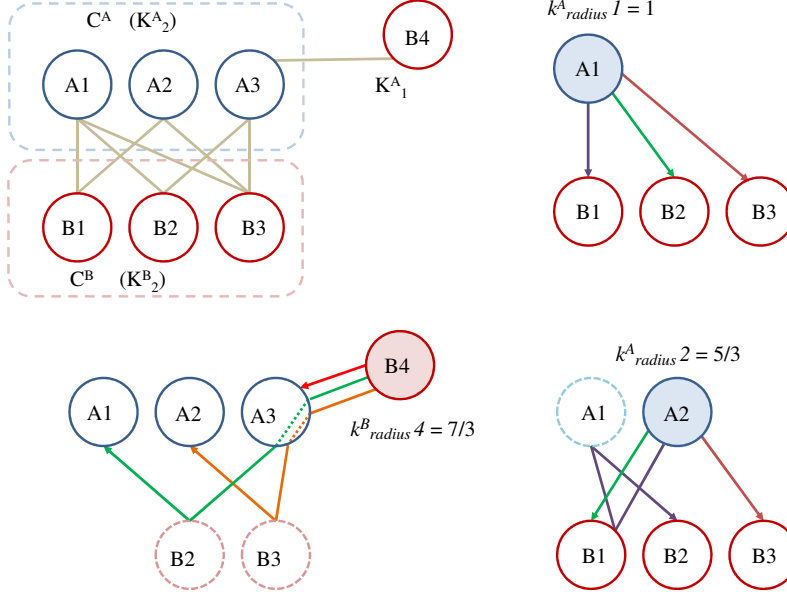


Figure 1: Examples of $k_{radius}$ in a fictional network.

Figure 1 is a toy bipartite network, with only seven nodes. The upper left graph shows the network structure. In the upper right figure, species $A1$ belongs to $C^A$. The distance to each node of $C^B$ is 1, so its $k_{radius1}(1)$ is 1. In the bottom right figure, node $A2$ also belongs to $C^A$ but there is not any direct link with $B2$, so the distance between them is 3 and $k_{radius}(2)$ is $\frac{5}{3}$. In the bottom left figure, node $B4$ is not part of $C^B$, and as may be expected, the value of its $k_{radius}$ is higher.

A global value can be defined averaging this magnitude across the network:

$$\overline{k}_{radius} = \frac{1}{\mid A \cup B \mid} \sum_{l \in A \cup B} k_{radius}(l) \tag{2}$$

For the network in Figure 1, the value is $11/7$.

$k_{radius}$ is a useful measure of network compactness but it does not work as measure of centrality. For instance, its value for an isolated specialist linked to the maximum core is low. To address this issue, we define a second $k$-magnitude, called $k_{degree}$:

$$k_{degree}^A(m) = \sum_{j} \frac{a_{mj}}{k_{radius}j} \quad m \in A, \forall j \in B \tag{3}$$

where $a_{mj}$ is the element of the interaction matrix that represents the link. So the $k_{degree}m$ is the sum of the inverse of $k_{radius}$ for each node linked to $m$. A node of the innermost shell will have a high degree, whereas specialists have only one or two links and so a low $k_{degree}$. In the example of Figure 1, this magnitude is $1 + 3/5 + 3/5 = 11/5$ for node $B3$, while only $3/7$ for node $B4$.

### Input file format

We use the file format of web of life ecological data collection [Bas09]. Data are stored as `.csv` files. Species of guild $a$ are distributed by colums, and those of guild $b$ by rows. First colum contains the labels of guild b nodes, and first row, the labels of guild a. 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 number.

The naming convention is $M\_XX\_NNN.csv$ where $XX$ is the type, $PL$ for pollinator networks and $SD$ for seed dispersers, and $NNN$ a serial number. Anyway, you are free to call your file in the most convenient way for you.

| | A | B | C | D | E |
|---|---|---|---|---|---|
| 1 | | Juniperus phoenicea | Osyris quadripartita | Corema album | Phillyrea angustifolia |
| 2 | Turdus merula | 1 | 1 | 1 | 1 |
| 3 | Turdus iliacus | 1 | 1 | 0 | 0 |
| 4 | Turdus philomelos | 1 | 1 | 0 | 0 |
| 5 | Turdus torquatus | 1 | 0 | 0 | 0 |
| 6 | Turdus viscivorus | 1 | 0 | 0 | 0 |
| 7 | | | | | |

Figure 2: Examples of input file, the seed disperser network 029 of web of life site.

From release 1.0 on, the input file may use semicolon or tabulator as field separator and lack species names as headers.

## Network analysis

The function `analyze_network` performs the *k-core decomposition* and analysis.

```
result_analysis <- analyze_network(namenetwork, directory="",
                    guild_a = "pl", guild_b = "pol",
                    plot_graphs = FALSE, only_NODF = FALSE,
                    sep=",",speciesinheader=TRUE
```

Arguments:

- `namenetwork`: name of the interaction matrix file.

- `directory`: folder where the network file is stored.

- `guild_a`: prefix for the guild of nodes stored in rows.

- `guild_b`: prefix for the guild of nodes stored in columns.

- `sep`: field separator character.

- `speciesinheader`: TRUE if species names are stored as row and column names inside the network data file.

- `plot_graphs`: plot kshell histogram and Kamada Kawai plots.

- `only_NODF`: just computes the $NODF$ measurement of nestedness.

The function returns:

- `calc_values`, a list containing the following objects:

    - `graph`: an igraph::graph object. Is stores additional information for each node:

        * `V(result_analysis$graph)`: list of node names

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* `V(result_analysis$graph)$kdegree`: list $k_{degree}$
* `V(result_analysis$graph)$kradius`: list $k_{radius}$
* `V(result_analysis$graph)$krisk`: list $k_{riks}$, a measurement of vulnerability (See [GA+17])

- `max_core`: maximum k shell index

- `nested_values`: a list containing the values provided by the bipartite::nested function, unless `only_NODF` set TRUE.

- `num_guild_a`: number of nodes of guild a.

- `num_guild_b`: number of nodes of guild b.

- `links`: number of network links.

- `meandist`: network average kradius.

- `meankdegree`: network average kdegree.

- `spaths_mat`: matrix with node to node shortest distance paths.

- `matrix`: interaction matrix with nodes of guild a by columns and guild b by rows.

- `g_cores`: list with the value of kshell for each node.

- `modularity_measure`: value of igraph::modularity function.

## The Ziggurat Plot

*Ziggurat* is a visualization created from scratch. Species are grouped by their $k$-*shells*, plotted as small ziggurats. The maximum $k$-*shell* lies on the left side, the other ones follow an almond-like distribution.

Species within the maximum shell are ordered, by default, by their $k_{degree}$ with the highest one leftmost. Areas do not convey meaning, nodes' height decreases just by convenience of visualization.
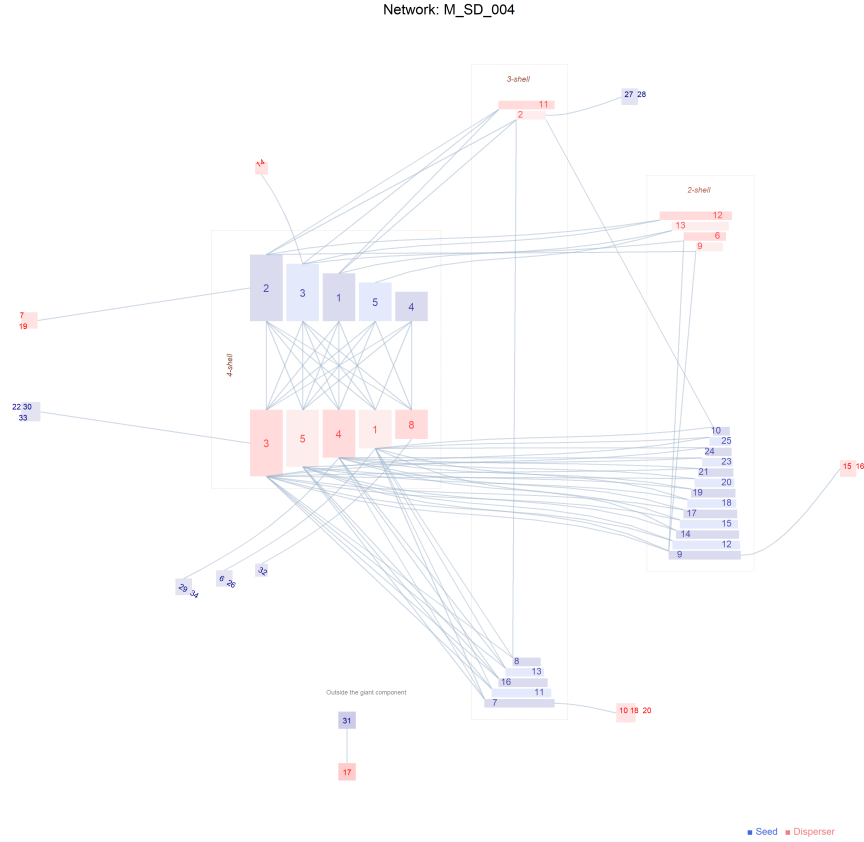


Figure 3: Ziggurat graph of an avian frugivore community in Puerto Rico with 54 species and 95 links [CCG03].

Nodes of 1-*shell* are scattered around the ziggurats. When multiple species of this shell are connected to the same node of any of the ziggurats they are clustered to reduce the number of lines. For instance, plants species 22, 30 and 33 are specialists linked to the generalist disperser 3. With this organization, we get a clear view of structure and interconnections. The almond shape leaves a wide space in the center of the graph to depict the links and they do not overcross the boxes of the different

species.
The function call prototype is:

```
ziggurat_graph <- function(datadir,filename, style='ziggurat',sep=",",
                           speciesinheader=TRUE, paintlinks = TRUE, print_to_file = FALSE,
                           plotsdir ="plotresults/", orderkcoremaxby = "kradius",
                           flip_results = FALSE, aspect_ratio = 1,
                           alpha_level = 0.2, color_guild_a = c("#4169E1","#00008B"),
                           color_guild_b = c("#F08080","#FF0000"),
                           color_link = "slategray3", alpha_link = 0.5, size_link = 0.5,
                           displace_y_b = rep(0,20),
                           displace_y_a = rep(0,20),
                           lsize_kcoremax = 3.5, lsize_zig = 3, lsize_kcore1 = 2.5,
                           lsize_legend = 4, lsize_core_box = 2.5,
                           labels_color = c(),
                           height_box_y_expand = 1, kcore2tail_vertical_separation = 1,
                           kcore1tail_disttocore = c(1,1), innertail_vertical_separation = 1,
                           factor_hop_x = 1, fattailjumphoriz = c(1,1),
                           fattailjumpvert = c(1,1),   coremax_triangle_height_factor = 1,
                           coremax_triangle_width_factor = 1, paint_outsiders = TRUE,
                           displace_outside_component = c(0,0), outsiders_separation_expand = 1,
                           outsiders_legend_expand = 1,
                           specialistskcore2_horizontal_dist_rootleaf_expand = 1,
                           specialistskcore2_vertical_dist_rootleaf_expand = 0,
                           specialists_boxes_separation_count = 1,
                           root_specialist_expand = c(1,1), hide_plot_border = TRUE,
                           rescale_plot_area = c(1,1),
                           kcore1specialists_leafs_vertical_separation = 1,
                           corebox_border_size = 0.2, kcore_species_name_display = c(),
                           kcore_species_name_break = c(), shorten_species_name = 0,
                           exclude_species_number = FALSE, label_strguilda = "",
                           label_strguildb = "", landscape_plot = TRUE,
                           backg_color = "white", show_title = TRUE, show_legend='BOTTOM',
                           use_spline =TRUE, spline_points = 10,
                           file_name_append = "", svg_scale_factor= 10, weighted_links = "none",
                           square_nodes_size_scale = 1, move_all_SVG_up = 0,
                           move_all_SVG_right = 0, progress=NULL
                           )
```

The configuration of ziggurat plots is rich and complex than that of polar graphs. There are just two mandatory parameters, `datadir` and `filename` that provide the directory and file name of the input file. The output file name is the same as the input file plus `_ziggurat.png` and the user mayo add the `file_name_append` suffix as well.

Graphical parameters provide a powerful toolset to improve visualizations. Figure  was created with the default call:
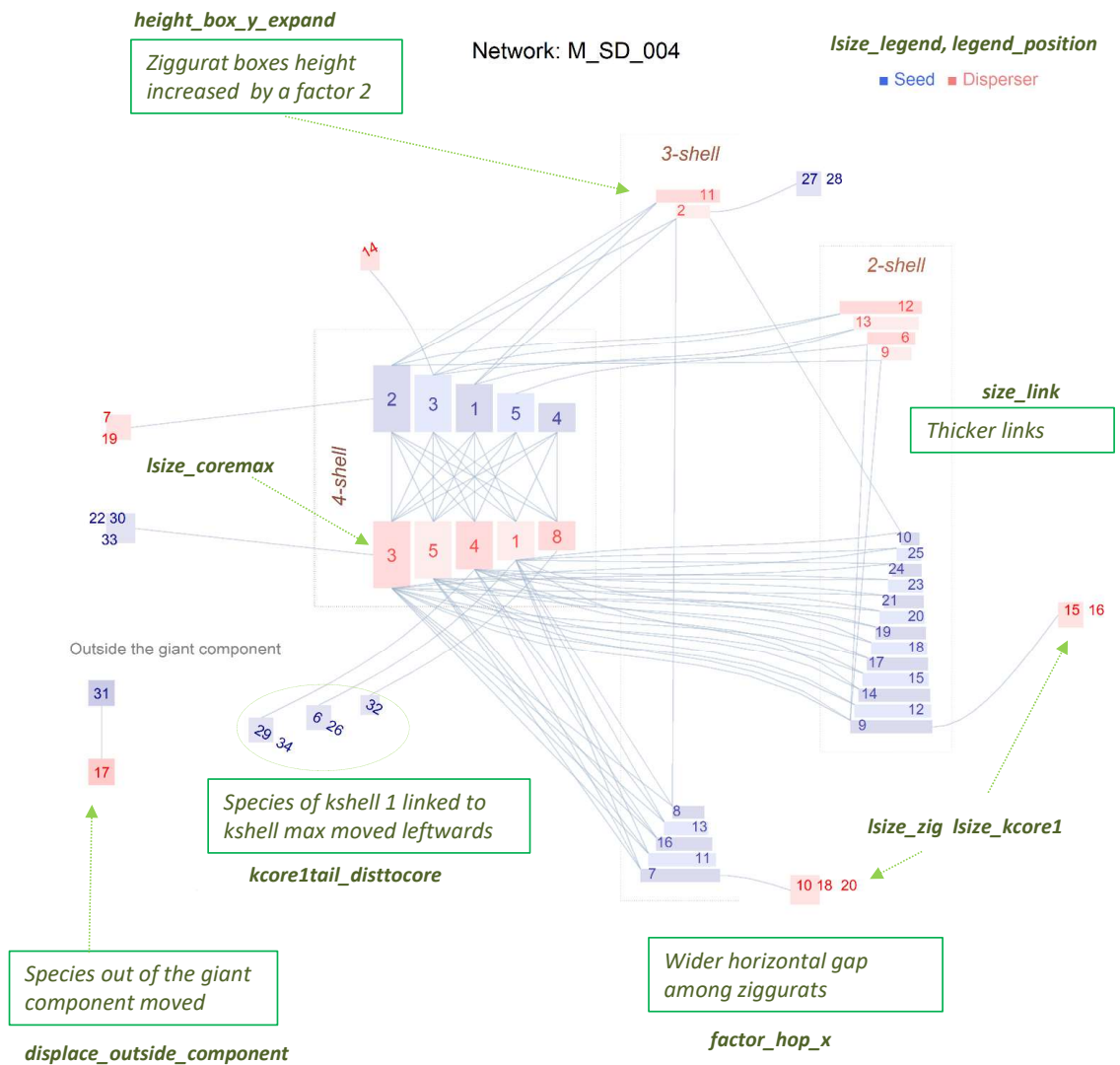
```
ziggurat_graph("data/","M_SD_004.csv",  plotsdir = "grafresults/",
               print_to_file = TRUE)
```

The same graph looks improved with some additional input data.

```
ziggurat_graph("../data/","M_SD_004.csv",print_to_file = TRUE,
                size_link = 0.5,lsize_kcoremax = 5.5 ,lsize_zig = 4.5,
                lsize_kcore1 = 4.5,lsize_legend = 6,
                lsize_core_box = 6 , height_box_y_expand = 1.6,
                factor_hop_x = 1.2,
                displace_outside_component = c(-1.4,0.6),
                kcore1tail_disttocore = c(1.2,1),  show_legend = "TOP")
```

**height_box_y_expand**

*Ziggurat boxes height increased by a factor 2*

Network: M_SD_004

**lsize_legend, legend_position**

■ Seed  ■ Disperser

*3-shell*

27  28

11
2

14

*2-shell*

12
13
6
9

**size_link**

*Thicker links*

7
19

2  3  1  5  4

*4-shell*

**lsize_coremax**

22 30
33

3  5  4  1  8

10
25
24
23
21
20
19
18
17
15
14
12
9

15  16

Outside the giant component

31

17

*Species of kshell 1 linked to kshell max moved leftwards*

29  34

6  26

32

8
13
16
11
7

10 18  20

**lsize_zig  lsize_kcore1**

**kcore1tail_disttocore**

*Species out of the giant component moved*

**displace_outside_component**

*Wider horizontal gap among ziggurats*

**factor_hop_x**

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Plot configuration may become hard when network size grows, but we will show now the usefulness of another set of input parameters with a midsized example. Default function call provides a quite readable ziggurat plot of pollinator network number 12.

```
ziggurat_graph("data/","M_PL_012.csv",  plotsdir = "grafresults/",
                print_to_file = TRUE)
```
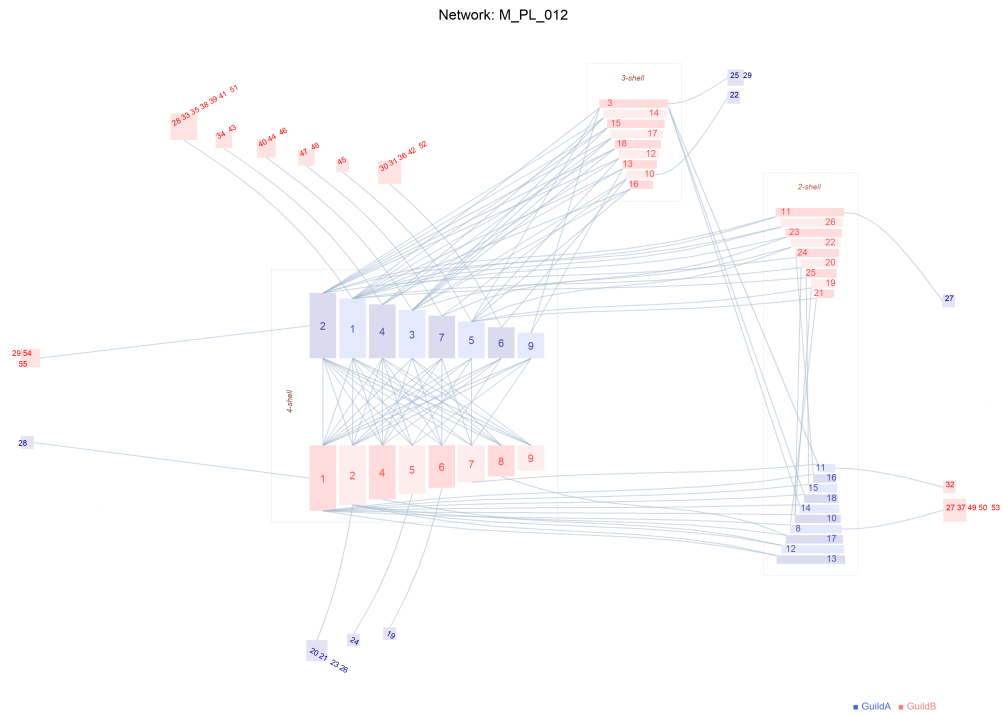


Figure 4: Ziggurat graph of a plant - pollinator network in Garajonay, La Palma (Spain). Olesen, unpublished.

This plot is nearly ready for publishing but fine tuning makes it look more professional.

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```
ziggurat_graph("../data/","M_PL_012.csv", height_box_y_expand = 2,
               factor_hop_x=1.3, plotsdir="grafresults",orderkcoremaxby="kdegree",
               color_link = "slategray3", alpha_link = 0.5,
               color_guild_a=c("darkolivegreen","darkolivegreen3"),
               color_guild_b=c("coral2","coral4"),
               labels_color= c("black","red"),backg_color = "snow",
               lsize_legend = 7, lsize_core_box = 6,
               innertail_vertical_separation = 2,lsize_kcoremax = 6,
               lsize_zig = 5,lsize_kcore1 = 5,
               displace_y_a=c(0,-0.5,0,0), show_legend ="TOP",
               displace_y_b=c(0,0,0.2,0),rescale_plot_area=c(1.4,2),
               coremax_triangle_width_factor = 1.15,
               coremax_triangle_height_factor = 1.1,
               fattailjumpvert = c(1.2,1.2),fattailjumphoriz = c(1.25,0.8),
               print_to_file = TRUE, hide_plot_border = FALSE,
               use_spline = FALSE, file_name_append = "improved")
```



Network: M_PL_012
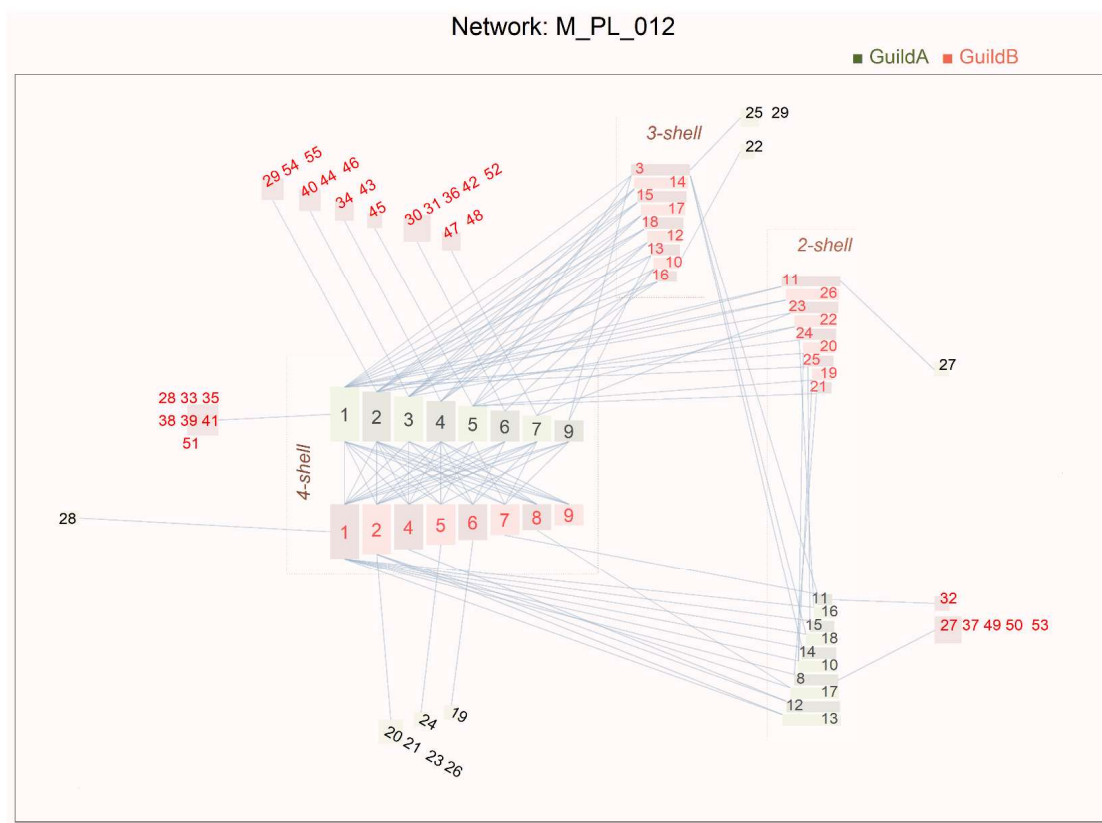
We do not repeat the meaning of those parameters that we have explained in the previous example. The role of some of the new ones are straightforward. We have changed the filling colors of ziggurats, providing the pairs `color_guild_a` and `color_guild_b`, and also the species label colors. A dime background is added as well. This trick shows the plotting area, that was increased with `rescale_plot_area`. This change only affects the plotting area, not the the figure. The aspect ratio may be modified to *flatten* the plot is is lesser than 1 or to *stretch* it if bigger. The default value is 1.

If you do not use splines, as in this example, links appear as straight lines. If you use splines you could also tell the function how many points they should have.

*Fat tails* are the two sets of *1-shell* species eventually linked to highest $k_{degree}$ generalists, those that are located leftmost in the max *k-shell*. The order of nodes within this max *k-shell* is now set to `kdegree` while the default choice is max *kradius*.

In the previous example we explained that `height_box_y_expand` controls the height of outer ziggurat boxes. It is possible to chnge the height and width of rectangles of the max *k-shell* with `coremax_triangle_height_factor` and `coremax_triangle_width_factor`.

The overall horizontal distance of *1-shell* species tied to the max *k-shell* (except fat tails) is increased or decreased with `horiz_kcoremax_tails_expand`.

Vectors `displace_y_a` and `displace_y_b` set the vertical separation of inner ziggurats.

Finally, `innertail_vertical_separation` controls the vertical separation of tails connected to these inner ziggurats. See plant species 22 and 25.

Next example shows how to manage *specialist tails* and *outsiders*. Specialist tails are chains of species of *1-shell.*. Outsiders are the species not connected to the giant component. Pollinator network 031 has species of both kinds.
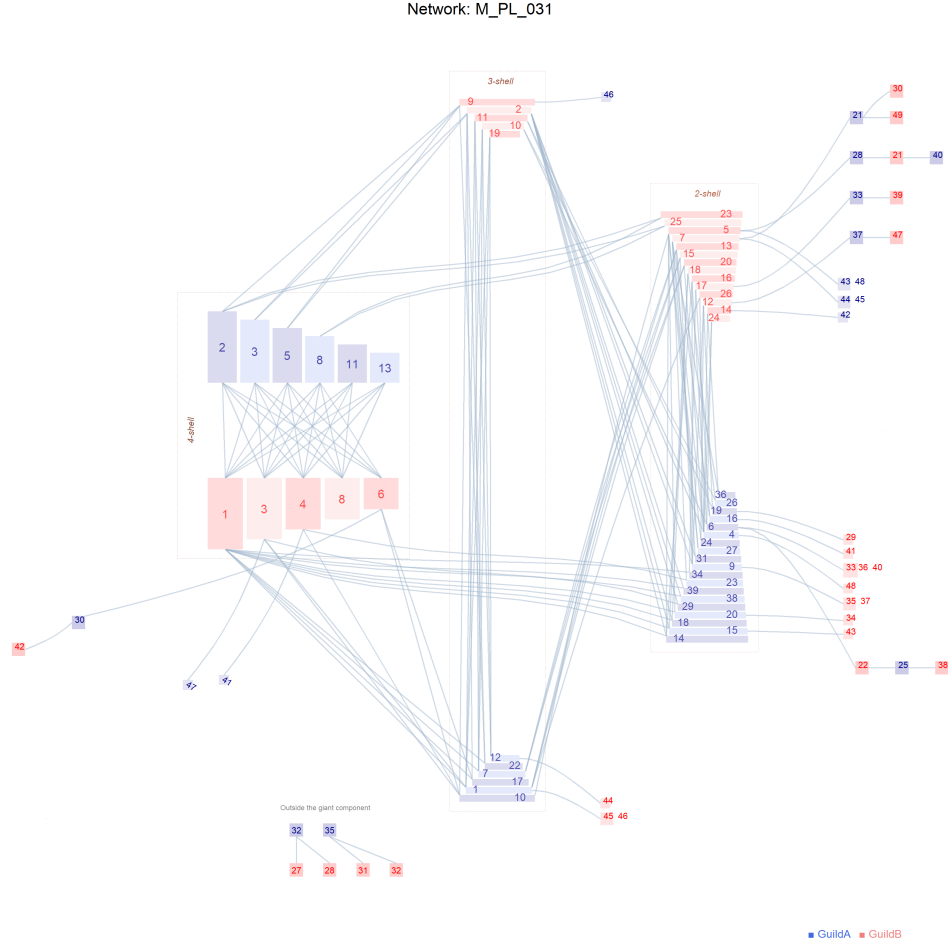
Figure 5: Default ziggurat graph of a plant - pollinator network in Alta Guyana (Venezuela) [Ram89].

Outsiders appear under the main plot. This network has a rich set of specialist chains, linked both to ziggurats of *2-shell* and to the max *shell*. If plant species 28 becomes extinct, it will also drag pollinator 21 and plant 40. This is an uncommon chain of specialists linked among them and very exposed to external perturbations.
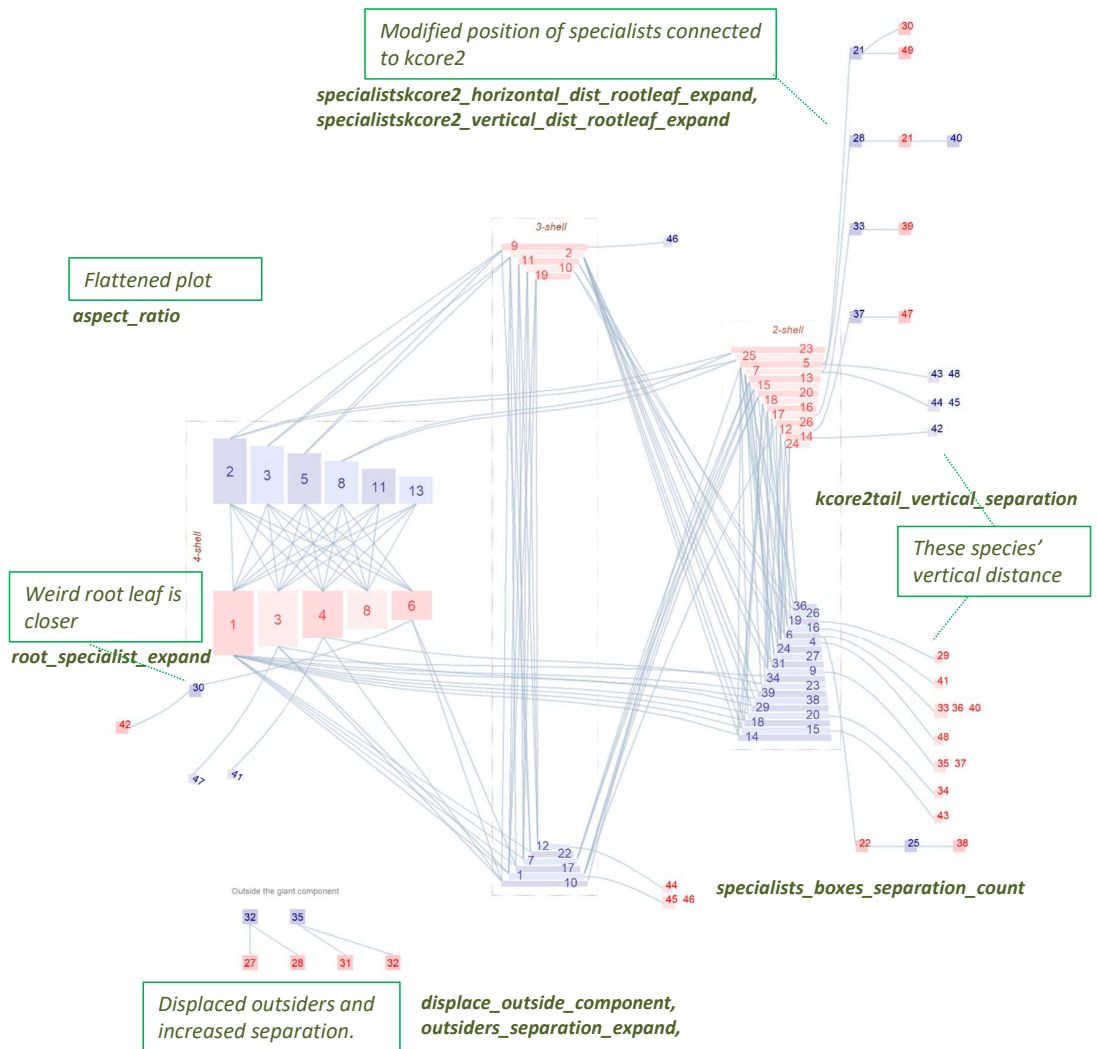
The `ziggurat_grap` function offers input fields to manage the appearance and position of these species.

```
ziggurat_graph("../data/","M_PL_031.csv",  plotsdir = "grafresults",
               print_to_file = TRUE, displace_outside_component = c(-0.2,0.5),
               kcore2tail_vertical_separation = 3,specialists_boxes_separation_count=3,
               root_specialist_expand = c(0.5,1),show_title = FALSE,
               show_legend = "TOP",
               specialistskcore2_horizontal_dist_rootleaf_expand = -0.1,
               specialistskcore2_vertical_dist_rootleaf_expand = 1.5,
               outsiders_separation_expand = 1.25,lsize_legend = 6,
               aspect_ratio= 0.8, file_name_append = "improved")
```



Modified position of specialists connected to kcore2

*specialistskcore2_horizontal_dist_rootleaf_expand,*
*specialistskcore2_vertical_dist_rootleaf_expand*

Flattened plot

*aspect_ratio*

Weird root leaf is closer

*root_specialist_expand*

*kcore2tail_vertical_separation*

These species' vertical distance

*specialists_boxes_separation_count*

Displaced outsiders and increased separation.

*displace_outside_component,*
*outsiders_separation_expand,*

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It is possible to display the names of the species inside the ziggurat rectangles. Be careful, because they may make hard to understand the structure, we do not encourage using this feature unless the network is tiny. Species names of *1-shell* cannot be displayed
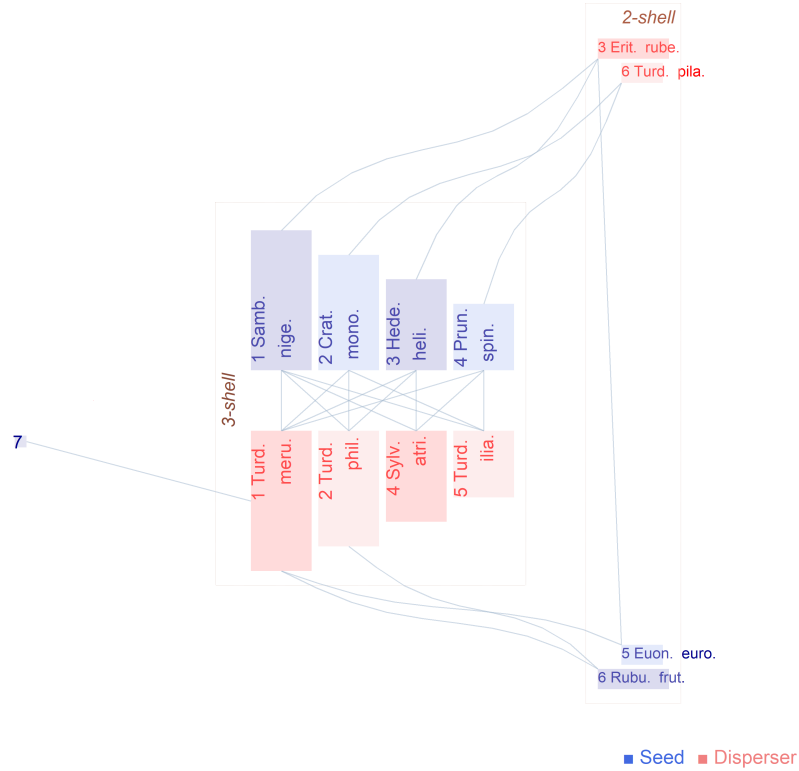
Network: M_SD_025



Figure 6: Ziggurat graph of a plant - disperser.

```
ziggurat_graph("./data/","M_SD_025.csv",plotsdir="grafresults/",
               shorten_species_name = 4, displace_legend = c(-0.2,0.2),
               height_box_y_expand = 2, coremax_triangle_width_factor = 1.25,
               coremax_triangle_height_factor = 2.25,lsize_core_box = 6,
               lsize_kcoremax = 6, lsize_legend= 7,lsize_kcore1 = 6,
               lsize_zig = 5, kcore_species_name_display = c(2,3),
               kcore_species_name_break = c(3), print_to_file = TRUE)
```

If the network is weighted, links width may be proportional to the interaction strength, as in figure 7. There are three options: square root, natural logarithm or decimal logarithm of the weight.
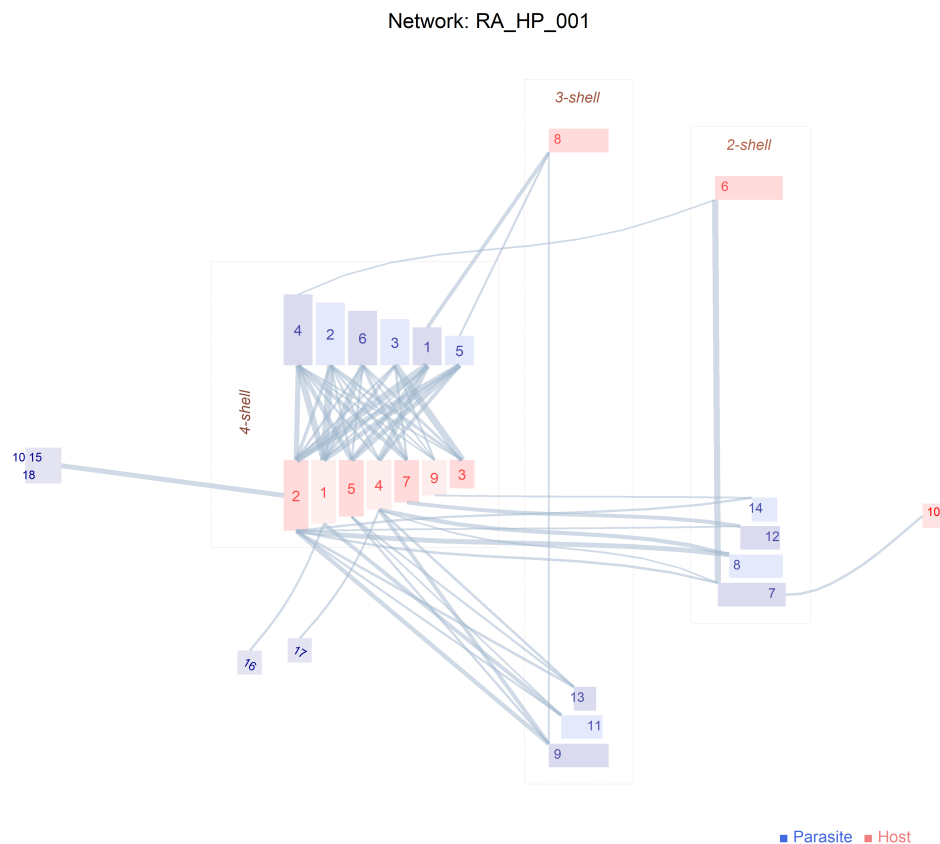


Figure 7: Ziggurat graph of a host - parasite network.

```
ziggurat_graph("../data/","RA_HP_001.csv" ,weighted_links = "ln",
    plotsdir = "grafresults", print_to_file = TRUE,
    label_strguilda = "Parasite" ,
    label_strguildb = "Host" ,lsize_kcoremax = 5 ,
    lsize_zig = 4.5 ,lsize_kcore1 = 4 ,lsize_legend = 6,
    lsize_core_box = 5 )
```

The function returns its own environment called **zgg** where configuration paramenters and results are stored. If you are developing an application, you can retrieve:

- **zgg$plot**: the ziggurat plot.

- **zgg$svg**: the ziggurat plot as an SVG object.

- **zgg$results_analysis**: the internal **analyze_network** call results.

The default **ziggurat_graph** prints the plot in **png** format with a resolution of $300dpi$, but you can save **zgg$plot** outside the function in any other format and resolution.
Finally, this is the meaning of all the input parameters:

- **datadir**: name of the file of the interaction matrix.

- **filename**: file with the interaction matrix.

- **sep**: field separator character.

- **speciesinheader**: TRUE if species names are stored as row and column names inside the network data file.

- **style**: equals 'ziggurat', do not modify.

- **paintlinks**: if set to FALSE links will be hidden. It is useful to test the plot appearance when the network is huge.

- **print_to_file**: if set to FALSE the plot is displayed in the R session window.

- **plotsdir**: the directory where the plot is stored.

- **flip_results**: displays the graph in portrait configuration.

- **aspect_ratio**: ziggurat plot default aspect ratio.

- **alpha_level**: transparency for ziggurats' filling.

- **color_guild_a**: default filling for nodes of guild_a.

- **color_guild_b**: default filling for nodes of guild_b.

- **color_link default**: link color.

- **alpha_link**: link transparency.

- **size_link**: width of links.

- **displace_y_b**: relative vertical displacement of guild_b inner ziggurats.

- **displace_y_a**: relative vertical displacement of guild_a inner ziggurats.

- **labels_size**: default node label size.

- `lsize_kcoremax`: nodes in *max–kshell* label size.

- `lsize_zig nodes`: in inner ziggurats label size.

- `lsize_kcore1`: labels of nodes in 1–*shell*.

- `lsize_legend`: legend label size.

- `lsize_kcorebox`: default *kshell* boxes label size.

- `labels_color`: default label colors.

- `height_box_y_expand`: expand inner ziggurat rectangles default height by this factor.

- `kcore2tail_vertical_separation`: expand vertical of 1–*shell* species linked to 2–*shell* by this factor.

- `kcore1tail_disttocore`: expand vertical separation of 1–*shell* species from *max–shell* (guild_a, guild,b).

- `innertail_vertical_separation`: expand vertical separation of *kshell* species connected to 2–*shell* < *kshell* < *max–shell*.

- `horiz_kcoremax_tails_expand`: expands horizontal separation of specialist tails connected to *max–shell*.

- `factor_hop_x expand inner`: expands ziggurats horizontal distance.

- `fattailjumphoriz`: displace species linked to leftmost *max–shell* species.

- `fattailjumpvert`: idem for vertical position.

- `coremax_triangle_width_factor`: expand khsell max rectangles width by this factor.

- `coremax_triangle_height_factor`: expand khsell max rectangles height by this factor.

- `paint_outsiders`: paint species disconnected of the giant component.

- `displace_outside_component`: displace outsider species (horizontal, vertical).

- `outsiders_separation_expand`: multiply by this factor outsiders' separation.

- `outsiders_legend_expand`: displace outsiders legend.

- `specialistskcore2_horizontal_dist_rootleaf_expand`: expand horizontal distance of specialist tail root node connected to 2–*shell*.

- `specialistskcore2_vertical_dist_rootleaf_expand`: expand vertical distance of specialist tails connected to 2–*shell*.

- `specialists_boxes_separation_count`: specialist species boxes separation count.

- **root_specialist_expand**: expand root specialist distances of tails connected to $kshell \neq 2$.

- **hide_plot_border**: hide border around the plot.

- **rescale_plot_area**: full plot area rescaling (horizontal, vertical).

- **kcore1specialists_leafs_vertical_separation**: expand vertical separation of specialist tails connected to 1–*shell* species.

- **corebox_border_size**: width of *kshell* boxes.

- **kcore_species_name_display**: display species names of shells listed in this vector.

- **kcore_species_name_break**: allow new lines in species names of shells listed in this vector.

- **shorten_species_names**: number of characters of species name to display.

- **label_strguilda**: string labels of guild a.

- **label_strguildb**: string labels of guild b.

- **landscape_plot**: paper landscape configuration.

- **backg_color**: plot background color.

- **show_title**: show plot title.

- **show_legend**: show plot legend position: "TOP","BOTTOM","NONE".

- **use_spline**: use splines to draw links.

- **spline_points**: number of points for each spline.

- **file_name_append**: a label that the user may append to the plot file name for convenience.

- **svg_scale_factor**: only for interactive apps, do not modify.

- **weighted_links**: weight function to display links, (`"none"`,`"log10"`,`"ln"`,`"sqrt"`)

- **square_nodes_size_scale**: scale the area of nodes in 1–*shell* or outsiders.

- **move_all_SVG_up**: only for interactive apps, do not modify.

- **move_all_SVG_right**: only for interactive apps, do not modify.

- **progress**: only for interactive apps, do not modify.

## The Polar Plot

The *Polar Plot* shows nodes (species) centrality and provides an overview of network distribution. It was inspired by the *fingerprint-like* graph, developed by Alvarez-Hamelin *et al.* [AH+05] to plot very large *k-decomposed* networks.

Nodes are depicted with their centers located at $k_{radius}$. Angles are assigned at random by the visualization algorithm and each guild lies inside one of the half planes. The size of each node is proportional to its $k_{degree}$ and the shape encodes 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.
The function call is:

```
polar_graph <- function( datadir, filename, sep=",",speciesinheader=TRUE,
                         plotsdir = "plot_results/polar/",
                         print_to_file = FALSE, pshowtext = FALSE,
                         show_histograms = TRUE,
                         glabels = c("Plant", "Pollinator"),
                         gshortened = c("pl","pol"),
                         lsize_title = 22, lsize_axis = 16,
                         lsize_legend = 16,lsize_axis_title = 16,
                         lsize_legend_title = 16,
                         file_name_append = "", print_title = TRUE,
                         printable_labels = 0, fill_nodes = TRUE,
                         alpha_nodes = 0.5,
                         max_kradius = 0, progress=NULL)
```

Arguments:

- `datadir`: folder where the network file is stored.

- `filename`: name of the interaction matrix file.

- `sep`: field separator character.

- `speciesinheader`: TRUE if species names are stored as row and column names inside the network data file.

- `plotsdir`: directory where plots are stored.

- `print_to_file`: store the plot in a file.

- `pshowtext`: useful for integration with interactive applications, do not modify.

- `show_histograms`: show histogram plots.

- `glabels`: guild labels.

- `gshortened`: guild shorthand.

- `size_title, lsize_axis, lsize_legend, lsize_axis_title, lsize_legend_title`: label sizes of the elements of the `ggplot2` object.

- `file_name_append`: optional suffix for the plot file.

- `print_title`: show network name as plot title.

- `printable_labels`: range of printable labels, from the innermost species. 0 means no node labels are displayed.

- `fill_nodes`: fill with solid grey color.

- `alpha_nodes`: node transparency ranging from 0 (fully transparent) to 1 (opaque).

- `max_kradius`: if bigger than 0 sets an upper limit different of the default. Useful to compare sibe by side networks of different sizes.

- `progress`: useful for integration with interactive applications, do not modify.

The parameters `datadir`, `filename` and `plotsdir` are the name of the interaction matrix, the directory where it is stored and the name of the plotting directory. If `print_to_file` is set to `FALSE` the polar plot will be displayed in the current R session. The name of the output file is that of the input file plus `_polar.png`. Paths are relative to the current working path in `R` but you may also specify absolute paths.

File plots have a default resolution of 300 dots per inch, and a size of 12 x 12 inches. If the user wants to display the result in the current R session, label sizes may appear different depending on the installed fonts and size of the plotting window.

The following command creates the file `M_PL_008_polar.png` in the directory `graphresults/`
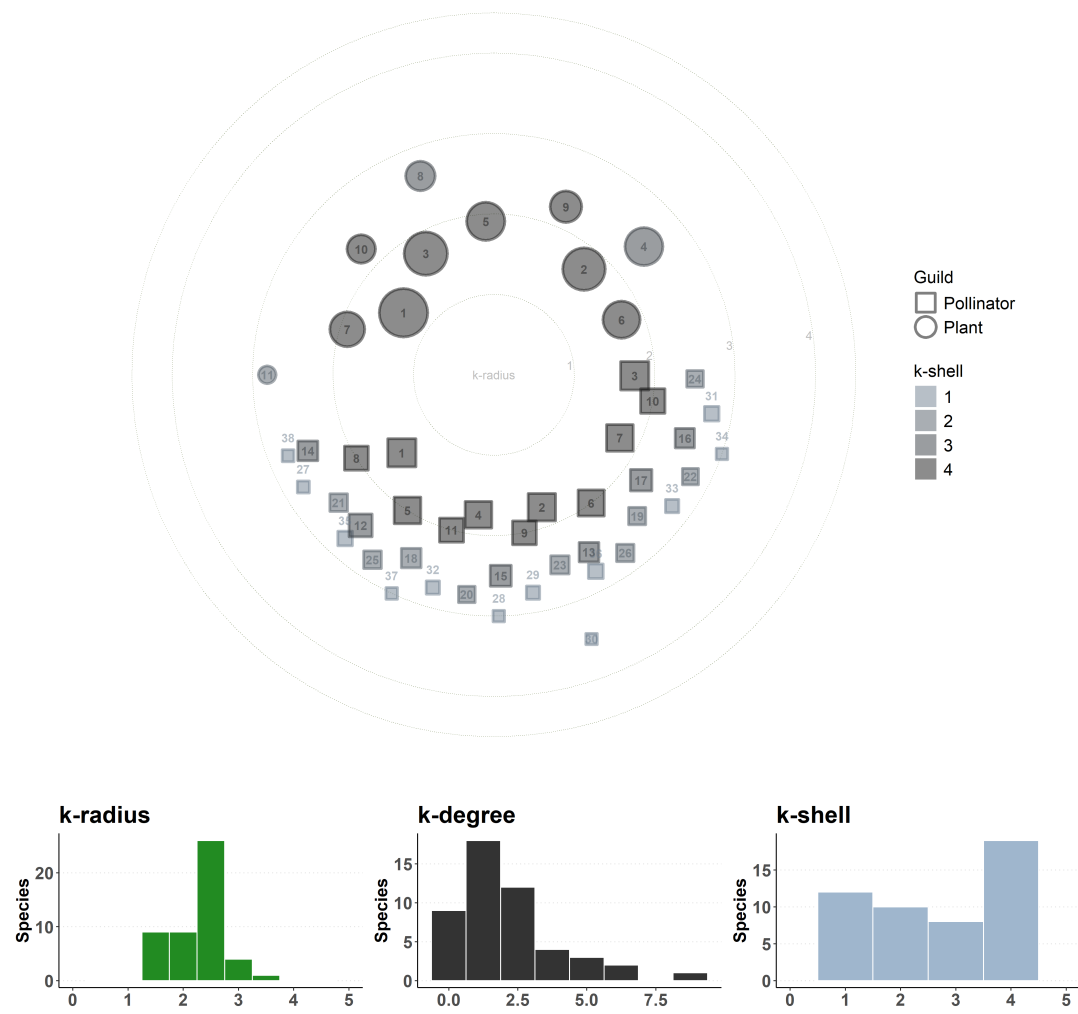
```
pgr <- polar_graph("../data/","M_PL_008.csv",plotsdir="grafresults/",
                   print_to_file = TRUE)
```
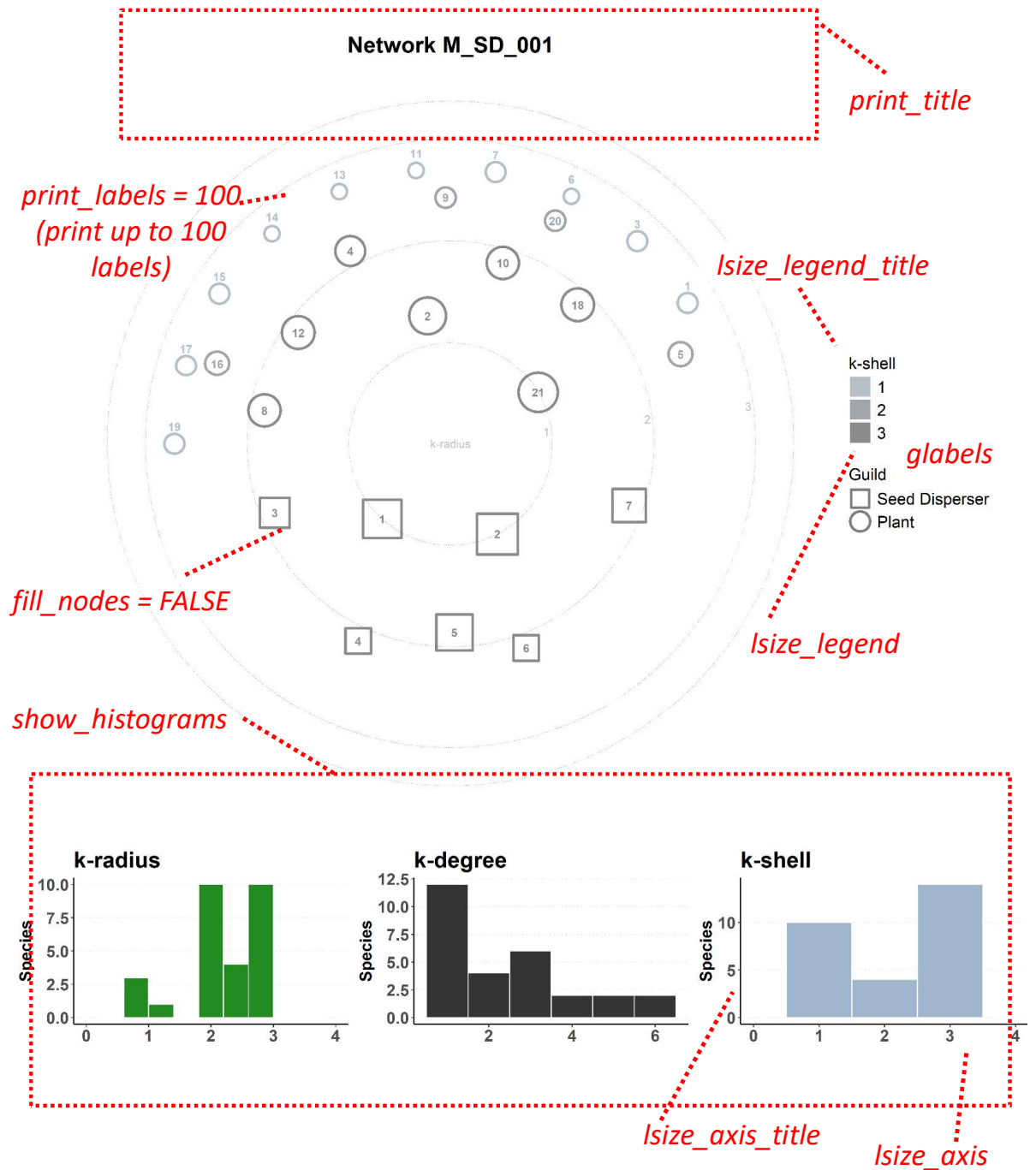
By default, nodes are unlabeled. You may choose to display some of them with the parameter `printable_labels`, but have in mind that the diagram may become messy. Guild labels are also configurable. The function will set automatically "Plant, Pollinator" and "Plant, Disperser" if the file follows the naming convention of the web of life site; you may choose any other pair of values with the input parameter `glabels`.

Three histrogams are displayed under the main plot, with the distributions of $k_{radius}$, $k_{degree}$ and $k_{shell}$.

The configuration of a polar graph is quite simple. The following picture shows how and where the different input parameters modify the plot.

**Network M_PL_008**

k-radius

Guild
□ Pollinator
○ Plant

k-shell
■ 1
■ 2
■ 3
■ 4

**k-radius**

**k-degree**

**k-shell**

**Network M_SD_001**

*print_title*

*print_labels = 100*
*(print up to 100 labels)*

*lsize_legend_title*

k-shell

*glabels*

*lsize_legend*

*fill_nodes = FALSE*

*show_histograms*

**k-radius**

**k-degree**

**k-shell**

*lsize_axis_title*

*lsize_axis*

```
polar_graph( "../data/", "M_SD_001.csv",plotsdir="plot_results/",
            print_title = TRUE, print_to_file = TRUE, lsize_axis = 16,
            lsize_legend = 16, lsize_axis_title = 16, lsize_legend_title = 16,
            glabels = c("Plant", "Seed Disperser"), gshortened = c("PL","SD"),
            fill_nodes = FALSE, printable_labels = 100,
            file_name_append = "showpars")
```

The `polar_graph` function returns a list with three objects:

- `polar_argg`: a list with the values of call arguments

- `result_analysis`: a list with the result of the network analysis. See `analyze_network` for details.

- `network_name`: network name.

# References

[AH+05]    José Ignacio Alvarez-Hamelin et al. "k-core decomposition: A tool for the visualization of large scale networks". In: *arXiv preprint cs/0504107* (2005).

[Bas09]    Jordi Bascompte. "Disentangling the web of life". In: *Science* 325 (2009), pp. 416–419.

[CCG03]    Tomás A Carlo, Jaime A Collazo, and Martha J Groom. "Avian fruit preferences across a Puerto Rican forested landscape: pattern consistency and implications for seed removal". In: *Oecologia* 134.1 (2003), pp. 119–131.

[GA+17]    Javier Garcia-Algarra et al. "Ranking of critical species to preserve the functionality of mutualistic networks using the k-core decomposition". In: *PeerJ* 5 (2017), e3321. DOI: 10.7717/peerj.3321. URL: http://dx.doi.org/10.7717/peerj.3321.

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[Ram89]    Nelson Ramirez. "Biología de polinización en una comunidad arbustiva tropical de la alta Guayana venezolana". In: *Biotropica* (1989), pp. 319–330.

[Sei83]    Stephen B Seidman. "Network structure and minimum degree". In: *Social networks* 5.3 (1983), pp. 269–287.